Molecular regulatory network of BRANCHED1 (BRC1) expression in axillary bud of Rpsa sp. in response to sugar and auxin

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« Réseau de régulation moléculaire de l'expression du gène *BRANCHED1* (*BRC1*) dans le bourgeon axillaire du rosier, en réponse au sucre et à l'auxine »

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Table des matières

INTRODUCTION

Ce travail de thèse a été réalisé dans le cadre d'une collaboration entre l'équipe ARCH-E (Biologie Intégrative de l'Architecture et Environnement) et l'équipe GDO (Génétique et Diversité des plantes Ornementales) de l'Institut de Recherche en Horticulture et Semences (UMR IRHS, INRA, Agrocampus Ouest et Université d'Angers). Les deux équipes, qui ont pour plante modèle le rosier, s'intéressent à des thématiques de recherche complémentaires (ramification, floraison, maladie du rosier, diversité génétique…) et déploient des approches pluridisciplinaires et multi-échelles.

Le débourrement des bourgeons ainsi que sa régulation le long de la tige aboutissent à des profils de ramifications qui sont à l'origine de l'architecture finale de la plante. Cette architecture correspond à l'organisation spatio-temporelle des différents axes qui la compose et s'agit d'un processus très complexe, qui contribue au fonctionnement globale de la plante en interaction avec son environnement. Elle lui permet de capter des ressources nécessaires à sa croissance et son développement, elle participe à l'élaboration du rendement des espèces cultivées, elle module la sensibilité à certaines maladies et elle prend part de la qualité esthétique des plantes ornementales (Boumaza *et al*., 2009; Valério *et al*., 2009; Simon *et al*., 2012). La maitrise de l'architecture des végétaux représente donc un enjeu majeur. De façon globale, les techniques classiques pour maitriser la ramification, notamment la taille ou l'utilisation de nanifiant, sont couteuses et/ou polluantes, aussi leur utilisation est très compromettante au regard de la nouvelle législation (Plan Ecophyto par exemple) qui est très soucieuse de la protection de l'environnement et de la santé humaine. Comprendre le déterminisme physiologique et moléculaire de la ramification et sa réponse aux différents facteurs environnementaux constitueraient une étape déterminante dans la définition de nouveaux itinéraires culturaux, basés sur des méthodes alternatives et innovantes.

Les recherches menées sur la modulation de la ramification ont montré le caractère multifactoriel de ce processus, car la ramification est sous le contrôle des hormones, des nutriments carbonés et azotés, de la nutrition minérale et des facteurs environnementaux (Huché-Thélier *et al*., 2011; Demotes-Mainard *et al*., 2013; Furet *et al*., 2014; Rameau *et al*., 2015; Le Moigne *et al*., 2018; Wang *et al*., 2019). De plus, sa régulation repose sur la perception et l'intégration des différents signaux, locaux ou systémiques, par le bourgeon lui-même (Rameau *et al*., 2015). Parmi les gènes intégrateurs au sein du bourgeon, le facteur de transcription *BRANCHED1* (*BRC1*), a fait l'objet de plusieurs études aussi bien chez les monocotylédones que chez les dicotylédones. Ces études ont montré que les mutants de ce gène (loss-of-function) présentent un phénotype hyper-ramifié et que son expression est très sensible aux facteurs endogènes et exogènes influençant la ramification (Rameau *et al*., 2015 ; Wang *et al*., 2019). Malgré ses données et son rôle majeur dans la régulation de la ramification, plusieurs lacunes persistent, notamment quant aux déterminismes moléculaires de la réponse de BRC1 à chacun de ses facteurs et à la nature des mécanismes conduisant à la convergence de l'action de ses facteurs au niveau BRC1.

L'objectif de ce travail de thèse s'inscrit dans ce contexte et vise à apporter des éléments de connaissances sur la régulation du facteur de transcription BRC1 par deux régulateurs majeurs de la ramification, l'auxine (hormone de la dominance apicale) et le saccharose (la principale forme de transport de photoassimilats chez les végétaux). Une attention particulière sera portée sur l'implication de la région promotrice et de la région 3'UTR (3' untranslated region) du gène *BRC1* du rosier. L'étude portera principalement sur l'effet combiné du sucre et de l'auxine sur le débourrement et la régulation du taux de transcrits *BRANCHED1* d'une part, et sur le rôle du métabolisme primaire (glycolyse/cycle de Krebs et la voie oxydative des pentoses phosphates (OPPP)) dans ce réseau moléculaire de régulation.

Ce manuscrit présente le travail de thèse en quatre parties :

La première partie développe, au travers d'une « analyse bibliographique », l'état des connaissances sur l'importance du gène *BRC1* dans le contrôle de la ramification, les voies de signalisation par les sucres et leurs interactions avec les hormones, et le rôle des protéines PUF (PUmilio RNA-binding protein Family), dans la régulation post-transcriptionnelle. Cette partie correspond à trois revues, dont deux sont parues en 2018 et une paraitra début 2019.

La deuxième partie présente sous la forme d'un article scientifique, le rôle de la région promotrice de *RhBRC1* (*Rosa hybrida BRANCHED1*) dans l'intégration de l'effet combinée auxine et sucre, et qui s'avère médié par la voie de la glycolyse/cycle de Krebs et par la voie OPPP. De plus, la perception du signal émanant de ces deux voies métaboliques impliquerait deux régions distinctes du promoteur *RhBRC1*. Pour cela, nous avons étudié l'effet combiné de l'auxine et de sucre sur des entre-nœuds, un segment de tige portant un bourgeon, prélevés sur la plante mère et placés sur un milieu gélosé avec différentes concentrations en sucre et en auxine. Une approche pluridisciplinaire intégrant des approches pharmacologiques (effecteurs des voies métaboliques d'intérêt), métabolomique, transcriptomique (RNA sequencing), a été réalisée ainsi que la transformation stable de cals de rosier avec des constructions présentant différentes régions de promoteurs de *BRC1*.

La troisième partie présente également sous forme d'un article scientifique, le rôle de la région 3'UTR du gène *RhBRC1* dans l'intégration de l'effet combinée auxine et sucre. Cette région a la particularité d'être plus sensible à la voie OPPP qu'à la voie de la glycolyse/cycle de Krebs, et ainsi contribuer à la régulation post-transcriptionnelle de *RhBRC1*, en provoquant la déstabilisation de son ARNm et en empêchant sa traduction. Une protéine de la famille des PUF, a été identifiée au niveau des bourgeons du rosier en étant sous le contrôle antagoniste auxine et sucre. Il s'agit de la protéine RhPUF4 (*Rosa hybrida* PUF4). La caractérisation de son expression en réponse à d'autres traitements (effecteurs des voies métaboliques) indique très fortement son rôle dans la régulation post-transcriptionnelle de *RhBRC1* médiée par la voie OPPP. Ces résultats s'appuient sur une stratégie

pluridisciplinaire et l'utilisation des cales de rosier transformés avec une construction partant une fusion traductionnelle de la GFP (Green Flurescent Protein) et de la région 3'UTR du gène *RhBRC1.*

Le dernier chapitre correspond à une discussion générale des principaux résultats de ce travail de thèse et leur déclinaison en perspectives. Ce chapitre s'appuie également sur des schémas illustratifs de ses résultats.

SYNTHESE BIBLIOGRAPHIQUE

I – Les enjeux de l'étude de la ramification des végétaux

Le marché de la rose et du rosier

En France, l'horticulture ornementale représente un enjeu économique important. La filière regroupe plus de 3600 entreprises en activité et 20 000 emplois directs fin 2015 pour un chiffre d'affaire total estimé à 1582 millions d'euros (FranceAgriMer, 2016). Dans la filière horticole, la culture du rosier a un impact économique sur deux types de marchés, la fleur coupée et les plantes en pot et à massif. En 2011, les français ont dépensé près d'un milliard d'euros en plantes ornementales d'extérieur, dont 8,4% pour les rosiers. Globalement 60% de la production nationale et 40% de la production européenne proviennent de la région de Doué-la-Fontaine (Maine-et-Loire), avec environ 7 millions de plants produits chaque année.

La rose est la fleur qui arrive en tête de la production florale sous serre en France, avec 300 hectares de surface permettant la production de 190 millions de tiges en 2007. Le Var, le Finistère et les Alpes Maritimes sont les principaux départements producteurs de roses en France, représentant, à eux trois, deux tiers de la production nationale. Le marché de la rose représente en France plus de la moitié des ventes en fleurs coupées et de la somme totale dépensée par les Français pour ce marché. Par conséquent, les marchés de la rose et du rosier représentent donc un enjeu économique de poids au niveau national. Maîtriser la culture du rosier afin d'en tirer une production optimale et développer des outils de production innovants et prédictifs s'avèrent central dans cette balance économique.

Impact de l'architecture du rosier sur sa valeur commerciale

Parmi les critères d'achat d'une plante ornementale, sa qualité visuelle est l'un des plus importants. Cette qualité visuelle repose principalement sur la forme de la plante, avec une préférence des consommateurs pour des plantes compactes et symétriques (Boumaza *et al*., 2009 et 2010). La forme résulte de l'organisation architecturale de la plante, qui elle-même

dépend de la croissance de la plante et de sa ramification. Comprendre et maîtriser l'établissement des ramifications et de l'architecture finale de la plante, permet donc de répondre aux attentes des consommateurs mais également aux exigences des différents acteurs de la filière de la fleur coupée et de plantes de jardin.

Habituellement, les rosiers buissons étaient vendus à l'automne en racines nues avec 2 à 4 tiges coupées, pour être transplantés en jardin en vue d'une première floraison au printemps suivant. Toutefois, l'attente du consommateur a fortement évolué notamment pour ceux qui vivent en zones urbaines et périurbaines et possèdent une surface destinée au jardin très limitée. Dans ce contexte, les consommateurs préfèrent l'achat de rosiers en pot au printemps, qui est de petite taille avec une architecture bien développée et prêt à fleurir. Cette nouvelle exigence souligne davantage l'intérêt de la qualité visuelle de la plante dans l'acte d'achat par le consommateur.

Importance de l'étude de la ramification chez les végétaux

Le rendement des plantes cultivées est étroitement lié à leur degré de ramification et à la dominance apicale. Ainsi, l'augmentation de la biomasse de la partie végétative et/ou du nombre de fruits a été mise en relation avec une dominance apicale faible chez différentes espèces (Irwin and Aarssen, 1996 pour revue). De plus, la ramification des espèces cultivées détermine leur compétitivité face aux adventices. Certaines études ont permis de corréler le nombre de ramifications de certaines variétés de céréales (riz, blé) à leur potentiel de compétitivité face aux adventices (Lemerle *et al*., 1996; Fischer *et al*., 1997; Zhao *et al*., 2006). La ramification des plantes peut modifier leur sensibilité à certaines maladies en influençant notamment les processus épidémiologiques. La ramification influence la densité de tissus, une variable déterminante dans l'établissement du microclimat au sein de la plante, la quantité de surface interceptrice des pathogènes et la facilité des pathogènes à se disperser de tissu en tissu. L'architecture de la plante affecte également la distribution des

photoassimilats au sein de la plante (Legrand and Barbosa, 2003; Robert *et al*., 2008; Gontijo *et al*., 2012).

II – Mise en place de la ramification chez les plantes

La forme générale des plantes est en partie due à leur architecture primaire, c'est-à-dire à l'organisation spatio-temporelle des différents axes qui la composent. La régulation de la ramification est sous le contrôle de facteurs endogènes (génétiques, hormonaux, nutriments carbonés et azotés) et exogènes (lumière, stress hydrique) permettant ainsi une certaine plasticité dans l'établissement de l'architecture des plantes. Ainsi, la variabilité génétique entre espèces peut conduire à l'établissement de profils de ramification différents entre individus (par exemple, basitone *versus* acrotone), tandis que des variations de conditions environnementales peuvent conduire à des profils architecturaux différents chez des plantes de fonds génétiques identiques (plasticité phénotypique). Cette variabilité du contrôle de la ramification des végétaux leur permet notamment de s'adapter de façon optimale aux contraintes auxquelles elles sont soumises. La ramification du rosier est en effet contrôlée par la qualité de la lumière (Girault *et al*., 2008 ; Mor and Halevy, 1984), l'intensité de la lumière (Demotes-Mainard *et al*., 2013), la température (Djennane *et al*., 2014), le statut hydrique (Demotes-Mainard *et al*., 2013) et la nutrition azotée (Huché-Thélier *et al*., 2011, Furet *et al*., 2014).

La croissance primaire des plantes se fait notamment grâce à la formation d'unités métamériques successives nommées phytomères. Chaque phytomère est constitué d'un nœud, d'un entre-nœud, d'une feuille à l'aisselle de laquelle se trouve un bourgeon axillaire. Le bourgeon est un ensemble d'organes végétatifs, correspondant à une plante « miniaturisée », car il est composé d'un méristème et de primordia foliaires. Il existe deux types de bourgeons. Les bourgeons sylleptiques se développent immédiatement après leur formation sans passer par une phase de dormance et les bourgeons proleptiques qui, au contraire, rentrent dans une phase de dormance après leur établissement.

Les axes issus de la croissance de bourgeons axillaires sont dénommés sous le terme de « ramifications » ou « branches ». Lors de leur formation, les bourgeons axillaires sont maintenus dormants par un ensemble de processus physiologiques, conduisant à trois types de dormances, qui peuvent se succéder dans le temps ou se superposer sur un même bourgeon (Horvath *et al*., 2003). Il y a la paradormance, liée à l'effet inhibiteur d'un organe de la plante (bourgeon apicale, tige, feuille) sur le bourgeon axillaire, l'endodormance, due à des signaux physiologiques et moléculaires internes au bourgeon lui-même qui empêchent sa croissance et sa levée requiert un passage par une période de froid, et enfin l'ecodormance, imposée par des facteurs environnementaux défavorables au débourrement des bourgeons.

Lorsque les conditions propices sont réunies, la dormance du bourgeon est levée, permettant ainsi à celui-ci de reprendre son activité. On parle alors de « débourrement » des bourgeons axillaires, décomposé en trois processus élémentaires, la formation de nouveaux organes (organogénèse), l'élongation des primordia préformés et des entre-nœuds, et la différenciation des tissus méristématiques au sein des organes.

III- Rôle intégrateur du *BRANCHED 1* dans la ramification

Comme nous l'avons décrit ci-dessous, la ramification est un processus physiologiquement très complexe mais important pour le fonctionnement globale et intégré de la plante. Il fait intervenir une multitude de facteurs endogènes et exogènes, dont les voies de signalisation doivent converger au niveau du bourgeon et y être convenablement perçues pour établir ou non la croissance du bourgeon et donc la formation de l'axe végétatif. Dans ce chapitre, nous nous sommes focalisés, sur l'identité et la régulation du gène *BRC1*, qui est un des « hub » clefs dans le réseau moléculaire contrôlant la ramification. Nous avons également décrit son rôle dans le processus de la ramification et souligné les lacunes qui restent à combler pour une meilleure compréhension du réseau de régulation moléculaire autour de ce gène.

BRANCHED1: a key hub of shoot branching

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Abstract:
Shoot branching is a key process for plant growth and fitness. Newly produced axes result from axillary bud outgrowth, which is at least partly mediated through the regulation of *BRANCHED1* gene expression (BRC1/TB1/FC1). *BRC1* encodes a pivotal bud-outgrowth-inhibiting transcription factor belonging to the TCP family. As the regulation of *BRC1* expression is a hub for many shoot-branching-related mechanisms, it is influenced by endogenous (phytohormones and nutrients) and exogenous (light) inputs, which involve so-far only partly identified molecular networks. This review highlights the central role of BRC1 in shoot branching and its responsiveness to different stimuli, and emphasizes the different knowledge gaps that should be addressed in the near future.

1. Introduction

Plants are sessile organisms that need to adjust their shape to suit the diversity of the changing environmental conditions in which they are growing. The regulation of shoot branching is a relevant strategy for plant survival and space occupancy, and involves an intricate regulatory network. Shoot branching depends on the status of bud dormancy, which is a temporary and reversible state (Shimizu and Mori, 1998). Shoot branching patterns, considered here as the distribution of branches along a parent stem, are generated during plant postembryonic development (Domagalska and Leyser, 2011). They depend on the ability of axillary vegetative buds located at the axil of each leaf to remain inactive or to produce a new branch in response to variable stimuli (Shinohara *et al*., 2013; Rameau *et al*., 2015; Wang and Jiao, 2018).

Shoot branching is an important feature of plant architecture that determines the interface between the plant and the surrounding environment. Shoot branching contributes to essential processes such as the establishment of leaf area and distribution that determine light interception and photosynthesis, which in turn influence the number of flowers and fruits, fruit filling and yield (Jiang and Egli, 1993; Richards, 2000). Branching also influences the plant competitiveness against weeds or the propagation of pests (Lemerle *et al*., 1996; Zhao *et al*., 2006; Simon *et al*., 2012). In ornamental plants, branching also determines plant visual quality, which drives consumers' preferences (Ta *et al*., 1987; Garbez *et al*., 2015; Boumaza *et al*., 2009, 2010).

Extensive studies have been undertaken for several decades to find out the mechanisms involved in branching. The currently accepted idea supports that endogenous, developmental, and environmental inputs converge into bud-located integrators, which are at the head of a network of mechanisms governing the ability of buds to grow out. Among these inputs, hormones, sugar, nitrogen, light, and water play a determining role in shoot branching regulation (McSteen, 2009; Niwa *et al*., 2013; González-Grandio *et al*., 2013; Teichmann and Muhr, 2015; Rameau *et al*., 2015; Li-Marchetti *et al*., 2015; Corot *et al*., 2017; Le Moigne *et al*., 2018). Those factors may influence shoot branching via various physiological and molecular mechanisms, targeting different branching-related genes and acting synergistically or antagonistically. *BRC1* (*BRANCHED 1)* is well known to act locally in buds and is considered to be an important hub of different signals controlling the ability of a bud to grow out in many species (Aguilar-Martínez *et al*., 2007; Dun *et al*., 2009; Leyser, 2009; Beveridge and Kyozuka, 2010; Rameau *et al*., 2015). *Arabidopsis thaliana* harbors two *BRANCHED* genes, namely *BRANCHED 1* (*BRC1*) and *BRANCHED 2* (*BRC2)*; they encode TCP transcription factors closely related to *TEOSINTE BRANCHED1* (*TB1*) in maize and *FINE CULM 1* (*FC1*) in rice. In addition, they are conserved in many species of the plant kingdom (Table 1). The corresponding mutants show an altered branching phenotype as compared to the wild type (Aguilar-Martínez *et al*., 2007; González-Grandío *et al*., 2013). This review addresses the molecular identity of *BRC1*, its involvement in shoot branching, and its regulation in response to endogenous inputs (hormones, nutrients) and exogenous cues (light).

We also discuss how *BRC1* can mechanistically govern bud outgrowth, and raise a few questions about future investigations.

2. BRC1 belongs to the TCP transcription factor family

AtBRC1 (also called *AtTCP18*) contains an open reading frame (ORF) made of *ca*.1,290-bp that encodes a protein with a TCP domain and an R domain. It belongs to the TCP gene family, an evolutionarily conserved family that first appeared in freshwater algae of the Charophyta family (Navaud *et al*., 2007). The TCP gene family was first described by Cubas *et al*., (1999) and is represented by four 'founding members': *TEOSINTE BRANCHED1* (*TB1*), *CYCLOIDEA* (*CYC*), *PROLIFERATING CELL NUCLEAR ANTIGEN FACTOR1* (*PCF1*), and *PCF2*, all identified on the basis of their functions in plant development or their DNA-binding capacities (for a review see Li, 2015; Danisman, 2016). In *Arabidopsis*, the TCP family comprises 24 genes encoding predicted proteins with a TCP domain (Cubas *et al*., 1999; Cubas, 2004; Kosugi and Ohashi, 2002; Palatnik *et al*., 2003) and categorized into two classes: class I (also known as PCF or TCP-P) is made up of 13 predicted proteins related to the PCF rice factors (Kosugi and Ohashi, 1997), and class II (also known as TCP-C) is made up of 11 predicted proteins related to the *Antirrhinum CYC* and *CIN* genes and to the *Zea mays TB1* gene (Luo *et al*., 1996; Doebley *et al*., 1997; Nath *et al*., 2003; Palatnik *et al*., 2003). All these transcription factors have the so-called TCP domain, a 59-amino-acid basic helix–loop–helix (bHLH), in common (Martín-Trillo and Cuba, 2010). Such a motif allows for DNA binding and protein–protein interactions in cells. The TCP domain is also necessary for nuclear localization (Kosugi and Ohashi, 1997; Cubas *et al*., 1999), and some TCP proteins can be targeted to the nucleus in heterologous systems (Suzuki *et al*., 2001; Qin *et al*., 2004).

Besides the TCP domain, a few class-II TCPs, including BRC1, display a functionally unknown arginine-rich motif, the R-domain, which is predicted to mediate protein interactions (Lupas *et al*., 1991; Cubas *et al*., 1999). The R domain may involve the phosphorylation process of BRC1 by a cAMP-dependent protein kinase (Dulhanty and Riordan, 1994; Martín-Trillo and Cubas, 2010). Additionally, most members of the *CYC/TB1* subclass, to which *BRC1* belongs, contain a conserved ECE (glutamic acid-cysteine-glutamic acid) motif that remains functionally uncharacterized and is located between their TCP and R domains (Howarth and Donoghue, 2006).

TCP proteins of various species regulate many biological processes, including seed germination, plant branching, lateral organ development, floral asymmetry, gametophyte development, leaf senescence, circadian rhythms, and defense responses (for a review see Li *et al*., 2015; Danisman, 2016). These TCP-dependent regulations could occur directly through their binding to the promoter of target genes or indirectly *via* their interactions with plant hormones (Danisman *et al*., 2012; Schommer *et al*., 2008; Guo *et al*., 2010; Li and Zachgo, 2013, Nicolas and Cubas, 2016). In *Arabidopsis*, the *CYC/TB1* clade consists of *AtBRC1*, *AtBRC2* (also called *AtTCP12*) and *AtTCP1*, and is mainly involved in the

development of axillary meristems, giving rise to either flowers or lateral shoots (Martín-Trillo and Cubas, 2010).

3. BRC1 is a central actor of shoot branching

The shoot axillary meristem produces a branch when the appropriate endogenous and exogenous inputs occur, so as to adapt plant architecture to environmental conditions. In monocots, *TB1* from *Zea mays* (Doebley *et al.*, 1997) and homologs of *TB1* in *Oryza sativa* (*OsTB1/FC1,* Takeda *et al.*, 2003) and *Sorghum bicolor* (*SbTB1,* Kebrom *et al.*, 2006) promote bud arrest locally, without affecting the number of buds, and thus lead to reduced tillering. Consistently, *TB1* and *OsTB1* are mainly expressed in axillary bud meristems (Hubbard *et al.*, 2002; Takeda *et al.*, 2003), and their mutants *tb1* and *fc1* exhibit over-tillering phenotypes (Doebley *et al.*, 1997; Wang *et al.*, 1999; Takeda *et al.*, 2003). The barley *TB1* ortholog, *INT-C,* has been shown to act mainly in the control of spike architecture, with a minor role in tillering (Ramsay et al., 2011). Moreover, modern maize displays less branching than the wild teosinte ancestor due to increased *TB1* expression (Studer *et al*., 2011; Zhou *et al*., 2011). However, the *intc* loss-of-function mutant showed less tillers in barley, whose phenotype is opposite to the recessive *tb1* mutant in maize (Liller et al., 2015; Dong et al., 2019).

In dicots, genes closely related to *TB1* have been studied in a variety of species. In *Arabidopsis, AtBRC1* and *AtBRC2* both negatively regulate the branching process (Aguilar-Martínez *et al.*, 2007; Poza-Carrión *et al*., 2007). However, *AtBRC1* seems to play a more pivotal role in axillary bud development than *AtBRC2*. The *AtBRC1* gene is predominantly expressed during the development of axillary buds (axillary meristems, bud leaf primordia and subtending vascular tissue). *AtBRC1* expression is inversely correlated with bud outgrowth and *brc1* mutant phenotypes are non-pleiotropic, while constitutive overexpression of *AtBRC1* reduces the growth of the whole plant (Aguilar-Martínez *et al.*, 2007). Moreover, many *AtBRC1*-homologous genes have also been found to be involved in shoot branching suppression (Table 1). In addition, repressed buds in pea have been found to be as metabolically active as growing buds, so BRC1 growth repression may not involve metabolism (Stafstrom and Sussex, 1988). Recent data demonstrate that *AtBRC1* is not always necessary for the complete inhibition of all buds in *Arabidopsis* (Seale *et al*., 2017).

Genomic sequences of *Solanum* species, including potato and tomato, also contain the *BRC1*-like gene, where it occurs under two forms (Brewer, 2015). More interestingly, in *Solanum tuberosum*, the *BRANCHED1a (StBRC1a)* gene encompasses an alternative splice site leading to the generation of two BRC1a protein isoforms, $BRC1a^{Long}$ and $BRC1a^{Short}$, with distinct C-terminal regions (Martín-Trillo *et al*., 2011; Nicolas *et al.*, 2015). The $BRC1a^{Long}$ C-terminal region has a strong activation domain and moves to the nucleus, whereas the $BRC1a^{Short}$ C-terminal region lacks an activation domain, which prevents the nuclear targeting of the protein (Nicolas *et al.*, 2015). These different splice variants of *AtBRC1* have also been found in *Arabidopsis* (data not shown), but whether the mechanism

mentioned above exists in *Arabidopsis* is still unknown. A central role of *BRC1* in shoot branching has also been revealed in pea (*PsBRC1,* Braun *et al.*, 2012), *Chrysanthemum* (*DgBRC1,* Chen *et al.*, 2013) and poplar (*BRC1*, Muhr *et al*., 2016). In *Rosa sp*., Li-Marchetti *et al*. (2017) carried out a Quantitative Trait Loci (QTL) analysis of the plant architecture, using a segregating, recurrent blooming population called 'The Fairy' x 'Old Blush'. They showed that the branching angle of order 2 long axes, the number of short axes (the type of axis that comprises one to four internodes), and stem elongation were correlated, with QTL located in the genomic region of *RhBRC1*, and assumed a pleiotropic role of *RhBRC1* in the establishment of the bushy shape of *Rosa sp*. Further work will be required to more accurately define the role of *BRC1* in the establishment of the plant complex architecture.

4. BRC1 is an integrator of diverse hormonal signaling networks

Auxin, cytokinins (CK) and strigolactones (SL) are implicated in the hormonal regulation of *BRC1* expression. In this regulation network, auxin and SL act as inducers while CK act as repressors (Teichmann and Muhr, 2015, Rameau *et al*., 2015). According to Ferguson *et al*. (2009), this kind of regulation could be involved in various metabolism pathways such as feedback regulation, long-distance hormone transport, and the interplay of plant hormone metabolism and signaling.

In apical dominance, the polar auxin transport (PAT) stream in the main stem, which is mediated by the PIN (PIN-FORMED) auxin-efflux facilitators located in xylem-associated cells (Petrasek and Friml, 2009), inhibits axillary bud outgrowth (Morris, 1977; Li and Bangerth, 1999; Balla *et al*., 2011). Auxin cannot directly regulate *BRC1* expression because it is not transported from the stem to the buds in great enough amounts (Hall and Hillman, 1975). It is hypothesized that PAT prevents the establishment of auxin canalization from axillary buds to the stem, and that this might be necessary for the buds to grow out (Li and Bangerth, 1999; Domagalska and Leyser, 2011; Chabikwa et al., 2018). The characterization of the auxin-resistant *Arabidopsis* mutant *axr1* indicated that such an auxin effect occurred after axillary meristem initiation through the inhibition of bud outgrowth (Stirnberg *et al*., 1999).

Auxin can indirectly promote *BRC1* expression in the bud (Aguilar-Martínez *et al*., 2007). Furthermore, auxin-mediated *BRC1* regulation through the control of two antagonistic factors, CK and SL, fine-tunes *BRC1* expression inside buds (Rameau et al., 2015). The role of CK, a collection of adenine-related compounds, in bud outgrowth was evidenced decades ago, when CK application to dormant buds was shown to promote bud outgrowth (Wickson and Thimann, 1958; Sachs and Thimann, 1967; Bangerth *et al*., 1994; Tanakea *et al*., 2006). In parallel, auxin indirectly inhibits bud outgrowth by decreasing systemic and local CK levels, which determines the CK supply to the buds (Müller and Leyser, 2001; Miyawaki *et al*., 2004; Nordström *et al*., 2004; Tanaka *et al*., 2006). CK can act to promote branching partly by promoting PIN3,4,7 cross-stem auxin transport between the bud and the adjoining stem, thereby potentially acting partly independently of *AtBRC1* repression directly in the bud

(Waldie and Leyser 2018). High CK levels in axillary buds lead to the activation of axillary buds through downregulation of *BRC1* expression (Braun *et al*., 2012), although *Psbrc1* (a pea *BRC1* mutant) remained sensitive to CK application. These findings might indicate that the branch-promoting hormone CK partly controls shoot branching by negatively regulating *BRC1* at the transcriptional level. In rice, transcript levels of *OsTB1*/*FC1* also decreased in a CK-dose-dependent manner (Minakuchi *et al*., 2010), and similar down-regulation of *DgBRC1* was reported in *Chrysanthemum* (Dierck *et al*., 2016). This CK-dependent *BRC1* regulation can be part of the light intensity-dependent bud outgrowth regulation in *Rosa sp* (Roman *et al*., 2016; Corot *et al*., 2017). The *Arabidopsis altered meristem program1* (*amp1*) mutants are characterized by higher levels of CK, more bud outgrowth, more axillary meristems, and reduced *BRC1* expression (Helliwell *et al*., 2001). Although CK are a powerful repressor of *BRC1*/*TB1*/*FC1* expression, the molecular mechanisms driven by this CK-dependent regulation still remain an open question (Figure 1).

Strigolactones (SL), a group of carotenoids derived from terpenoid lactones (Lin *et al*., 2009; Alder *et al*., 2012), act as endogenous shoot branching inhibitors (Gomez-Roldan *et al*., 2008). Direct application of GR24 - an SL analog - on buds inhibited outgrowth on intact and decapitated plants (Brewer *et al*., 2009), and auxin application elevated the transcription levels of SL biosynthesis genes (Sorefan *et al*., 2003, Foo *et al*., 2005; Johnson *et al*., 2006; Zou *et al*., 2006; Arite *et al*., 2007 and 2009; Hayward *et al*., 2009). These findings support that auxin-mediated bud outgrowth inhibition involves the promotion of systemic and local SL synthesis in the stem and thereby of SL levels inside buds. Consistently, different SL mutants exhibited a highly branched phenotype in pea (*ramosus* (*rms*)), petunia (*decreased apical dominance* (*dad*)) and *Arabidopsis* (*more axillary growth* (*max*)) (Crawford *et al*., 2010). A role for BRC1 downstream of SL was first reported in *Arabidopsis* and pea, where *BRC1* expression was upregulated by SL, and shoot branching in the *brc1* mutant was insensitive to SL (Aguilar-Martínez *et al*., 2007; Dun *et al*., 2012; Revel *et al*., 2015). However, SL application did not change the transcriptional activation of *OsTB1/FC1* expression in rice. (Minakuchi *et al*., 2010). Recent investigations showed that *DWARF 53* (*D53*)*/ SUPPRESSOR OF MAX2 1-LIKE* genes (*SMXL6*, *7*, *8*) acted downstream of SL as repressors of SL-dependent *BRC1* upregulation and thereby promoted shoot branching (Zhou *et al*., 2013; Jiang *et al*., 2013; Kong *et al*., 2014; Wang *et al*., 2015). Mutants deficient in *D53*-like genes indeed displayed constitutive *BRC1* upregulation (Seale *et al*., 2017; Soundappan *et al*., 2015; Wang *et al*., 2015). Moreover, SL perception by D14 (α/β hydrolase) and the recruitment of the SCF complex resulted in the polyubiquitination and 26S-proteasome–mediated degradation of D53 (Waters *et al*., 2017; Kerr and Beveridge, 2017). D53 physically interacts with IPA1 (IDEAL PLANT ARCHITECTURE1), a repressor of shoot branching, and prevents it from upregulating *TB1* expression (Figure 1) (Song *et al*., 2017). IPA1, also named OsSPL14, is a member of the SQUAMOSA PROMOTER BINDING PROTEIN-LIKE (SPL) family of plant-specific transcription factors (Miura *et al*., 2010) that directly binds to the *TB1* promoter in rice and activates *TB1*transcriptional activity (Figure 1; Jiao *et al*., 2010; Lu *et al*., 2013). Further support for the relevance of the "*IPA-1*-related genes and *TB1*" module in shoot branching comes from a study in wheat, where

TaD53 physically interacted with TaSPL3 and prevented TaSPL3 upregulation of *TaTB1* gene expression (Liu *et al*., 2017). Although the *Arabidopsis* homologs of *IPA1* have been identified as being *SPL9/15*, further work will be required to confirm whether this mechanism is involved in the SL-dependent regulation of *AtBRC1*.

Besides auxin, CK, and SL, gibberellin (GA) might also be involved in the regulation of *BRC1* expression, even if the mechanism is still unknown (Lantzouni *et al*., 2017). GAs (diterpenoid tetracyclin molecules) are plant hormones that regulate various developmental processes, including stem elongation, germination, dormancy, flowering, flower development, and leaf and fruit senescence (Hedden and Sponsel, 2015). In *Rosa sp*., GA biosynthesis strongly increases during bud outgrowth (Choubane *et al*., 2012). In the perennial woody plant *Jatropha curcas*, GA and CK synergistically promote lateral bud outgrowth, and both hormones negatively influence *BRC1* and *BRC2* expression (Ni *et al*., 2015). Simultaneously altered GA and SL levels positively influenced the expression of the *GA2 OXIDASE2* gene which encodes a GA-catabolic enzyme, and the expression of *BRC1* (Figure 1) (Lantzouni *et al*., 2017). Furthermore, GA is required for CK-mediated axillary bud outgrowth in *Arabidopsis thaliana* (Jasinski *et al*., 2005; Lo *et al*., 2008).

5. BRC1 expression is regulated by light

Shoot branching is negatively affected by low light intensity and low ratios of red/far red (R:FR) light in many species (Kebrom *et al*., 2006; Finlayson *et al*., 2010; Su *et al*., 2011; Revel *et al*., 2015). In this process, light acts both as a driver of photosynthesis for the supply of sugars to axillary buds and as a photomorphogenic signal (Su *et al*., 2011). The signaling role of light in plant branching was first unraveled by Kebrom *et al*. (2006). In 2006 and 2010, these authors showed that active PHYB suppressed the expression of the *SbTB1* gene in sorghum, leading to high plant branching, whereas environmental conditions that inactivate phyB (low R/FR ratio) increased *SbTB1* expression and in turn repressed bud outgrowth. Additional experiments carried out in *Arabidopsis* confirmed these findings: a low R/FR ratio favored *AtBRC1* upregulation through the PHYB pathway, which is required for shoot branching reduction (Figure 1; González-Grandío *et al*., 2013). This effect seems to be reversible, as evidenced by the rapid and local downregulation of *AtBRC1* after increasing the R/FR ratio (Holalu and Finlayson 2017). Such a response may contribute to the rapid adaptation of plants to fluctuations in the R/FR light ratio.

Besides light quality, a slight decrease of the photosynthetic leaf area is associated with a stimulation of *TB1* expression in sorghum seedlings and consequently a lower propensity of tiller buds to grow out (Kebrom and Mullet, 2015). In addition, darkness-exposed *Rosa sp.* exhibited no bud outgrowth and higher levels of *RhBRC1* transcripts than plants placed under light (Roman *et al*., 2016). All these findings indicate that *BRC1* expression is very sensitive to both light intensity and quality. However, this regulation may involve distinct mechanisms (Kebrom *et al*., 2010).

6. BRC1 is regulated by nutrients

Sugars are well known to promote bud outgrowth in many species (Leduc *et al*., 2014; Rameau *et al*., 2015; Kebrom, 2017; Tarancón *et al*., 2017), and the relationship between sugars and bud outgrowth has been investigated for years (Maurel *et al*., 2004; Chao *et al*., 2007; Girault *et al.*, 2010; Kebrom *et al.*, 2010 and 2012; Henry *et al.*, 2011; Rabot *et al.*, 2012; Mason *et al*., 2014; Barbier *et al.*, 2015; Fichtner *et al*., 2017). Sugar effects are seemingly dependent on environmental conditions (Corot *et al*., 2017). Sugars not only serve as a carbon source for plant metabolism, but also as an important signaling entity that affects many developmental processes including *BRC1* gene expression (Price *et al*., 2004; Hellmann and Smeekens, 2014; Barbier *et al*., 2015; Sakr *et al*., 2018). In an interesting study, Mason *et al.* (2014) demonstrated that the initial signal responsible for the release of bud outgrowth after decapitation in pea was an increase in sugar availability rather than a decrease in apically supplied auxin, as traditionally thought. This is in line with the earlier proposal by Morris and collaborators (Morris *et al.*, 2005), who assumed the existence of an auxin-independent "fast-decapitation signal" leading to bud outgrowth initiation after decapitation. Furthermore, Mason *et al.* (2014) also reported that the timing of the increase of the sugar flux inside buds and bud outgrowth tightly coincided with the downregulation of *BRC1* expression. In this process, sugar acts more likely as a signaling entity, because many non-metabolizable sugar analogs can trigger bud outgrowth (Rabot *et al*., 2012) and repress *BRC1* expression (Barbier *et al*., 2015). In addition, this effect of sugar on *BRC1* transcription could be mediated indirectly *via* sugar regulation of CK biosynthesis and SL signaling (Barbier *et al*., 2015) and/or directly (irrespective of hormonal action). Decapitation led to a rapid and sustained rise in trehalose-6 phosphate (T6P) levels in axillary buds and a decreased expression level of *BRC1*, which supports that T6P could partly mediate the sugar-dependent down-regulation of *BRC1* (Figure 1) (Fichtner *et al*., 2017). Further works are required to further unravel this molecular regulatory network. In the present state of knowledge, we cannot rule out that the transcriptional regulation of *BRC1* in response to sugars could involve many sugar-signaling pathways and also that *BRC1* expression is sensitive to the plant carbon status and/or energy levels (Martín-Fontecha *et al*., 2018).

Mineral nutrition influences tiller bud outgrowth in barley (Fletcher and Dale, 1974). In wheat, phosphorus deficiency directly altered the normal pattern of tiller emergence by reducing the rate of tiller emergence for each tiller (Rodríguez *et al*., 1999). Although several links exist between phosphate and the branching-related hormones (auxin, SL, CK), no direct effect of the phosphate status on *BRC1*/*TB1*/*FC1* gene expression is documented. Low-phosphate growth conditions enhance SL production in many species (Yoneyama *et al*., 2007; López-Ráez *et al*., 2008; Kohlen *et al*., 2011; Umehara *et al*., 2008; Domagalska and Leyser, 2011; Yamada *et al*., 2014). This situation leads to the repression of shoot branching (Umehara *et al*., 2008; Kohlen *et al*., 2011), but also to the stimulation of lateral root formation for soil foraging (Ruyter-Spira *et al*., 2011; Yoneyama *et al*., 2007). In contrast to SL, low levels of inorganic phosphate reduce CK production, which correlates with a reduced number of branches (Horgan and Wareing, 1980).

In herbaceous and woody plants, high levels of nitrogen fertilization (nitrate and /or

ammonium) result in (i) a large number of outgrowing buds (Lortie and Aarssen, 1997; Médiène *et al*., 2002; Cline *et al*., 2006; Emarat-Pardaz *et al*., 2013; Furet *et al*., 2013; Pal *et al*., 2013), and (ii) improved secondary axis elongation (Thitithanakul *et al*., 2012; Thitithanakul, 2012). Luo *et al*. (2017) confirmed that nitrogen deficiency did not affect the initiation of tiller buds, but suppressed tiller bud outgrowth in *Oryza sativa*. In *Arabidopsis*, low nitrate delayed axillary bud activation, and this process involved an effect of the plant nitrogen status rather than a direct nitrate-signaling pathway (De Jong *et al*. 2014). Recent results demonstrated a relationship between nitrogen fertilization and *BRC1* expression in rice (Li *et al*., 2016). They showed that high ammonium nitrate intake in the root environment induced a reduction of apical dominance through overexpression of miRNA393 in the buds; miRNA393 inhibits the expression of the genes involved in auxin synthesis and signaling (*OsTIR1*, *OsAFB2* and *OsIAA6*) as well as *OsTB1*. In *Arabidopsis*, the *brc1-2*/*brc2-1* double mutant exhibited a higher number of branches than the wild type, but low availability of nitrate reduced this effect (Seale *et al*., 2017). As root nitrate is widely known to induce CK biosynthesis and signaling events in the whole plant (Crawford, 1995; Sakakibara *et al*., 1998; Takei *et al*., 2001; Forde, 2002a, 2002b; Takei *et al*., 2002), and CK repress *BRC1* expression, we cannot exclude that nitrate may affect *BRC1* expression through CK modulation. In rice, the supply of a CK analog (BAP) or ammonium nitrate regulated SL amounts in the stem and the bud within three hours after treatment, but nothing has been reported regarding *BRC1* expression (Xu *et al*., 2015).

In Rosaceae as in many woody plants, nitrate is reduced and assimilated into amino acids directly in the roots; consequently, asparagine, arginine, aspartate, and glutamine are the main forms of nitrogen translocated to the buds via the xylem sap (Millard *et al*., 1998; Malaguti *et al*., 2001; Grassi *et al*., 2002; Guak *et al*., 2003; Le Moigne *et al*., 2018). In rose, asparagine is a major nitrogen form involved in bud outgrowth (Le Moigne *et al*., 2018); this is in accordance with previous data showing that application of asparagine on the soil of olive trees or on the leaves of poplar trees contributed to enhance bud outgrowth and secondary axis elongation (Cline *et al*., 2006; Proietti and Tombesi, 1996). In rice, a lack of cytosolic glutamine synthetase1;2 in the vascular tissues of axillary buds severely reduced their outgrowth (Funayama *et al*., 2013; Ohashi *et al*., 2015) independently of the SL level (Ohashi *et al*., 2015). In rose bush, sucrose, glucose, and fructose had to be associated to asparagine to allow for the buds to grow out *in vitro* (Le Moigne *et al*., 2018). This effect involved the upregulation of *IPT3* gene expression in the stem and in the vicinity of the bud (Le Moigne *et al*., 2018) and the downregulation of *BRC1* (Barbier *et al*., 2015). In addition to a nutritional role, asparagine might also be a signal representing the nitrogen status of the plant, so as to counteract *BRC1* expression through CK stimulation.

7. A BRC1-related regulatory mechanism

Many studies ascribe an inhibitory function of mitotic cell activity to BRC1 (Poza-Carrión *et al*., 2007; Kieffer *et al*., 2011). This is because early results of EMSA (Electrophoresis Mobility Shift Assay) revealed the capacity of the TCP domain to associate specifically with

the promoter element of the rice proliferating cell nuclear antigen (PCNA) gene (Kosugi and Ohashi, 1997; Kosugi and Ohashi, 2002). These cis-regulatory modules are indispensable for the transcriptional activation of the PCNA gene in rice meristem tissues (Kosugi and Ohashi, 1997), which seems to be an ancient and prevalent role of TCP transcription factors (Ortiz-Ramírez *et al*., 2016).

BRC1-mediated branching is repressed by the regulation of abscisic acid (ABA) metabolism (Figure 1). ABA is a plant hormone that plays important roles in many phases of the plant life cycle (Seo and Koshiba, 2002; Wang *et al*., 2018; Hayes, 2018). Evidence for a role of ABA in regulating bud growth comes from the positive correlation between a reduction of ABA levels in buds and their release from dormancy (Cline, 1991). Moreover, the *Arabidopsis era1* (*ENHANCED RESPONSE TO ABA 1*) mutant exhibited high sensitivity to ABA and reduced branching (Pei *et al*., 1998). In *brc1 Arabidopsis* mutants, the ABA-signaling pathway showed a significantly reduced response as compared to the wild type. Additional data revealed that the expression levels of two ABA markers, *ABA-RESPONSE PROTEIN* (*ABR*) and *UDP-GLUCOSYL TRANSFERASE 74D1* (*UGT74D1*), were significantly upregulated in the wild type but not in *brc1* mutants treated with low R:FR light (González-Grandío *et al*., 2013). González-Grandío and Cubas (2014) support a model in which ABA acts rather downstream of BRC1, because *ABRE-BINDING FACTOR 3* (*ABF3*) and *ABA INSENSITIVE 5* (*ABI5*), two key regulators of the ABA response that contain TCP-binding sites in their promoters (Finkelstein *et al*., 2000; Yoshida *et al*., 2010; González-Grandío *et al*., 2014; Nicolas and Cubas, 2016), are upregulated in axillary buds upon *BRC1* induction (González-Grandío and Cubas, 2014). They also indicated that BRC1 bound to and positively regulated three transcription factors: *HOMEOBOX PROTEIN 21* (*HB21*), *HOMEOBOX PROTEIN 40* (*HB40*), and *HOMEOBOX PROTEIN 53*(*HB53*). These three proteins, together with BRC1, enhanced *NINE-CIS-EPOXICAROTENOID DIOXIGENASE 3* (*NCED3*) expression, the main ABA-biosynthesis enzyme, leading in turn to ABA accumulation in buds (González-Grandío *et al*., 2017). This finding demonstrates a direct relationship between *BRC1* and ABA signaling, and places ABA downstream of *BRC1*. Consistently, *BRC1* expression was found to be insensitive to exogenous ABA application (Yao and Scott, 2015).

TCP genes generally act by positively or negatively regulating the cell cycle (Sarvepalli and Nath, 2018). As a transcription factor, BRC1 could bind to the promoter region of various genes to regulate the branching process and participate to many regulatory mechanisms (González-Grandio *et al*., 2013). In maize, TB1 can directly activate the *tassels replace upper ears1* (*tru1*) gene that encodes an ankyrin-repeat-domain protein by binding to the promoter region of *tru1* (Dong *et al.* 2017). In *Arabidopsis*, bioinformatic analysis indicates that the promoter sequences of 1,950 genes expressed in the shoot bear the TCP-cis regulatory motif (5'-RRVMMMV-3') and could be putatively regulated by *AtBRC1*. Based on Gene Ontology (GO) enrichment analysis, these putative target genes are thought to be mainly involved in metabolic processes, including amino acid metabolism (*e.g*. *ALANINE-2-OXOGLUTARATE AMINOTRANSFERASE 1* (*AOAT1*); *HYDROXYPYRUVATE REDUCTASE* (*ATHPR1*)) and

sulfur (*e.g*. *sulfate transmembrane transporter* (*MOT2*), *sulfate transporter 1;2* (*SULTR1;2*)) (data not shown). We can therefore speculate that BRC1/TB1 might control bud outgrowth via various pathways, such as stimulating the ABA-signaling pathway and inhibiting cell division and cell metabolism.

8. Conclusion and perspectives

BRC1/*TB1*/*FC1* is an integrator gene involved in shoot branching, which fits well with the ability of *BRC1*/*TB1*/*FC1* expression to integrate many endogenous and exogenous inputs (Figure 1). However, the detailed mechanism whereby these stimuli regulate *BRC1* expression is still puzzling, and many mechanistic scenarios are plausible. Many questions are thus still open and include how CK and SL, the main two branching-related hormones, antagonistically regulate *BRC1* expression, and which molecular actors could be involved. Similar questions concern the sugar-mediated downregulation of BRC1, and the molecular mechanism behind the combined effect of nutrients and hormones on *BRC1* expression (Sakr *et al*. 2018). In addition, the regulation of gene expression includes many aspects, such as epigenetic regulation, transcriptional regulation, post-transcriptional regulation, translational and post-translational regulation. The relevance of these mechanisms in the regulation of *BRC1* expression deserves to be investigated in different biological contexts. Recent data showed that the protein interaction process also influences *BRC1* expression. For example, the florigen proteins FLOWERING LOCUS T (FT) and TWIN SISTER OF FT (TSF) influence axillary meristem development via their interaction with AtBRC1 (Niwa *et al*., 2013); TIE1 (TCP interactor containing EAR motif protein 1), a transcriptional repressor identified as involved in the control of leaf development, controls shoot branching by interacting with BRC1 (Yang *et al*., 2018). Additional protein partners may also interact with BRC1, including those related to the energy and nutrient statuses (Sucrose non fermenting-related kinase (SnRK1)/Target of Ramapacin (TOR kinase)) (Martín-Fontecha *et al*., 2018). Meanwhile, our knowledge about the molecular network governing the BRC1-dependent reduction of plant branching is still limited, and the only available data report that BRC1 action could be related to different biological functions such as cell proliferation, cell metabolism, hormone biosynthesis, ribosome biosynthesis, *etc*.. All these findings indicate that further work is required to fully investigate the regulatory network behind the regulation and function of *BRC1* in shoot branching.

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Table 1. The publication of *BRC1* homologue genes in different species

Species		Name of the gene	References
Monocots	*Zea mays*	*TB1*	Doebley et al., 1997
	Oryza sativa	*Ostb1*/*FC1*	Takeda et al., 2003
	Sorghum bicolor	*SbTB1*	Kebrom et al., 2006
	Hordeum vulgare	*INTERMEDIUM-C*	Ramsay et al., 2011
	Triticum aestivum	*TB-D1*	Dixon et al., 2018
Eudicots	*Solanum tuberosum*	*StBRC1*	Nicolas et al., 2015
	Pisum sativum	*PsBRC1*	Braun et al., 2012
	Dendranthema grandiflora	*DgBRC1*	Chen et al., 2013
	Arabidopsis thaliana	*AtBRC1*	Aguilar-Martínez et al., 2007
	Solanum lycopersicum	*SlBRC1*	Martín-Trillo et al., 2011
	Rosa hybrida	*RhBRC1*	Barbier et al., 2015
	Nicotiana tabacum	*NtBRC1a; NtBRC1b;NtBRC1c;NtBRC1d*	Chen et al., 2016
	Populus canescens	*PcBRC1*	Muhr et al., 2018

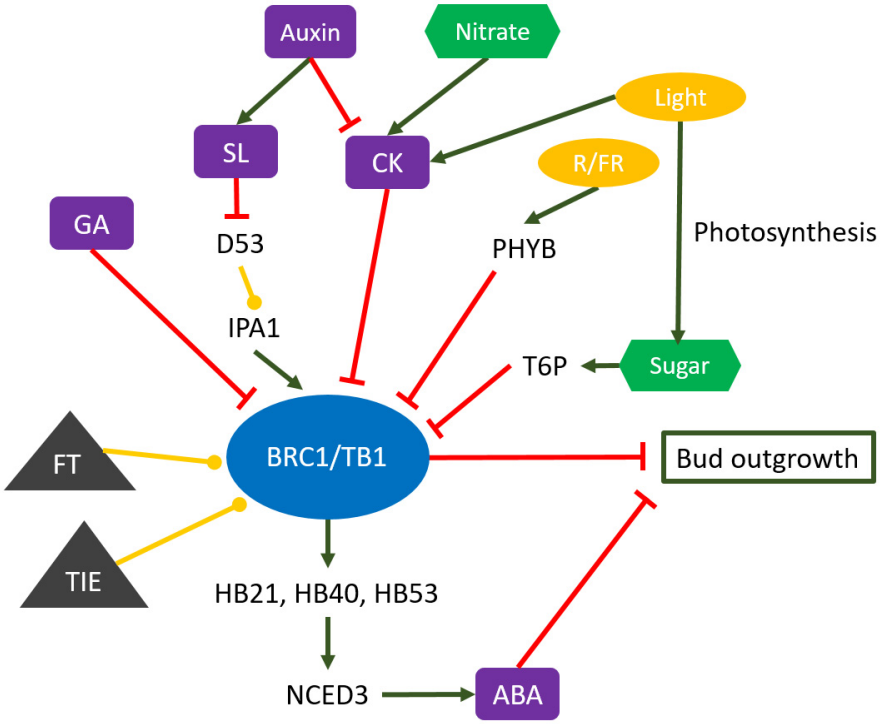

Figure 1. Many factors influence the expression of *BRC1*, including developmental, positional, genetic, hormonal, sugar signal and environmental factors. Auxin, cytokinin (CK), and strigolactones (SL) are implicated in the hormonal regulation of *BRC1* expression; auxin and SLs as inhibitors of *BRC1* and CK as a promoter of *BRC1*. The red line, inhibition effect; The green arrow, stimulation effect; The yellow bullet-end lines, protein interaction; The violet element, plant hormones; The green element, plant nutrition; The green element, The yellow element, exogenous influence factor; The grey triangle, the proteins that interact with BRC1/TB1; D53, DWARF 53; HB21, HOMEOBOX PROTEIN 21; HB40, HOMEOBOX PROTEIN 40; HB53, HOMEOBOX PROTEIN 53; IPA1, IDEAL PLANT ARCHITECTURE1; NCED3, NINE-CIS-EPOXICAROTENOID DIOXIGENASE 3; PHYB, PHYTOCHROME B; T6P, trehalose-6 phosphate.

References:

Aguilar-Martínez, J. A., Poza-Carrión, C., and Cubas, P. (2007). Arabidopsis *BRANCHED1* acts as an integrator of branching signals within axillary buds. *The Plant Cell*, 19(2), 458-472. doi: 10.1105/tpc.106.048934

Alder, A., Jamil, M., Marzorati, M., Bruno, M., Vermathen, M., Bigler, P., et al. (2012). The path from β-carotene to carlactone, a strigolactone-like plant hormone. *Science*, 335(6074), 1348-1351. DOI: 10.1126/science.1218094

Arite, T., Iwata, H., Ohshima, K., Maekawa, M., Nakajima, M., Kojima, M., et al. (2007). *DWARF10*, an RMS1/MAX4/DAD1 ortholog, controls lateral bud outgrowth in rice. *The Plant Journal*, 51(6), 1019-1029.doi: 10.1111/j.1365-313X.2007.03210.x

Arite, T., Umehara, M., Ishikawa, S., Hanada, A., Maekawa, M., Yamaguchi, S., et al. (2009). *d14*, a strigolactone-insensitive mutant of rice, shows an accelerated outgrowth of tillers. *Plant and Cell Physiology*, 50(8), 1416-1424.doi: 10.1093/pcp/pcp091

Balla, J., Kalousek, P., Reinöhl, V., Friml, J., and Procházka, S. (2011). Competitive canalization of PIN-dependent auxin flow from axillary buds controls pea bud outgrowth. *The Plant Journal*, 65(4), 571-577. doi: 10.1111/j.1365-313X.2010.04443.x

Bangerth, F. (1994). Response of cytokinin concentration in the xylem exudate of bean (*Phaseolus vulgaris* L.) plants to decapitation and auxin treatment, and relationship to apical dominance. *Planta*, 194(3), 439-442. doi:10.1007/BF00197546

Barbier, F., Peron, T., Lecerf, M., Perez-Garcia, M.-D., Barriere, Q., Rol ik, J., et al. (2015). Sucrose is an early modulator of the key hormonal mechanisms controlling bud outgrowth in *Rosa hybrida*. *J. Exp. Bot*. 66, 2569–2582. doi: 10.1093/jxb/erv047

Bate, N., and Twell, D. (1998). Functional architecture of a late pollen promoter: pollen-specific transcription is developmentally regulated by multiple stage-specific and co-dependent activator elements. *Plant molecular biology*, 37(5), 859-869. doi:10.1023/A:1006095023050

Beveridge, C. A., and Kyozuka, J. (2010). New genes in the strigolactone-related shoot branching pathway. *Current opinion in plant biology*, 13(1), 34-39. doi: 10.1016/j.pbi.2009.10.003

Boumaza, R., Demotes-Mainard, S., Huché-Thellier, L. and Guérin, V. (2009). Visual characterization of the esthetic quality of the rosebush. *Journal of Sensory Studies*, 24, 774-796. doi: 10.1111/j.1745-459X.2009.00238.x

Boumaza, R., Huché-Thélier, L., Demotes-Mainard, S., Le Coz, E., Leduc, N., Pelleschi-Travier, S., et al. (2010). Sensory profiles and preference analysis in ornamental horticulture: the case of the rosebush. *Food quality and preference*, 21(8), 987-997. doi: 10.1016/j.foodqual.2010.05.003

Braun, N., de Saint Germain, A., Pillot, J. P., Boutet-Mercey, S., Dalmais, M., Antoniadi, I., et al. (2012). The pea TCP transcription factor PsBRC1 acts downstream of strigolactones to control shoot branching. *Plant Physiology*, 158(1), 225-238. doi: 10.1104/pp.111.182725

Brewer, P. B. (2015). Plant Architecture: The Long and the Short of Branching in Potato. *Current Biology*, 25(16), R724-R725. doi: 10.1016/j.cub.2015.06.066

Brewer, P. B., Dun, E. A., Ferguson, B. J., Rameau, C., and Beveridge, C. A. (2009). Strigolactone acts downstream of auxin to regulate bud outgrowth in pea and Arabidopsis. *Plant Physiology*, 150(1), 482-493. doi: 10.1104/pp.108.134783

Chabikwa, T. G., Brewer, P. B., and Beveridge, C. A. (2019). Initial bud outgrowth occurs independent of auxin flow out of buds. *Plant physiology*, pp-00519.doi: 10.1104/pp.18.00519

Chao, W. S., Foley, M. E., Horvath, D. P., and Anderson, J. V. (2007). Signals regulating dormancy in vegetative buds. *International Journal of Plant Developmental Biology*, 1(1), 49-56.

Chen, X. J., Xia, X. J., Guo, X., Zhou, Y. H., Shi, K., Zhou, J., and Yu, J. Q. (2016). Apoplastic H_2O_2 plays a critical role in axillary bud outgrowth by altering auxin and cytokinin homeostasis in tomato plants. *New Phytologist*, 211(4), 1266-1278. doi: 10.1111/nph.14015

Chen, X., Zhou, X., Xi, L., Li, J., Zhao, R., Ma, N., and Zhao, L. (2013). Roles of *DgBRC1* in regulation of lateral branching in chrysanthemum (Dendranthema× grandiflora cv. Jinba). *PLoS One*, 8(4), e61717. doi: 10.1371/journal.pone.0061717

Choubane, D., Rabot, A., Mortreau, E., Legourrierec, J., Péron, T., Foucher, F., et al. (2012). Photocontrol of bud burst involves gibberellin biosynthesis in Rosa sp. *Journal of plant physiology*, 169(13), 1271-1280. doi: 10.1016/j.jplph.2012.04.014

Chow, C. N., Zheng, H. Q., Wu, N. Y., Chien, C. H., Huang, H. D., Lee, T. Y., et al. (2015). PlantPAN 2.0: an update of plant promoter analysis navigator for reconstructing transcriptional regulatory networks in plants. *Nucleic acids research*, 44(D1), D1154-D1160. doi: 10.1093/nar/gkv1035

Cline, M. G. (1991). Apical dominance. *The Botanical Review*, 57(4), 318-358. doi:10.1007/BF02858771

Cline, M.G., Thangavelu, M., Dong-Il, K., (2006). A possible role of cytokinin in mediating long-distance nitrogen signaling in the promotion of sylleptic branching in hybrid poplar. *Journal of. Plant Physiology*. 163, 684–688. doi: 10.1016/j.jplph.2005.06.005

Corot, A., Roman, H., Douillet, O., Autret, H., Perez-Garcia, M.D., Citerne, S., et al. (2017). Cytokinins and Abscisic Acid Act Antagonistically in the Regulation of the Bud Outgrowth Pattern by Light Intensity. *Frontiers in Plant Science*, 8: 1724 doi: 10.3389/fpls.2017.01724

Crawford, N. M. (1995). Nitrate: nutrient and signal for plant growth. *The plant cell*, 7(7), 859-868 doi:10.1105/tpc.7.7.859

Crawford, S., Shinohara, N., Sieberer, T., Williamson, L., George, G., Hepworth, J., et al. (2010). Strigolactones enhance competition between shoot branches by dampening auxin transport. *Development*, 137(17), 2905-2913. doi: 10.1242/dev.051987

Cubas, P. (2004). Role of TCP genes in the evolution of morphological characters in angiosperms. In Developmental genetics and plant evolution (Boca Raton, FL: CRC Press), 262-281

Cubas, P., Lauter, N., Doebley, J., and Coen, E. (1999). The TCP domain: a motif found in proteins regulating plant growth and development. *The Plant Journal*, 18(2), 215-222. doi:10.1046/j.1365-313X.1999.00444.x

Danisman, S. (2016). TCP transcription factors at the interface between environmental challenges and the plant's growth responses. *Frontiers in plant science*, 7, 1930. doi: 10.3389/fpls.2016.01930

Danisman, S., Van der Wal, F., Dhondt, S., Waites, R., de Folter, S., Bimbo, A., et al. (2012). Arabidopsis class I and class II TCP transcription factors regulate jasmonic acid metabolism and leaf development antagonistically. *Plant physiology*, pp-112. doi: 10.1104/pp.112.200303

De Jong, F., Thodey, K., Lejay, L. V., and Bevan, M. W. (2014). Glucose elevates NITRATE TRANSPORTER2. 1 protein levels and nitrate transport activity independently of its HEXOKINASE1-mediated stimulation of *NITRATE TRANSPORTER2. 1* expression. *Plant Physiology*, 164(1), 308-320. doi: 10.1104/pp.113.230599

Dierck, R., De Keyser, E., De Riek, J., Dhooghe, E., Van Huylenbroeck, J., Prinsen, E., et al. (2016).Change in auxin and cytokinin levels coincides with altered expression of branching genes during axillary bud outgrowth in Chrysanthemum. *PloS one*, 11(8), e0161732. doi: 10.1371/journal.pone.0161732

Doebley, J., Stec, A., and Hubbard, L. (1997). The evolution of apical dominance in maize. *Nature*, 386(6624), 485-488. doi: 10.1038/386485a0

Domagalska, M. A., and Leyser, O. (2011). Signal integration in the control of shoot branching. *Nature Reviews Molecular Cell Biology*, 12(4), 211-221. doi: 10.1038/nrm3088

Donald, R. G., and Cashmore, A. R. (1990). Mutation of either G box or I box sequences profoundly affects expression from the Arabidopsis rbcS-1A promoter. *The EMBO Journal*, 9(6), 1717-1726. doi:10.1002/j.1460-2075.1990.tb08295.x

Dong, Z., Alexander, M., and Chuck, G. (2019). Understanding Grass Domestication through Maize Mutants. *Trends in Genetics*, 35(2), 118-128. doi: 10.1016/j.tig.2018.10.007

Dong, Z., Li, W., Unger-Wallace, E., Yang, J., Vollbrecht, E., and Chuck, G. (2017). Ideal crop plant architecture is mediated by *tassels replace upper ears1*, a BTB/POZ ankyrin repeat gene directly targeted by TEOSINTE BRANCHED1. Proceedings of the National Academy of Sciences, 114(41), E8656-E8664. doi:10.1073/pnas.1714960114

Dixon, L. E., Greenwood, J. R., Bencivenga, S., Zhang, P., Cockram, J., Mellers, G., et al. (2018). *TEOSINTE BRANCHED1* regulates inflorescence architecture and development in bread wheat (*Triticum aestivum* L.). *The Plant Cell*, tpc-00961. doi: 10.1105/tpc.17.00961

Dulhanty, A. M., and Riordan, J. R. (1994). Phosphorylation by cAMP-dependent protein kinase causes a conformational change in the R domain of the cystic fibrosis transmembrane conductance regulator. *Biochemistry*, 33(13), 4072-4079.

Dun, E. A., Brewer, P. B., and Beveridge, C. A. (2009). Strigolactones: discovery of the elusive shoot branching hormone. *Trends in plant science*, 14(7), 364-372. doi: 10.1016/j.tplants.2009.04.003

Dun, E. A., de Saint Germain, A., Rameau, C., and Beveridge, C. A. (2012). Antagonistic action of strigolactone and cytokinin in bud outgrowth control. *Plant Physiology*, 158(1), 487-498. doi: 10.1104/pp.111.186783

Ellenberger, T., Fass, D., Arnaud, M., and Harrison, S. C. (1994). Crystal structure of transcription factor E47: E-box recognition by a basic region helix-loop-helix dimer. *Genes and development*, 8(8), 970-980. doi:10.1101/gad.8.8.970

Emarat-Pardaz, J., Shakiba, M. R., Toorchi, M., and Mohammadinasab, A. D. (2013). The influence of light intensities and nitrogen on growth of *Hypericum perforatum* L. *International Journal of Agriculture*, 3(4), 775–781.

Ferguson, B. J., and Beveridge, C. A. (2009). Roles for auxin, cytokinin, and strigolactone in regulating shoot branching. *Plant physiology*, 149(4), 1929-1944. doi: 10.1104/pp.109.135475

Ferreira, D. A., Soldi, M. C. M., Cheavegatti Gianotto, A., Carneiro, M. S., Amadeu, R. R., Aricetti, J. A., et al. (2018). Metabolite Profiles of Sugarcane Culm Reveal the Relationship Among Metabolism and Axillary Bud Outgrowth in Genetically Related Sugarcane Commercial Cultivars. *Frontiers in plant science*, 9, 857. doi: 10.3389/fpls.2018.00857

Fichtner, F., Barbier, F. F., Feil, R., Watanabe, M., Annunziata, M. G., Chabikwa, T. G., et al. (2017). Trehalose 6-phosphate is involved in triggering axillary bud outgrowth in garden pea (*Pisum sativum* L.). *The Plant Journal*, 92(4), 611-623. doi: 10.1111/tpj.13705

Finkelstein, R. R., and Lynch, T. J. (2000). The Arabidopsis abscisic acid response gene *ABI5* encodes a basic leucine zipper transcription factor. *The Plant Cell*, 12(4), 599-609. doi: 10.1105/tpc.12.4.599

Finlayson, S. A., Krishnareddy, S. R., Kebrom, T. H., and Casal, J. J. (2010). Phytochrome regulation of branching in Arabidopsis. *Plant physiology*, 152(4), 1914-1927. doi: 10.1104/pp.109.148833

Fletcher, G. M., and Dale, J. E. (1974). Growth of tiller buds in barley: effects of shade treatment and mineral nutrition. *Annals of Botany*, 38(1), 63-76. doi:10.1093/oxfordjournals.aob.a084802

Foo, E., Bullier, E., Goussot, M., Foucher, F., Rameau, C., and Beveridge, C. A. (2005). The branching gene *RAMOSUS1* mediates interactions among two novel signals and auxin in pea. *The Plant Cell*, 17(2), 464-474.doi: 10.1105/tpc.104.026716

Forde, B. G. (2002a). Local and long-range signaling pathways regulating plant responses to nitrate. *Annual Review of Plant Biology*, 53(1), 203-224. doi:10.1146/annurev.arplant.53.100301.135256

Forde, B. G. (2002b). The role of long-distance signalling in plant responses to nitrate and other nutrients. *Journal of Experimental Botany*, 53(366), 39-43. doi: 10.1093/jexbot/53.366.39

Funayama, K., Kojima, S., Tabuchi-Kobayashi, M., Sawa, Y., Nakayama, Y., Hayakawa, T., et al. (2013). Cytosolic glutamine synthetase1; 2 is responsible for the primary assimilation of ammonium in rice roots. *Plant and cell physiology*, 54(6), 934-943. doi: 10.1093/pcp/pct046

Furet, P. M., Lothier, J., Demotes-Mainard, S., Travier, S., Henry, C., Guérin, V., et al. (2014). Light and nitrogen nutrition regulate apical control in *Rosa hybrida* L. *Journal of plant physiology*, 171(5), 7-13. doi: 10.1016/j.jplph.2013.10.008

Garbez, M., Galopin, G., Sigogne, M., Favre, P., Demotes-Mainard, S. and Symoneaux, R. (2015). Assessing the visual aspect of rotating virtual rose bushes by a labeled sorting task. *Food Quality and Preference*, 40, Part B, 287-295. doi: 10.1016/j.foodqual.2014.06.008

Girault, T., Abidi, F., Sigogne, M., PELLESCHI-TRAVIER, S. A. N. D. R. I. N. E., Boumaza, R., Sakr, S., and Leduc, N. (2010). Sugars are under light control during bud burst in Rosa sp. *Plant, cell and environment*, 33(8), 1339-1350. doi: 10.1111/j.1365-3040.2010.02152.x

Giuliano, G., Pichersky, E., Malik, V. S., Timko, M. P., Scolnik, P. A., and Cashmore, A. R. (1988). An evolutionarily conserved protein binding sequence upstream of a plant light-regulated gene. *Proceedings of the National Academy of Sciences*, 85(19), 7089-7093. doi:10.1073/pnas.85.19.7089

Gomez-Roldan, V., Fermas, S., Brewer, P. B., Puech-Pagès, V., Dun, E. A., Pillot, J. P., et al. (2008). Strigolactone inhibition of shoot branching. *Nature*, 455(7210), 189. doi: 10.1038/nature07271

González-Grandío, E., and Cubas, P. (2014). Identification of gene functions associated to active and dormant buds in Arabidopsis. *Plant signaling and behavior*, 9(2), e27994. doi: 10.4161/psb.27994

González-Grandío, E., Pajoro, A., Franco-Zorrilla, J. M., Tarancón, C., Immink, R. G., and Cubas, P. (2017). Abscisic acid signaling is controlled by a BRANCHED1/HD-ZIP I cascade in Arabidopsis axillary buds. *Proceedings of the National Academy of Sciences*, 114(2), E245-E254. doi: 10.1073/pnas.1613199114

González-Grandío, E., Poza-Carrión, C., Sorzano, C. O. S., and Cubas, P. (2013). *BRANCHED1* promotes axillary bud dormancy in response to shade in Arabidopsis. *The Plant Cell*, tpc-112. doi: 10.1105/tpc.112.108480

Gordân, R., Shen, N., Dror, I., Zhou, T., Horton, J., Rohs, R., et al. (2013). Genomic regions flanking E-box binding sites influence DNA binding specificity of bHLH transcription factors through DNA shape. *Cell reports*, 3(4), 1093-1104. doi: 10.1016/j.celrep.2013.03.014

Grassi, G., Millard, P., Wendler, R., Minotta, G., and Tagliavini, M. (2002). Measurement of xylem sap amino acid concentrations in conjunction with whole tree transpiration estimates spring N remobilization by cherry (*Prunus avium* L.) trees. *Plant, Cell and Environment*, 25(12), 1689-1699. doi: 10.1046/j.1365-3040.2002.00949.x

Guak, S., Neilsen, D., Millard, P., Wendler, R., and Neilsen, G. H. (2003). Determining the role of N remobilization for growth of apple (*Malus domestica* Borkh.) trees by measuring xylem-sap N flux. *Journal of experimental botany*, 54(390), 2121-2131. doi: 10.1093/jxb/erg228

Guo, Z., Fujioka, S., Blancaflor, E. B., Miao, S., Gou, X., and Li, J. (2010). TCP1 modulates brassinosteroid biosynthesis by regulating the expression of the key biosynthetic gene *DWARF4* in *Arabidopsis thaliana*. *The Plant Cell*, tpc-109. doi: 10.1105/tpc.109.069203

Hall, S. M., and Hillman, J. R. (1975). Correlative inhibition of lateral bud growth in Phaseolus vulgaris L. Timing of bud growth following decapitation. Planta, 123(2), 137-143. doi: 10.1007/BF00383862

Han, Y. J., Kwon, Y. G., Chung, H. T., Lee, S. K., Simmons, R. L., Billiar, T. R., et al. (2001). Antioxidant enzymes suppress nitric oxide production through the inhibition of NF-κB activation: role of H_2O_2 and nitric oxide in inducible nitric oxide synthase expression in macrophages. *Nitric Oxide*, 5(5), 504-513. doi: 10.1006/niox.2001.0367

Hartmann, U., Sagasser, M., Mehrtens, F., Stracke, R., and Weisshaar, B. (2005). Differential combinatorial interactions of cis-acting elements recognized by R2R3-MYB, BZIP, and BHLH factors control light-responsive and tissue-specific

activation of phenylpropanoid biosynthesis genes. *Plant molecular biology*, 57(2), 155-171. doi: 10.1007/s11103-004-6910-0

Hayes, S. (2018). Revealing the Invisible: A Synthetic Reporter for ABA. *Plant physiology*, 177(4), 1346-1347. doi: 10.1104/pp.18.00646

Hayward, A., Stirnberg, P., Beveridge, C., and Leyser, O. (2009). Interactions between auxin and strigolactone in shoot branching control. *Plant physiology*, 151(1), 400-412. doi: 10.1104/pp.109.137646

Hedden, P., and Sponsel, V. (2015). A century of gibberellin research. *Journal of plant growth regulation*, 34(4), 740-760. doi: 10.1007/s00344-015-9546-1

Helliwell, C. A., Chin-Atkins, A. N., Wilson, I. W., Chapple, R., Dennis, E. S., and Chaudhury, A. (2001). The Arabidopsis *AMP1* gene encodes a putative glutamate carboxypeptidase. *The Plant Cell*, 13(9), 2115-2125. doi: 10.1105/TPC.010146

Hellmann, H. A., and Smeekens, S. (2014). Sugar sensing and signaling in plants. *Frontiers in plant science*, 5, 113. doi: 10.3389/fpls.2014.00113

Henry, C., Rabot, A., Laloi, M., Mortreau, E., Sigogne, M., Leduc, N., . et al. (2011). Regulation of RhSUC2, a sucrose transporter, is correlated with the light control of bud burst in *Rosa* sp. *Plant, cell and environment*, 34(10), 1776-1789. doi: 10.1111/j.1365-3040.2011.02374.x

Higo, K., Ugawa, Y., Iwamoto, M., and Higo, H. (1998). PLACE: a database of plant cis-acting regulatory DNA elements. *Nucleic acids research*, 26(1), 358-359. doi: 10.1093/nar/26.1.358

Holalu, S. V., and Finlayson, S. A. (2017). The ratio of red light to far red light alters Arabidopsis axillary bud growth and abscisic acid signalling before stem auxin changes. *Journal of experimental botany*, 68(5), 943-952. doi: 10.1093/jxb/erw479

Honma, T., and Goto, K. (2001). Complexes of MADS-box proteins are sufficient to convert leaves into floral organs. *Nature*, 409(6819), 525. doi: 10.1038/35054083

Horgan, J. M., and Wareing, P. F. (1980). Cytokinins and the growth responses of seedlings of *Betula pendula* Roth. and *Acer pseudoplatanus* L. to nitrogen and phosphorus deficiency. *Journal of Experimental Botany*, 31(2), 525-532. doi:10.1093/jxb/31.2.525

Howarth, D. G., and Donoghue, M. J. (2006). Phylogenetic analysis of the "ECE"(CYC/TB1) clade reveals duplications predating the core eudicots. *Proceedings of the National Academy of Sciences*, 103(24), 9101-9106. doi: 10.1073/pnas.0602827103

Hubbard, L., McSteen, P., Doebley, J., and Hake, S. (2002). Expression patterns and mutant phenotype of teosinte branched1 correlate with growth suppression in maize and teosinte. *Genetics*, 162(4), 1927-1935.

Jasinski, S., Piazza, P., Craft, J., Hay, A., Woolley, L., Rieu, I., et al. (2005). KNOX action in Arabidopsis is mediated by coordinate regulation of cytokinin and gibberellin activities. *Current Biology*, 15(17), 1560-1565. doi: 10.1016/j.cub.2005.07.023

Jian, Z., Li, K., Song, P., Zhu, G., Zhu, L., Cui, T., et al. (2014). Impaired activation of the Nrf2-ARE signaling pathway undermines H_2O_2-induced oxidative stress response: a possible mechanism for melanocyte degeneration in vitiligo. *Journal of Investigative Dermatology*, 134(8), 2221-2230. doi: 10.1038/jid.2014.152

Jiang, H. and Egli, D. B. (1993). Shade Induced Changes in Flower and Pod Number and Flower and Fruit Abscission in Soybean. *Agronomy Journal*, 85, 221-225. doi:10.2134/agronj1993.00021962008500020011x

Jiang, L., Liu, X., Xiong, G., Liu, H., Chen, F., Wang, L., et al. (2013). DWARF 53 acts as a repressor of strigolactone signalling in rice. *Nature*,504(7480), 401-405. doi: 10.1038/nature12870

Jiao, Y., Wang, Y., Xue, D., Wang, J., Yan, M., Liu, G., et al. (2010). Regulation of OsSPL14 by OsmiR156 defines ideal plant architecture in rice. *Nature genetics*, 42(6), 541. doi: 10.1038/ng.591

Johnson, X., Brcich, T., Dun, E. A., Goussot, M., Haurogné, K., Beveridge, C. A., et al. (2006). Branching genes are conserved across species. Genes controlling a novel signal in pea are coregulated by other long-distance signals. *Plant physiology*, 142(3), 1014-1026. doi: 10.1104/pp.106.087676

Jones, D. T., Taylor, W. R., and Thornton, J. M. (1992). The rapid generation of mutation data matrices from protein sequences. *Bioinformatics*, 8(3), 275-282. doi:10.1093/bioinformatics/8.3.275

Kebrom, T. H. (2017). A growing stem inhibits bud outgrowth-the overlooked theory of apical dominance. *Frontiers in plant science*, 8, 1874. doi: 10.3389/fpls.2017.01874

Kebrom, T. H., and Mullet, J. E. (2015). Photosynthetic leaf area modulates tiller bud outgrowth in sorghum. *Plant, cell and environment*, 38(8), 1471-1478. doi: 10.1111/pce.12500

Kebrom, T. H., Brutnell, T. P., and Finlayson, S. A. (2010). Suppression of sorghum axillary bud outgrowth by shade, phyB and defoliation signalling pathways. *Plant, cell and environment*, 33(1), 48-58. doi: 10.1111/j.1365-3040.2009.02050.x

Kebrom, T. H., Burson, B. L., and Finlayson, S. A. (2006). Phytochrome B represses *Teosinte Branched1* expression and induces sorghum axillary bud outgrowth in response to light signals. *Plant Physiology*, 140(3), 1109-1117. doi: 10.1104/pp.105.074856

Kebrom, T., Chandler, P., Swain, S., King, R., Richards, R., and Spielmeyer, W. (2012). Inhibition of tiller bud outgrowth in the tin mutant of wheat is associated with precocious internode development. *Plant Physiology*, pp-112. doi: 10.1104/pp.112.197954

Kerr, S. C., and Beveridge, C. A. (2017). IPA1: a direct target of SL signaling. *Cell research*, 27(10), 1191. doi: 10.1038/cr.2017.114

Kieffer, M., Master, V., Waites, R., and Davies, B. (2011). TCP14 and TCP15 affect internode length and leaf shape in Arabidopsis. *The Plant Journal*, 68(1), 147-158. doi: 10.1111/j.1365-313X.2011.04674.x

Kohlen, W., Charnikhova, T., Liu, Q., Bours, R., Domagalska, M.A., Beguerie, S., et al. (2011). Strigolactones are transported through the xylem and play a key role in shoot architectural response to phosphate deficiency in nonarbuscular mycorrhizal host Arabidopsis. *Plant Physiology*. 155, 974–987. doi: 10.1104/pp.110.164640

Kong, X., Zhang, M., and Ding, Z. (2014). D53: the missing link in strigolactone signaling. *Molecular plant*, 7(5), 761-763. doi: 10.1093/mp/ssu016

Kosugi, S., and Ohashi, Y. (1997). PCF1 and PCF2 specifically bind to cis elements in the rice proliferating cell nuclear antigen gene. *The Plant Cell*, 9(9), 1607-1619. doi: 10.1105/tpc.9.9.1607

Kosugi, S., and Ohashi, Y. (2002). DNA binding and dimerization specificity and potential targets for the TCP protein family. *The Plant Journal*, 30(3), 337-348. doi: 10.1046/j.1365-313X.2002.01294.x

Kumar, S., Stecher, G., and Tamura, K. (2016). MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Molecular biology and evolution*, 33(7), 1870-1874. doi: 10.1093/molbev/msw054

Lantzouni, O., Klermund, C., and Schwechheimer, C. (2017). Largely additive effects of gibberellin and strigolactone on gene expression in Arabidopsis thaliana seedlings. *The Plant Journal*, 92(5), 924-938. doi: https://doi.org/10.1111/tpj.13729

Le Moigne, M.A., Guérin, V., Furet, P.M., Billard, V., Lebrec, A., Spíchal, L., et al. (2018). Asparagine and sugars are both required to sustain secondary axis elongation after bud outgrowth in *Rosa hybrid*. *Journal of Plant Physiology*, 222: 17-27. doi: 10.1016/j.jplph.2017.12.013

Leduc, N., Roman, H., Barbier, F., Péron, T., Huché-Thélier, L., Lothier, J., et al. (2014). Light signaling in bud outgrowth and branching in plants. *Plants*, 3(2), 223-250. doi: 10.3390/plants3020223

Lemerle, D., Verbeek, B., Cousens, R. d., and Coombes, N.E. (1996). The potential for selecting wheat varieties strongly competitive against weeds. *Weed Research*, 36, 505–513. doi: 10.1111/j.1365-3180.1996.tb01679.x

Leyser, O. (2008). Strigolactones and shoot branching: a new trick for a young dog. *Developmental cell*, 15(3), 337-338. doi: 10.1016/j.devcel.2008.08.008

Leyser, O. (2009). The control of shoot branching: an example of plant information processing. *Plant, cell and environment*, 32(6), 694-703. doi: 10.1111/j.1365-3040.2009.01930.x

Li, C. J., and Bangerth, F. (1999). Autoinhibition of indoleacetic acid transport in the shoots of two-branched pea (*Pisum sativum*) plants and its relationship to correlative dominance. *Physiologia Plantarum*, 106(4), 415-420. doi: 10.1034/j.1399-3054.1999.106409.x

Li, S. (2015). The Arabidopsis thaliana TCP transcription factors: a broadening horizon beyond development. *Plant signaling and behavior*, 10(7), e1044192. doi: 10.1080/15592324.2015.1044192

Li, S., and Zachgo, S. (2013). TCP3 interacts with R2R3-MYB proteins, promotes flavonoid biosynthesis and negatively regulates the auxin response in *Arabidopsis thaliana*. *The Plant Journal*, 76(6), 901-913. doi: 10.1111/tpj.12348

Li, X., Xia, K., Liang, Z., Chen, K., Gao, C., and Zhang, M. (2016). MicroRNA393 is involved in nitrogen-promoted rice tillering through regulation of auxin signal transduction in axillary buds. *Scientific reports*, 6, 32158. doi: 10.1038/srep32158

Liang, M. H., Lu, Y., Chen, H. H., and Jiang, J. G. (2017). The salt-regulated element in the promoter of lycopene β-cyclase gene confers a salt regulatory pattern in carotenogenesis of *Dunaliella bardawil*. *Environmental microbiology*, 19(3), 982-989. doi: 10.1111/1462-2920.13539

Li-Marchetti, C., Le Bras, C., Chastellier, A., Relion, D., Morel, P., Sakr, S., et al. (2017). 3D phenotyping and QTL analysis of a complex character: rose bush architecture. *Tree Genetics and Genomes*, 13(5), 112. doi: 10.1007/s11295-017-1194-0

Li-Marchetti, C., Le Bras, C., Relion, D., Citerne, S., Huché-Thélier, L., Sakr, S., et al. (2015). Genotypic differences in architectural and physiological responses to water restriction in rose bush. *Frontiers in plant science*, 6, 355. doi: 10.3389/fpls.2015.00355

Liller, C. B., Neuhaus, R., Von Korff, M., Koornneef, M., and Van Esse, W. (2015). Mutations in barley row type genes have pleiotropic effects on shoot branching. *PloS one*, 10(10), e0140246. doi:10.1371/journal.pone.0140246

Lin, H., Wang, R., Qian, Q., Yan, M., Meng, X., Fu, Z., et al. (2009). DWARF27, an iron-containing protein required for the biosynthesis of strigolactones, regulates rice tiller bud outgrowth. *The Plant Cell*, 21(5), 1512-1525. doi: 10.1105/tpc.109.065987

Liu, J., Cheng, X., Liu, P., and Sun, J. (2017). miR156-targeted SBP-Box transcription factors interact with DWARF53 to regulate *TEOSINTE BRANCHED1* and *BARREN STALK1* expression in bread wheat. *Plant physiology*, 174(3), 1931-1948. doi: 10.1104/pp.17.00445

Lo, S. F., Yang, S. Y., Chen, K. T., Hsing, Y. I., Zeevaart, J. A., Chen, L. J., et al. (2008). A novel class of gibberellin 2-oxidases control semidwarfism, tillering, and root development in rice. *The Plant Cell*, 20(10), 2603-2618. doi: 10.1105/tpc.108.060913

López-Ráez, J.A., Charnikhova, T., Gómez-Roldán, V., Matusova, R., Kohlen, W., De Vos, R., et al. (2008). Tomato strigolactones are derived from carotenoids and their biosynthesis is promoted by phosphate starvation. *New Phytologist*. 178, 863–874. doi: 10.1111/j.1469-8137.2008.02406.x

Lortie, C. J., and Aarssen, L. W. (1997). Apical dominance as an adaptation in Verbascum thapsus: effects of water and nutrients on branching. *International Journal of Plant Sciences*, 158(4), 461-464.

Lu, S., Zhuo, C., Wang, X., and Guo, Z. (2014). Nitrate reductase (NR)-dependent NO production mediates ABA-and H_2O_2-induced antioxidant enzymes. *Plant physiology and biochemistry*, 74, 9-15. doi: 10.1016/j.plaphy.2013.10.030

Lu, Z., Yu, H., Xiong, G., Wang, J., Jiao, Y., Liu, G., et al. (2013). Genome-wide binding analysis of the transcription activator ideal plant architecture1 reveals a complex network regulating rice plant architecture. *The Plant Cell*, tpc-113. doi: 10.1105/tpc.113.113639

Luo, D., Carpenter, R., Vincent, C., Copsey, L., and Coen, E. (1996). Origin of floral asymmetry in Antirrhinum. *Nature*, 383, 794-799. doi: 10.1038/383794a0

Luo, L., Pan, S., Liu, X., Wang, H., and Xu, G. (2017). Nitrogen deficiency inhibits cell division-determined elongation, but not initiation, of rice tiller buds. *Israel Journal of Plant Sciences*, 1-9. doi: 10.1080/07929978.2016.1275367

Lupas, A., Van Dyke, M., and Stock, J. (1991). Predicting coiled coils from protein sequences. *Science*, 1162-1164.

Malaguti, D., Millard, P., Wendler, R., Hepburn, A., and Tagliavini, M. (2001). Translocation of amino acids in the xylem of apple (*Malus domestica* Borkh.) trees in spring as a consequence of both N remobilization and root uptake. *Journal of Experimental Botany*, 52(361), 1665-1671. doi: 10.1093/jexbot/52.361.1665

Martín-Fontecha, E. S., Tarancón, C., and Cubas, P. (2018). To grow or not to grow, a power-saving program induced in dormant buds. *Current opinion in plant biology*, 41, 102-109. doi: 10.1016/j.pbi.2017.10.001

Martín-Trillo, M., and Cubas, P. (2010). TCP genes: a family snapshot ten years later. *Trends in plant science*, 15(1), 31-39. doi: 10.1016/j.tplants.2009.11.003

Martín-Trillo, M., Grandío, E. G., Serra, F., Marcel, F., Rodríguez-Buey, M. L., Schmitz, G., et al. (2011). Role of tomato *BRANCHED1*-like genes in the control of shoot branching. *The Plant Journal*, 67(4), 701-714. doi: 10.1111/j.1365-313X.2011.04629.x

Mason, M. G., Ross, J. J., Babst, B. A., Wienclaw, B. N., and Beveridge, C. A. (2014). Sugar demand, not auxin, is the initial regulator of apical dominance. *Proceedings of the National Academy of Sciences*, 111(16), 6092-6097. doi: 10.1073/pnas.1322045111

Maurel, K., Sakr, S., Gerbe, F., Guilliot, A., Bonhomme, M., Rageau, R., and Pétel, G. (2004). Sorbitol uptake is regulated by glucose through the hexokinase pathway in vegetative peach-tree buds. *Journal of experimental botany*, 55(398), 879-888. doi: 10.1093/jxb/erh087

McSteen, P. (2009). Hormonal regulation of branching in grasses. *Plant Physiology*, 149(1), 46-55. doi: 10.1104/pp.108.129056

Médiène, S., Pagès, L., Jordan, M. O., Le Bot, J., and Adamowicz, S. (2002). Influence of nitrogen availability on shoot development in young peach trees [*Prunus persica* (L.) Batsch]. *Trees*, 16(8), 547-554. doi: 10.1007/s00468-002-0204-4

Millard, P., Wendler, R., Hepburn, A., and Smith, A. (1998). Variations in the amino acid composition of xylem sap of Betula pendula Roth. trees due to remobilization of stored N in the spring. *Plant, Cell and Environment*, 21(7), 715-722. doi: 10.1046/j.1365-3040.1998.00313.x

Minakuchi, K., Kameoka, H., Yasuno, N., Umehara, M., Luo, L., Kobayashi, K., et al. (2010). *FINE CULM1* (*FC1*) works downstream of strigolactones to inhibit the outgrowth of axillary buds in rice. *Plant and Cell Physiology*, 51(7), 1127-1135. doi: 10.1093/pcp/pcq083

Miura, K., Ikeda, M., Matsubara, A., Song, X. J., Ito, M., Asano, K., et al. (2010). OsSPL14 promotes panicle branching and higher grain productivity in rice. *Nature genetics*, 42(6), 545. doi: 10.1038/ng.592

Miyawaki, K., Matsumoto-Kitano, M., and Kakimoto, T. (2004). Expression of cytokinin biosynthetic isopentenyltransferase genes in Arabidopsis: tissue specificity and regulation by auxin, cytokinin, and nitrate. *The Plant Journal*,37(1), 128-138. doi: 10.1046/j.1365-313X.2003.01945.x

Morris, D. A. (1977). Transport of exogenous auxin in two-branched dwarf pea seedlings (*Pisum sativum* L.). *Planta*, 136(1), 91-96. doi:10.1007/BF00387930

Morris, S. E., Cox, M. C., Ross, J. J., Krisantini, S., and Beveridge, C. A. (2005). Auxin dynamics after decapitation are not correlated with the initial growth of axillary buds. *Plant Physiology*, 138(3), 1665-1672. doi: 10.1104/pp.104.058743

Muhr, M., Prüfer, N., Paulat, M., and Teichmann, T. (2016). Knockdown of strigolactone biosynthesis genes in Populus affects *BRANCHED1* expression and shoot architecture. *New Phytologist*, 212(3), 613-626. doi: 10.1111/nph.14076

Muhr, M., Paulat, M., Awwanah, M., Brinkkötter, M., and Teichmann, T. (2018). CRISPR/Cas9-mediated knockout of *Populus BRANCHED1* and *BRANCHED2* orthologs reveals a major function in bud outgrowth control. Tree physiology, 38(10), 1588-1597. doi: 10.1093/treephys/tpy088

Müller, D., and Leyser, O. (2011). Auxin, cytokinin and the control of shoot branching. *Annals of Botany*, 107(7), 1203-1212. doi: 10.1093/aob/mcr069

Nath, U., Crawford, B. C., Carpenter, R., and Coen, E. (2003). Genetic control of surface curvature. *Science*, 299(5611), 1404-1407. doi: 10.1126/science.1079354

Navaud, O., Dabos, P., Carnus, E., Tremousaygue, D., and Hervé, C. (2007). TCP transcription factors predate the emergence of land plants. *Journal of molecular evolution*, 65(1), 23-33. doi: 10.1007/s00239-006-0174-z

Ni, J., Gao, C., Chen, M. S., Pan, B. Z., Ye, K., and Xu, Z. F. (2015). Gibberellin promotes shoot branching in the perennial woody plant *Jatropha curcas*. *Plant and Cell Physiology*, 56(8), 1655-1666. doi: 10.1093/pcp/pcv089

Nicolas, M., and Cubas, P. (2016). TCP factors: new kids on the signaling block. *Current opinion in plant biology*, 33, 33-41. doi: 10.1016/j.pbi.2016.05.006

Nicolas, M., Rodríguez-Buey, M. L., Franco-Zorrilla, J. M., and Cubas, P. (2015). A recently evolved alternative splice site in the *BRANCHED1a* gene controls potato plant architecture. *Current Biology*, 25(14), 1799-1809. doi: 10.1016/j.cub.2015.05.053

Niwa, M., Daimon, Y., Kurotani, K. I., Higo, A., Pruneda-Paz, J. L., Breton, G., et al. (2013). BRANCHED1 interacts with FLOWERING LOCUS T to repress the floral transition of the axillary meristems in Arabidopsis. *The Plant Cell*, 25(4), 1228-1242. doi: 10.1105/tpc.112.109090

Nordström, A., Tarkowski, P., Tarkowska, D., Norbaek, R., Åstot, C., Dolezal, K., et al. (2004). Auxin regulation of cytokinin biosynthesis in *Arabidopsis thaliana*: a factor of potential importance for auxin-cytokinin-regulated development. *Proceedings of the National Academy of Sciences*, 101(21), 8039-8044. doi: 10.1073/pnas.0402504101

Ohashi, M., Ishiyama, K., Kusano, M., Fukushima, A., Kojima, S., Hanada, A., et al. (2015). Lack of cytosolic glutamine synthetase1; 2 in vascular tissues of axillary buds causes severe reduction in their outgrowth and disorder of metabolic balance in rice seedlings. *The Plant Journal*, 81(2), 347-356. doi: 10.1111/tpj.12731

Ortiz-Ramírez, C., Hernandez-Coronado, M., Thamm, A., Catarino, B., Wang, M., Dolan, L., et al. (2016). A transcriptome atlas of Physcomitrella patens provides insights into the evolution and development of land plants. *Molecular plant*, 9(2), 205-220. doi: 10.1016/j.molp.2015.12.002

Pal, P. K., Prasad, R., and Pathania, V. (2013). Effect of decapitation and nutrient applications on shoot branching, yield, and accumulation of secondary metabolites in leaves of Stevia rebaudiana Bertoni. *Journal of plant physiology*, 170(17), 1526-1535. doi: 10.1016/j.jplph.2013.06.017

Palatnik, J. F., Allen, E., Wu, X., Schommer, C., Schwab, R., Carrington, J. C., et al. (2003). Control of leaf morphogenesis by microRNAs. *Nature*, 425(6955), 257-263. doi: 10.1038/nature01958

Pei, Z. M., Ghassemian, M., Kwak, C. M., McCourt, P., and Schroeder, J. I. (1998). Role of farnesyltransferase in ABA regulation of guard cell anion channels and plant water loss. *Science*, 282(5387), 287-290. doi: 10.1126/science.282.5387.287

Petrášek, J., and Friml, J. (2009). Auxin transport routes in plant development. *Development*, 136(16), 2675-2688. doi: 10.1242/dev.030353

Plesch, G., Ehrhardt, T., and Mueller-Roeber, B. (2001). Involvement of TAAAG elements suggests a role for Dof transcription factors in guard cell-specific gene expression. *The Plant Journal*, 28(4), 455-464. doi: 10.1046/j.1365-313X.2001.01166.x

Poza-Carrión, C., Aguilar-Martínez, J. A., and Cubas, P. (2007). Role of TCP gene *BRANCHED1* in the control of shoot branching in Arabidopsis. *Plant signaling and behavior*, 2(6), 551-552. doi: 10.4161/psb.2.6.4811

Price, J., Laxmi, A., Martin, S. K. S., and Jang, J. C. (2004). Global transcription profiling reveals multiple sugar signal transduction mechanisms in Arabidopsis. *The Plant Cell*, 16(8), 2128-2150. doi: 10.1105/tpc.104.022616

Proietti, P., and Tombesi, A. (1996). Effects of gibberellic acid, asparagine and glutamine on flower bud induction in olive. *Journal of Horticultural Science*, 71(3), 383-388. doi: 10.1080/14620316.1996.11515418

Qin, L. J., Guo, X. Z., Feng, X. Z., Weng, L., Yan, J., Hu, X. H., et al. (2004). Cloning of *LjCYC1* gene and nuclear localization of LjCYC1 protein in Lotus japonicus. *Journal of Plant Physiology and Molecular Biology*, 30(5), 523-532.

Rabot, A., Henry, C., Baaziz, K. B., Mortreau, E., Azri, W., Lothier, J., et al. (2012). Insight into the role of sugars in bud burst under light in the rose. *Plant and Cell Physiology*, 53(6), 1068-1082. doi: 10.1093/pcp/pcs051

Rameau, C., Bertheloot, J., Leduc, N., Andrieu, B., Foucher, F., et al. (2015). Multiple pathways regulate shoot branching. *Frontiers in plant science*, 5, 741. doi: 10.3389/fpls.2014.00741

Ramsay, L., Comadran, J., Druka, A., Marshall, D. F., Thomas, W. T., Macaulay, M., et al. (2011). *INTERMEDIUM-C*, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene *TEOSINTE BRANCHED 1*. Nature genetics, 43(2), 169-172. doi: 10.1038/ng.745

Revel, S. M., Bart, J. J., Luo, Z., Oplaat, C., Susan, E. L., Mark, W. W., et al. (2015). Environmental control of branching in petunia. *Plant physiology*, pp-00486. doi: 10.1104/pp.15.00486

Richards, R. A. (2000). Selectable traits to increase crop photosynthesis and yield of grain crops. *Journal of Experimental Botany*, 51, 447-458. doi: 10.1093/jexbot/51.suppl_1.447

Rodríguez, D., Andrade, F. H., and Goudriaan, J. (1999). Effects of phosphorus nutrition on tiller emergence in wheat. *Plant and Soil*, 209(2), 283-295. doi: 10.1023/A:1004690404870

Rogers, H. J., Bate, N., Combe, J., Sullivan, J., Sweetman, J., Swan, C., et al. (2001). Functional analysis of *cis*-regulatory elements within the promoter of the tobacco late pollen gene g10. *Plant molecular biology*, 45(5), 577-585. doi: 10.1023/A:1010695226241

Roman, H., Girault, T., Barbier, F., Péron, T., Brouard, N., Pencik, A., et al. (2016). Cytokinins are initial targets of light in the control of bud outgrowth. *Plant physiology*, pp-00530. doi: 10.1104/pp.16.00530

Ruyter-Spira, C., Kohlen, W., Charnikhova, T., van Zeijl, A., van Bezouwen, L., de Ruijter, N., et al. (2010). Physiological effects of the synthetic strigolactone analog GR24 on root system architecture in Arabidopsis: Another below-ground role for strigolactones?. *Plant physiology*, pp-110. doi: 10.1104/pp.110.166645

Sachs, T., and Thimann, K. V. (1967). The role of auxins and cytokinins in the release of buds from dominance. *American Journal of Botany*, 136-144. doi:10.1002/j.1537-2197.1967.tb06901.x

Sakakibara, H., Suzuki, M., Takei, K., Deji, A., Taniguchi, M., and Sugiyama, T. (1998). A response-regulator homologue possibly involved in nitrogen signal transduction mediated by cytokinin in maize. *The Plant Journal*, 14(3), 337-344. doi: 10.1046/j.1365-313X.1998.00134.x

Sakr, S., Wang, M., Dédaldéchamp, F., Perez-Garcia, M. D., Ogé, L., Hamama, L., and Atanassova, R. (2018). The Sugar-Signaling Hub: Overview of Regulators and Interaction with the Hormonal and Metabolic Network. *International journal of molecular sciences*, 19(9), 2506. doi: 10.3390/ijms19092506

Sarvepalli, K., & Nath, U. (2018). CIN-TCP transcription factors: Transiting cell proliferation in plants. *IUBMB life*, 70(8), 718-731. doi:10.1002/iub.1874

Schommer, C., Palatnik, J. F., Aggarwal, P., Chételat, A., Cubas, P., Farmer, E. E., et al. (2008). Control of jasmonate biosynthesis and senescence by miR319 targets. *PLoS biology*, 6(9), e230. doi: 10.1371/journal.pbio.0060230

Seale, M., Bennett, T., and Leyser, O. (2017). *BRC1* expression regulates bud activation potential, but is not necessary or sufficient for bud growth inhibition in Arabidopsis. *Development*, dev-145649. doi: 10.1242/dev.145649

Seo, M., and Koshiba, T. (2002). Complex regulation of ABA biosynthesis in plants. Trends in plant science, 7(1), 41-48. doi: 10.1016/S1360-1385(01)02187-2

Shimizu, S., and Mori, H. (1998). Analysis of cycles of dormancy and growth in pea axillary buds based on mRNA accumulation patterns of cell cycle-related genes. *Plant and cell physiology*, 39(3), 255-262. doi:10.1093/oxfordjournals.pcp.a029365

Shinohara, N., Taylor, C., and Leyser, O. (2013). Strigolactone can promote or inhibit shoot branching by triggering rapid depletion of the auxin efflux protein PIN1 from the plasma membrane. *PLoS biology*, 11(1), e1001474. doi: 10.1371/journal.pbio.1001474

Shore, P., and Sharrocks, A. D. (1995). The MADS-box family of transcription factors. *The FEBS Journal*, 229(1), 1-13. doi: 10.1111/j.1432-1033.1995.0001l.x

Simon, S., Morel, K., Durand, E., Brevalle, G., Girard, T., and Lauri, P.-É. (2011). Aphids at crossroads: when branch architecture alters aphid infestation patterns in the apple tree. *Trees,* 26, 273–282. doi: 10.1007/s00468-011-0629-8

Song, X., Lu, Z., Yu, H., Shao, G., Xiong, J., Meng, X., et al. (2017). IPA1 functions as a downstream transcription factor repressed by D53 in strigolactone signaling in rice. *Cell research*, 27(9), 1128. doi: 10.1038/cr.2017.102

Sorefan, K., Booker, J., Haurogné, K., Goussot, M., Bainbridge, K., Foo, E., et al. (2003). *MAX4* and *RMS1* are orthologous dioxygenase-like genes that regulate shoot branching in Arabidopsis and pea. *Genes and development*, 17(12), 1469-1474. doi: 10.1101/gad.256603

Soundappan, I., Bennett, T., Morffy, N., Liang, Y., Stanga, J. P., Abbas, A., et al. (2015). SMAX1-LIKE/D53 family members enable distinct MAX2-dependent responses to strigolactones and karrikins in Arabidopsis. *The Plant Cell*, tpc-15. doi: 10.1105/tpc.15.00562

Stålberg, K., Ellerström, M., Ezcurra, I., Ablov, S., and Rask, L. (1996). Disruption of an overlapping E-box/ABRE motif abolished high transcription of the napA storage-protein promoter in transgenic *Brassica napus* seeds. *Planta*, 199(4), 515-519. doi: 10.1007/BF00195181

Stafstrom, J. P., and Sussex, I. M. (1988). Patterns of protein synthesis in dormant and growing vegetative buds of pea. *Planta*, 176(4), 497-505. doi:10.1007/BF00397656

Stirnberg, P., Chatfield, S. P., and Leyser, H. O. (1999). AXR1 acts after lateral bud formation to inhibit lateral bud growth in Arabidopsis. *Plant Physiology*,121(3), 839-847. doi: 10.1104/pp.121.3.839

Studer, A., Zhao, Q., Ross-Ibarra, J., and Doebley, J. (2011). Identification of a functional transposon insertion in the maize domestication gene *tb1*. *Nature genetics*, 43(11), 1160. doi:10.1038/ng.942

Su, H., Abernathy, S. D., White, R. H., and Finlayson, S. A. (2011). Photosynthetic photon flux density and phytochrome B interact to regulate branching in Arabidopsis. *Plant, cell and environment*, 34(11), 1986-1998. doi: 10.1111/j.1365-3040.2011.02393.x

Suzuki, T., Sakurai, K., Ueguchi, C., and Mizuno, T. (2001). Two Types of Putative Nuclear Factors that Physically Interactwith Histidine-Containing Phosphotransfer (Hpt) Domains, Signaling Mediators in His-to-Asp Phosphorelay, in *Arabidopsis thaliana*. *Plant and Cell Physiology*, 42(1), 37-45. doi: 10.1093/pcp/pce011

Swaraj, K., Laura, J. S., and Bishnoi, N. R. (1993). Nitrate induced nodule senescence and changes in activities of enzymes scavenging H_2O_2 in clusterbean (*Cyamopsis tetragonaloba* Taub.). *Journal of plant physiology*, 141(2), 202-205. doi: 10.1016/S0176-1617(11)80760-1

Ta, T. C., MacDowall, F. D. H., and Faris, M. A. (1987). Utilization of carbon from shoot photosynthesis and nodule CO_2 fixation in the fixation and assimilation of nitrogen by alfalfa root nodules. *Canadian journal of botany*, 65(12), 2537-2541.

Takeda, T., Suwa, Y., Suzuki, M., Kitano, H., Ueguchi-Tanaka, M., Ashikari, M., et al. (2003). The *OsTB1* gene negatively regulates lateral branching in rice. *The Plant Journal*, 33(3), 513-520. doi: 10.1046/j.1365-313X.2003.01648.x

Takei, K., Sakakibara, H., Taniguchi, M., and Sugiyama, T. (2001). Nitrogen-dependent accumulation of cytokinins in root and thetranslocation to leaf: Implication of cytokinin species that induces geneexpression of maize responseregulator. *Plant and Cell Physiology*, 42(1), 85-93. doi: 10.1093/pcp/pce009

Takei, K., Takahashi, T., Sugiyama, T., Yamaya, T., and Sakakibara, H. (2002). Multiple routes communicating nitrogen availability from roots to shoots: a signal transduction pathway mediated by cytokinin. *Journal of Experimental Botany*, 53(370), 971-977. doi: 10.1093/jexbot/53.370.971

Tanaka, M., Takei, K., Kojima, M., Sakakibara, H., and Mori, H. (2006). Auxin controls local cytokinin biosynthesis in the nodal stem in apical dominance. *The Plant Journal*, 45(6), 1028-1036. doi: 10.1111/j.1365-313X.2006.02656.x

Tanaka, Y. (2006). Flower colour and cytochromes P450. *Phytochemistry Reviews*, 5(2-3), 283-291. doi: 10.1007/s11101-006-9003-7

Tarancón, C., González-Grandío, E., Oliveros, J. C., Nicolas, M., and Cubas, P. (2017). A conserved carbon starvation response underlies bud dormancy in woody and Herbaceous Species. *Frontiers in plant science*, 8, 788. doi: 10.3389/fpls.2017.00788

Teichmann, T., and Muhr, M. (2015). Shaping plant architecture. *Frontiers in plant science*, 6, 233. doi: 10.3389/fpls.2015.00233

Thitithanakul, S. (2012). Effect of nitrogen supply before bud break on early development of the young hybrid poplar [Doctoral dissertation]. Université Blaise Pascal-Clermont-Ferrand II.

Thitithanakul, S., Pétel, G., Chalot, M., and Beaujard, F. (2012). Supplying nitrate before bud break induces pronounced changes in nitrogen nutrition and growth of young poplars. *Functional Plant Biology*, 39(9), 795-803. doi: 10.1071/FP12129

Umehara, M., Hanada, A., Yoshida, S., Akiyama, K., Arite, T., Takeda-Kamiya, N., et al. (2008). Inhibition of shoot branching by new terpenoid plant hormones. *Nature*, 455, 195-200. doi: 10.1038/nature07272

Waldie, T., and Leyser, O. (2018). Cytokinin targets auxin transport to promote shoot branching. *Plant physiology*, pp-01691. doi: 10.1104/pp.17.01691

Wang, R. L., Stec, A., Hey, J., Lukens, L., and Doebley, J. (1999). The limits of selection during maize domestication. *Nature*, 398(6724), 236-239. doi: 10.1038/18435

Wang, L., Wang, B., Jiang, L., Liu, X., Li, X., Lu, Z., et al. (2015). Strigolactone signaling in Arabidopsis regulates shoot development by targeting D53-like SMXL repressor proteins for ubiquitination and degradation. *The Plant Cell*, 27(11), 3128-3142. doi: 10.1105/tpc.15.00605

Wang, P., Zhao, Y., Li, Z., Hsu, C. C., Liu, X., Fu, L., et al. (2018). Reciprocal regulation of the TOR kinase and ABA receptor balances plant growth and stress response. *Molecular cell*, 69(1), 100-112. doi: 10.1016/j.molcel.2017.12.002

Wang, Y., and Jiao, Y. (2018). Axillary meristem initiation-a way to branch out. *Current opinion in plant biology*, 41, 61-66. doi: 10.1016/j.pbi.2017.09.001

Wang, Y., Sun, S., Zhu, W., Jia, K., Yang, H., and Wang, X. (2013). Strigolactone/MAX2-induced degradation of brassinosteroid transcriptional effector BES1 regulates shoot branching. *Developmental cell*, 27(6), 681-688. doi: 10.1016/j.devcel.2013.11.010

Waters, M. T., Gutjahr, C., Bennett, T., and Nelson, D. C. (2017). Strigolactone signaling and evolution. *Annual Review of Plant Biology*, 68, 291-322. doi: 10.1146/annurev-arplant-042916-040925

Wickson, M., and Thimann, K. V. (1958). The antagonism of auxin and kinetin in apical dominance. *Physiologia Plantarum*, 11(1), 62-74. doi:10.1111/j.1399-3054.1958.tb08426.x

Xu, J., Zha, M., Li, Y., Ding, Y., Chen, L., Ding, C., and Wang, S. (2015). The interaction between nitrogen availability and auxin, cytokinin, and strigolactone in the control of shoot branching in rice (*Oryza sativa* L.). *Plant cell reports*, 34(9), 1647-1662. doi: 10.1007/s00299-015-1815-8

Yamada, Y., Furusawa, S., Nagasaka, S., Shimomura, K., Yamaguchi, S., and Umehara, M. (2014). Strigolactone signaling regulates rice leaf senescence in response to a phosphate deficiency. *Planta*, 240(2), 399-408. doi: 10.1007/s00425-014-2096-0

Yang, Y., Nicolas, M., Zhang, J., Yu, H., Guo, D., Yuan, R., et al. (2018). The TIE1 transcriptional repressor controls shoot branching by directly repressing *BRANCHED1* in Arabidopsis. *PLoS genetics*, 14(3), e1007296. doi: 10.1371/journal.pgen.1007296

Yao, C., and Scott, A. F. (2015). Abscisic acid is a general negative regulator of Arabidopsis axillary bud growth. *Plant physiology*, pp-00682. doi: 10.1104/pp.15.00682

Yao, L. L., Pei, B. L., Zhou, Q., and Li, Y. Z. (2012). NO serves as a signaling intermediate downstream of H_2O_2 to modulate dynamic microtubule cytoskeleton during responses to VD-toxins in Arabidopsis. *Plant signaling and behavior*, 7(2), 174-177. doi: 10.4161/psb.18768

Yoneyama, K., Yoneyama, K., Takeuchi, Y., and Sekimoto, H. (2007). Phosphorus deficiency in red clover promotes exudation of orobanchol, the signal for mycorrhizal symbionts and germination stimulant for root parasites. *Planta*, 225(4), 1031-1038. doi: 10.1007/s00425-006-0410-1

Yoshida, T., Fujita, Y., Sayama, H., Kidokoro, S., Maruyama, K., Mizoi, J., et al. (2010). AREB1, AREB2, and ABF3 are master transcription factors that cooperatively regulate ABRE-dependent ABA signaling involved in drought stress tolerance and require ABA for full activation. *The Plant Journal*, 61(4), 672-685. doi: 10.1111/j.1365-313X.2009.04092.x

Zhang, H., and Forde, B. G. (1998). An Arabidopsis MADS box gene that controls nutrient-induced changes in root architecture. *Science*, 279(5349), 407-409. doi: 10.1126/science.279.5349.407

Zhang, Z. B., Yang, G., Arana, F., Chen, Z., Li, Y., and Xia, H. J. (2007). Arabidopsis inositol polyphosphate 6-/3-kinase (*AtIpk2β*) is involved in axillary shoot branching via auxin signaling. *Plant physiology*, 144(2), 942-951. doi: 10.1104/pp.106.092163

Zhao, D.L., Atlin, G.N., Bastiaans, L., and Spiertz, J.H.J. (2006). Developing selection protocols for weed competitiveness in aerobic rice. *Field Crops Research* 97, 272–285. doi: 10.1016/j.fcr.2005.10.008

Zhou, F., Lin, Q., Zhu, L., Ren, Y., Zhou, K., Shabek, N., et al. D14-SCF^{D3}-dependent degradation of D53 regulates strigolactone signalling. *Nature*, 504(7480), 406. doi: 10.1038/nature12878

Zhou, L., Zhang, J., Yan, J., and Song, R. (2011). Two transposable element insertions are causative mutations for the major domestication gene *teosinte branched 1* in modern maize. *Cell research*, 21(8), 1267. doi:10.1038/cr.2011.104

Zou, J., Zhang, S., Zhang, W., Li, G., Chen, Z., Zhai, W., et al. The rice *HIGH-TILLERING DWARF1* encoding an ortholog of Arabidopsis MAX3 is required for negative regulation of the outgrowth of axillary buds. *The Plant Journal*, 48(5), 687-698. doi: 10.1111/j.1365-313X.2006.02916.x

IV- Voies de signalisations des sucres et interactions avec les hormones et l'azote

Il est bien établi que les sucres (saccharose et hexoses) et les hormones (notamment l'auxine, les cytokinines (CK) et les strigolactones (SL)) jouent un rôle important dans le contrôle de la ramification. Les sucres sont des molécules particulièrement déterminantes dans la croissance et le développement des végétaux, pour lesquels ils jouent non seulement un rôle de source de carbone et d'énergie, dédié aux besoins du métabolisme cellulaire, mais également une entité « signal » perçue par des récepteurs spécifiques et donc apte à réguler plusieurs processus, y compris la ramification.

Chez le rosier, l'implication des sucres dans le processus du débourrement des bourgeons axillaires a fait l'objet de plusieurs travaux, notamment par notre équipe de recherche ARCH-E (Girault *et al*., 2010; Henry *et al*., 2011; Rabot *et al*., 2012; Rabot *et al*., 2014; Barbier *et al*., 2015 et Corot *et al*., 2017). Ces études ont permis de montrer une étroite corrélation entre la capacité du bourgeon à débourrer et la disponibilité du sucre pour le bourgeon. Par ailleurs, et sur la base d'utilisation des analogues non métabolisables de saccharose et d'hexoses, un rôle signal de sucre dans le contrôle du débourrement a été proposé. Un autre résultat marquant, récemment obtenu chez le pois (Mason *et al*., 2014), a montré que l'effet inhibiteur exercé par la dominance apicale serait associé à un détournement des ressources carbonées (photoassimilats) par le bourgeon apical en croissance (force puits importante) au détriment des bourgeons axillaires (force puits faible). Cette situation d'inhibition corrélative est levée par l'apport direct du sucre exogène au bourgeon axillaire par l'intermédiaire du pétiole, alors que la concentration de l'auxine au voisinage du bourgeon restant inchangée (indépendamment de la dominance apicale). Ce résultat souligne la possibilité que la ramification pourrait être sous le contrôle combiné de l'auxine et du sucre, et vient étayer les données obtenues par Barbier *et al*. (2015) montrant que le saccharose est capable de réguler, de façon antagoniste par rapport à l'auxine, les CK et les SL, deux hormones centrales de la ramification. Alors que l'auxine, à l'origine de la

dominance apicale, réprime la synthèse des CK (stimulatrice de la ramification) et stimule la synthèse des SL (inhibitrice de la ramification), le saccharose affecte négativement la voie de signalisation des SL et positivement la synthèse des CK.

Au vue de ces données et la possibilité d'une interaction entre le saccharose et l'auxine dans la régulation de la ramification, cette revue a pour objectif de réaliser un état de l'art sur l'importance des voies de signalisations des sucres dans le fonctionnement de la plante et leurs interactions avec la majorité des phytohormones. Ceci permet également de bien souligner l'originalité de la question abordée dans le cadre de ce travail de thèse.

The Sugar-Signaling Hub: Overview of Regulators and Interaction with the Hormonal and Metabolic Network

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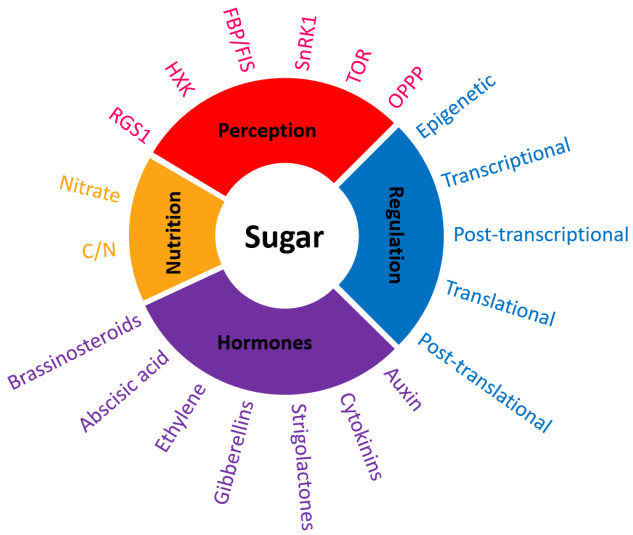
Abstract: Plant growth and development has to be continuously adjusted to the available resources. Their optimization requires the integration of signals conveying the plant metabolic status, its hormonal balance, and its developmental stage. Many investigations have recently been conducted to provide insights into sugar signaling and its interplay with hormones and nitrogen in the fine-tuning of plant growth, development, and survival. The present review emphasizes the diversity of sugar signaling integrators, the main molecular and biochemical mechanisms related to the sugar-signaling dependent regulations, and to the regulatory hubs acting in the interplay of the sugar-hormone and sugar-nitrogen networks. It also contributes to compiling evidence likely to fill a few knowledge gaps, and raises new questions for the future.

Graphical Abstract:



Sugar signaling in plant: Perception, regulation, crosstalk with hormones and nitrogen. RGS1 (Regulator of G-protein signaling 1), SnRK1(Sucrose non-Fermenting related protein kinase 1), FBP/FIS(Fructose 1-6-bisphosphatase/Fructose-Insensitive 1), HXK(Hexokinase), TOR(Target of rapamycin kinase), OPPP(Oxidative pentose phosphate pathway), C/N(Carbon/Nitrogen ratio).

Keywords: sugar; pathway; sensing; crosstalk; regulation; hormone; nitrogen

1. Introduction

Plant growth and development are regulated by many factors including light, temperature, water, sugars, and plant hormones. As plants are autotrophic organisms, they produce their carbon skeletons through photosynthesis in the form of sugars that serve as structural components and energy sources throughout their life [1]. Sugars are also signaling entities; therefore, perception and management of sugar levels by plants are critical for their survival. Plants have evolved a complex mechanistic system to sense different sugars, including sucrose, hexoses, and trehalose. These sugars elicit adequate responses, some of which are specific to the type of sugar [2–6]. Sugar signaling is also a mechanism that plants use to integrate various internal and external cues to achieve nutrient homeostasis, mediate developmental programs, and orchestrate stress responses [6]. In addition, the carbon and nitrogen metabolisms are closely connected with each other at almost all stages of plant growth and development. The coordination and the integration of the C and N metabolic and signaling pathways appear crucial for the improvement of plant performances [7,8]. Besides nutrients, plant hormones play a determining role in plant development and are key transmitters of developmental programs [9]. In addition, the interaction between sugars and plant hormones is orchestrated to finely regulate the main biological processes throughout the plant life cycle. In this context, and with a view to understanding the mechanisms involved in the sugar and plant hormone networks, it is important to decipher their crosstalk with sugars during plant development. The present review emphasizes the emerging understanding of the main sugar signaling pathways in plants and the array of molecular and biochemical mechanisms that mediate the effects of the sugar signal. To provide a comprehensive idea about the relevance of the sugar-signaling-dependent regulation of plant functioning, this review also addresses the interplay between sugar, nitrogen, and the main plant hormones, while focusing on certain biological contexts. This work also underlines a few emerging linker molecular actors that deserve to be further investigated.

2. Sugar Signaling Pathways

2.1. Disaccharide Signaling Pathways

Sucrose is the main sugar for systemic source-to-sink transport in plants. The dual role of sucrose, i.e., as an energy source and a signaling entity, was evidenced by many experiments showing that non-metabolizable sucrose analogs could mimic the effect of sucrose while its derivative hexoses (glucose and fructose) have very low efficiency [10–13]. The best-known example is the sucrose-specific down-regulation of *BvSUT1* (*Beta vulgaris* Sucrose Transporter 1), encoding the phloem-located proton-sucrose symporter, which is neither elicited by hexoses nor affected by mannoheptulose, a hexokinase inhibitor [10]. By doing so, sucrose signaling regulates the expression of its own transporter at the site of phloem loading and thereby may control photo-assimilated partitioning between source and sink. Sucrose signaling controls not only plant metabolism but also plant development [6,14–18]. However, the mechanism of sucrose perception remains unknown. Barker et al. (2000) proposed the plasma membrane sucrose transporter AtSUT2/SUC3 as a putative sucrose sensor (Figure 1) [19]. AtSUT2/SUC3 shares structural features with the yeast glucose sensors Snf3 and Rgt2. The tonoplast low-affinity sucrose transporter SUT4 that interacts with five cytochrome b5 family members may also mediate sugar signaling [20]. Downstream of sucrose sensing, calcium, calcium dependent-protein kinases (CDPKs), and protein phosphatases could transmit sucrose signals [21,22]. All these findings show clearly that the questions of sucrose sensors and the sucrose signaling pathway are still open, and future research could investigate whether other actors such as sucrose synthase (a sucrose-degrading enzyme) [23] or BZR1-BAM (a transcription factor containing a non-catalytic-amylase (BAM)-like domain [24]) might be part of this mechanism.

Like sucrose, trehalose 6P (T6P) is a non-reducing disaccharide, synthesized from UDP-glucose (UDPG) and glucose 6-phosphate (Glc6P) by trehalose 6P synthase (TPS), and then dephosphorylated into trehalose by trehalose 6P phosphatase (TPP, Figure 1) [25]. *Arabidopsis thaliana* has 11 TPS and 10 TPP genes [26], and large TPS and TPP gene families are present in other flowering plants [27–29]. The T6P pathway has emerged as an important regulatory mechanism in plants that affects cell metabolism, plant growth, and abiotic stress responses [30–33]. More interestingly, T6P levels appear to follow sucrose levels, which makes it an essential

signal metabolite in plants, linking growth and development to carbon availability [34]. These findings led to the proposal of the Suc-T6P nexus model, assuming that T6P is both a signal and a negative feedback regulator of sucrose levels [31,32,35]. This tight relationship between T6P and sucrose contributes to maintaining sucrose levels within an optimal range depending on cell type, developmental stages, and environmental cues [31,32,35].

2.2. Hexose-Dependent Pathways

Plant cells possess intracellular and extracellular sugar sensors. In many plants, the regulator of G-protein signaling 1 (RGS1), a seven-transmembrane-domain protein located on the plasma membrane, plays a critical role as an external sugar sensor (Figure 1) [36]. It could function as a plasma membrane sensor or partner responding to changes in glucose, fructose, and sucrose levels [37]. RGS1 proteins deactivate G-protein and sugars accelerates GTP hydrolysis by Gα subunits, and leads to RGS1 phosphorylation by WINK [with no lysine8 (K)] kinase. As a result, RGS1 is internalized by endocytosis, associated with sustained activation of G-protein-mediated sugar signaling [38]. High concentrations of D-glucose rapidly induce RGS endocytosis through AtWNK8 and AtWNK10, whereas low sustained sugar concentrations slowly activate the AtWNK1pathway [39], allowing the cells to respond adequately to high and low intensities of sugar signals.

The first intracellular glucose sensor demonstrated in plants was AtHXK1, an *Arabidopsis thaliana* mitochondrion-associated (type B) hexokinase [40–43]. AtHXK1 is involved in the regulation of many processes [6,44], and its function as a glucose sensor was confirmed by the characterization of the *Arabidopsis gin2* (*glucose insensitive 2*) mutant [42]. When the metabolic activity of AtHXK1 was uncoupled from its signaling activity, its glucose-sensing function was found to be independent of its catalytic activity [42]. Moreover, AtHXK1 has a nuclear signaling function [43], where it interacts with two unconventional partners, the vacuolar H^+-ATPase B1 (VHA-B1) and the 19S regulatory particle of the proteasome subunit (RPT5B) to form a hetero-multimeric complex for the recruitment of hypothetical transcription factors. Such a multimeric complex may bind to the promoters of glucose-inducible genes to modulate their expression. The sensing role of AtHXK1 appears to have been evolutionarily conserved and to be shared by HXK in many other species including potato (StHXK1 and 2) and rice (OsHXK5 and 6) [45,46]. In addition, Hexokinase-Like1 (HKL1, a mitochondrion-associated non-catalytic homolog of *AtHXK1*) [47,48] and AtHXK3 (a plastidial hexokinase) [49] may also be part of hexose signaling. Irrespectively of its well-known sensor function, recent studies have revealed new physiological functions of glucose phosphorylation by AtHXK [50,51].

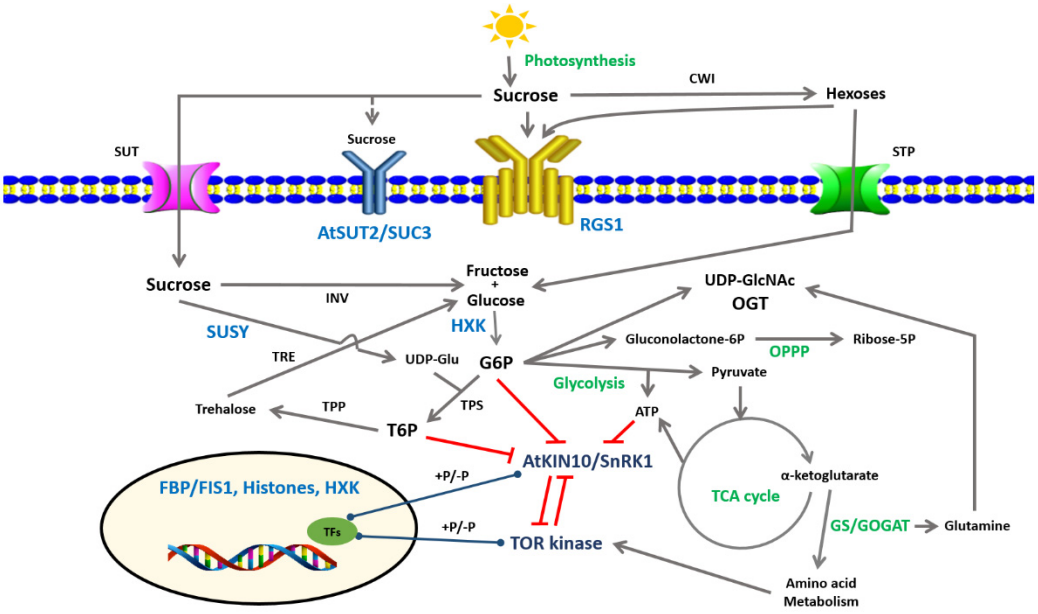


Figure 1. Schematic representation of the sugar metabolism (green) and signaling (blue) pathways. Sugar sensing involves for example glucose sensors (HXK: Hexokinase, OGT: O-Glucose *N*-acetyl transferase); fructose sensors (i.e., FBP/FIS1, fructose-1,6-bisphosphatase), sucrose and hexose sensors (RGS1, regulator of G-protein signaling), and putative sucrose sensors (SUSY, SUcrose SYnthase, putative sucrose transporter AtSUT2/SUC3). Downstream of sugar perception are two energy sensors: AtKIN10/SnRK1 (sucrose-non-fermentation-related protein kinase1) and TOR-kinase (target of rapamycin kinase). CWI: cell wall invertase; G6P: glucose 6-phosphate; GS/GOGAT: glutamine synthetase/glutamate oxoglutarate aminotransferase; INV, invertase; OPPP: oxidative pentose phosphate pathway; STP: Sugar transport protein; SUT: sucrose transporter; TCA cycle: Tricarboxylic acid cycle; TFs: transcription factors; TPS: T6P synthase; TPP: trehalose 6P phosphatase; T6P, trehalose 6-phosphate; UDPGlc: Uridine diphosphate glucose; UDPGlc-NAC: UDP *N*-acetylglucosamine.

We currently have no evidence of the role of fructokinase (FRK), which catalyzes the irreversible phosphorylation of fructose, in the fructose-sensing process [44]. However, combining cell-based functional screen and genetic mutations, Cho and Yoo (2011) identified the nuclear-localized fructose 1-6-bisphosphatase (FBP/FIS1, Fructose-Insensitive 1) as a putative fructose sensor uncoupled from its catalytic activity [52]. Meanwhile, Li et al. (2011) characterized the ANAC089 transcription factor as a fructose-sensitivity repressor in *Arabidopsis* [53]. Other researchers isolated two FRK-like proteins (FLN1 and FLN2) that are components of the thylakoid-bound PEP (plastid-encoded polymerase) complex in *Arabidopsis thaliana*, regulate plastidial gene expression, and are essential for plant growth and development [54]. It will be interesting to determine whether there is a connection between these different fructose sensors and how these two hexose pathways could interact.

2.3. Energy and Metabolite Sensors

2.3.1. SnRK 1: Sucrose Non-Fermenting Related Protein Kinase 1

AtKIN10/AtKIN11/SnRK1 is a serine/threonine kinase that shares high sequence identity with yeast SnF1 and mammal AMPK (5′ AMP-activated Protein Kinase), and is considered as the energy-signaling hub controlling many regulatory proteins [55,56]. The evolutionary conservation of this protein function is demonstrated by its heterotrimeric structure, with one catalytic α-subunit and two regulatory ß and γ subunits [57], as well as the functional complementation of the yeast *snf1* mutant with the rye orthologue [58]. In plants, SnRK1 plays a crucial role in the reprogramming of metabolism, the adjustment of growth and development, and plant responses to different biotic and abiotic stresses [55]. SnRK1 controls the expression of more than one thousand genes coding for transcription factors and proteins involved in chromatin remodeling, and also acts through post-translational regulation of several key metabolic enzymes and certain transcription factors [59– 63]. There exists a positive correlation between the expression profile of genes regulated by AtKIN10 and the profile of genes regulated by sugar starvation [61]. These authors reported that the regulation of SnRK1 activity and signaling required the phosphorylation of a highly conserved threonine residue close to the active site in the catalytic α-subunit. The dephosphorylation of SnRK1α by PP2C phosphatases may reverse the activation loop and provide mechanisms for the integration of environmental cues [64]. The complex interplay of SnRK1 and SnRK2/ABA with the clade of PP2C phosphatases has been demonstrated in the ABA signaling pathway, where both types of protein kinases encompass common downstream targets such as different bZIP transcription factors [63]. In addition, the involvement of micro RNAs in SnRK1-mediated signal transduction appears plausible [65]. It is noteworthy that at least part of the gene responses related to the SnRK1 pathway might be independent of HXK1 signaling.

2.3.2. TOR Kinase: A Target of Rapamycin Kinase

TOR-kinase is evolutionarily conserved in all eukaryotic organisms, and plays a central role in the integration of endogenous (energy and nutrient status) and exogenous (environmental factors) signals to modulate growth and development. In plants, TOR-kinase has been identified only as the TORC1 complex, whose organization is similar in animals and yeast. The complex encompasses the TOR partners RAPTOR (kontroller of growth protein 1 (KOG1)/regulatory-associated protein of mTOR) and LST8 (small lethal with SEC13 protein 8) [66]. The crucial function of TOR-kinase lies in the positive regulation of metabolism and growth through the synthesis of proteins [16]. TOR-kinase activity seems to control nitrogen and carbon assimilation, and has a fundamental role in embryogenesis, meristem activity, leaf and root growth, senescence, and life span through the inhibition of autophagy [67–70]. As a result of TOR activation, growth is resumed, and reserve compounds, starch, lipids, and proteins are stored [71].

Sugars generally induce the activity of TOR kinase [16,69,72,73]. The glucose-enhanced activity of AtTOR was evidenced by the stimulation of root meristem activity [74]. Inversely, specific inhibitors of AtTOR reduced root growth. TOR activates glycolysis to enhance carbon skeleton production, which is further needed for amino acid and protein synthesis. AtTOR interaction with the RAPTOR protein is involved in the regulation of the ribosomal protein kinase S6K1, which represses the cell cycle by phosphorylating the Retino-Blastoma-Related (RBR) protein under unfavorable conditions [75]. Furthermore, it has been suggested that RBR is involved in the transition from heterotrophic to autotrophic plant development, which requires the expression-

inhibition of cell cycle genes, and the persistent inactivation of late embryonic genes through the modification of the epigenetic landscape, namely the trimethylation of lysine 27 of histone H3 (H3K27met3) [76].

Both the SnRK1 and TOR-kinase regulators act antagonistically. Energy and nutrient (C and N) scarcity activates SnRK1 to promote energy-saving and nutrient remobilization processes, while TOR is active under favorable conditions, when nutrients are available to enhance growth, development, and the anabolic metabolism. Such a crosstalk between TOR-kinase and SnRK1 is central for plants to adapt protein synthesis and metabolism to the available resources [77–79]. TOR and SnRK1 act downstream of sugar sensing and theirs activities are modulated by the sugar status of plants (Figure 1) [16]. T6P potentially inhibits AtSnRK1, supporting the model that T6P reflects cell sugar availability and promotes growth by repressing SnRK1 activity in sink tissues [31,32,35,80–83].

2.3.3. The OPPP: The Oxidative Pentose Phosphate Pathway

Specific investigations of sugar sensing, downstream of HXK, highlighted the occurrence of the OPPP in plants (Figure 1). This pathway seems to govern nitrogen and sulfur acquisition in response to the carbon status of the plant [84]. This integration would be critical for the coordination of amino-acid biosynthesis with the availability of these three important components.

2.4. Sugar Signaling in the Regulation of Sugar Transporters

AtSTP1 (*Arabidopsis thaliana* sugar transporter 1) was the earliest-discovered sugar transporter gene regulated by light [85]. Two other STP genes (*AtSTP13* and *AtSTP14*) have been reported to be sensitive to light conditions. They display diurnal regulation, which may result from a direct light effect or from the sensing of photosynthesis-derived sugars [86]. As sugar sensing plays a significant role in the establishment of different developmental stages, sugar transport and signaling appear crucial for these transitions. The latter assumption is corroborated by the changes in the transcriptional control of many sugar transporter genes in distinct mutants such as the Arabidopsis mutant “sweetie”, which is strongly affected in carbohydrate metabolism and displays an upregulated *STP1* gene [87]. The tight connection between sugar signaling and the regulation of sugar transporters fits with the impact of SnRK1 alteration on the expression of several *STPs* (*AtSTP1*, *AtSTP3*, *AtSTP4*, *AtSTP7*, and *AtSTP14*) by transient expression in mesophyll protoplasts [61].

Glucose-dependent down-regulation has been suggested for several STP genes (*STP1*, *STP4*, *STP13*, and *STP14*), but there appears to be different pathways for sugar control of *STP* expression [4,86,88–90]. Based on the demonstrated down-regulation of *STP4* and *STP10* in two independent hexokinase1 mutants, it has been suggested that their transcriptional control requires the glucose sensor HXK1. Inversely, *STP1*, one of the genes most repressed by sugars as revealed by large-scale genome analyses, displays glucose-dependent regulation independent of HXK1 [89]. The high responsiveness of *STP1* to sugars is corroborated by the rapid modulation of its expression in response to minor fluctuations of sugar levels (5 mM glucose) [4,88].

3. Molecular Mechanisms Involved in Regulation by Sugars

3.1. Epigenetic Regulation

Epigenetic mechanisms (DNA methylation, histone posttranslational modifications), as well as small RNAs, histone variants, chromatin remodeling, and higher-order chromatin organization control chromatin structure and thereby influence gene expression. Combinations of these epigenetic marks reflect the active (accessible) and repressive (inaccessible) chromatin state according to the “histone code hypothesis” [91]. A growing body of evidence from yeast and mammals suggests that metabolic signals also play crucial roles in determining chromatin structure [92]. In plants, histones act as metabolic sensors and may affect sensitivity/resistance to glucose and sucrose in link with germination. In *Arabidopsis*, the enzyme encoded by HISTONE ACETYLTRANSFERASE1 (HAC1), was efficiently involved in histone acetylation and protein–protein interactions required for transcriptional activation of gene expression [93–95]. Mutations in HAC1 cause a sugar-response defect, and lead to decreased expression of genes, *AtPV42a* and *AtPV42b*, which encode cystathionine-β-synthase (CBS) domain-containing proteins that belong to the PV42 class of γ-type subunits of the plant SnRK1 complexes [96]. This pioneer finding resulted from a screen for sugar-insensitive mutants. It highlights the fact that *hac1* mutants are resistant to high glucose and sucrose concentrations. The authors discussed the possible role of this histone acetyltransferase in the plant sugar response through long-term effects

of the nutritional status on the expression of a specific set of genes. The detailed phenotyping of these mutants revealed delayed flowering times possibly related to the indirectly increased expression of the central floral repressor FLC (FLOWERING LOCUS C) by HAC1 [97,98], and a low productivity, namely a reduced number of seeds per silique [96]. The importance of sugar levels for the induction of flowering [99–101] suggests a putative involvement of HAC1 in the link between the sugar response and flowering time.

The fine-tuning of the cell fate between proliferation and differentiation in shoot and root apices relies on the balance of antagonistic effects of auxin and cytokinins, but also on glucose and light. All these signals are integrated by TOR kinase. Furthermore, the mutation of transcriptional corepressor TOPLESS, which is required to repress root formation at the shoot pole in late embryogenesis, may be suppressed by a mutation in HAC1. These data suggest that the stable switching-off of auxin-inducible genes (i.e., prevention of their activation), needs to be done through chromatin remodeling [102]. We may also speculate that epigenetic regulation seems required in the complex interplay between metabolic and hormonal signaling. New data arguing in favor of this statement concerns a small family of proteins interacting with ABA INSENSITIVE 5 (ABI5), named (ABI5)-binding proteins AFPs. They may interact with the TOPLESS co-repressor to inhibit ABA- and stress-responses, conferring strong resistance to ABA-mediated inhibition of germination in *Arabidopsis* overexpressing lines [103]. Using a yeast two-hybrid system, the authors demonstrated the direct interaction of AFP2 with histone deacetylase (HDAC) subunits and thereby suggested the possible involvement of some AFPs in the regulation of gene expression through chromatin remodeling.

A new histone modification was reported recently, the *N*-acetylglucosamine (GlcNAc) can be O-linked to the serine 112 of H2B by the enzyme O-GlcNAc transferase (OGT) and produces the O-GlcNAcylation mark [104]. The activated sugar UDP-GlcNAc (Uridine diphosphate *N*-acetylglucosamine) acting as co-substrate, is synthesized from extracellular glucose via the hexosamine biosynthesis pathway. For a first time, the activity of a histone-modifying enzyme is directly linked to the extracellular glucose concentration. Fujiki et al. demonstrated that O-GlcNAcylation of histone H2B at Ser112 fluctuates in response to extracellular glucose. Through a genome-wide analysis, they revealed that H2B Ser112 O-GlcNAcylation was frequently located nearby transcribed genes, suggesting that histone H2B O-GlcNAcylation facilitates gene transcription [104]. GlcNAc is a key signaling metabolite that can coordinate the glucose and glutamine metabolisms in cells through glycosylation of growth factor receptors [105]. Although the transcriptional implication of histone GlcNAcylation remains to be fully elucidated, it is likely that a flux through the hexosamine biosynthesis pathway affects the levels of this novel epigenetic mark. Therefore, nutrient sensing by OGT may be pivotal in the modulation of chromatin remodeling and in the regulation of gene expression [106,107].

In *Drosophila melanogaster*, OGTs act as part of chromatin-remodeling complexes (CRCs) called polycomb group (PcG) proteins [108,109]. Switch/Sucrose-Nonfermenting-(SWI/SNF) type CRCs are constituted of a central Snf2-type ATPase associated with several non-catalytic core subunits evolutionarily conserved in eukaryotes. In *Arabidopsis*, the BRAHMA (BRM) ATPase and SWI3C CRC subunits act within a common complex to fulfill most of their functions, i.e., regulation of transcription, DNA replication and repair, and cell cycling. In addition, the *swi3c* mutation inhibits DELLA-dependent transcriptional activation of GIBBERELLIN-INSENSITIVE DWARF1 (GID1) GA-receptor and GA3ox (active GA biosynthesis) genes [110]. SWI3C also interacts with the O-GlcNAc transferase SPINDLY (SPY) required for the functioning of DELLAs in the GA-response pathway. Physical protein–protein interactions of SWI3C with DELLA and SPY have been demonstrated and further supposed to be required for certain DELLA-mediated effects such as transcriptional activation of the GID1 and GA3ox genes. The established pivotal role of DELLA proteins as a hub in the hormonal crosstalk between gibberellins, auxins, abscisic acid, ethylene, and brassinosteroids has been further supported by their direct physical interaction with SWI/SNF-type CRCs [111]. In the same context, it appears tantalizing to decipher the roles of sugar signaling because it interacts so tightly with hormone signaling. Moreover, it is possibly involved in the linking of the energy metabolism with epigenetic regulation through the expression of specific sets of genes in plant growth, development, and stress responses.

3.2. Transcriptional Regulation

Sugars affect the expression level of many genes in plants. Approximately 10% of *Arabidopsis* genes are sugar-responsive [4,112]. Based on the functional characterization of many sugar-regulated plant promoters, different cis-acting elements have emerged as crucial components of sugar-regulated gene expression. Such cis-acting elements transduce signals of sugar starvation [113,114] or sugar supply [115–119]. The GC-box

(GGAGAACCGGG), G-box (CTACGTG), TA-box (TATCAA), and their variants are associated with sugar starvation promoting the expression of α-Amy3 (α-amylase 3, an endo-amylolytic enzyme catalyzing starch degradation in higher plants) [113,114]. By contrast, Sporamin Promoters 8 [SP8a (ACTGTGTA) and SP8b (TACTATT)] and SUgar REsponsive-elements SURE1 (AATAGAAAA) and SURE2 (AATACTAAT) are involved in sugar induction of sporamin and patatin expression, respectively [117,120]. Other cis-acting elements such as the B-box (GCTAAACAAT), the CGACG element, the TGGACGG element, and the W-box (TGACT), S box (CACCTCCA), and TTATC element also participate in plant sugar signaling [117–119,121]. Sugar-responsive transcription factors include members of the ERF/AP2 [122], MYB [123], WRKY [124], and bZIP [125] families (Table 1). The first to be identified were SPF8 and SUSIBA2 (SUgar SIgnaling in BArley) [120,124], two members of the plant-specific WRKY family [126]. SUSIBA2 has a high relevance in plant sugar signaling because it is specifically sugar inducible, binds to SURE and W-box elements of the isoamylase (iso1) promoter, a key amylopectin-synthesizing enzyme, and induces carbohydrate accumulation in barley endosperm [124]. This regulation is biologically important, and makes the activity of SUSIBA2 a major component of the high sink strength of seeds. In agreement with this, SUSIBA2-expressing rice preferentially reallocates photosynthates towards aboveground tissues (stem and seeds); this offers sustainable means of increasing starch contents for food production and limits root-related greenhouse gas emission during rice cultivation [127]. In barley leaves, SUSIBA1 and SUSIBA2 are involved in an antagonistic SUSIBA regulatory network that ultimately leads to the coordination of starch and fructan synthesis in response to sugar availability [128]. Low sucrose concentrations generally upregulate SUSIBA1 expression, which acts as a repressor of both fructan synthesis and SUSIBA2 expression, while high sucrose levels induce SUSIBA2 expression, which stimulates starch accumulation in leaves but represses SUSIBA1 expression. This intertwined regulation shows that SUSIBA2 expression depends on the competitive binding of SUSIBA1 (repressor)/SUSIBA2 (inducer) to the target site (W-box) of the SUSIBA2 promoter, building up an autoregulatory system for the sequential regulation of starch and fructan synthesis [128]. Noteworthy, we do not know as yet whether the SUSIBA-related function in sugar signaling is evolutionarily conserved in eudicots. Besides the WRKY family, transcription factors from the bZIP and MYB families are also involved in sugar-regulated gene expression. bZIP is one of the largest transcription factor families in higher plants, characterized by a leucine zipper and a basic region necessary for their specific binding activity to various ACGT elements in plant promoters [129]. This bZIP family regulates the expression of genes involved in an array of plant biological processes and environmental stresses [130–136]. Early investigations based on transcriptomic analysis identified 10 sugar-responsive bZIP transcription factors in *Arabidopsis*. Amongst them, *AtbZIP1* is transcriptionally and post-translationally repressed by glucose through a hexokinase-dependent pathway [4], which explains its high expression under conditions of sugar and energy depletion [137]. Besides its negative role in early seedling growth, *bZIP1* acts as a master regulator gene for the sugar-signaling pathway: most of the genes identified as *AtbZIP1*-regulated are also sugar sensitive, and it could probably mediate sugar signaling by binding to the C- or G-boxes in the promoters of its target genes [125,137]. Unlike SUSIBA2, AtbZIP1 is involved in other signaling pathways, especially those elicited by light, nutrients, and stress signaling [125,138]. Some transcription factors of the MYB family also mediate sugar signaling, as shown for sugar-induced anthocyanin biosynthesis. Out of the transcription factors involved in this process, MYB71/PAP1, whose expression is upregulated by sucrose availability [139], stimulates the anthocyanin biosynthesis pathway [140,141] through sugar signaling. In fact, the myb71/pap1mutant is defective in sucrose-induced DRF (dihydroflavonol reductase) expression; DRF encodes a key enzymatic function in anthocyanin accumulation, and the alteration of MYB71/PAP1 protein-binding activity related to natural variation in *Arabidopsis* accessions impairs sugar inducibility [13]. Other MYB transcription factors contribute to the sugar-dependent regulation of α-amylase expression. In rice suspension cells and barley aleurone, three structurally related OsMYB transcription factors (OsMYB1, OsMYB2, and OsMYB3) bind to the same target site (a TA-box), share overlapping sequences, but display different biological functions, with a prominent role of OsMYB1 in sugar-starvation-induced α-amylase gene expression [123]. These OsMYBs are also involved in GA-induced expression of α-amylase. This raises the question of their multifunctional roles in many signaling pathways [123]. More recently, Chen et al. (2017) identified two homologs of OsMYB1 in *Arabidopsis* (MYB1 and MYB2) that also recognize the sugar-response element TA-box, but play opposite roles in glucose signaling in *Arabidopsis* [142].

Table 1. The transcription factors that are involved in sugar signaling in *Arabidopsis thaliana.*

Gene ID	Gene Symbol	Transcription Factor Family	Main Process/Function	Binding Site	References
AT1G69780	ATHB13	HD-ZIP	Response to sugar signaling pathways. Control cotyledon and leaf morphogenesis	5′-CAATNATTG-3′	[100,389–391]
AT5G28770	AtbZIP63	bZIP	Response to glucose and ABA signaling pathways	5′-CACGTG-3′ *	[392,393]
AT1G45249	ABF2	bZIP	Involved in ABA and glucose signaling pathways. Response to salt stress	5′-CACGTG-3′; 5′-ACGTGKC-3′	[394–399]
AT2G40220	ABI4	AP2/ERF	Response to ABA, ethylene, cytokinin, and sugar signaling pathways. Involved in osmotic stress, defense response and root development, and stomatal movement	5′-CACTTCCA-3′	[121,311,400–405]
AT5G24800	AtbZIP9	bZIP	Response to sugar signaling pathway	5′-CACGTG-3′	[406,407]
AT4G34590	AtbZIP11	bZIP	Involved in sugar, auxin signaling pathways. Affect root growth and amino acid metabolism	5′-CACGTG-3′	[162,165,167,212,408]
AT3G20770	AtEIN3	EIL	Response to ethylene and sugar signaling pathways	5′-GGATTCAAGGGGCA TGTATCTTGAATCC-3′	[298,409–411]
AT2G28350	ARF10	ARF	Involved in auxin, and ABA signaling pathways. Control cell division, seed germination and developmental growth, and root cap development	5′-TGTCTC-3′ *	[412–418]
AT1G56650	AtMYB75	MYB	Response to sugar, jasmonic acid, auxin, ethylene signaling pathways. Regulation of anthocyanin biosynthetic process and removal of superoxide radicals. Involved in cell wall formation	5′-CACGTG-3′, 5′-ACACGT-3′	[13,239,289,419–425]
AT2G36270	ABI5	bZIP	Involved in ABA, sugar signaling pathways during seed germination	5′-CACGTG-3′	[103,122,289,426–431]
AT2G30470	HSI2	B3	Repressor of the sugar-inducible genes involved in the seed maturation. Plays an essential role in regulating the transition from seed maturation to seedling growth. Involved in embryonic pathways and ABA signaling	5′-CATGCA-3′	[432–437]
AT5G49450	AtbZIP1	bZIP	Involved in sugar (nutrients) signaling pathway. Response to salt and osmotic stress	5′-CACGTG-3′	[125,136,138,210,406,438]
AT3G23210	bHLH34	bHLH	Response to glucose and ABA signaling	5′-(GA)n-3′; 5′-CANNTG-3′	[107,406]
AT3G44290	NAC060	NAC	Response to sugar-and ABA signaling cascade	Unknown	[315,439]
AT4G00238	AtSTKL1	GeBP	Involved in mediating certain glucose responses	5′-GCCT-3′	[440]
AT5G08790	ATAF2	NAC	Response to sugar, jasmonic signaling pathways. Seedling photomorphogenesis and leaf senescence	5′-RTKVCGTR-3′ *	[441–446]

AT5G56860	GATA21	GATA	Response to Gibberellic acid and sugar signaling pathways. Involved in regulation of nitrogen compound metabolic process, flower development, cell differentiation, and chlorophyll biosynthetic process	5′-GATA-3′	[447–452]
AT3G54320	AtWRI1	AP2/ERF	Response to sugar signaling pathway. Involved in triglyceride biosynthetic process, lipid metabolic process, regulation of glycolytic process, and seed development	5′-CACRNNTHCCRADG-3′ *	[453–459]
AT4G14410	bHLH104	bHLH	Response to sugar signaling pathway and iron homeostasis	5′-(GA)n-3′	[460–462]
AT5G64750	ABR1	AP2/ERF	Involved in ABA and sugar signaling pathways. Response to osmotic stress and salt	5′-GCCGCC-3′	[463–465]
AT4G00250	ATSTKL2	GeBP	Response to sugar signaling	5′-GCCT-3′	[440]

The code of bind site follows the IUPAC role. * The binding sites are predicted by PlantPAN database (http://plantpan2.itps.ncku.edu.tw/index.html) [466].

3.3. Post-Transcriptional Level

Gene post-transcriptional regulation plays a determining role in plant growth and represents a powerful strategy for plants to flexibly adapt their growth and development to endogenous and exogenous stimuli. This could involve regulation of the rate of mRNA turnover. Extensive investigations have reported that RNA-binding proteins (RBPs) regulate many aspects of RNA processing [143]. In rice cell cultures, nuclear run-on transcription. and mRNA half-life analyses revealed that sugar starvation led to reduced mRNA transcription rates and stability of a large set of genes [144]. Using microarray experiments, Nicolai et al. (2006) identified 268 mRNAs and 224 mRNAs under transcriptional and post-transcriptional regulation, respectively, in response to sugar starvation [145]. Most of them were sugar-starvation-repressed and related to the plant cell cycle and plant cell growth, supporting a rapid adaptability of cell metabolic activity to a low sugar status. Another example that links sugar availability to mRNA destabilization resides in the sugar-induced instability of α-Amy3 [146], probably through the 3′UTR sequence of α-Amy3 RNA [147,148]. Although such post-transcriptional regulation is involved in sugar-controlled mRNA stability, much remains to be understood about the molecular mechanisms involved in this process. UPF RNA helicase, a key component of NMD (nonsense-mediated RNA decay) in *Arabidopsis*, takes part in the sugar-signaling pathway [149], as demonstrated by the low-β-amylase1 (*lba1*) phenotype of the AtUP-1 RNA helicase mutant [150]. Consistently, many sugar-inducible genes were upregulated when the *lba1* mutant was complemented with the wild type AtUPF1, suggesting that AtUPF RNA helicase might optimize sugar inducibility [149]. Similarly, AtTZF1, which encodes an *Arabidopsis thaliana* tandem zinc finger protein, is sugar responsive and might confer sugar-dependent post-transcriptional regulation [151]. This family of proteins plays a critical role in plant growth, development, and stress responses, probably via regulation RNA processing [152].

An emerging process behind sugar-dependent post-transcriptional regulation is mediated by miRNA. miRNAs are regarded as the most important gene regulators that hinder much of gene expression [153]. Many studies have demonstrated that sugars induced the juvenile-to-adult transition by repressing the levels of two members of miR156 (miR156A and miR156C) in *Arabidopsis* seedlings [154,155]. miR156 is known to promote leaf juvenility by impeding the function of SPL (SQUAMOSA PROMOTER BINDING PROTEIN-Like) transcription factor [156]. This sugar effect implies the AtHXK1 signaling pathway and T6P [154,157], and occurs cooperatively with the Mediator Cyclin-Dependent Kinase 8 (CDK8) module [158]. All these findings indicate that sugar-dependent post-transcriptional regulation is far from being a neglected mechanism, but rather involves a diversity of complex processes that requires more investment to decipher the regulatory molecular network.

3.4. Translational and Post-Translational Regulation

Regulation of mRNA translation can operate at multiple stages, including through regulatory elements in the 5′ and 3′ untranslated regions (UTRs) of mRNA. Upstream of the open reading frame (uORF), 30% to 40% of eukaryotic mRNAs are located in the 5′UTR [159] and involved in many developmental and growth-related processes [160,161]. Such regulation concerns the *Arabidopsis* basic leucine zipper *AtbZIP11*, which orchestrates metabolic reprogramming in response to cellular sugar status and energy deprivation conditions [162–165]. Under high sucrose conditions, *AtbZIP11* is induced at the transcriptional level, while it is repressed at the translational level [4,112,166,167]. This translational regulation requires the second uORF of *bZIP11* mRNA, named sucrose-induced repression of translation (SIRT), which is evolutionarily conserved among all groups of S1 members [167–171]. Data from frame-shift mutation and amino-acid substitution indicate that sucrose specifically causes ribosome stalling during translation of the second uORF, impeding the translation of the bZIP main ORF [167]. Using a cell-free translation model, Yamashita et al. (2017) demonstrated that SIRT was critical for specific sucrose-induced ribosome stalling, and probably acted as an intracellular sensor of sucrose [172]. In heterotrophic maize suspension cells, Cheng et al. (1999) ascribed a determining role to the length of the 3′UTR sequence of Incw1, a cell wall invertase, in sugar-mediated translational control [173]. Incw1 encodes two transcripts that only diverge in the length of their 3′UTR (Incw1-Small RNA and Incw 1-Large RNA) and are differentially regulated by sugars. The 3′UTR of the Incw1 genes may act as a regulatory sensor of carbon starvation and as a link between sink metabolism and cellular translation in plants.

Sugar signaling can also be mediated by different mechanisms of post-translational regulation. The 14-3-3 proteins are phosphoserine-binding proteins that regulate a wide array of targets via direct protein–protein

interactions [174]. They are involved in sugar-mediated post-translational regulation. In suspension-cultured cell models, sugar supply promotes both protein phosphorylation and their interaction with 14-3-3 proteins, while sugar depletion induces the dissociation of this protein complex, ultimately leading to selective degradation of these 14-3-3-regulated proteins [175]. This coordinated post-translational regulation could establish a new steady-state balance of metabolic activity adapted to sugar starvation conditions. Energy depletion (sugar starvation) due to the application of 2-deoxyglucose, a powerful blocker of the glycolysis pathway [74], led to the inhibition of key metabolic enzymes [60] related to their coordinated phosphorylation by SnRK1 and recognition by 14-3-3 proteins [57,59,60]. More recently, Okumura et al. (2016) demonstrated that sugar accumulation in photosynthetic leaves induced the activation of the plasma membrane H^+-ATPase through the phosphorylation of the penultimate threonine of the C-terminal region and the binding of 14-3-3 proteins [176,177]. Accordingly, light-induced phosphorylation of H^+-ATPase was strongly suppressed in mutants impaired in endogenous sugar accumulation. Such activation of H^+-ATPase may stimulate sucrose export from leaves and thereby avoid inhibition of photosynthesis by high sugar accumulation [178,179]. Additional mechanisms of sugar-elicited posttranslational regulation come from the regulation of AGPase (ADP gluco-pyrophosphorylase), a key enzyme of the starch biosynthesis pathway [180]. Starch synthesis can increase via allosteric activation of AGPase, as a result of a higher 3PGA (3-phosphoglycerate) to Pi (inorganic phosphate) ratio [181] and/or through its post-translational redox activation in response to light or high sugar treatment in *Arabidopsis* [182–185]. This latter regulation is dependent on T6P [186,187]. All these findings show that post-transcriptional regulation is prevalent for sugar signaling, and extensive investigations are required to get more information about the molecular mechanisms and the relevance of additional post-transcriptional mechanisms such as sumoylation, protein–protein interactions, or unfolded cytoplasmic proteins.

4. Crosstalk between Sugar and Hormone Signaling

4.1. Sugars and Auxin

Auxin has been chemically identified as indole-3-acetic acid (IAA). It plays a pivotal role in almost all processes of plant growth and development [188–190]. Growing evidence suggests a crosstalk between sugar and auxin that involves metabolism [191–193], transport [194–197], and signaling pathways [198–201]. The first link between sugar and auxin came from *Arabidopsis* hypocotyl explants of *hxk*/*gin2*, which is insensitive to auxin induction of cell proliferation and root formation [42]. Accordingly, auxin-resistant mutants (*axr1*, *axr2*, *tir1*) are insensitive to high glucose concentrations [42]. Sugar and auxin represent a highly complex and central signaling network in various aspects of plant development, including cell proliferation, cell expansion, cell differentiation, hypocotyl elongation, or anther development [179,202–206]. A novel allele of the hookless1 gene (*hls1*) was found resistant to both sugar and auxin responses in excised leaf petioles, suggesting that it may be part of the negative effects of auxin on sugar-responsive gene expression [199]. One of the best examples is their major contributing role in root system architecture, whereby sugar works individually or cooperatively with auxin [200,203,207–209]. Transcriptomic experiments on seedling roots revealed that glucose regulates the expression of many auxin-related genes (e.g., YUCCA, TIR1); more interestingly, a number of these genes are insensitive to glucose alone, but become glucose-responsive in the presence of auxin (e.g., AUX/IAA) [200]. In addition, exogenous glucose supply enhances defects in the induction of lateral root growth, root hair elongation, and gravitropism in mutants of auxin sensing (*tir1*) and signaling (*axr2* and *axr3*), suggesting that glucose-regulated root architecture may occur through auxin-based signal transduction [200]. Gonzali et al. (2005) showed that auxin and turanose, a non-metabolizable analogue of sucrose, regulated the expression of the WOX5 transcription factor, a Wushel-related homeobox gene required for sustaining local auxin maxima in the root apical meristem [198]. Additional insights into the interactions between auxin and sugar come from the elegant work conducted in *Arabidopsis* by Weiste et al. (2017): they demonstrated a new function of S_1bZIP11-related TFs (bZIP1,-11 and -44) as negative regulators of auxin-mediated primary root growth (Figure 2) [165]. These transcription factors are downregulated by sugar and upregulated by low energy levels through SnRK1 kinase activity [61,162,167,170,171,210,211]. In this context, bZIP11 and closely related TFs directly up-regulate the expression of IAA3/SHY2, a key negative regulator of root growth. By repressing transcription of PIN1 and PIN3—major auxin efflux facilitators—IAA3/SHY2 restricts polar auxin transport (PAT) to the root apical meristem and thereby blocks auxin-driven primary root growth. These findings support that *bZIP11* and closely related transcription factors are a gateway for integrating low-energy-related stimuli into auxin-mediated root growth responses [165]. A close interaction between bZIP11 and auxin signaling was

also demonstrated when the highly homologous bZIP11-related TFs were found to quantitatively modulate auxin-responsive gene expression by recruiting the histone acetylation machinery to target promoters [212]. Repression of PIN1 accumulation and consequently reduction of PAT in roots explains the inhibition of root elongation in response to high glucose concentrations, through *ABI5* (ABA insensitive 5) [213]. Part of the glucose and auxin interplay in root growth and development is thought to result from the glucose-dependent activation of the heterotrimeric G-protein [214] and the auxin-activated TOR-kinase signaling pathway [215]. Based on genetic analysis, Raya-González et al. (2017) proposed a new mechanism involving MED12 or MED13, two subunits of the MEDIATOR complex responsible for the connection of RNA polymerase II to specific transcription factors [216], and thus controlling gene transcription [217]. The loss-of-function mutants *med12* and *med13* displayed short and thin primary roots associated with decreased auxin responsiveness and a reduction of cell proliferation and elongation in primary roots. This behavior was fully alleviated by exogenous sugar. Further analysis supports that MED12 and MED13 can operate as positive linkers of sugar sensing to the auxin response pathway, and that MED12 acts upstream of AUXIN RESISTANT 1 (AUX1), an auxin influx carrier central for the spatio-temporal transport of auxin within the root tissue. An interesting connection between sugar signaling and polar auxin transport also results from hypocotyl elongation; it involves the PIF (Phytochrome interacting family) transcriptional regulators (Figure 2). PIFs (e.g., PIF4) induces the expression of many auxin biosynthesis genes (e.g., YUCCA) by binding to their promoter [218], and its upregulation by sucrose leads to auxin accumulation and thereby to hypocotyl elongation [195]. The regulation mechanism between sugar and PIF seems to be complex: other works showed that PIFs could act as negative regulators of sugar-induced IAA biosynthesis [196], and that the auxin response acts upstream of PIFs [197]. Additionally, the role of PIFs in linking sugar signaling to auxin accumulation is central during another development in response to high temperature [204]. Although the sugar and auxin interplay plays a coordinated role in the control of many plant developmental processes, extensive investigations are still required to understand whether these so-far described pathways are interconnected or correlated with each other.

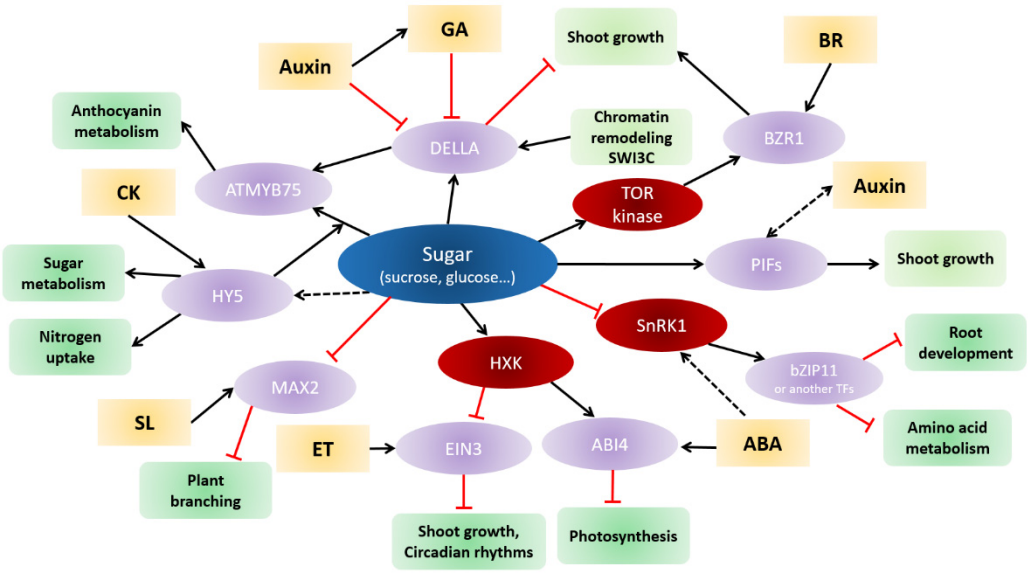


Figure 2. Schematic representation of the crosstalk between the sugar and hormone signaling pathways (orange frame) in the regulation of certain physiological processes (green frame). Light-purple circles represent hub regulators, including transcription factors (ABI4: ABA insensitive 4; ATMYB75/PAP1; bZIP11; EIN3: ETHYLENE-INSENSITIVE 3; HY5: Elongated Hypocotyl 5: PIFs: Phytochrome interacting factors), F-box (MAX2: MORE AXILLARY 2) and key regulators of the hormone signaling pathways (DELLA and BZR1: BRASSINAZOLE RESISTANT). Red circles represent glucose sensors (HXK: hexokinase) and energy sensors (SnRK1: Sucrose non-fermenting related kinase 1; TOR-kinase: Target of Rapamycin kinase). ABA: Abscisic acid; BR: Brassinosteroid; CK: Cytokinin; GA: Gibberellin; SL: Strigolactone. Black arrows indicate stimulating effects and red blunts indicate repressing effects.

4.2. Sugar and Cytokinins

Cytokinins (CKs) are underlying factors of the regulation of plant development. They influence many central processes including cell proliferation, source/sink relationships, leaf senescence, apical dominance, root growth, nutritional signaling, and responses to abiotic and biotic stresses [219–223]. Many examples indicate that CKs and sugars can cross-influence their metabolism and transport [193,222,224–229], which may impinge on signaling pathways. Based on transcript profiling of *Arabidopsis* seedlings after glucose and cytokinin treatment, Kushwah and Laxmi (2014) showed that glucose and CKs acted both agonistically and antagonistically on gene expression, and glucose had a strong effect on genes involved in cytokinin metabolism and signaling [229]. The first direct interplay between sugar and CKs came from the characterization of the hxk1/gin2 mutant, which displays decreased sensitivity to sugar and increased sensitivity to CKs [42], suggesting an antagonistic effect of CKs. In accordance with this, a constitutive CK response mutant was insensitive to high glucose-dependent seedling development repression [230], and a CK receptor mutant (ahk3) exhibited CK resistance but increased sucrose sensitivity during plant growth assays [231]. The cytokinin-resistant (cnr1) mutant exhibited a number of altered auxin responses as well as hypersensitivity to sugars, as evidenced by high levels of chlorophyll and anthocyanins as compared to the wild type [232]. Further proof came from the fact that sucrose downregulates WPK4, that is activated by CK and encodes a putative protein kinase belonging to the SnF1 kinase subfamily [233,234]. Other responses rather revealed synergistic effects. In *Arabidopsis* seedlings, CKs and glucose positively regulate root elongation via an HXK1-dependent pathway [235], involving *Arabidopsis* cytokinin receptor AHK4 (ARABIDOPSIS HISTIDINE KINASE 4) and three *Arabidopsis* type-B response regulators (ARR1, ARR10, and ARR11) [235,236]. In that case, glucose only boosts CK-dependent root elongation, which occurs upstream of the effect of auxin on root development [235,236]. CKs and sugar also play important roles in the regulation of different cell cycle phases, including the G1/S transition via the sucrose induction of *cycD3* expression [15] and the G2/M transition [237]. Another synergistic action between CKs and glucose resides in their combinatorial effect on anthocyanin accumulation in *Arabidopsis* leaves: sugar-induced anthocyanin biosynthesis is enhanced by CKs via the redundant action of three type-B ARRs (ARR1, ARR10, and ARR12) [238]. This signaling cascade involves transcriptional upregulation of MYB75/PAP1 by LONG HYPOCOTYL 5 (HY5) (Figure 2) [239].

In *Arabidopsis*, a balance between the antagonistic effects of auxin—which mediates cell division—and CKs—which mediate cell differentiation—establishes the root meristem [240]. Inversely, in the shoot meristem, CKs seem to promote the proliferation of stem cells and inhibit their differentiation, whereas auxin triggers organ primordia initiation [102]. It is noteworthy that the activation of root and shoot apical meristems relies on distinct glucose and light signals [241]. The authors provide arguments that glucose is required and sufficient to activate TOR kinase in the root apex, whereas neither glucose nor light alone can efficiently activate this central integrator of the cell nutrient and energy status in the shoot apex.

4.3. Sugars and Strigolactones

Strigolactones (SLs) were first considered as rhizosphere-signaling molecules that promote the germination of root-parasitic weeds and the symbiotic interactions between plants and soil microorganisms [242–244]. Since then, SLs have been revealed as mobile phytohormones controlling plant development and plant adaptation to environmental stress [245–253]. In addition, genes involved in SL biosynthesis and signaling are known in many plants [254]. Only a few studies have addressed how sugar signaling and SL signaling interplay to regulate plant functioning. Wu et al. (2017) showed that an *smxl4*/*smxl5* double mutant of *Arabidopsis* caused defective phloem transport of sugar and enhanced starch accumulation [255]. Li et al. (2016) reported that both mutants of *MAX1* and *MAX2*, involved in SL biosynthesis and signaling, respectively, were hyposensitive to glucose repression of seedling establishment; this suggests that this repression is under the cooperative effect of SLs and glucose, probably via the hexokinase-independent pathway [256]. Conversely, an antagonistic effect between the sugar- and SL-signaling pathways has been reported for plant branching. In that case, SLs act as inhibitors while sugars act as inducers [257]. In accordance with this, *Arabidopsis* plants overexpressing cyanobacterial fructose-1,6-bisphosphatase-II in the cytosol exhibited an over-branching phenotype associated with high sugar contents and repression of *MAX1* and *MAX4*, two SL-biosynthesis genes [258]. These findings fit with those reported by Barbier et al. (2015) in Rosa sp. buds, in which both metabolizable and non-metabolizable analogs of sucrose or hexoses down-regulated *MAX2* expression, and this

effect coincided with the ability of buds to grow out [193]. Further investigations should be led to ascertain the components through which these two signals interact.

4.4. Sugars and Gibberellins

Gibberellins (GAs) constitute a large group of molecules with a tetracyclic diterpenoid structure. They function as plant hormones and influence photosynthesis, the carbohydrate metabolism, plant growth (cell and stem length elongation) and development processes (germination, flowering etc.), and responses to biotic and abiotic stresses [259–268]. GAs directly regulate the plant carbon status through their effect on photosynthetic activity [269–271] and sugar metabolic activity [272–279]. Sugar can also affect the GA metabolism in different biological contexts [49,280]. A first direct interaction between sugar and GA signaling was revealed by the sugar-insensitive1 (*sis1*) mutant, which was also insensitive to gibberellins during seed germination [281], suggesting a cooperative effect between sugars and GAs. However, other data provide evidence for an antagonistic crosstalk. Sugar and GA signaling compete to regulate the expression of α-amylase in many cereal seeds [282–285], which involves spatiotemporal transcriptional regulation of GAMYB [285,286]. Li et al. (2014) reported that sucrose stabilizes DELLA proteins [287], supporting the importance of GAs in dark-induced hypocotyl elongation [288] and their negative effect on the sucrose-dependent induction of the anthocyanin biosynthesis pathway [289]. DELLA proteins are central repressors of the GA response [290]. In this context, Loreti et al. (2008) showed that GA repressed the expression of several sucrose-induced genes involved in anthocyanin synthesis, and this repressive effect was noticeably absent in *gai*, a mutant expressing a stabilized DELLA protein [289]. DELLA acts by inducing the upregulation of PAP1/MYB75 [291], a sucrose-induced transcription factor that mediates anthocyanin synthesis (Figure 2) [13]. DELLA proteins could be one of the main convergent actors of the hormonal and sucrose-dependent molecular networks.

4.5. Sugars and Ethylene

Ethylene regulates a host of plant processes, ranging from seed germination to organ senescence and plant responses to biotic and abiotic cues [292–294]. In higher plants, the pathways of ethylene metabolism and signaling are well established [295]. As evidenced by genetic and phenotypic analyses of many *Arabidopsis* mutants, there is a tight, but generally antagonistic, interaction between sugar and ethylene signaling. Mutants displaying nonfunctional ethylene receptors (*etr1*, *ein4*) or alteration of signal transduction proteins (*ein2* and *ein3*), are hypersensitive to sugar-mediated photosynthesis repression, while constitutive triple response 1 (*ctr1*), a negative regulator of ethylene signaling, is glucose insensitive [281,296–298]. Consistently, the ethylene-insensitive *etr1* and *ein2* mutants both exhibit *glo* (glucose-oversensitive) phenotypes, whereas the constitutive ethylene signaling mutant *ctr1* is allelic to *gin4*, a glucose-insensitive mutant [296,299]. Such an antagonistic interaction explains the ability of glucose to stimulate the degradation of ETHYLENE-INSENSITIVE3 (EIN3), a key positive transcriptional regulator in ethylene signaling, through the hexokinase-signaling pathway, and thereby promote plant growth [298]. The antagonistic interplay between the sucrose and ethylene pathways is involved in sustaining sugar-dependent circadian rhythms in darkness through post-transcriptional regulation of the circadian oscillator GIGANTEA (GI) [300]. According to these authors, sugars maintain circadian rhythms in the evening/night transition by stabilizing the GIGANTEA (GI) protein depending on the activity of the F-Box protein ZEITLUPE (ZTL), and by destabilizing EIN3 (Figure 2) [300]. The ethylene- and sugar-signaling pathways can also work cooperatively: both ethylene-insensitive (*ein2-1*) and ethylene-constitutive response (*sis1/ctr1)* mutants displayed only a slight modification of sugar-dependent chlorophyll accumulation and growth, but higher impairment of the sugar-induced tolerance to atrazine (an inhibitor of electron transport in photosystem-II photosynthesis) [301]. It appears that the mechanism of sucrose-dependent protection against atrazine requires active ethylene signaling and may rather involve a hexokinase-independent pathway.

4.6. Sugars and Abscisic Acid

Abscisic Acid (ABA) regulates many plant adaptive responses to environmental constraints [302–304]. Among plant hormones, ABA is one of major importance in the interaction with sugar signals since many mutations affecting sugar sensing and signaling are allelic to genes encoding components of the ABA synthesis or ABA transduction pathways. In *Arabidopsis*, ABA-deficient (*aba2*, *aba3*) and ABA-insensitive (*abi4*) mutants are allelic to glucose insensitive1 (*gin1*)/impaired sucrose induction 4 (*isi4*)/sugar insensitive1 (*sis1*) [305,306], and *gin6*/*isi3*/*sis5*/*sun6* [122], respectively. The *abi8* mutants are resistant to glucose-mediated

developmental arrest of wild-type seedlings [307]. The crosstalk between sugar and ABA can involve synergistic effects with ApL3 (ADP pyrophosphorylase large subunit) [306,308], ASR (ABA, stress and ripening-induced protein) in grape [309] and many photosynthesis-related genes [121,310,311]; but it can also involve agonistic effects, e.g., on the expression of Rab16A [312], Amy3D [115], and OsTIP3.1, a tonoplast intrinsic protein [313]. ABI4, a transcription factor of the AP2/ERF family, plays a prominent role in glucose and ABA signaling [121,122,314,315]. Many investigations underline the key role of SnRK1 in glucose and ABA signaling, since plants over-expressing SnRK1.1 displayed hypersensitivity to glucose and ABA during early seedling development [316], and SnRK1 was required for ABA-mediated maturation of pea seeds [317]. In addition, mutants disrupted in the three SnRK1 subunits displayed full ABA insensitivity, supporting that SnRK-mediated protein phosphorylation is necessary for all aspects of ABA functioning [318]. Exogenous ABA application resulted in the fine-tuning of SnRK1 activity [319]. Overlapping between the ABA and sucrose pathways was also confirmed by the phenotype of *aip* (a null mutant of AIP1), a member of group A PP2C serving as a positive actor in ABA signaling. This mutant exhibited lower sensitivity to ABA and glucose during seed germination and early seedling development [320]. More recently, Carvalho et al. (2016) identified a negative regulator of the glucose signaling pathway corresponding to the plant-specific SR45, belonging to the highly conserved family of serine/arginine-rich (SR) proteins [321]. Phenotypic and molecular characterization of the *sr45-1* mutant revealed hypersensitivity to glucose during early seedling growth, and over-induction of ABA-biosynthesis and ABA-signaling genes in response to glucose as compared to the wild type.

4.7. Sugars and Brassinosteroids

Brassinosteroids (BRs) are a class of polyhydroxylated sterol derivatives that regulate many plant growth processes [322–326]. Glucose affects BR biosynthesis, perception, transduction, and homeostasis [327–329]. On the other hand, BRs influence CO_2 assimilation, metabolism, and sugar fluxes [330–339]. BRs and sugars interplay cooperatively to regulate certain developmental processes, including etiolated hypocotyl elongation and LR development in *Arabidopsis* seedlings [340–342]. Analysis of glucose and BR sensitivity in both hexokinase-dependent and hexokinase-independent pathways complete this picture, providing evidence that glucose and BRs act via HXK1 pathway and BRs act downstream of this glucose sensor [329,341,342]. BZR1 (BRASSINAZOLE RESISTANT 1) protein can represent a converging hub between sugar and BR signaling (Figure 2) [341,343], and its stability is positively and synergistically controlled by TOR-dependent and BR signaling pathways in hypocotyls [343]. According to these authors, such TOR-mediated regulation allows carbon availability to control the hormonal growth promotion programs, ensuring a supply-demand balance in plant growth. Synergetic overlapping between sugar and BR signaling might also take place in the regulation of floral signal transduction, with a downstream effect of BZR1 and BZR2 [263]. This assumption is linked to the fact that many BR-deficient mutants (*brs1*, *det2*, *cpd*, *bls1*) display a late-flowering phenotype, and the *bls1* (*brassinosteroid*, *light and sugar1*) mutant is hypersensitive to sugars [344].

4.8. Crosstalk between Sugar and Nitrate Signaling

4.8.1. a—Interactions between Sugars and Nitrogen

The control of C and N interactions involves various endogenous signals, NO_3^- and NH_4^+ ions, amino acids, as well as sugars issued from the carbon metabolism [345–349]. Nitrate acts as a positive signal for the induction of proper sugar uptake and assimilation, while the metabolites resulting from sugar assimilation—e.g., glutamate, glutamine, aspartate, and to a lesser extend glycine and serine—serve as negative signals [350–356]. NR (nitrate reductase) and PEPc (phosphoenolpyruvate carboxylase) are two enzymes that link primary N and C assimilation in plants [357]. The interdependence of the C and N metabolisms supports their roles in the regulation of gene expression that can occur at the cell, organ, or whole plant levels [358]. Furthermore, nitrate uptake is enhanced by the CO_2 level through the availability of carbohydrates, and inversely a reduction of carbon storage by defoliation impairs nitrate uptake [345,349,359–363]. In line with this, the dark-dependent decrease of N uptake is reversed by addition of sucrose, which transcriptionally affects high- and low-affinity nitrate transporters [364]. Moreover, the regulation of nitrate uptake by light and sucrose is strongly linked [365], and NR gene expression appears to be regulated by photosynthesis through glucose synthesis [366]. Taken together, these results strongly suggest that the C/N ratio affects NR and NiR gene expression as well as

the related enzyme activities. Nitrogen starvation of wheat seedlings significantly decreased both the transcript levels and enzyme activities of NR, NiR, GS, and GOGAT, while potassium nitrate and ammonium nitrate restored gene expression and the catalytic activities of these enzymes [367]. In *Brassica juncea*, the expression of most of the N-pathway genes is significantly modulated under exogenous supply of sucrose or of sucrose and nitrogen [368]. These data emphasize the importance of C/N ratio signaling in the regulation of gene expression.

4.8.2. b—C/N Regulation

Many transcription factors—bZIP, Dof, Nin-like protein 7—as well as proteins such as kinases/phosphorylases are involved in regulating both the carbon and nitrogen metabolisms. Besides TOR kinases, other regulatory hubs between sugars and the nitrogen metabolism have been identified in plants. Among them, Elongated Hypocotyl 5 (HY5) is a bZIP transcription factor involved in a great number of signaling pathways such as hormonal, metabolic, or abiotic stress pathways [369]. It may operate in combination with the circadian rhythm to adjust levels of photosynthetic gene expression in the daytime [370]. HY5 is a shoot-to-root phloem-mobile signal and it mediates the regulation of root growth and nitrate uptake by light [369,371,372]. In the shoot, HY5 promotes carbon assimilation and translocation, whereas in the root it mediates the activation *NRT2.1* expression, supporting the fact that it coordinates plant nutrition and growth in response to fluctuating light environments (Figure 2). Furthermore, HY5 regulates the sucrose metabolism and sucrose movement into phloem cells for shoot-to-root translocation by increasing the expression levels of *SWEET11* and *SWEET12*, two genes encoding sucrose efflux transporters required for sucrose phloem loading [371,373]. Taken together, all these results strongly suggest that HY5 mediates the homeostatic regulation of the whole-plant C status versus the whole-plant N status [371]. Furthermore, the master clock control gene CCA1 targets the transcription factor bZIP1, which itself targets ASN1 involved in asparagine synthesis, and the nitrate transporter 2.1 (NRT2.1) [4,138]. SnRK1 phosphorylates NR [374,375] supporting the impact of both SnRK1 and bZIP1 on nitrogen signaling. Dröge-Laser and Weiste (2018) recently highlighted the importance of bZIPs in the control of metabolic gene expression according to the plant nutritional status [376].

The Dof1 (DNA binding with one finger) transcription factor from maize (*ZmDof1*) up-regulates the expression of PEPc and thereby modulates the C/N network. Overexpression of *ZmDof1* in *Arabidopsis* and potato was accompanied by the promotion of nitrogen assimilation and plant growth under low nitrogen conditions [377–379], and up-regulation of multiple genes involved in carbon skeleton synthesis [378]. In agreement with this, expression of *ZmDof1* regulates the expression of genes involved in organic acid metabolism, leading to the accumulation of amino acids and to increased growth under N-limiting conditions. These effects suggest that nitrogen use efficiency (NUE) could also be improved by manipulating the carbon metabolism pathways [363]. An analysis of the *cis*-regulatory element in the promoter of *AtSUC2*, which encodes a companion-cell-specific proton-sucrose symporter, identified a putative binding site for HD-Zip and a binding site for DOF transcription factors [380]. Furthermore, Skirycz et al. (2006) reported the phloem-specific localization of a member of the DOF transcription factor family [381]. In *Oryza sativa*, OsDOF11 modulates sugar transport by regulating the expression of SUT (SUT1, 3, 4, and 5) and SWEET (SWEET11 and SWEET14) genes [382].

Proteins from the Nodule inception-like protein (NIN-Like Protein—NLP) family appear as master regulators of nitrate signaling. NLP7 and NLP6 bind and activate the promoters of several nitrate-induced genes [78,383–386]. The only known actor of the signaling mechanisms involved in the induction of *NRT2.1* and *NRT1.1* expression by carbon is the OPPP [84,387,388]. Otherwise, NLP7 is involved in the regulation of the gene coding for 6-phosphogluconate dehydrogenase, a key enzyme of the OPPP [385]. Glucose increases NRT2.1 protein levels and transport activity independently of its hexokinase1-mediated stimulation of NRT2.1 expression, demonstrating another possible post-transcriptional mechanism influencing nitrate uptake [387]. These authors also established that photosynthate availability in the form of glucose is coupled to nitrate uptake and assimilation through glucose metabolism by HXK1 in the OPPP, transcriptional control of NRT2.1, and post-translational regulation of NRT2.1 protein levels and transport activities [387].

5. Conclusions

The complex processes of plant growth and development rely on the integration of inputs about nutrient availability, the energy status, and the hormonal balance under variable conditions at the level of whole

organisms. Sugar signaling downstream of signal-specific sensors (e.g., hexokinase, RGS1, fructose 1,6 bisphosphatase, O-GlcNAc transferase) converge to hub regulators of the nutrient and energy status (SnRK1 and TOR kinase). These key integrators might mediate the balance between the anabolic and catabolic metabolisms, as well as accumulation of reserves versus remobilization of reserves through epigenetic reprogramming, transcriptional/post-transcriptional regulation, ribosome biogenesis, translational activity, and protein modifications. Extensive investigations are required to identify additional hub regulators with original/unexpected functions. In this regard, the relevance of "non-canonical" sensors including histone modifiers, microRNAs, transcription factors, and many others (small peptides etc.) should not be overlooked. The complexity of sugar-responsiveness processes further requires the approaches of systems biology. The diversity of sugar sensors and the emerging transduction pathways are tightly interconnected with the hormone and nitrate signaling networks. At present, there is still a knowledge gap about the interconnections between all these signal transduction pathways, while the identity of the molecular actors involved in convergence points remains mostly unknown.

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All the authors have significant contribution to this manuscript.

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References:

1. Chiariello, N.R.; Mooney, H.A.; Williams, K. Growth, carbon allocation and cost of plant tissues. In *Plant Physiological Ecology*; Springer Netherlands: New York, NY, USA, 2000; pp. 327–365.
2. Sheen, J.; Zhou, L.; Jang, J.C. Sugars as signaling molecules. *Curr. Opin. Plant Biol.* **1999**, *2*, 410–418.
3. Eastmond, P.J.; Graham, I.A. Trehalose metabolism: A regulatory role for trehalose-6-phosphate? *Curr. Opin. Plant Biol.* **2003**, *6*, 231–235.
4. Price, J.; Laxmi, A.; Martin, S.K.S.; Jang, J.C. Global transcription profiling reveals multiple sugar signal transduction mechanisms in *Arabidopsis*. *Plant Cell* **2004**, *16*, 2128–2150.
5. Wind, J.; Smeekens, S.; Hanson, J. Sucrose: Metabolite and signaling molecule. *Phytochemistry* **2010**, *71*, 1610–1614.
6. Li, L.; Sheen, J. Dynamic and diverse sugar signaling. *Curr. Opin. Plant Biol.* **2016**, *33*, 116–125.
7. Funk, J.L.; Glenwinkel, L.A.; Sack, L. Differential Allocation to Photosynthetic and Non-Photosynthetic Nitrogen Fractions among Native and Invasive Species. *PLoS ONE* **2013**, *8*, E64502.
8. Zhang, X.; Li, K.; Xing, R.; Liu, S.; Li, P. Metabolite profiling of wheat seedlings induced by chitosan: Revelation of the enhanced carbon and nitrogen metabolism. *Front. Plant Sci.* **2017**, *8*, doi:10.3389/fpls.2017.02017.
9. Ljung, K.; Nemhauser, J.L.; Perata, P. New mechanistic links between sugar and hormone signalling networks. *Curr. Opin. Plant Biol.* **2015**, *25*, 130–137.
10. Chiou, T.J.; Bush, D.R. Sucrose is a signal molecule in assimilate partitioning. *Proc. Natl. Acad. Sci. USA* **1998**, *95*, 4784–4788.
11. Loreti, E.; Alpi, A.; Perata, P. Glucose and disaccharide-sensing mechanisms modulate the expression of *α-amylase* in barley embryos. *Plant Physiol.* **2000**, *123*, 939–948.
12. Fernie, A.R.; Roscher, A.; Ratcliffe, R.G.; Kruger, N.J. Fructose 2, 6-bisphosphate activates pyrophosphate: Fructose-6-phosphate 1-phosphotransferase and increases triose phosphate to hexose phosphate cycling in heterotrophic cells. *Planta* **2001**, *212*, 250–263.
13. Teng, S.; Keurentjes, J.; Bentsink, L.; Koornneef, M.; Smeekens, S. Sucrose-specific induction of anthocyanin biosynthesis in *Arabidopsis* requires the *MYB75/PAP1* gene. *Plant Physiol.* **2005**, *139*, 1840–1852.
14. Roldán, M.; Gómez-Mena, C.; Ruiz-García, L.; Salinas, J.; Martínez-Zapater, J.M. Sucrose availability on the aerial part of the plant promotes morphogenesis and flowering of *Arabidopsis* in the dark. *Plant J.* **1999**, *20*, 581–590.
15. Riou-Khamlichi, C.; Menges, M.; Healy, J.S.; Murray, J.A. Sugar control of Plant Cell cycle: Differential regulation of Arabidopsis D-type cyclin gene expression. *Mol. Cell. Biol.* **2000**, *20*, 4513–4521.
16. Lastdrager, J.; Hanson, J.; Smeekens, S. Sugar signals and the control of plant growth and development. *J. Exp. Bot.* **2014**, *65*, 799–807.
17. Ruan, Y.L. Sucrose metabolism: Gateway to diverse carbon use and sugar signaling. *Annu. Rev. Plant Biol.* **2014**, *65*, 33–67.
18. Mason, M.G.; Ross, J.J.; Babst, B.A.; Wienclaw, B.N.; Beveridge, C.A. Sugar demand, not auxin, is the initial regulator of apical dominance. *Proc. Natl. Acad. Sci. USA* **2014**, *111*, 6092–6097.
19. Barker, L.; Kühn, C.; Weise, A.; Schulz, A.; Gebhardt, C.; Hirner, B.; Hellmann, H.; Schulze, W.; Ward, JM.; Frommer, W.B. SUT2, a putative sucrose sensor in sieve elements. *Plant Cell.* **2000**, *12*, 1153–1164.
20. Li, Y.; Li, L.L.; Fan, R.C.; Peng, C.C.; Sun, H.L.; Zhu, S.Y.; Wang, X.F.; Zhang, L.Y.; Zhang, D.P. *Arabidopsis* sucrose transporter SUT4 interacts with cytochrome b5-2 to regulate seed germination in response to sucrose and glucose. *Mol. Plant* **2012**, *5*, 1029–1041.
21. Vitrac, X.; Larronde, F.; Krisa, S.; Decendit, A.; Deffieux, G.; Mérillon, J.M. Sugar sensing and Ca^{2+}-calmodulin requirement in *Vitis vinifera* cells producing anthocyanins. *Phytochemistry.* **2000**, *53*, 659–665.
22. Martinez-Noel, G.; Tognetti, J.A.; Salerno, G.; Horacio, P. Sugar signaling of fructan metabolism: New insights on protein phosphatases in sucrose-fed wheat leaves. *Plant Signal. Behav.* **2010**, *5*, 311–313.
23. Nguyen, D.M.; Zhang, Z.; Doherty, W.O. Degradation of hydroxycinnamic acid mixtures in aqueous sucrose solutions by the Fenton process. *J. Agric. Food Chem.* **2015**, *63*, 1582–1592.
24. Soyk, S.; Šimková, K.; Zürcher, E.; Luginbühl, L.; Brand, L.H.; Vaughan, C.K.;Wanke, D.; Zeeman, S.C. The enzyme-like domain of Arabidopsis nuclear *β-amylases* is critical for DNA sequence recognition and transcriptional activation. *Plant Cell.* **2014**, *26*, 1746–1763.
25. Cabib, E.; Leloir, L.F. The biosynthesis of trehalose phosphate. *J. Biol. Chem.* **1958**, *231*, 259–275.
26. Leyman, B.; Van Dijck, P.; Thevelein, J.M. An unexpected plethora of trehalose biosynthesis genes in *Arabidopsis thaliana*. *Trends Plant Sci.* **2001**, *6*, 510–513.

27. Ramon, M.; De Smet, I.V.E.; Vandesteene, L.; Naudts, M.; Leyman, B.; Van Dijck, P.; Rolland, F.; Beeckman, T.; Thevelein, J.M. Extensive expression regulation and lack of heterologous enzymatic activity of the Class II trehalose metabolism proteins from *Arabidopsis thaliana*. *Plant Cell Environ.* **2009**, *32*, 1015–1032.
28. Vandesteene, L.; López-Galvis, L.; Vanneste, K.; Feil, R.; Maere, S.; Lammens, W.; Rolland, F.; Lunn, J.E; Avonce, N.; Beeckman,T.; et al. Expansive evolution of the trehalose-6-phosphate phosphatase gene family in *Arabidopsis*. *Plant Physiol.* **2012**, *160*, 884–896.
29. Vandesteene, L.; Ramon, M.; Le Roy, K.; Van Dijck, P.; Rolland, F. A single active trehalose-6-P synthase (TPS) and a family of putative regulatory TPS-like proteins in *Arabidopsis*. *Mol. Plant.* **2010**, *3*, 406–419.
30. Paul, M.J.; Primavesi, L.F.; Jhurreea, D.; Zhang, Y. Trehalose metabolism and signaling. *Annu. Rev. Plant Biol*. **2008**, *59*, 417–441.
31. Yadav, U.P.; Ivakov, A.; Feil, R.; Duan, G.Y.; Walther, D.; Giavalisco, P.; Piques, M.;Carillo, P., Hubberten, H.M.; Stitt, M.; et al. The sucrose–trehalose 6-phosphate (Tre6P) nexus: Specificity and mechanisms of sucrose signalling by Tre6P. *J. Exp. Bot.* **2014**, *65*, 1051–1068.
32. Figueroa, C.M.; Lunn, J.E. A tale of two sugars: Trehalose 6-phosphate and sucrose. *Plant Physiol.* **2016**, *172*, 7–27.
33. Fichtner, F.; Barbier, F.F.; Feil, R.; Watanabe, M.; Annunziata, M.G.; Chabikwa, T.G.; Höfgen, R.; Stitt, M.; Beveridge, C.A.; Lunn, J.E. Trehalose 6-phosphate is involved in triggering axillary bud outgrowth in garden pea (*Pisum sativum* L.). *Plant J.* **2017**, *92*, 611–623.
34. Carillo, P.; Feil, R.; Gibon, Y.; Satoh-Nagasawa, N.; Jackson, D.; Bläsing, O.E.; Stitt, M.; Lunn, J.E. A fluorometric assay for trehalose in the picomole range. *Plant Methods.* **2013**, *9*, 21.
35. Lunn, J.E.; Delorge, I.; Figueroa, C.M.; Van Dijck, P.; Stitt, M. Trehalose metabolism in plants. *Plant J.* **2014**, *79*, 544–567.
36. Phan, N.; Urano, D.; Srba, M.; Fischer, L.; Jones, A.M. Sugar-induced endocytosis of plant 7TM-RGS proteins. *Plant Signal. Behav.* **2013**, *8*, e22814.
37. Grigston, J.C.; Osuna, D.; Scheible, W.R.; Liu, C.; Stitt, M.; Jones, A.M. D-Glucose sensing by a plasma membrane regulator of G signaling protein, AtRGS1. *FEBS Lett.* **2008**, *582*, 3577–3584.
38. Urano, D.; Phan, N.; Jones, J.C.; Yang, J.; Huang, J.; Grigston, J.; Taylor, J.P.; Jones, A.M. Endocytosis of the seven-transmembrane RGS1 protein activates G-protein-coupled signalling in *Arabidopsis*. *Nat. Cell Biol.* **2012**, *14*, 1079–1088.
39. Fu, Y.; Lim, S.; Urano, D.; Tunc-Ozdemir, M.; Phan, N.G.; Elston, T.C.; Jones, A.M. Reciprocal encoding of signal intensity and duration in a glucose-sensing circuit. *Cell.* **2014**, *156*, 1084–1095.
40. Jang, J.C.; Sheen, J. Sugar sensing in higher plants. *Plant Cell* **1994**, *6*, 1665–1679.
41. Jang, J.C.; León, P.; Zhou, L.; Sheen, J. Hexokinase as a sugar sensor in higher plants. *Plant Cell.* **1997**, *9*, 5–19.
42. Moore, B.; Zhou, L.; Rolland, F.; Hall, Q.; Cheng, W.H.; Liu, Y.X.; Hwang, I.; Jones, T.; Sheen, J. Role of the *Arabidopsis* glucose sensor HXK1 in nutrient, light, and hormonal signaling. *Science.* **2003**, *300*, 332–336.
43. Cho, Y.H.; Yoo, S.D.; Sheen, J. Regulatory functions of nuclear hexokinase1 complex in glucose signaling. *Cell.* **2006**, *127*, 579–589.
44. Granot, D.; Kelly, G.; Stein, O.; David-Schwartz, R. Substantial roles of hexokinase and fructokinase in the effects of sugars on Plant Physiol. and development. *J. Exp. Bot.* **2013**, *65*, 809–819.
45. Veramendi, J.; Fernie, A.R.; Leisse, A.; Willmitzer, L.; Trethewey, R.N. Potato hexokinase 2 complements transgenic *Arabidopsis* plants deficient in hexokinase 1 but does not play a key role in tuber carbohydrate metabolism. *Plant Mol. Biol.* **2002**, *49*, 491–501.
46. Cho, J.I.; Ryoo, N.; Hahn, T.R.; Jeon, J.S. Evidence for a role of hexokinases as conserved glucose sensors in both monocot and dicot plant species. *Plant Signal. Behav.* **2009**, *4*, 908–910.
47. Karve, A.; Moore, B.D. Function of *Arabidopsis* hexokinase-like1 as a negative regulator of plant growth. *J. Exp. Bot.* **2009**, *60*, 4137–4149.
48. Karve, A.; Xia, X.; Moore, B.D. *Arabidopsis* Hexokinase-Like1 and Hexokinase1 form a critical node in mediating plant glucose and ethylene responses. *Plant Physiol.* **2012**, *158*, 1965–1975.
49. Zhang, Y.; Liu, Z.; Wang, L.; Zheng, S.; Xie, J.; Bi, Y. Sucrose-induced hypocotyl elongation of *Arabidopsis* seedlings in darkness depends on the presence of gibberellins. *J. Plant Physiol.* **2010**, *167*, 1130–1136.
50. Fukumoto, T.; Kano, A.; Ohtani, K.; Inoue, M.; Yoshihara, A.; Izumori, K.; Tajima, S.; Shigematsu, Y.; Tanaka, K.; Ohkouchi, T.; et al. Phosphorylation of d-allose by hexokinase involved in regulation of *OsABF1* expression for growth inhibition in *Oryza sativa* L. *Planta* **2013**, *237*, 1379–1391.

51. Bruggeman, Q.; Prunier, F.; Mazubert, C.; de Bont, L.; Garmier, M.; Lugan, R.; Benhamed, M.; Bergounioux, C.; Raynaud, C.; Delarue, M. Involvement of *Arabidopsis* hexokinase1 in cell death mediated by myo-inositol accumulation. *Plant Cell* **2015**, doi:10.1105/tpc.15.00068.
52. Cho, Y.H.; Yoo, S.D. Signaling role of fructose mediated by FINS1/FBP in *Arabidopsis thaliana*. *PLoS Genet.* **2011**, *7*, e1001263.
53. Li, P.; Wind, J.J.; Shi, X.; Zhang, H.; Hanson, J.; Smeekens, S.C.; Teng, S. Fructose sensitivity is suppressed in *Arabidopsis* by the transcription factor ANAC089 lacking the membrane-bound domain. *Proc. Natl. Acad. Sci. USA* **2011**, *108*, 3436–3441.
54. Gilkerson, J.; Perez-Ruiz, J.M.; Chory, J.; Callis, J. The plastid-localized pfkB-type carbohydrate kinases FRUCTOKINASE-LIKE 1 and 2 are essential for growth and development of Arabidopsis thaliana. *BMC Plant Biol.* **2012**, *12*, 102.
55. Broeckx, T.; Hulsmans, S.; Rolland, F. The plant energy sensor: Evolutionary conservation and divergence of SnRK1 structure, regulation, and function. *J. Exp. Bot.* **2016**, *67*, 6215–6252.
56. Simon, N.M.; Sawkins, E.; Dodd, A.N. Involvement of the SnRK1 subunit KIN10 in sucrose-induced hypocotyl elongation. *Plant Signal. Behav.* **2018**, doi:10.1080/15592324.2018.1457913.
57. Polge, C.; Thomas, M. SNF1/AMPK/SnRK1 kinases, global regulators at the heart of energy control? *Trends Plant Sci.* **2007**, *12*, 20–28.
58. Alderson, A.; Sabelli, P.A.; Dickinson, J.R.; Cole, D.; Richardson, M.; Kreis, M.; Halford, N.G. Complementation of *snf1*, a mutation affecting global regulation of carbon metabolism in yeast, by a plant protein kinase cDNA. *Proc. Natl. Acad. Sci. USA* **1991**, *88*, 8602–8605.
59. Sugden, C.; Crawford, R.M.; Halford, N.G.; Hardie, D.G. Regulation of spinach SNF1-related (SnRK1) kinases by protein kinases and phosphatases is associated with phosphorylation of the T loop and is regulated by 5′-AMP. *Plant J.* **1999**, *19*, 433–439.
60. Harthill, J.E.; Meek, S.E.; Morrice, N.; Peggie, M.W.; Borch, J.; Wong, B.H.; MacKintosh, C. Phosphorylation and 14-3-3 binding of *Arabidopsis* trehalose-phosphate synthase 5 in response to 2-deoxyglucose. *Plant J.* **2006**, *47*, 211–223.
61. Baena-González, E.; Rolland, F.; Thevelein, J.M.; Sheen, J. A central integrator of transcription networks in plant stress and energy signalling. *Nature* **2007**, *448*, 938–942.
62. Coello, P.; Hey, S.J.; Halford, N.G. The sucrose non-fermenting-1-related (SnRK) family of protein kinases: Potential for manipulation to improve stress tolerance and increase yield. *J. Exp. Bot.* **2010**, *62*, 883–893.
63. Hey, S.J.; Byrne, E.; Halford, N.G. The interface between metabolic and stress signalling. *Ann. Bot.* **2009**, *105*, 197–203.
64. Rodrigues, A.; Adamo, M.; Crozet, P.; Margalha, L.; Confraria, A.; Martinho, C.; Elias, A.; Rabissi, A.; Lumbreras, V.; González-Guzmán, M.; et al. ABI1 and PP2CA phosphatases are negative regulators of Snf1-related protein kinase1 signaling in *Arabidopsis*. *Plant Cell* **2013**, doi:10.1105/tpc.113.114066.
65. Confraria, A.; Martinho, C.S.D.S.; Elias, A.; Rubio-Somoza, I.; Baena-González, E. miRNAs mediate SnRK1-dependent energy signaling in *Arabidopsis*. *Front. Plant Sci.* **2013**, *4*, 197.
66. Kravchenko, A.; Citerne, S.; Jéhanno, I.; Bersimbaev, R.I.; Veit, B.; Meyer, C.; Leprince, A.S. Mutations in the *Arabidopsis* Lst8 and Raptor genes encoding partners of the TOR complex, or inhibition of TOR activity decrease abscisic acid (ABA) synthesis. *Biochem. Biophys. Res. Commun.* **2015**, *467*, 992–997.
67. Menand, B.; Desnos, T.; Nussaume, L.; Berger, F.; Bouchez, D.; Meyer, C.; Robaglia, C. Expression and disruption of the *Arabidopsis* TOR (target of rapamycin) gene. *Proc. Natl. Acad. Sci. USA* **2002**, *99*, 6422–6427.
68. Liu, Y.; Bassham, D.C. TOR is a negative regulator of autophagy in *Arabidopsis thaliana*. *PLoS ONE* **2010**, *5*, e11883.
69. Dobrenel, T.; Marchive, C.; Sormani, R.; Moreau, M.; Mozzo, M.; Montané, M.H.; Menand, B.; Robaglia, C.; Meyer, C. Regulation of plant growth and metabolism by the TOR kinase. *Biochem. Soc. Trans.* **2011**, *39*, 477–481.
70. Xiong, Y.; Sheen, J. TOR signaling networks in plant growth and metabolism. *Plant Physiol.* **2014**, doi:10.1104/pp.113.229948.
71. Dobrenel, T.; Marchive, C.; Azzopardi, M.; Clément, G.; Moreau, M.; Sormani, R.; Robaglia, C.; Meyer, C. Sugar metabolism and the plant target of rapamycin kinase: A sweet opera TOR?. *Front. Plant Sci.* **2013**, *4*, 93.
72. Robaglia, C.; Thomas, M.; Meyer, C. Sensing nutrient and energy status by SnRK1 and TOR kinases. *Curr. Opin. Plant Biol.* **2012**, *15*, 301–307.
73. Ren, M.; Venglat, P.; Qiu, S.; Feng, L.; Cao, Y.; Wang, E.; Xiang, D.; Wang, J.; Alexander, D.; Chalivendra, S.; et al. Target of rapamycin signaling regulates metabolism, growth, and life span in *Arabidopsis*. *Plant Cell* **2012**, doi:10.1105/tpc.112.107144.

74. Xiong, Y.; McCormack, M.; Li, L.; Hall, Q.; Xiang, C.; Sheen, J. Glucose–TOR signalling reprograms the transcriptome and activates meristems. *Nature* **2013**, *496*, 181–186.
75. Henriques, R.; Magyar, Z.; Monardes, A.; Khan, S.; Zalejski, C.; Orellana, J.; Szabados, L.; Torre, C.; Koncz, C.; Bögre, L. *Arabidopsis* S6 kinase mutants display chromosome instability and altered RBR1–E2F pathway activity. *EMBO J.* **2010**, *29*, 2979–2993.
76. Gutzat, R.; Borghi, L.; Fütterer, J.; Bischof, S.; Laizet, Y.H.; Hennig, L.; Feil, R.; Lunn, J.; Gruissem, W. Retinoblastoma-Related Protein controls the transition to autotrophic plant development. *Development* **2011**, *138*, 2977–2986.
77. Baena-González, E. Energy signaling in the regulation of gene expression during stress. *Mol. Plant* **2010**, *3*, 300–313.
78. Krapp, A.; David, L.C.; Chardin, C.; Girin, T.; Marmagne, A.; Leprince, A.S.; Chaillou, S.; Ferrario-Méry, S.; Meyer, C.; Daniel-Vedele, F. Nitrate transport and signalling in *Arabidopsis*. *J. Exp. Bot.* **2014**, *65*, 789–798.
79. Baena-González, E.; Hanson, J. Shaping plant development through the SnRK1–TOR metabolic regulators. *Curr. Opin. Plant Biol.* **2017**, *35*, 152–157.
80. Zhang, Y.; Primavesi, L.F.; Jhurreea, D.; Andralojc, P.J.; Mitchell, R.A.; Powers, S.J.; Schluepmann, H.; Delatte, T.; Wingler, A.; Paul, M.J. Inhibition of SNF1-related protein kinase1 activity and regulation of metabolic pathways by trehalose-6-phosphate. *Plant Physiol.* **2009**, *149*, 1860–1871.
81. Paul, M.J.; Jhurreea, D.; Zhang, Y.; Primavesi, L.F.; Delatte, T.; Schluepmann, H.; Wingler, A. Up-regulation of biosynthetic processes associated with growth by trehalose 6-phosphate. *Plant Signal. Behav.* **2010**, *5*, 386–392.
82. Smeekens, S.; Ma, J.; Hanson, J.; Rolland, F. Sugar signals and molecular networks controlling plant growth. *Curr. Opin. Plant Biol.* **2010**, *13*, 273–278.
83. O'hara, L.E.; Paul, M.J.; Wingler, A. How do sugars regulate plant growth and development? New insight into the role of trehalose-6-phosphate. *Mol. Plant* **2013**, *6*, 261–274.
84. Lejay, L.; Wirth, J.; Pervent, M.; Cross, J.M.F.; Tillard, P.; Gojon, A. Oxidative pentose phosphate pathway-dependent sugar sensing as a mechanism for regulation of root ion transporters by photosynthesis. *Plant Physiol.* **2008**, *146*, 2036–2053.
85. Stadler, R.; Büttner, M.; Ache, P.; Hedrich, R.; Ivashikina, N.; Melzer, M.; Shearson, S.M.; Smith, S.M.; Sauer, N. Diurnal and light-regulated expression of *AtSTP1* in guard cells of *Arabidopsis*. *Plant Physiol.* **2003**, *133*, 528–537.
86. Büttner, M. The *Arabidopsis* sugar transporter (AtSTP) family: An update. *Plant Biol.* **2010**, *12*, 35–41.
87. Veyres, N.; Danon, A.; Aono, M.; Galliot, S.; Karibasappa, Y.B.; Diet, A.; Grandmottet, F.; Tamaoki, M.; Lesur, D.; Pilard, S.; et al. The *Arabidopsis* sweetie mutant is affected in carbohydrate metabolism and defective in the control of growth, development and senescence. *Plant J.* **2008**, *55*, 665–686.
88. Villadsen, D.; Smith, S. Identification of more than 200 glucose-responsive *Arabidopsis* genes none of which responds to 3-*O*-methylglucose or 6-deoxyglucose. *Plant Mol. Biol.* **2004**, *55*, 467–477.
89. Cordoba, E.; Aceves-Zamudio, D.L.; Hernández-Bernal, A.F.; Ramos-Vega, M.; León, P. Sugar regulation of *SUGAR TRANSPORTER PROTEIN 1* (*STP1*) expression in *Arabidopsis thaliana*. *J. Exp. Bot.* **2014**, *66*, 147–159.
90. Rottmann, T.; Zierer, W.; Subert, C.; Sauer, N.; Stadler, R. *STP10* encodes a high-affinity monosaccharide transporter and is induced under low-glucose conditions in pollen tubes of *Arabidopsis*. *J. Exp. Bot.* **2016**, *67*, 2387–2399.
91. Strahl, B.D.; Allis, C.D. The language of covalent histone modifications. *Nature* **2000**, *403*, 41–45.
92. Lu, C.; Thompson, C.B. Metabolic regulation of epigenetics. *Cell Metab.* **2012**, *16*, 9–17.
93. Bordoli, L.; Netsch, M.; Lüthi, U.; Lutz, W.; Eckner, R. Plant orthologs of p300/CBP: Conservation of a core domain in metazoan p300/CBP acetyltransferase-related proteins. *Nucleic Acids Res.* **2001**, *29*, 589–597.
94. Pandey, R.; MuÈller, A.; Napoli, C.A.; Selinger, D.A.; Pikaard, C.S.; Richards, E.J.; Bender, J.; Mount, D.; Jorgensen, R.A. Analysis of histone acetyltransferase and histone deacetylase families of *Arabidopsis thaliana* suggests functional diversification of chromatin modification among multicellular eukaryotes. *Nucleic Acids Res.* **2002**, *30*, 5036–5055.
95. Bharti, K.; von Koskull-Döring, P.; Bharti, S.; Kumar, P.; Tintschl-Körbitzer, A.; Treuter, E.; Nover, L. Tomato heat stress transcription factor HsfB1 represents a novel type of general transcription coactivator with a histone-like motif interacting with the plant CREB binding protein ortholog HAC1. *Plant Cell* **2004**, *16*, 1521–1535.
96. Heisel, T.J.; Li, C.Y.; Grey, K.M.; Gibson, S.I. Mutations in HISTONE ACETYLTRANSFERASE1 affect sugar response and gene expression in *Arabidopsis*. *Front. Plant Sci.* **2013**, *4*, 245.
97. Deng, W.; Liu, C.; Pei, Y.; Deng, X.; Niu, L.; Cao, X. Involvement of the histone acetyltransferase AtHAC1 in the regulation of flowering time via repression of FLOWERING LOCUS C in *Arabidopsis*. *Plant Physiol.* **2007**, *143*, 1660–1668.

98. Han, S.K.; Song, J.D.; Noh, Y.S.; Noh, B. Role of plant CBP/p300-like genes in the regulation of flowering time. *Plant J.* **2007**, *49*, 103–114.
99. Corbesier, L.; Lejeune, P.; Bernier, G. The role of carbohydrates in the induction of flowering in *Arabidopsis thaliana*: Comparison between the wild type and a starchless mutant. *Planta* **1998**, *206*, 131–137.
100. Gibson, S.I. Control of plant development and gene expression by sugar signaling. *Curr. Opin. Plant Biol.* **2005**, *8*, 93–102.
101. Xing, L.B.; Zhang, D.; Li, Y.M.; Shen, Y.W.; Zhao, C.P.; Ma, J.J.; An, N.; Han, M.Y. Transcription profiles reveal sugar and hormone signaling pathways mediating flower induction in apple (*Malus domestica* Borkh.). *Plant Cell Physiol.* **2015**, *56*, 2052–2068.
102. Wolters, H.; Jürgens, G. Survival of the flexible: Hormonal growth control and adaptation in plant development. *Nat. Rev. Genet.* **2009**, *10*, 305–317.
103. Lynch, T.J.; Erickson, B.J.; Miller, D.R.; Finkelstein, R.R. ABI5-binding proteins (AFPs) alter transcription of ABA-induced genes via a variety of interactions with chromatin modifiers. *Plant Mol. Biol.* **2017**, *93*, 403–418.
104. Fujiki, R.; Hashiba, W.; Sekine, H.; Yokoyama, A.; Chikanishi, T.; Ito, S.; Imai, Y.;Kim, J.; He, H.H.; Igarashi, K.; et al. GlcNAcylation of histone H2B facilitates its monoubiquitination. *Nature* **2011**, *480*, 557–560.
105. Wellen, K.E.; Hatzivassiliou, G.; Sachdeva, U.M.; Bui, T.V.; Cross, J.R.; Thompson, C.B. ATP-citrate lyase links cellular metabolism to histone acetylation. *Science* **2009**, *324*, 1076–1080.
106. Dehennaut, V.; Leprince, D.; Lefebvre, T. O-GlcNAcylation, an epigenetic mark. Focus on the histone code, TET family proteins, and polycomb group proteins. *Front. Endocrinol.* **2014**, *5*, 155.
107. Wu, D.; Cai, Y.; Jin, J. Potential coordination role between O-GlcNAcylation and epigenetics. *Protein Cell* **2017**, *8*, 713–723.
108. Gambetta, M.C.; Oktaba, K.; Müller, J. Essential role of the glycosyltransferase sxc/Ogt in polycomb repression. *Science* **2009**, *325*, 93–96.
109. Sinclair, D.A.; Syrzycka, M.; Macauley, M.S.; Rastgardani, T.; Komljenovic, I.; Vocadlo, D.J.; Brock, H.W.; Honda, B.M. Drosophila O-GlcNAc transferase (OGT) is encoded by the Polycomb group (PcG) gene, super sex combs (sxc). *Proc. Natl. Acad. Sci. USA* **2009**, *106*, 13427–13432.
110. Sarnowska, E.A.; Rolicka, A.T.; Bucior, E.; Cwiek, P.; Tohge, T.; Fernie, A.R.; Jikumaru, Y.; Kamiya, Y.; Franzen, R.; Schmelzer, E.; et al. DELLA-interacting SWI3C core subunit of SWI/SNF chromatin remodeling complex modulates gibberellin responses and hormonal crosstalk in *Arabidopsis*. *Plant Physiol.* **2013**, doi:10.1104/pp.113.223933.
111. Sarnowska, E.; Gratkowska, D.M.; Sacharowski, S.P.; Cwiek, P.; Tohge, T.; Fernie, A.R.; Siedlecki, J.A.; Koncz, C.; Sarnowski, T.J. The role of SWI/SNF chromatin remodeling complexes in hormone crosstalk. *Trends Plant Sci.* **2016**, *21*, 594–608.
112. Bläsing, O.E.; Gibon, Y.; Günther, M.; Höhne, M.; Morcuende, R.; Osuna, D.; Thimm, O.; Usadel, B.; Scheible, R.; Stitt, M. Sugars and circadian regulation make major contributions to the global regulation of diurnal gene expression in *Arabidopsis*. *Plant Cell* **2005**, *17*, 3257–3281.
113. Lu, C.A.; Lim, E.K.; Yu, S.M. Sugar response sequence in the promoter of a rice *α-amylase* gene serves as a transcriptional enhancer. *J. Biol. Chem.* **1998**, *273*, 10120–10131.
114. Chen, W.; Provart, N.J.; Glazebrook, J.; Katagiri, F.; Chang, H.S.; Eulgem, T.; Mauch, F.; Luan, S.; Zou, G.; Whitham, S.A.; et al. Expression profile matrix of *Arabidopsis* transcription factor genes suggests their putative functions in response to environmental stresses. *Plant Cell* **2002**, *14*, 559–574.
115. Hwang, Y.S.; Karrer, E.E.; Thomas, B.R.; Chen, L.; Rodriguez, R.L. Three cis-elements required for rice *α-amylase Amy3D* expression during sugar starvation. *Plant Mol. Biol.* **1998**, *36*, 331–341.
116. Ishiguro, S.; Nakamura, K. The nuclear factor SP8BF binds to the 5′-upstream regions of three different genes coding for major proteins of sweet potato tuberous roots. *Plant Mol. Biol.* **1992**, *18*, 97–108.
117. Grierson, C.; Du, J.S.; De Torres Zabala, M.; Beggs, K.; Smith, C.; Holdsworth, M.; Bevan, M. Separate cis sequences and trans factors direct metabolic and developmental regulation of a potato tuber storage protein gene. *Plant J.* **1994**, *5*, 815–826.
118. Maeo, K.; Tomiya, T.; Hayashi, K.; Akaike, M.; Morikami, A.; Ishiguro, S.; Nakamura, K. Sugar-responsible elements in the promoter of a gene for *β-amylase* of sweet potato. *Plant Mol. Biol.* **2001**, *46*, 627–637.
119. Zourelidou, M.; De Torres-Zabala, M.; Smith, C.; Bevan, M.W. Storekeeper defines a new class of plant-specific DNA-binding proteins and is a putative regulator of patatin expression. *Plant J.* **2002**, *30*, 489–497.
120. Ishiguro, S.; Nakamura, K. Characterization of a cDNA encoding a novel DNA-binding protein, SPF1, that recognizes SP8 sequences in the 5′ upstream regions of genes coding for sporamin and *β-amylase* from sweet potato. *Mol. Gen. Genet.* **1994**, *244*, 563–571.

121. Acevedo-Hernández, G.J.; León, P.; Herrera-Estrella, L.R. Sugar and ABA responsiveness of a minimal RBCS light-responsive unit is mediated by direct binding of ABI4. *Plant J.* **2005**, *43*, 506–519.
122. Arenas-Huertero, F.; Arroyo, A.; Zhou, L.; Sheen, J.; Leon, P. Analysis of *Arabidopsis* glucose insensitive mutants, *gin5* and *gin6*, reveals a central role of the plant hormone ABA in the regulation of plant vegetative development by sugar. *Genes Dev.* **2000**, *14*, 2085–2096.
123. Lu, C.A.; Ho, T.H.D.; Ho, S.L.; Yu, S.M. Three novel MYB proteins with one DNA binding repeat mediate sugar and hormone regulation of *α-amylase* gene expression. *Plant Cell* **2002**, *14*, 1963–1980.
124. Sun, C.; Palmqvist, S.; Olsson, H.; Borén, M.; Ahlandsberg, S.; Jansson, C. A novel WRKY transcription factor, SUSIBA2, participates in sugar signaling in barley by binding to the sugar-responsive elements of the *iso1* promoter. *Plant Cell* **2003**, *15*, 2076–2092. .
125. Kang, S.G.; Price, J.; Lin, P.C.; Hong, J.C.; Jang, J.C. The *Arabidopsis* bZIP1 transcription factor is involved in sugar signaling, protein networking, and DNA binding. *Mol. Plant* **2010**, *3*, 361–373.
126. Eulgem, T.; Rushton, P.J.; Robatzek, S.; Somssich, I.E. The WRKY superfamily of plant transcription factors. *Trends Plant Sci.* **2000**, *5*, 199–206.
127. Su, J.; Hu, C.; Yan, X.; Jin, Y.; Chen, Z.; Guan, Q.; Wang, Y.; Zhong, D.; Jansson, C,; Wang, F.; et al. Expression of barley SUSIBA2 transcription factor yields high-starch low-methane rice. *Nature* **2015**, *523*, 602–606.
128. Jin, Y.; Fei, M.; Rosenquist, S.; Jin, L.; Gohil, S.; Sandström, C.; Olsson, H.; Persson, C.; Höglund, A.; Fransson, G.; et al. A dual-promoter gene orchestrates the sucrose-coordinated synthesis of starch and fructan in barley. *Mol. Plant* **2017**, *10*, 1556–1570.
129. Izawa, T.; Foster, R.; Chua, N.H. Plant bZIP protein DNA binding specificity. *J. Mol. Biol.* **1993**, *230*, 1131–1144.
130. Jakoby, M.; Weisshaar, B.; Dröge-Laser, W.; Vicente-Carbajosa, J.; Tiedemann, J.; Kroj, T.; Parcy, F. bZIP transcription factors in *Arabidopsis*. *Trends Plant Sci.* **2002**, *7*, 106–111.
131. Kim, S.Y. The role of ABF family bZIP class transcription factors in stress response. *Physiol. Plant.* **2006**, *126*, 519–527.
132. Alves, M.S.; Dadalto, S.P.; Gonçalves, A.B.; De Souza, G.B.; Barros, V.A.; Fietto, L.G. Plant bZIP transcription factors responsive to pathogens: A review. *Int. J. Mol. Sci.* **2013**, *14*, 7815–7828.
133. Lockhart, J. Frenemies: Antagonistic bHLH/bZIP transcription factors integrate light and reactive oxygen species signaling in *Arabidopsis*. *Plant Cell* **2013**, doi:10.1105/tpc.113.250510.
134. Sun, L.; Yang, Z.T.; Song, Z.T.; Wang, M.J.; Sun, L.; Lu, S.J.; Liu, J.X. The plant-specific transcription factor gene *NAC103* is induced by bZIP60 through a new *cis*-regulatory element to modulate the unfolded protein response in *Arabidopsis*. *Plant J.* **2013**, *76*, 274–286.
135. Cookson, S.J.; Yadav, U.P.; Klie, S.; Morcuende, R.; Usadel, B.; Lunn, J.E.; Stitt, M. Temporal kinetics of the transcriptional response to carbon depletion and sucrose readdition in *Arabidopsis* seedlings. *Plant Cell Environ.* **2016**, *39*, 768–786.
136. Dash, M.; Yordanov, Y.S.; Georgieva, T.; Tschaplinski, T.J.; Yordanova, E.; Busov, V. Poplar *PtabZIP1-like* enhances lateral root formation and biomass growth under drought stress. *Plant J.* **2017**, *89*, 692–705.
137. Dietrich, K.; Weltmeier, F.; Ehlert, A.; Weiste, C.; Stahl, M.; Harter, K.; Dröge-Laser, W. Heterodimers of the *Arabidopsis* transcription factors bZIP1 and bZIP53 reprogram amino acid metabolism during low energy stress. *Plant Cell* **2011**, doi:10.1105/tpc.110.075390.
138. Para, A.; Li, Y.; Marshall-Colón, A.; Varala, K.; Francoeur, N.J.; Moran, T.M.; Edwards, M.B.; Hackley, C.; Bargmann, B.O.; Birnbaum, K.D.; et al. Hit-and-run transcriptional control by bZIP1 mediates rapid nutrient signaling in *Arabidopsis*. *Proc. Natl. Acad. Sci. USA* **2014**, doi:10.1073/pnas.1404657111.
139. Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Leyva, A.; Meissner, R.C.; Petroni, K.; Urzainqui, A.; Bevan, M.; Martin, C.; et al. Towards functional characterisation of the members of the R2R3-MYB gene family from *Arabidopsis thaliana*. *Plant J.* **1998**, *16*, 263–276.
140. Borevitz, J.O.; Xia, Y.; Blount, J.; Dixon, R.A.; Lamb, C. Activation tagging identifies a conserved MYB regulator of phenylpropanoid biosynthesis. *Plant Cell* **2000**, *12*, 2383–2393.
141. Tohge, T.; Nishiyama, Y.; Hirai, M.Y.; Yano, M.; Nakajima, J.I.; Awazuhara, M.; Inoue, E.; Takahashi, H.; Goodenowe, D.B.; Kitayama, M.; et al. Functional genomics by integrated analysis of metabolome and transcriptome of *Arabidopsis* plants over-expressing an MYB transcription factor. *Plant J.* **2005**, *42*, 218–235.
142. Chen, Y.S.; Chao, Y.C.; Tseng, T.W.; Huang, C.K.; Lo, P.C.; Lu, C.A. Two MYB-related transcription factors play opposite roles in sugar signaling in *Arabidopsis*. *Plant Mol. Biol.* **2017**, *93*, 299–311.
143. Wang, M.; Ogé, L.; Perez-Garcia, M.D.; Hamama, L.; Sakr, S. The PUF Protein Family: Overview on PUF RNA targets, biological functions, and post transcriptional regulation. *Int. J. Mol. Sci.* **2018**, *19*, 410.

144. Ho, S.L.; Chao, Y.C.; Tong, W.F.; Yu, S.M. Sugar coordinately and differentially regulates growth-and stress-related gene expression via a complex signal transduction network and multiple control mechanisms. *Plant Physiol.* **2001**, *125*, 877–890.
145. Nicolai, M.; Roncato, M.A.; Canoy, A.S.; Rouquie, D.; Sarda, X.; Freyssinet, G.; Robaglia, C. Large-scale analysis of mRNA translation states during sucrose starvation in *Arabidopsis* cells identifies cell proliferation and chromatin structure as targets of translational control. *Plant Physiol.* **2006**, *141*, 663–673.
146. Sheu, J.J.; Jan, S.P.; Lee, H.T.; Yu, S.M. Control of transcription and mRNA turnover as mechanisms of metabolic repression of *α-amylase* gene expression. *Plant J.* **1994**, *5*, 655–664.
147. Chan, M.T.; Yu, S.M. The 3′ untranslated region of a rice *α-amylase* gene functions as a sugar-dependent mRNA stability determinant. *Proc. Natl. Acad. Sci. USA* **1998**, *95*, 6543–6547.
148. Chan, M.T.; Yu, S.M. The 3′ untranslated region of a rice *α-amylase* gene mediates sugar-dependent abundance of mRNA. *Plant J.* **1998**, *15*, 685–695.
149. Yoine, M.; Ohto, M.A.; Onai, K.; Mita, S.; Nakamura, K. The lba1 mutation of UPF1 RNA helicase involved in nonsense-mediated mRNA decay causes pleiotropic phenotypic changes and altered sugar signalling in *Arabidopsis*. *Plant J.* **2006**, *47*, 49–62.
150. Mita, S.; Murano, N.; Akaike, M.; Nakamura, K. Mutants of *Arabidopsis thaliana* with pleiotropic effects on the expression of the gene for *β-amylase* and on the accumulation of anthocyanin that are inducible by sugars. *Plant J.* **1997**, *11*, 841–851.
151. Pomeranz, M.C.; Hah, C.; Lin, P.C.; Kang, S.G.; Finer, J.J.; Blackshear, P.J.; Jang, J.C. The *Arabidopsis* tandem zinc finger protein AtTZF1 traffics between the nucleus and cytoplasmic foci and binds both DNA and RNA. *Plant Physiol.* **2010**, *152*, 151–165.
152. Bogamuwa, S.P.; Jang, J.C. Tandem CCCH zinc finger proteins in plant growth, development and stress response. *Plant Cell Physiol.* **2014**, *55*, 1367–1375.
153. Barrera-Figueroa, B.E.; Gao, L.; Wu, Z.; Zhou, X.; Zhu, J.; Jin, H.; Liu, L.; Zhu, J.K. High throughput sequencing reveals novel and abiotic stress-regulated microRNAs in the inflorescences of rice. *BMC Plant Biol.* **2012**, *12*, 132.
154. Yang, L.; Xu, M.; Koo, Y.; He, J.; Poethig, R.S. Sugar promotes vegetative phase change in *Arabidopsis thaliana* by repressing the expression of *MIR156A* and *MIR156C*. *eLife* **2013**, *2*, e00260.
155. Yu, S.; Cao, L.; Zhou, C.M.; Zhang, T.Q.; Lian, H.; Sun, Y.; Wu, J.; Huang, J.; Wang, G.; Wang, J.W. Sugar is an endogenous cue for juvenile-to-adult phase transition in plants. *eLife* **2013**, *2*, e00269.
156. Yamaguchi, A.; Wu, M.F.; Yang, L.; Wu, G.; Poethig, R.S.; Wagner, D. The microRNA-regulated SBP-Box transcription factor SPL3 is a direct upstream activator of LEAFY, FRUITFULL, and APETALA1. *Dev. Cell* **2009**, *17*, 268–278.
157. Wahl, V.; Ponnu, J.; Schlereth, A.; Arrivault, S.; Langenecker, T.; Franke, A.; Feil, R.; Lunn, J.E.; Stitt, M.; Schmid, M. Regulation of flowering by trehalose-6-phosphate signaling in *Arabidopsis thaliana*. *Science* **2013**, *339*, 704–707.
158. Buendía-Monreal, M.; Gillmor, C.S. Convergent repression of miR156 by sugar and the CDK8 module of *Arabidopsis* mediator. *Dev. Biol.* **2017**, *423*, 19–23.
159. Churbanov, A.; Rogozin, I.B.; Babenko, V.N.; Ali, H.; Koonin, E.V. Evolutionary conservation suggests a regulatory function of AUG triplets in 5′-UTRs of eukaryotic genes. *Nucleic Acids Res.* **2005**, *33*, 5512–5520.
160. Von Arnim, A.G.; Jia, Q.; Vaughn, J.N. Regulation of plant translation by upstream open reading frames. *Plant Sci.* **2014**, *214*, 1–12.
161. Wethmar, K. The regulatory potential of upstream open reading frames in eukaryotic gene expression. *Wiley Interdiscip. Rev. RNA* **2014**, *5*, 765–768.
162. Hanson, J.; Hanssen, M.; Wiese, A.; Hendriks, M.M.; Smeekens, S. The sucrose regulated transcription factor bZIP11 affects amino acid metabolism by regulating the expression of *ASPARAGINE SYNTHETASE1* and *PROLINE DEHYDROGENASE2*. *Plant J.* **2008**, *53*, 935–949.
163. Ma, J.; Hanssen, M.; Lundgren, K.; Hernández, L.; Delatte, T.; Ehlert, A.; Liu, C.M.; Schluepmann, H.; Dröge-Laser, W.; Moritz, T; et al. The sucrose-regulated *Arabidopsis* transcription factor bZIP11 reprograms metabolism and regulates trehalose metabolism. *New Phytol.* **2011**, *191*, 733–745.
164. Juntawong, P.; Girke, T.; Bazin, J.; Bailey-Serres, J. Translational dynamics revealed by genome-wide profiling of ribosome footprints in *Arabidopsis*. *Proc. Natl. Acad. Sci. USA* **2014**, *111*, E203–E212.
165. Weiste, C.; Pedrotti, L.; Selvanayagam, J.; Muralidhara, P.; Fröschel, C.; Novák, O.; Ljung, K.; Hanson, J.; Dröge-Laser, W. The *Arabidopsis* bZIP11 transcription factor links low-energy signalling to auxin-mediated control of primary root growth. *PLoS Genet.* **2017**, *13*, e1006607.

166. Thum, K.E.; Shin, M.J.; Palenchar, P.M.; Kouranov, A.; Coruzzi, G.M. Genome-wide investigation of light and carbon signaling interactions in *Arabidopsis*. *Genome Biol.* **2004**, *5*, R10.
167. Rahmani, F.; Hummel, M.; Schuurmans, J.; Wiese-Klinkenberg, A.; Smeekens, S.; Hanson, J. Sucrose control of translation mediated by an upstream open reading frame-encoded peptide. *Plant Physiol.* **2009**, *150*, 1356–1367.
168. Wiese, A.; Elzinga, N.; Wobbes, B.; Smeekens, S. A conserved upstream open reading frame mediates sucrose-induced repression of translation. *Plant Cell* **2004**, *16*, 1717–1729.
169. Wiese, A.; Elzinga, N.; Wobbes, B.; Smeekens, S. Sucrose-induced translational repression of plant bZIP-type transcription factors. *Biochem. Soc. Trans.* **2005**, *33*, 272–275.
170. Hummel, M.; Rahmani, F.; Smeekens, S.; Hanson, J. Sucrose-mediated translational control. *Ann. Bot.* **2009**, *104*, 1–7.
171. Weltmeier, F.; Rahmani, F.; Ehlert, A.; Dietrich, K.; Schütze, K.; Wang, X.; Chaban, C.; Hanson, J.; Teige, M.; Harter, K.; et al. Expression patterns within the *Arabidopsis* C/S1 bZIP transcription factor network: Availability of heterodimerization partners controls gene expression during stress response and development. *Plant Mol. Biol.* **2009**, *69*, 107–119.
172. Yamashita, Y.; Takamatsu, S.; Glasbrenner, M.; Becker, T.; Naito, S.; Beckmann, R. Sucrose sensing through nascent peptide-meditated ribosome stalling at the stop codon of *Arabidopsis* bZIP11 uORF2. *FEBS Lett.* **2017**, *591*, 1266–1277.
173. Cheng, W.H.; Taliercio, E.W.; Chourey, P.S. Sugars modulate an unusual mode of control of the cell-wall invertase gene (*Incw1*) through its 3′ untranslated region in a cell suspension culture of maize. *Proc. Natl. Acad. Sci. USA* **1999**, *96*, 10512–10517.
174. Camoni, L.; Visconti, S.; Aducci, P.; Marra, M. 14-3-3 proteins in plant hormone signaling: Doing several things at once. *Front. Plant Sci.* **2018**, *9*, 297.
175. Moorhead, G.; Douglas, P.; Cotelle, V.; Harthill, J.; Morrice, N.; Meek, S.; Deiting, U.; Stitt, M.; Scarabel, M.; Aitken, A.; et al. Phosphorylation-dependent interactions between enzymes of plant metabolism and 14-3-3 proteins. *Plant J.* **1999**, *18*, 1–12.
176. Okumura, M.; Inoue, S.I.; Kuwata, K.; Kinoshita, T. Photosynthesis activates plasma membrane H^+-ATPase via sugar accumulation in *Arabidopsis* leaves. *Plant Physiol.* **2016**, doi:10.1104/pp.16.00355.
177. Fuglsang, A.T.; Visconti, S.; Drumm, K.; Jahn, T.; Stensballe, A.; Mattei, B.; Jensen, O.N.; Aducci, P.; Palmgren, M.G. Binding of 14-3-3 protein to the plasma membrane H^+-ATPase AHA2 involves the three C-terminal residues Tyr946-Thr-Val and requires phosphorylation of Thr947. *J. Biol. Chem.* **1999**, *274*, 36774–36780.
178. Lemoine, R.; La Camera, S.; Atanassova, R.; Dédaldéchamp, F.; Allario, T.; Pourtau, N.; Bonnemain, J.L.; Laloi, M.; Coutos-Thévenot, P.; Maurousset, L.; et al. Source-to-sink transport of sugar and regulation by environmental factors. *Front. Plant Sci.* **2013**, *4*, 272.
179. Wang, L.; Ruan, Y.L. Regulation of cell division and expansion by sugar and auxin signaling. *Front. Plant Sci.* **2013**, *4*, 163.
180. Saripalli, G.; Gupta, P.K. AGPase: Its role in crop productivity with emphasis on heat tolerance in cereals. *Theor. Appl. Genet.* **2015**, *128*, 1893–1916.
181. Preiss, J. Biosynthesis of starch and its regulation. *Biochem. Plants* **1988**, *14*, 181–254.
182. Hendriks, J.H.; Kolbe, A.; Gibon, Y.; Stitt, M.; Geigenberger, P. ADP-glucose pyrophosphorylase is activated by posttranslational redox-modification in response to light and to sugars in leaves of *Arabidopsis* and other plant species. *Plant Physiol.* **2003**, *133*, 838–849.
183. Tiessen, A.; Prescha, K.; Branscheid, A.; Palacios, N.; McKibbin, R.; Halford, N.G.; Geigenberger, P. Evidence that SNF1-related kinase and hexokinase are involved in separate sugar-signalling pathways modulating post-translational redox activation of ADP-glucose pyrophosphorylase in potato tubers. *Plant J.* **2003**, *35*, 490–500.
184. Gibson, S.I. Sugar and phytohormone response pathways: Navigating a signalling network. *J. Exp. Bot.* **2004**, *55*, 253–264.
185. Geigenberger, P.; Kolbe, A.; Tiessen, A. Redox regulation of carbon storage and partitioning in response to light and sugars. *J. Exp. Bot.* **2005**, *56*, 1469–1479.
186. Kolbe, A.; Tiessen, A.; Schluepmann, H.; Paul, M.; Ulrich, S.; Geigenberger, P. Trehalose 6-phosphate regulates starch synthesis via posttranslational redox activation of ADP-glucose pyrophosphorylase. *Proc. Natl. Acad. Sci. USA* **2005**, *102*, 11118–11123.
187. Lunn, J.E.; Feil, R.; Hendriks, J.H.; Gibon, Y.; Morcuende, R.; Osuna, D.; Scheible, W.; Carillo, P.; Hajirezaei, M.R.; Stitt, M. Sugar-induced increases in trehalose 6-phosphate are correlated with redox activation of ADPglucose pyrophosphorylase and higher rates of starch synthesis in *Arabidopsis thaliana*. *Biochem. J.* **2006**, *397*, 139–148.

188. Olatunji, D.; Geelen, D.; Verstraeten, I. Control of endogenous auxin levels in plant root development. *Int. J. Mol. Sci.* **2017**, *18*, 2587.
189. Majda, M.; Robert, S. The role of auxin in cell wall expansion. *Int. J. Mol. Sci.* **2018**, *19*, 951.
190. Tian, H.; Lv, B.; Ding, T.; Bai, M.; Ding, Z. Auxin-BR interaction regulates plant growth and development. *Front. Plant Sci.* **2018**, *8*, 2256.
191. LeClere, S.; Schmelz, E.A.; Chourey, P.S. Sugar levels regulate tryptophan-dependent auxin biosynthesis in developing maize kernels. *Plant Physiol.* **2010**, *153*, 306–318.
192. Sagar, M.; Chervin, C.; Mila, I.; Hao, Y.; Roustan, J.P.; Benichou, M.; Gibon, Y.; Biais, B.; Maury, P.; Latche, A.; et al. SlARF4, an auxin response factor involved in the control of sugar metabolism during tomato fruit development. *Plant Physiol.* **2013**, *161*, 1362–1374.
193. Barbier, F.; Péron, T.; Lecerf, M.; Perez-Garcia, M.D.; Barrière, Q.; Rolčík, J.; Boutet-Mercey, S.; Citerne, S.; Lemoine, R.; Porcheron, B.; et al. Sucrose is an early modulator of the key hormonal mechanisms controlling bud outgrowth in *Rosa hybrida*. *J. Exp. Bot.* **2015**, *66*, 2569–2582.
194. Long, J.C.; Zhao, W.; Rashotte, A.M.; Muday, G.K.; Huber, S.C. Gravity-stimulated changes in auxin and invertase gene expression in maize pulvinal cells. *Plant Physiol.* **2002**, *128*, 591–602.
195. Stewart, J.L.; Maloof, J.N.; Nemhauser, J.L. PIF genes mediate the effect of sucrose on seedling growth dynamics. *PLoS ONE* **2011**, *6*, e19894.
196. Sairanen, I.; Novák, O.; Pěnčík, A.; Ikeda, Y.; Jones, B.; Sandberg, G.; Ljung, K. Soluble carbohydrates regulate auxin biosynthesis via PIF proteins in *Arabidopsis*. *Plant Cell* **2012**, doi:10.1105/tpc.112.104794.
197. Lilley, J.L.; Gee, C.W.; Sairanen, I.; Ljung, K.; Nemhauser, J.L. An endogenous carbon-sensing pathway triggers increased auxin flux and hypocotyl elongation. *Plant Physiol.* **2012**, doi:10.1104/pp.112.205575.
198. Gonzali, S.; Novi, G.; Loreti, E.; Paolicchi, F.; Poggi, A.; Alpi, A.; Perata, P. A turanose-insensitive mutant suggests a role for WOX5 in auxin homeostasis in *Arabidopsis thaliana*. *Plant J.* **2005**, *44*, 633–645.
199. Ohto, M.A.; Hayashi, S.; Sawa, S.; Hashimoto-Ohta, A.; Nakamura, K. Involvement of HLS1 in sugar and auxin signaling in *Arabidopsis* leaves. *Plant Cell Physiol.* **2006**, *47*, 1603–1611.
200. Mishra, B.S.; Singh, M.; Aggrawal, P.; Laxmi, A. Glucose and auxin signaling interaction in controlling *Arabidopsis thaliana* seedlings root growth and development. *PLoS ONE* **2009**, *4*, e4502.
201. Lin, X.Y.; Ye, Y.Q.; Fan, S.K.; Jin, C.W.; Zheng, S.J. Increased sucrose accumulation regulates iron-deficiency responses by promoting auxin signaling in *Arabidopsis* plants. *Plant Physiol.* **2016**, *170*, 907–920.
202. Altman, A.; Wareing, P.F. The Effect of IAA on Sugar Accumulation and Basipetal Transport of 14C-labelled Assimilates in Relation to Root Formation in Phaseolus vulgaris Cuttings. *Physiol. Plant.* **1975**, *33*, 32–38.
203. Eveland, A.L.; Jackson, D.P. Sugars, signalling, and plant development. *J. Exp. Bot.* **2011**, *63*, 3367–3377.
204. Min, L.; Li, Y.; Hu, Q.; Zhu, L.; Gao, W.; Wu, Y.; Ding, Y.; Liu, S.; Yang, X.; Zhang, X.; et al. Sugar and auxin signaling pathways respond to high temperature stress during anther development as revealed by transcript profiling analysis in cotton. *Plant Physiol.* **2014**, doi:10.1104/pp.113.232314.
205. Li, G.; Ma, J.; Tan, M.; Mao, J.; An, N.; Sha, G.; Zhang, D.; Zhao, C.; Han, M. Transcriptome analysis reveals the effects of sugar metabolism and auxin and cytokinin signaling pathways on root growth and development of grafted apple. *BMC Genom.* **2016**, *17*, 150.
206. Moreno-Ortega, B.; Chandezon, E.; Fort, G.; Guédon, Y.; Muller, B.L. Why is lateral root growth so variable? A framework to analyze growth variability among lateral roots and the possible roles of auxin and carbon. In Proceedings of the 7th International Symposium on Root Development, Weimar, Germany, 15–19 September 2014.
207. Jain, A.; Poling, M.D.; Karthikeyan, A.S.; Blakeslee, J.J.; Peer, W.A.; Titapiwatanakun, B.; Murphy, A.S.; Raghothama, K.G. Differential effects of sucrose and auxin on localized phosphate deficiency-induced modulation of different traits of root system architecture in *Arabidopsis*. *Plant Physiol.* **2007**, *144*, 232–247.
208. MacGregor, D.R.; Deak, K.I.; Ingram, P.A.; Malamy, J.E. Root system architecture in *Arabidopsis* grown in culture is regulated by sucrose uptake in the aerial tissues. *Plant Cell* **2008**, *20*, 2643–2660.
209. Kircher, S.; Schopfer, P. Photosynthetic sucrose acts as cotyledon-derived long-distance signal to control root growth during early seedling development in *Arabidopsis*. *Proc. Natl. Acad. Sci. USA* **2012**, *109*, 11217–11221.
210. Hartmann, L.; Pedrotti, L.; Weiste, C.; Fekete, A.; Schierstaedt, J.; Göttler, J.; Kempa, S.; Krischke, M.; Dietrich, K.; Mueller, M.J.; et al. Crosstalk between two bZIP signaling pathways orchestrates salt-induced metabolic reprogramming in *Arabidopsis* roots. *Plant Cell* **2015**, doi:10.1105/tpc.15.00163.
211. Mair, A.; Pedrotti, L.; Wurzinger, B.; Anrather, D.; Simeunovic, A.; Weiste, C.; Valerio, C.; Dietrich, K.; Kirchler, T.; Nagele, T.; et al. SnRK1-triggered switch of bZIP63 dimerization mediates the low-energy response in plants. *eLife* **2015**, *4*, e05828.

212. Weiste, C.; Dröge-Laser, W. The *Arabidopsis* transcription factor bZIP11 activates auxin-mediated transcription by recruiting the histone acetylation machinery. *Nat. Commun.* **2014**, *5*, 3883.
213. Yuan, T.T.; Xu, H.H.; Zhang, K.X.; Guo, T.T.; Lu, Y.T. Glucose inhibits root meristem growth via ABA INSENSITIVE 5, which represses PIN1 accumulation and auxin activity in *Arabidopsis*. *Plant Cell Environ.* **2014**, *37*, 1338–1350.
214. Booker, K.S.; Schwarz, J.; Garrett, M.B.; Jones, A.M. Glucose attenuation of auxin-mediated bimodality in lateral root formation is partly coupled by the heterotrimeric G protein complex. *PLoS ONE* **2010**, *5*, e12833.
215. Barrada, A.; Montané, M.H.; Robaglia, C.; Menand, B. Spatial regulation of root growth: Placing the plant TOR pathway in a developmental perspective. *Int. J. Mol. Sci.* **2015**, *16*, 19671–19697.
216. Raya-González, J.; López-Bucio, J.S.; Prado-Rodríguez, J.C.; Ruiz-Herrera, L.F.; Guevara-García, Á.A.; López-Bucio, J. The MEDIATOR genes *MED12* and *MED13* control *Arabidopsis* root system configuration influencing sugar and auxin responses. *Plant Mol. Biol.* **2017**, *95*, 141–156.
217. Malik, S.; Roeder, R.G. The metazoan Mediator co-activator complex as an integrative hub for transcriptional regulation. *Nat. Rev. Genet.* **2010**, *11*, 761.
218. Franklin, K.A.; Lee, S.H.; Patel, D.; Kumar, S.V.; Spartz, A.K.; Gu, C.; Ye, S.; Yu, P.; Breen, G.; Cohen, J.D.; et al. Phytochrome-interacting factor 4 (PIF4) regulates auxin biosynthesis at high temperature. *Proc. Natl. Acad. Sci. USA* **2011**, *108*, 20231–20235.
219. Kuiper, D. Sink strength: Established and regulated by plant growth regulators. *Plant Cell Environ.* **1993**, *16*, 1025–1026.
220. Hirose, N.; Takei, K.; Kuroha, T.; Kamada-Nobusada, T.; Hayashi, H.; Sakakibara, H. Regulation of cytokinin biosynthesis, compartmentalization and translocation. *J. Exp. Bot.* **2007**, *59*, 75–83.
221. Eviatar-Ribak, T.; Shalit-Kaneh, A.; Chappell-Maor, L.; Amsellem, Z.; Eshed, Y.; Lifschitz, E. A cytokinin-activating enzyme promotes tuber formation in tomato. *Curr. Biol.* **2013**, *23*, 1057–1064.
222. Wang, G.; Zhang, G.; Wu, M. CLE peptide signaling and crosstalk with phytohormones and environmental stimuli. *Front. Plant Sci.* **2016**, *6*, 1211.
223. Kieber, J.J.; Schaller, G.E. Cytokinin signaling in plant development. *Development* **2018**, *145*, dev149344.
224. Lara, M.E.B.; Garcia, M.C.G.; Fatima, T.; Ehneß, R.; Lee, T.K.; Proels, R.; Tanner, T.; Roitsch, T. Extracellular invertase is an essential component of cytokinin-mediated delay of senescence. *Plant Cell* 2004, 16, 1276–1287.
225. Werner, T.; Holst, K.; Pörs, Y.; Guivarch, A.; Mustroph, A.; Chriqui, D.; Grimm, B.; Schmülling, T. Cytokinin deficiency causes distinct changes of sink and source parameters in tobacco shoots and roots. *J. Exp. Bot.* **2008**, *59*, 2659–2672.
226. Lefebre, R.; Vasseur, J.; Backoula, E.; Coullerot, J.P. Participation of carbohydrate metabolism in the organogenic orientation of Chicorium intybus tissues cultivated in vitro. *Can. J. Bot* **1992**, *70*, 1897–1902.
227. Reguera, M.; Peleg, Z.; Abdel-Tawab, Y.M.; Tumimbang, E.; Delatorre, C.A.; Blumwald, E. Stress-Induced CK Synthesis Increases Drought Tolerance through the Coordinated Regulation of Carbon and Nitrogen Assimilation in Rice. *Plant Physiol.* **2013**, doi:10.1104/pp.113.227702.
228. Albacete, A.; Cantero-Navarro, E.; Balibrea, M.E.; Großkinsky, D.K.; de la Cruz González, M.; Martínez-Andújar, C.; Smigocki, A.C.; Roitsch, T.; Pérez-Alfocea, F. Hormonal and metabolic regulation of tomato fruit sink activity and yield under salinity. *J. Exp. Bot.* **2014**, *65*, 6081–6095.
229. Kushwah, S.; Laxmi, A. The interaction between glucose and cytokinin signal transduction pathway in *Arabidopsis thaliana*. *Plant Cell Environ.* **2014**, *37*, 235–253.
230. Rolland, F.; Baena-Gonzalez, E.; Sheen, J. Sugar sensing and signaling in plants: Conserved and novel mechanisms. *Annu. Rev. Plant Biol*. **2006**, *57*, 675–709.
231. Franco-Zorrilla, J.M.; Martín, A.C.; Leyva, A.; Paz-Ares, J. Interaction between phosphate-starvation, sugar, and cytokinin signaling in *Arabidopsis* and the roles of cytokinin receptors CRE1/AHK4 and AHK3. *Plant Physiol.* **2005**, *138*, 847–857.
232. Laxmi, A.; Paul, L.K.; Raychaudhuri, A.; Peters, J.L.; Khurana, J.P. *Arabidopsis* cytokinin-resistant mutant, *cnr1*, displays altered auxin responses and sugar sensitivity. *Plant Mol. Biol.* **2006**, *62*, 409–425.
233. Sano, H.; Youssefian, S. Light and nutritional regulation of transcripts encoding a wheat protein kinase homolog is mediated by cytokinins. *Proc. Natl. Acad. Sci. USA* **1994**, *91*, 2582–2586.
234. Ikeda, Y.; Koizumi, N.; Kusano, T.; Sano, H. Sucrose and cytokinin modulation of WPK4, a gene encoding a SNF1-related protein kinase from wheat. *Plant Physiol.* **1999**, *121*, 813–820.
235. Kushwah, S.; Jones, A.M.; Laxmi, A. Cytokinin interplay with ethylene, auxin and glucose signaling controls *Arabidopsis* seedling root directional growth. *Plant Physiol.* **2011**, doi:10.1104/pp.111.175794.

236. Kushwah, S.; Laxmi, A. The interaction between glucose and cytokinin signaling in controlling *Arabidopsis thaliana* seedling root growth and development. *Plant Signal. Behav.* **2017**, *12*, e1312241.
237. Dewitte, W.; Riou-Khamlichi, C.; Scofield, S.; Healy, J.S.; Jacqmard, A.; Kilby, N.J.; Murray, J.A. Altered cell cycle distribution, hyperplasia, and inhibited differentiation in *Arabidopsis* caused by the D-type cyclin CYCD3. *Plant Cell* **2003**, *15*, 79–92.
238. Das, P.K.; Shin, D.H.; Choi, S.B.; Yoo, S.D.; Choi, G.; Park, Y.I. Cytokinins enhance sugar-induced anthocyanin biosynthesis in *Arabidopsis*. *Mol. Cells* **2012**, doi:10.1007/s10059-012-0114-2.
239. Shin, D.H.; Choi, M.; Kim, K.; Bang, G.; Cho, M.; Choi, S.B.; Choi, G.; Park, Y.I. HY5 regulates anthocyanin biosynthesis by inducing the transcriptional activation of the MYB75/PAP1 transcription factor in *Arabidopsis*. *FEBS Lett.* **2013**, *587*, 1543–1547.
240. Ioio, R.D.; Linhares, F.S.; Scacchi, E.; Casamitjana-Martinez, E.; Heidstra, R.; Costantino, P.; Sabatini, S. Cytokinins determine *Arabidopsis* root-meristem size by controlling cell differentiation. *Curr. Biol.* **2007**, *17*, 678–682.
241. Li, C.; Wang, H.; Ming, J.; Liu, M.; Fang, P. Hydrogen generation by photocatalytic reforming of glucose with heterostructured CdS/MoS2 composites under visible light irradiation. *Int. J. Hydrogen Energy* **2017**, *42*, 16968–16978.
242. Xie, X.; Yoneyama, K.; Yoneyama, K. The strigolactone story. *Annu. Rev. Phytopathol.* **2010**, *48*, doi:10.1146/annurev-phyto-073009-114453.
243. Czarnecki, O.; Yang, J.; Weston, D.J.; Tuskan, G.A.; Chen, J.G. A dual role of strigolactones in phosphate acquisition and utilization in plants. *Int. J. Mol. Sci.* **2013**, *14*, 7681–7701.
244. Smith, S.M.; Li, J. Signalling and responses to strigolactones and karrikins. *Curr. Opin. Plant Biol.* **2014**, *21*, 23–29.
245. Gomez-Roldan, V.; Fermas, S.; Brewer, P.B.; Puech-Pagès, V.; Dun, E.A.; Pillot, J.P.; Letisse, F.; Matusova, R.; Danoun, S.; Portais, J.; et al. Strigolactone inhibition of shoot branching. *Nature* **2008**, *455*, 189–194.
246. Umehara, M.; Hanada, A.; Yoshida, S.; Akiyama, K.; Arite, T.; Takeda-Kamiya, N.; Magome, H.; Kamiya, Y.; Shirasu, K.; Yoneyama, K.; et al. Inhibition of shoot branching by new terpenoid plant hormones. *Nature* **2008**, *455*, 195–200.
247. Koltai, H. Strigolactones are regulators of root development. *New Phytol.* **2011**, *190*, 545–549.
248. Ruyter-Spira, C.; Al-Babili, S.; Van Der Krol, S.; Bouwmeester, H. The biology of strigolactones. *Trends Plant Sci.* **2013**, *18*, 72–83.
249. Van Ha, C.; Leyva-González, M.A.; Osakabe, Y.; Tran, U.T.; Nishiyama, R.; Watanabe, Y.; Tanaka, M.; Seki, M.; Yamaguchi, S.; Dong, N.V.; et al. Positive regulatory role of strigolactone in plant responses to drought and salt stress. *Proc. Natl. Acad. Sci. USA* **2014**, *111*, 851–856.
250. Kapulnik, Y.; Koltai, H. Strigolactone involvement in root development, response to abiotic stress and interactions with the biotic soil environment. *Plant Physiol.* **2014**, doi:10.1104/pp.114.244939.
251. Saeed, W.; Naseem, S.; Ali, Z. Strigolactones biosynthesis and their role in abiotic stress resilience in plants: A critical review. *Front. Plant Sci.* **2017**, *8*, 1487.
252. Hu, Q.; Zhang, S.; Huang, B. Strigolactones and interaction with auxin regulating root elongation in tall fescue under different temperature regimes. *Plant Sci.* **2018**, *271*, 34–39.
253. Luo, L.; Wang, H.; Liu, X.; Hu, J.; Zhu, X.; Pan, S.; Qin, R.; Wang, Y.; Zhao, P.; Fan, X.; et al. Strigolactones affect the translocation of nitrogen in rice. *Plant Sci.* **2018**, *270*, 190–197.
254. Waters, M.T.; Gutjahr, C.; Bennett, T.; Nelson, D.C. Strigolactone signaling and evolution. *Annu. Rev. Plant Biol.* **2017**, *68*, 291–322.
255. Wu, Y.Y.; Hou, B.H.; Lee, W.C.; Lu, S.H.; Yang, C.J.; Vaucheret, H.; Chen, H.M. DCL2-and RDR6-dependent transitive silencing of SMXL4 and SMXL5 in *Arabidopsis dcl4* mutants causes defective phloem transport and carbohydrate over-accumulation. *Plant J.* **2017**, *90*, 1064–1078.
256. Li, G.D.; Pan, L.N.; Jiang, K.; Takahashi, I.; Nakamura, H.; Xu, Y.W.; Asami, T.; Shen, R.F. Strigolactones are involved in sugar signaling to modulate early seedling development in *Arabidopsis*. *Plant Biotechnol.* **2016**, *33*, 87–97.
257. Rameau, C.; Bertheloot, J.; Leduc, N.; Andrieu, B.; Foucher, F.; Sakr, S. Multiple pathways regulate shoot branching. *Front. Plant Sci.* **2015**, *5*, 741.
258. Otori, K.; Tamoi, M.; Tanabe, N.; Shigeoka, S. Enhancements in sucrose biosynthesis capacity affect shoot branching in *Arabidopsis*. *Biosci. Biotechnol. Biochem.* **2017**, *81*, 1470–1477.
259. Richards, D.E.; King, K.E.; Ait-ali, T.; Harberd, N.P. How gibberellin regulates plant growth and development: A molecular genetic analysis of gibberellin signaling. *Annu. Rev. Plant Biol.* **2001**, *52*, 67–88.
260. Biemelt, S.; Tschiersch, H.; Sonnewald, U. Impact of altered gibberellin metabolism on biomass accumulation, lignin biosynthesis, and photosynthesis in transgenic tobacco plants. *Plant Physiol.* **2004**, *135*, 254–265.

261. Ueguchi-Tanaka, M.; Nakajima, M.; Motoyuki, A.; Matsuoka, M. Gibberellin receptor and its role in gibberellin signaling in plants. *Annu. Rev. Plant Biol.* **2007**, *58*, 183–198.
262. Huerta, L.; Forment, J.; Gadea, J.; Fagoaga, C.; Peña, L.; Pérez-Amador, M.A.; García-Martínez, J.L. Gene expression analysis in citrus reveals the role of gibberellins on photosynthesis and stress. *Plant Cell Environ.* **2008**, *31*, 1620–1633.
263. Matsoukas, I.G. Interplay between sugar and hormone signaling pathways modulate floral signal transduction. *Front. Genet.* **2014**, *5*, 218.
264. Xu, H.; Liu, Q.; Yao, T.; Fu, X. Shedding light on integrative GA signaling. *Curr. Opin. Plant Biol.* **2014**, *21*, 89–95.
265. Ševčíková, H.; Mašková, P.; Tarkowská, D.; Mašek, T.; Lipavská, H. Carbohydrates and gibberellins relationship in potato tuberization. *J. Plant Physiol.* **2017**, *214*, 53–63.
266. Wang, B.; Wei, H.; Xue, Z. The role of gibberellin in iron homeostasis in rice. *Ann. Bot.* **2017**, *119*, 945–956.
267. Conti, L. Hormonal control of the floral transition: Can one catch them all? *Dev. Biol.* **2017**, *430*, 288–301.
268. Shu, K.; Zhou, W.; Yang, W. APETALA 2-domain-containing transcription factors: Focusing on abscisic acid and gibberellins antagonism. *New Phytol.* **2018**, *217*, 977–983.
269. Yuan, L.; Xu, D.Q. Stimulation effect of gibberellic acid short-term treatment on leaf photosynthesis related to the increase in Rubisco content in broad bean and soybean. *Photosynth. Res.* **2001**, *68*, 39–47.
270. Tuna, A.L.; Kaya, C.; Dikilitas, M.; Higgs, D. The combined effects of gibberellic acid and salinity on some antioxidant enzyme activities, plant growth parameters and nutritional status in maize plants. *Environ. Exp. Bot.* **2008**, *62*, 1–9.
271. Jiang, X.; Li, H.; Wang, T.; Peng, C.; Wang, H.; Wu, H.; Wang, X. Gibberellin indirectly promotes chloroplast biogenesis as a means to maintain the chloroplast population of expanded cells. *Plant J.* **2012**, *72*, 768–780.
272. Miyamoto, K.; Ueda, J.; Kamisaka, S. Gibberellin-enhanced sugar accumulation in growing subhooks of etiolated *Pisum sativum* seedlings. Effects of gibberellic acid, indoleacetic acid and cycloheximide on invertase activity, sugar accumulation and growth. *Physiol. Plant.* **1993**, *88*, 301–306.
273. Chen, W.S.; Liu, H.Y.; Liu, Z.H.; Yang, L.; Chen, W.H. Geibberllin and temperature influence carbohydrate content and flowering in *Phalaenopsis*. *Physiol. Plant.* **1994**, *90*, 391–395.
274. Mehouachi, J.; Tadeo, F.R.; Zaragoza, S.; Primo-Millo, E.; Talon, M. Effects of gibberellic acid and paclobutrazol on growth and carbohydrate accumulation in shoots and roots of citrus rootstock seedlings. *J. Hortic. Sci.* **1996**, *71*, 747–754.
275. Miyamoto, K.; Ito, E.; Yamamoto, H.; Ueda, J.; Kamisaka, S. Gibberellin-enhanced growth and sugar accumulation in growing subhooks of etiolated *Pisum sativum* seedlings: Effects of actinomycin D on invertase activity, soluble sugars and stem elongation. *J. Plant Physiol.* **2000**, *156*, 449–453.
276. Ranwala, A.P.; Miller, W.B. Gibberellin-mediated changes in carbohydrate metabolism during flower stalk elongation in tulips. *Plant Growth Regul.* **2008**, *55*, 241–248.
277. Choubane, D.; Rabot, A.; Mortreau, E.; Legourrierec, J.; Péron, T.; Foucher, F.; Ahcène, Y.; Pelleschi-Travierc, S.; Leduc, N.; Hamama, L.; et al. Photocontrol of bud burst involves gibberellin biosynthesis in Rosa sp. *J. Plant Physiol.* **2012**, *169*, 1271–1280.
278. Liu, S.S.; Chen, J.; Li, S.C.; Zeng, X.; Meng, Z.X.; Guo, S.X. Comparative transcriptome analysis of genes involved in GA-GID1-DELLA regulatory module in symbiotic and asymbiotic seed germination of *Anoectochilus roxburghii* (Wall.) Lindl.(Orchidaceae). *Int. J. Mol. Sci.* **2015**, *16*, 30190–30203.
279. Machado, R.A.; Baldwin, I.T.; Erb, M. Herbivory-induced jasmonates constrain plant sugar accumulation and growth by antagonizing gibberellin signaling and not by promoting secondary metabolite production. *New Phytol.* **2017**, *215*, 803–812.
280. Paparelli, E.; Parlanti, S.; Gonzali, S.; Novi, G.; Mariotti, L.; Ceccarelli, N.; Dongen, J.T.; Kölling, K.; Zeeman, S.C.; Perata, P. Nighttime sugar starvation orchestrates gibberellin biosynthesis and plant growth in *Arabidopsis*. *Plant Cell* **2013**, doi:10.1105/tpc.113.115519.
281. Gibson, S.I.; Laby, R.J.; Kim, D. The *sugar-insensitive1* (*sis1*) mutant of *Arabidopsis* is allelic to *ctr1*. *Biochem. Biophys. Res. Commun.* **2001**, *280*, 196–203.
282. Karrer, E.E.; Rodriguez, R.L. Metabolic regulation of rice *α-amylase* and sucrose synthase genes in *planta*. *Plant J.* **1992**, *2*, 517–523.
283. Perata, P.; Matsukura, C.; Vernieri, P.; Yamaguchi, J. Sugar repression of a gibberellin-dependent signaling pathway in barley embryos. *Plant Cell* **1997**, *9*, 2197–2208.
284. Morita, A.; Umemura, T.A.; Kuroyanagi, M.; Futsuhara, Y.; Perata, P.; Yamaguchi, J. Functional dissection of a sugar-repressed *α-amylase* gene (RAmy1A) promoter in rice embryos. *FEBS Lett.* **1998**, *423*, 81–85.

285. Chen, P.W.; Chiang, C.M.; Tseng, T.H.; Yu, S.M. Interaction between rice MYBGA and the gibberellin response element controls tissue-specific sugar sensitivity of *α-amylase* genes. *Plant Cell* **2006**, *18*, 2326–2340.
286. Gubler, F.; Kalla, R.; Roberts, J.K.; Jacobsen, J.V. Gibberellin-regulated expression of a myb gene in barley aleurone cells: Evidence for Myb transactivation of a high-pI *alpha-amylase* gene promoter. *Plant Cell* **1995**, *7*, 1879–1891.
287. Li, Y.; Van den Ende, W.; Rolland, F. Sucrose induction of anthocyanin biosynthesis is mediated by DELLA. *Mol. Plant* **2014**, *7*, 570–572.
288. Alabadí, D.; Gil, J.; Blázquez, M.A.; García-Martínez, J.L. Gibberellins repress photomorphogenesis in darkness. *Plant Physiol.* **2004**, *134*, 1050–1057.
289. Loreti, E.; Povero, G.; Novi, G.; Solfanelli, C.; Alpi, A.; Perata, P. Gibberellins, jasmonate and abscisic acid modulate the sucrose-induced expression of anthocyanin biosynthetic genes in *Arabidopsis*. *New Phytol.* **2008**, *179*, 1004–1016.
290. Davière, J.M.; Achard, P. A pivotal role of DELLAs in regulating multiple hormone signals. *Mol. Plant* **2016**, *9*, 10–20.
291. Gallego-Bartolomé, J.; Alabadí, D.; Blázquez, M.A. DELLA-induced early transcriptional changes during etiolated development in *Arabidopsis thaliana*. *PLoS ONE* **2011**, *6*, e23918.
292. Yin, C.C.; Zhao, H.; Ma, B.; Chen, S.Y.; Zhang, J.S. Diverse roles of ethylene in regulating agronomic traits in rice. *Front. Plant Sci.* **2017**, *8*, 1676.
293. Dubois, M.; Van den Broeck, L.; Inzé, D. The pivotal role of ethylene in plant growth. *Trends Plant Sci.* **2018**, *23*, 311–323.
294. Nascimento, F.X.; Rossi, M.J.; Glick, B.R. Ethylene and 1-Aminocyclopropane-1-carboxylate (ACC) in plant–bacterial interactions. *Front. Plant Sci.* **2018**, *9*, 114.
295. Larsen, P.B. Mechanisms of ethylene biosynthesis and response in plants. *Essays Biochem.* **2015**, *58*, 61–70.
296. Zhou, L.; Jang, J.C.; Jones, T.L.; Sheen, J. Glucose and ethylene signal transduction crosstalk revealed by an *Arabidopsis* glucose-insensitive mutant. *Proc. Natl. Acad. Sci. USA* **1998**, *95*, 10294–10299.
297. León, P.; Sheen, J. Sugar and hormone connections. *Trends Plant Sci.* **2003**, *8*, 110–116.
298. Yanagisawa, S.; Yoo, S.D.; Sheen, J. Differential regulation of EIN3 stability by glucose and ethylene signalling in plants. *Nature* **2003**, *425*, 521–525.
299. Cheng, W.H.; Endo, A.; Zhou, L.; Penney, J.; Chen, H.C.; Arroyo, A.; Leon, P.; Nambara, E.; Asami, T.; Seo, M.; et al. A unique short-chain dehydrogenase/reductase in *Arabidopsis* glucose signaling and abscisic acid biosynthesis and functions. *Plant Cell* **2002**, *14*, 2723–2743.
300. Haydon, M.J.; Mielczarek, O.; Frank, A.; Román, Á.; Webb, A.A. Sucrose and ethylene signaling interact to modulate the circadian clock. *Plant Physiol.* **2017**, pp-00592.
301. Sulmon, C.; Gouesbet, G.; El Amrani, A.; Couée, I. Involvement of the ethylene-signalling pathway in sugar-induced tolerance to the herbicide atrazine in *Arabidopsis thaliana* seedlings. *J. Plant Physiol.* **2007**, *164*, 1083–1092.
302. Rohde, A.; Kurup, S.; Holdsworth, M. ABI3 emerges from the seed. *Trends Plant Sci.* **2000**, *5*, 418–419.
303. Finkelstein, R.R.; Gampala, S.S.; Rock, C.D. Abscisic acid signaling in seeds and seedlings. *Plant Cell* **2002**, *14* (Suppl. 1), S15–S45.
304. Vishwakarma, K.; Upadhyay, N.; Kumar, N.; Yadav, G.; Singh, J.; Mishra, R.K.; Kumar, V.; Verma, R.; Upadhyay, R.G.; Pandey, M.; et al. Abscisic acid signaling and abiotic stress tolerance in plants: A review on current knowledge and future prospects. *Front. Plant Sci.* **2017**, *8*, 161.
305. Laby, R.J.; Kincaid, M.S.; Kim, D.; Gibson, S.I. The *Arabidopsis* sugar-insensitive mutants *sis4* and *sis5* are defective in abscisic acid synthesis and response. *Plant J.* **2000**, *23*, 587–596.
306. Rook, F.; Corke, F.; Card, R.; Munz, G.; Smith, C.; Bevan, M.W. Impaired sucrose-induction mutants reveal the modulation of sugar-induced starch biosynthetic gene expression by abscisic acid signalling. *Plant J.* **2001**, *26*, 421–433.
307. Brocard-Gifford, I.; Lynch, T.J.; Garcia, M.E.; Malhotra, B.; Finkelstein, R.R. The *Arabidopsis thaliana ABSCISIC ACID-INSENSITIVE 8* locus encodes a novel protein mediating abscisic acid and sugar responses essential for growth. *Plant Cell* **2004**, *16*, 406–421.
308. Akihiro, T.; Mizuno, K.; Fujimura, T. Gene expression of ADP-glucose pyrophosphorylase and starch contents in rice cultured cells are cooperatively regulated by sucrose and ABA. *Plant Cell Physiol.* **2005**, *46*, 937–946.
309. Çakir, B.; Agasse, A.; Gaillard, C.; Saumonneau, A.; Delrot, S.; Atanassova, R. A grape ASR protein involved in sugar and abscisic acid signaling. *Plant Cell* **2003**, *15*, 2165–2180.
310. Susek, R.E.; Ausubel, F.M.; Chory, J. Signal transduction mutants of *Arabidopsis* uncouple nuclear *CAB* and *RBCS* gene expression from chloroplast development. *Cell* **1993**, *74*, 787–799.

311. Huijser, C.; Kortstee, A.; Pego, J.; Weisbeek, P.; Wisman, E.; Smeekens, S. The *Arabidopsis SUCROSE UNCOUPLED-6* gene is identical to *ABSCISIC ACID INSENSITIVE-4*: Involvement of abscisic acid in sugar responses. *Plant J.* **2000**, *23*, 577–585.
312. Toyofuku, K.; Loreti, E.; Vernieri, P.; Alpi, A.; Perata, P.; Yamaguchi, J. Glucose modulates the abscisic acid-inducible Rab16A gene in cereal embryos. *Plant Mol. Biol.* **2000**, *42*, 451–460.
313. Han, C.S.; Kim, S.; Lee, S.E.; Choi, S.; Kim, S.H.; sun Yoon, I.; Hwang, Y.S. Cross-talk between ABA and sugar signaling is mediated by the ACGT core and CE1 element reciprocally in *OsTIP3;1* promoter. *J. Plant Physiol.* **2018**, *224*, 103–111.
314. Wind, J.J.; Peviani, A.; Snel, B.; Hanson, J.; Smeekens, S.C. ABI4: Versatile activator and repressor. *Trends Plant Sci.* 2013, 18, 125–132.
315. Li, P.; Zhou, H.; Shi, X.; Yu, B.; Zhou, Y.; Chen, S.; Wang, Y.; Peng, Y.; Meyer, R.C.; Smeekens, S.C.; et al. The ABI4-induced *Arabidopsis* ANAC060 transcription factor attenuates ABA signaling and renders seedlings sugar insensitive when present in the nucleus. *PLoS Genet.* **2014**, *10*, e10.
316. Jossier, M.; Bouly, J.P.; Meimoun, P.; Arjmand, A.; Lessard, P.; Hawley, S.; Hardie, D.G.; Thomas, M. SnRK1 (SNF1-related kinase 1) has a central role in sugar and ABA signalling in *Arabidopsis thaliana*. *Plant J.* **2009**, *59*, 316–328.
317. Radchuk, R.; Emery, R.N.; Weier, D.; Vigeolas, H.; Geigenberger, P.; Lunn, J.E.; Feil, R.; Weschke, W.; Weber, H. Sucrose non-fermenting kinase 1 (SnRK1) coordinates metabolic and hormonal signals during pea cotyledon growth and differentiation. *Plant J.* **2010**, *61*, 324–338.
318. Fujii, H.; Zhu, J.K. *Arabidopsis* mutant deficient in 3 abscisic acid-activated protein kinases reveals critical roles in growth, reproduction, and stress. *Proc. Natl. Acad. Sci. USA* **2009**, *106*, 8380–8385.
319. Coello, P.; Hirano, E.; Hey, S.J.; Muttucumaru, N.; Martinez-Barajas, E.; Parry, M.A.; Halford, N.G. Evidence that abscisic acid promotes degradation of SNF1-related protein kinase (SnRK) 1 in wheat and activation of a putative calcium-dependent SnRK2. *J. Exp. Bot.* **2011**, *63*, 913–924.
320. Lim, C.W.; Kim, J.H.; Baek, W.; Kim, B.S.; Lee, S.C. Functional roles of the protein phosphatase 2C, AtAIP1, in abscisic acid signaling and sugar tolerance in *Arabidopsis*. *Plant Sci.* **2012**, *187*, 83–88.
321. Carvalho, R.F.; Szakonyi, D.; Simpson, C.G.; Barbosa, I.C.; Brown, J.W.; Baena-González, E.; Duque, P. The *Arabidopsis* SR45 splicing factor, a negative regulator of sugar signaling, modulates SNF1-related protein kinase 1 (SnRK1) stability. *Plant Cell* **2016**, doi:10.1105/tpc.16.00301.
322. Bajguz, A. Metabolism of brassinosteroids in plants. *Plant Physiol. Biochem.* **2007**, *45*, 95–107.
323. Wang, Z.Y. Brassinosteroids modulate plant immunity at multiple levels. *Proc. Natl. Acad. Sci. USA* **2012**, *109*, 7–8.
324. Wang, W.; Bai, M.Y.; Wang, Z.Y. The brassinosteroid signaling network-a paradigm of signal integration. *Curr. Opin. Plant Biol.* **2014**, *21*, 147–153.
325. Nolan, T.M.; Brennan, B.; Yang, M.; Chen, J.; Zhang, M.; Li, Z.; Wang, X.; Bassham, D.C.; Walley, J.; Yin, Y. Selective autophagy of BES1 mediated by DSK2 balances plant growth and survival. *Dev. Cell* **2017**, *41*, 33–46.
326. Li, Z.; Ou, Y.; Zhang, Z.; Li, J.; He, Y. Brassinosteroid signaling recruits histone 3 lysine-27 demethylation activity to FLOWERING LOCUS C chromatin to inhibit the floral transition in *Arabidopsis*. *Mol. Plant*. **2018**, doi:10.1016/j.molp.2018.06.007.
327. Szekeres, M.; Németh, K.; Koncz-Kálmán, Z.; Mathur, J.; Kauschmann, A.; Altmann, T.; Rédei, G.P.; Nagy, F.; Schell, J.; Koncz, C. Brassinosteroids rescue the deficiency of CYP90, a cytochrome P450, controlling cell elongation and de-etiolation in *Arabidopsis*. *Cell* **1996**, *85*, 171–182.
328. Smeekens, S. Sugar regulation of gene expression in plants. *Curr. Opin. Plant Biol.* **1998**, *1*, 230–234.
329. Gupta, A.; Singh, M.; Laxmi, A. The interaction between glucose and brassinosteroid signal transduction pathway in *Arabidopsis thaliana*. *Plant Physiol.* **2015**, doi:10.1104/pp.15.00495.
330. Goetz, M.; Godt, D.E.; Roitsch, T. Tissue-specific induction of the mRNA for an extracellular invertase isoenzyme of tomato by brassinosteroids suggests a role for steroid hormones in assimilate partitioning. *Plant J.* **2000**, *22*, 515–522.
331. Schlüter, U.; Köpke, D.; Altmann, T.; Müssig, C. Analysis of carbohydrate metabolism of CPD antisense plants and the brassinosteroid-deficient *cbb1* mutant. *Plant Cell Environ.* **2002**, *25*, 783–791.
332. Lisso, J.; Altmann, T.; Müssig, C. Metabolic changes in fruits of the tomato *dx* mutant. *Phytochemistry* **2006**, *67*, 2232–2238.
333. Wu, C.Y.; Trieu, A.; Radhakrishnan, P.; Kwok, S.F.; Harris, S.; Zhang, K.; Wang, J.; Wan, J.; Zhai, H.; Takatsuto, S.; et al. Brassinosteroids regulate grain filling in rice. *Plant Cell* **2008**, *20*, 2130–2145.
334. Vicentini, R.; de Maria Felix, J.; Dornelas, M.C.; Menossi, M. Characterization of a sugarcane (*Saccharum* spp.) gene homolog to the brassinosteroid insensitive1-associated receptor kinase 1 that is associated to sugar content. *Plant Cell Rep.* **2009**, *28*, 481–491.

335. Jiang, Y.P.; Cheng, F.; Zhou, Y.H.; Xia, X.J.; Mao, W.H.; Shi, K.; Chen, Z.; Yu, J.Q. Cellular glutathione redox homeostasis plays an important role in the brassinosteroid-induced increase in CO_2 assimilation in *Cucumis sativus*. *New Phytol.* **2012**, *194*, 932–943.
336. Bitterlich, M.; Krügel, U.; Boldt-Burisch, K.; Franken, P.; Kühn, C. The sucrose transporter Sl SUT 2 from tomato interacts with brassinosteroid functioning and affects arbuscular mycorrhiza formation. *Plant J.* **2014**, *78*, 877–889.
337. Schröder, F.; Lisso, J.; Obata, T.; Erban, A.; Maximova, E.; Giavalisco, P.; Kopka, J.; Fernie, A.R.; Willmitzer, L.; Müssig, C. Consequences of induced brassinosteroid deficiency in *Arabidopsis* leaves. *BMC Plant Biol.* **2014**, *14*, 309.
338. Xu, W.; Dubos, C.; Lepiniec, L. Transcriptional control of flavonoid biosynthesis by MYB–bHLH-WDR complexes. *Trends Plant Sci.* **2015**, *20*, 176–185.
339. Nie, S.; Huang, S.; Wang, S.; Cheng, D.; Liu, J.; Lv, S.; Li, Q.; Wang, X. Enhancing brassinosteroid signaling via overexpression of tomato (*Solanum lycopersicum*) SlBRI1 improves major agronomic traits. *Front. Plant Sci.* **2017**, *8*, 1386.
340. Zhang, Y.; Liu, Z.; Wang, J.; Chen, Y.; Bi, Y.; He, J. Brassinosteroid is required for sugar promotion of hypocotyl elongation in *Arabidopsis* in darkness. *Planta* **2015**, *242*, 881–893.
341. Zhang, Y.; He, J. Sugar-induced plant growth is dependent on brassinosteroids. *Plant Signal. Behav.* **2015**, *10*, e1082700.
342. Gupta, A.; Singh, M.; Laxmi, A. Interaction between glucose and brassinosteroid during regulation of lateral root development in *Arabidopsis thaliana*. *Plant Physiol.* **2015**, doi:10.1104/pp.114.256313.
343. Zhang, G.; Song, X.; Guo, H.; Wu, Y.; Chen, X.; Fang, R. A small G protein as a novel component of the rice brassinosteroid signal transduction. *Mol. Plant* **2016**, *9*, 1260–1271.
344. Laxmi, A.; Paul, L.K.; Peters, J.L.; Khurana, J.P. *Arabidopsis* constitutive photomorphogenic mutant, *bls1*, displays altered brassinosteroid response and sugar sensitivity. *Plant Mol. Biol.* **2004**, *56*, 185–201.
345. Stitt, M.; Krapp, A. The interaction between elevated carbon dioxide and nitrogen nutrition: The physiological and molecular background. *Plant Cell Environ.* **1999**, *22*, 583–621.
346. Coruzzi, G.M.; Zhou, L. Carbon and nitrogen sensing and signaling in plants: Emerging 'matrix effects'. *Curr. Opin. Plant Biol.* **2001**, *4*, 247–253.
347. Miller, A.J.; Fan, X.; Shen, Q.; Smith, S.J. Amino acids and nitrate as signals for the regulation of nitrogen acquisition. *J. Exp. Bot.* **2007**, *59*, 111–119.
348. Nunes-Nesi, A.; Fernie, A.R.; Stitt, M. Metabolic and signaling aspects underpinning the regulation of plant carbon nitrogen interactions. *Mol. Plant* **2010**, *3*, 973–996.
349. Guo, Q.; Turnbull, M.H.; Song, J.; Roche, J.; Novak, O.; Späth, J.; Jameson, P.E.; Love, J. Depletion of carbohydrate reserves limits nitrate uptake during early regrowth in *Lolium perenne* L. *J. Exp. Bot.* **2017**, *68*, 1569–1583.
350. Muller, B.; Touraine, B. Inhibition of NO_3^- uptake by various phloem translocated amino acids in soybean seedlings. *J. Exp. Bot.* **1992**, *43*, 617–623.
351. Crawford, N.M. Nitrate: Nutrient and signal for plant growth. *Plant Cell* **1995**, *7*, 859–868.
352. Forde, B.G.; Clarkson, D.T. Nitrate and ammonium nutrition of plants: Physiological and molecular perspectives. In *Advances in Botanical Research*; Academic Press: London, UK, 1999; Volume 30, pp. 1–90.
353. Coruzzi, G.; Bush, D.R. Nitrogen and carbon nutrient and metabolite signaling in plants. *Plant Physiol.* **2001**, *125*, 61–64.
354. Stitt, M.; Müller, C.; Matt, P.; Gibon, Y.; Carillo, P.; Morcuende, R.; Scheible, W.; Krapp, A. Steps towards an integrated view of nitrogen metabolism. *J. Exp. Bot.* **2002**, *53*, 959–970.
355. Coruzzi, G.M. Primary N-assimilation into amino acids in *Arabidopsis*. *Arabidopsis Book* **2003**, *2*, e0010.
356. Geβler, A.; Kopriva, S.; Rennenberg, H. Regulation of nitrate uptake at the whole-tree level: Interaction between nitrogen compounds, cytokinins and carbon metabolism. *Tree Physiol.* **2004**, *24*, 1313–1321.
357. Foyer, C.H.; Parry, M.; Noctor, G. Markers and signals associated with nitrogen assimilation in higher plants. *J. Exp. Bot.* **2003**, *54*, 585–593.
358. Stitt, M. Nitrate regulation of metabolism and growth. *Curr. Opin. Plant Biol.* **1999**, *2*, 178–186.
359. Pace, G.M.; Volk, R.J.; Jackson, W.A. Nitrate reduction in response to CO_2-limited photosynthesis: Relationship to carbohydrate supply and nitrate reductase activity in maize seedlings. *Plant Physiol.* **1990**, *92*, 286–292.
360. Rufty, T.W.; MacKown, C.T.; Volk, R.J. Effects of altered carbohydrate availability on whole-plant assimilation of $^{15}NO_3^-$. *Plant Physiol.* **1989**, *89*, 457–463.
361. Delhon, P.; Gojon, A.; Tillard, P.; Passama, L. Diurnal regulation of NO_3^- uptake in soybean plants. IV. Dependence on current photosynthesis and sugar availability to the roots. *J. Exp. Bot.* **1996**, *47*, 893–900.

362. Constable, J.V.; Bassirirad, H.; Lussenhop, J.; Zerihun, A. Influence of elevated CO_2 and mycorrhizae on nitrogen acquisition: Contrasting responses in *Pinus taeda* and *Liquidambar styraciflua*. *Tree Physiol.* **2001**, *21*, 83–91.
363. Masclaux-Daubresse, C.; Daniel-Vedele, F.; Dechorgnat, J.; Chardon, F.; Gaufichon, L.; Suzuki, A. Nitrogen uptake, assimilation and remobilization in plants: Challenges for sustainable and productive agriculture. *Ann. Bot.* **2010**, *105*, 1141–1157.
364. Lejay, L.; Tillard, P.; Lepetit, M.; Olive, F.D.; Filleur, S.; Daniel-Vedele, F.; Gojon, A. Molecular and functional regulation of two NO_3^- uptake systems by N-and C-status of *Arabidopsis* plants. *Plant J.* **1999**, *18*, 509–519.
365. Lejay, L.; Gansel, X.; Cerezo, M.; Tillard, P.; Müller, C.; Krapp, A.; Wirén, N.; Daniel-Vedele, F.; Gojon, A. Regulation of root ion transporters by photosynthesis: Functional importance and relation with hexokinase. *Plant Cell* **2003**, *15*, 2218–2232.
366. Chow, F.; Capociama, F.V.; Faria, R.; Oliveira, M.C.D. Characterization of nitrate reductase activity in vitro in *Gracilaria caudata* J. Agardh (Rhodophyta, Gracilariales). *Braz. J. Bot.* **2007**, *30*, 123–129.
367. Balotf, S.; Kavoosi, G.; Kholdebarin, B. Nitrate reductase, nitrite reductase, glutamine synthetase, and glutamate synthase expression and activity in response to different nitrogen sources in nitrogen-starved wheat seedlings. *Biotechnol. Appl. Biochem.* **2016**, *63*, 220–229.
368. Goel, P.; Bhuria, M.; Kaushal, M.; Singh, A.K. Carbon: Nitrogen interaction regulates expression of genes involved in n-uptake and assimilation in *Brassica juncea* L. *PLoS ONE* **2016**, *11*, e0163061.
369. Gangappa, S.N.; Botto, J.F. The multifaceted roles of HY5 in plant growth and development. *Mol. Plant* **2016**, *9*, 1353–1365.
370. Toledo-Ortiz, G.; Johansson, H.; Lee, K.P.; Bou-Torrent, J.; Stewart, K.; Steel, G.; Rodríguez-Concepción, M.; Halliday, K.J. The HY5-PIF regulatory module coordinates light and temperature control of photosynthetic gene transcription. *PLoS Genet.* **2014**, *10*, e100441.
371. Chen, X.; Yao, Q.; Gao, X.; Jiang, C.; Harberd, N.P.; Fu, X. Shoot-to-root mobile transcription factor HY5 coordinates plant carbon and nitrogen acquisition. *Curr. Biol.* **2016**, *26*, 640–646.
372. Palme, K.; Teale, W.; Dovzhenko, A. Plant signaling: HY5 synchronizes resource supply. *Curr. Biol.* **2016**, *26*, R328–R329.
373. Chen, L.Q.; Qu, X.Q.; Hou, B.H.; Sosso, D.; Osorio, S.; Fernie, A.R.; Frommer, W.B. Sucrose efflux mediated by SWEET proteins as a key step for phloem transport. *Science* **2012**, *335*, 207–211.
374. Nukarinen, E.; Nägele, T.; Pedrotti, L.; Wurzinger, B.; Mair, A.; Landgraf, R.; Börnke, F.; Hanson, J.; Teige, M.; Baena-Gonzalez, E.; et al. Quantitative phosphoproteomics reveals the role of the AMPK plant ortholog SnRK1 as a metabolic master regulator under energy deprivation. *Sci. Rep.* **2016**, *6*, 31697.
375. Emanuelle, S.; Doblin, M.S.; Stapleton, D.I.; Bacic, A.; Gooley, P.R. Molecular insights into the enigmatic metabolic regulator, SnRK1. *Trends Plant Sci.* **2016**, *21*, 341–353.
376. Dröge-Laser, W.; Weiste, C. The C/S 1 bZIP network: A regulatory hub orchestrating plant energy homeostasis. *Trends Plant Sci.* **2018**, *23*, 422–433.
377. Yanagisawa, S. Dof1 and Dof2 transcription factors are associated with expression of multiple genes involved in carbon metabolism in maize. *Plant J.* **2000**, *21*, 281–288.
378. Yanagisawa, S.; Akiyama, A.; Kisaka, H.; Uchimiya, H.; Miwa, T. Metabolic engineering with Dof1 transcription factor in plants: Improved nitrogen assimilation and growth under low-nitrogen conditions. *Proc. Natl. Acad. Sci. USA* **2004**, *101*, 7833–7838.
379. Peña, P.A.; Quach, T.; Sato, S.; Ge, Z.; Nersesian, N.; Changa, T.; Dweikat, I.; Soundararajan, M.; Clemente, T.E. Expression of the maize Dof1 transcription factor in wheat and sorghum. *Front. Plant Sci.* **2017**, *8*, 434.
380. Schneidereit, A.; Imlau, A.; Sauer, N. Conserved *cis*-regulatory elements for DNA-binding-with-one-finger and homeo-domain-leucine-zipper transcription factors regulate companion cell-specific expression of the *Arabidopsis thaliana SUCROSE TRANSPORTER 2* gene. *Planta* **2008**, *228*, 651.
381. Skirycz, A.; Reichelt, M.; Burow, M.; Birkemeyer, C.; Rolcik, J.; Kopka, J.; Zanor, M.I.; Gershenzon, J.; Strnad, M.; Szopa, J.; et al. DOF transcription factor AtDof1.1 (OBP2) is part of a regulatory network controlling glucosinolate biosynthesis in *Arabidopsis*. *Plant J.* **2006**, *47*, 10–24.
382. Wu, Y.; Lee, S.K.; Yoo, Y.; Wei, J.; Kwon, S.Y.; Lee, S.W.; Jeon, J.S.; An, G. Rice transcription factor OsDOF11 modulates sugar transport by promoting expression of sucrose transporter and *SWEET* genes. *Mol. Plant* **2018**, *11*, 833–845.
383. Castaings, L.; Camargo, A.; Pocholle, D.; Gaudon, V.; Texier, Y.; Boutet-Mercey, S.; Taconnat, L.; Renou, J.P.; Daniel-Vedele, F.; Fernandez, E.; et al. The nodule inception-like protein 7 modulates nitrate sensing and metabolism in *Arabidopsis*. *Plant J.* **2009**, *57*, 426–435.

384. Konishi, M.; Yanagisawa, S. *Arabidopsis* NIN-like transcription factors have a central role in nitrate signalling. *Nat. Commun.* **2013**, *4*, 1617.
385. Marchive, C.; Roudier, F.; Castaings, L.; Bréhaut, V.; Blondet, E.; Colot, V.; Meyer, C.; Krapp, A. Nuclear retention of the transcription factor NLP7 orchestrates the early response to nitrate in plants. *Nat. Commun.* **2013**, *4*, 1713.
386. Medici, A.; Krouk, G. The primary nitrate response: A multifaceted signalling pathway. *J. Exp. Bot.* **2014**, *65*, 5567–5576.
387. De Jong, F.; Thodey, K.; Lejay, L.V.; Bevan, M.W. Glucose elevates NITRATE TRANSPORTER2. 1 protein levels and nitrate transport activity independently of its HEXOKINASE1-mediated stimulation of *NITRATE TRANSPORTER2.1* expression. *Plant Physiol.* **2014**, *164*, 308–320.
388. Ruffel, S.; Gojon, A.; Lejay, L. Signal interactions in the regulation of root nitrate uptake. *J. Exp. Bot.* **2014**, *65*, 5509–5517.
389. Johannesson, H.; Wang, Y.; Engström, P. DNA-binding and dimerization preferences of *Arabidopsis* homeodomain-leucine zipper transcription factors in vitro. *Plant Mol. Biol.* **2001**, *45*, 63–73.
390. Hanson, J.; Johannesson, H.; Engström, P. Sugar-dependent alterations in cotyledon and leaf development in transgenic plants expressing the HDZhdip gene *ATHB13*. *Plant Mol. Biol.* **2001**, *45*, 247–262.
391. Ribone, P.A.; Capella, M.; Chan, R.L. Functional characterization of the homeodomain leucine zipper I transcription factor AtHB13 reveals a crucial role in *Arabidopsis* development. *J. Exp. Bot.* **2015**, *66*, 5929–5943.
392. Matiolli, C.C.; Tomaz, J.P.; Duarte, G.T.; Prado, F.M.; Del Bem, L.E.V.; Silveira, A.B.; Gauer, L.; Corrêa, L.G.; Drumond, R.D.; Viana, A.J.C.; et al. The *Arabidopsis* bZIP gene *AtbZIP63* is a sensitive integrator of transient ABA and glucose signals. *Plant Physiol.* **2011**, doi:10.1104/pp.111.181743.
393. Kunz, S.; Gardeström, P.; Pesquet, E.; Kleczkowski, L.A. Hexokinase 1 is required for glucose-induced repression of *bZIP63*, *At5g22920*, and *BT2* in *Arabidopsis*. *Front. Plant Sci.* **2015**, *6*, 525.
394. Seok, H.Y.; Woo, D.H.; Nguyen, L.V.; Tran, H.T.; Tarte, V.N.; Mehdi, S.M.M.; Lee, S.Y.; Moon, Y.H. *Arabidopsis* AtNAP functions as a negative regulator via repression of AREB1 in salt stress response. *Planta* **2017**, *245*, 329–341.
395. Sakuraba, Y.; Kim, Y.S.; Han, S.H.; Lee, B.D.; Paek, N.C. The *Arabidopsis* transcription factor NAC016 promotes drought stress responses by repressing AREB1 transcription through a trifurcate feed-forward regulatory loop involving NAP. *Plant Cell* **2015**, doi:10.1105/tpc.15.00222.
396. Des Marais, D.L.; Skillern, W.D.; Juenger, T.E. Deeply diverged alleles in the *Arabidopsis* AREB1 transcription factor drive genome-wide differences in transcriptional response to the environment. *Mol. Biol. Evol.* **2015**, *32*, 956–969.
397. García, M.N.M.; Stritzler, M.; Capiati, D.A. Heterologous expression of *Arabidopsis* ABF4 gene in potato enhances tuberization through ABA-GA crosstalk regulation. *Planta* **2014**, *239*, 615–631.
398. Jia, W.; Zhang, L.; Wu, D.; Liu, S.; Gong, X.; Cui, Z.; Cui, N.; Cao, H.; Rao, L.; Wang, C. Sucrose transporter AtSUC9 mediated by a low sucrose level is involved in *Arabidopsis* abiotic stress resistance by regulating sucrose distribution and ABA accumulation. *Plant Cell Physiol.* **2015**, *56*, 1574–1587.
399. Shinozaki, K.; Yamaguchi-Shinozaki, K. Gene expression and signal transduction in water-stress response. *Plant Physiol.* **1997**, *115*, 327–334.
400. Barczak-Brzyżek, A.; Kiełkiewicz, M.; Górecka, M.; Kot, K.; Karpińska, B.; Filipecki, M. Abscisic Acid Insensitive 4 transcription factor is an important player in the response of *Arabidopsis thaliana* to two-spotted spider mite (*Tetranychus urticae*) feeding. *Exp. Appl. Acarol.* **2017**, *73*, 317–326.
401. Liu, S.; Hao, H.; Lu, X.; Zhao, X.; Wang, Y.; Zhang, Y.; Xie, Z.; Wang, R. Transcriptome profiling of genes involved in induced systemic salt tolerance conferred by *Bacillus amyloliquefaciens* FZB42 in *Arabidopsis thaliana*. *Sci. Rep.* **2017**, *7*, 10795.
402. Hsiao, Y.C.; Hsu, Y.F.; Chen, Y.C.; Chang, Y.L.; Wang, C.S. A WD40 protein, AtGHS40, negatively modulates abscisic acid degrading and signaling genes during seedling growth under high glucose conditions. *J. Plant Res.* **2016**, *129*, 1127–1140.
403. Huang, X.; Zhang, X.; Gong, Z.; Yang, S.; Shi, Y. ABI4 represses the expression of type-A ARRs to inhibit seed germination in *Arabidopsis*. *Plant J.* **2017**, *89*, 354–365.
404. Ramon, M.; Rolland, F.; Thevelein, J.M.; Van Dijck, P.; Leyman, B. ABI4 mediates the effects of exogenous trehalose on *Arabidopsis* growth and starch breakdown. *Plant Mol. Biol.* **2007**, *63*, 195–206.
405. Shkolnik-Inbar, D.; Adler, G.; Bar-Zvi, D. ABI4 downregulates expression of the sodium transporter HKT1; 1 in *Arabidopsis* roots and affects salt tolerance. *Plant J.* **2013**, *73*, 993–1005.
406. Ezer, D.; Shepherd, S.J.; Brestovitsky, A.; Dickinson, P.; Cortijo, S.; Charoensawan, V.; Box, M.S.; Biswas, S.; Jaeger, K.; Wigge, P.A. The G-box transcriptional regulatory code in *Arabidopsis*. *Plant Physiol.* **2017**, doi:10.1104/pp.17.01086.

407. Pedrotti, L.; Weiste, C.; Nägele, T.; Wolf, E.; Lorenzin, F.; Dietrich, K.; Mair, A.; Weckwerth, W.; Teige, M.; Baena-González, E.; et al. Snf1-RELATED KINASE1-controlled C/S1-bZIP signaling activates alternative mitochondrial metabolic pathways to ensure plant survival in extended darkness. *Plant Cell* **2018**, doi:10.1105/tpc.17.00414.
408. Thalor, S.K.; Berberich, T.; Lee, S.S.; Yang, S.H.; Zhu, X.; Imai, R.; Takahashi, Y.; Kusano, T. Deregulation of sucrose-controlled translation of a bZIP-type transcription factor results in sucrose accumulation in leaves. *PLoS ONE* **2012**, *7*, e33111.
409. Guo, H.; Ecker, J.R. Plant responses to ethylene gas are mediated by SCFEBF1/EBF2-dependent proteolysis of EIN3 transcription factor. *Cell* **2003**, *115*, 667–677.
410. Nie, H.; Zhao, C.; Wu, G.; Wu, Y.; Chen, Y.; Tang, D. SR1, a calmodulin-binding transcription factor, modulates plant defense and ethylene-induced senescence by directly regulating NDR1 and EIN3. *Plant Physiol.* **2012**, *158*, 1847–1859.
411. Solano, R.; Stepanova, A.; Chao, Q.; Ecker, J.R. Nuclear events in ethylene signaling: A transcriptional cascade mediated by *ETHYLENE-INSENSITIVE3* and *ETHYLENE-RESPONSE-FACTOR1*. *Genes Dev.* **1998**, *12*, 3703–3714.
412. Wojcikowska, B.; Gaj, M.D. High activity of auxin response factors (ARF5, ARF6, ARF10 and ARF16) in somatic embryogenesis of *Arabidopsis*. *BioTechnol. J. Biotechnol. Comput. Biol. Bionanotechnol.* **2013**, *94*, 336–352.
413. Liu, X.; Zhang, H.; Zhao, Y.; Feng, Z.; Li, Q.; Yang, H.Q.; Luan, S.; Li, J.; He, Z.H. Auxin controls seed dormancy through stimulation of abscisic acid signaling by inducing ARF-mediated ABI3 activation in *Arabidopsis*. *Proc. Natl. Acad. Sci. USA* **2013**, *110*, 15485–15490.
414. Ding, Z.; Friml, J. Auxin regulates distal stem cell differentiation in *Arabidopsis* roots. *Proc. Natl. Acad. Sci. USA* **2010**, *107*, 12046–12051.
415. Liu, P.P.; Montgomery, T.A.; Fahlgren, N.; Kasschau, K.D.; Nonogaki, H.; Carrington, J.C. Repression of *AUXIN RESPONSE FACTOR10* by microRNA160 is critical for seed germination and post-germination stages. *Plant J.* **2007**, *52*, 133–146.
416. Wang, J.W.; Wang, L.J.; Mao, Y.B.; Cai, W.J.; Xue, H.W.; Chen, X.Y. Control of root cap formation by microRNA-targeted auxin response factors in *Arabidopsis*. *Plant Cell* **2005**, *17*, 2204–2216.
417. Wójcikowska, B.; Gaj, M.D. Expression profiling of *AUXIN RESPONSE FACTOR* genes during somatic embryogenesis induction in *Arabidopsis*. *Plant Cell Rep.* **2017**, *36*, 843–858.
418. Mei, L.; Yuan, Y.; Wu, M.; Gong, Z.; Zhang, Q.; Yang, F.; Zhang, Q.; Luo, Y.; Xu, X.; Zhang, W.; et al. SlARF10, an auxin response factor, is required for chlorophyll and sugar accumulation during tomato fruit development. *bioRxiv* **2018**, doi:10.1101/253237.
419. Liang, J.; He, J. Protective role of anthocyanins in plants under low nitrogen stress. *Biochem. Biophys. Res. Commun.* **2018**, *498*, 946–953.
420. Broeckling, B.E.; Watson, R.A.; Steinwand, B.; Bush, D.R. Intronic sequence regulates sugar-dependent expression of *Arabidopsis thaliana* production of anthocyanin pigment-1/MYB75. *PLoS ONE* **2016**, *11*, e0156673.
421. Jeong, S.W.; Das, P.K.; Jeoung, S.C.; Song, J.Y.; Lee, H.K.; Kim, Y.K.; Kim, W.J.; Park, Y.I.; Yoo, S.D.; Choi, S.B.; et al. Ethylene suppression of sugar-induced anthocyanin pigmentation in *Arabidopsis*. *Plant Physiol.* **2010**, *154*, 1514–1531.
422. Kwon, Y.; Oh, J.E.; Noh, H.; Hong, S.W.; Bhoo, S.H.; Lee, H. The ethylene signaling pathway has a negative impact on sucrose-induced anthocyanin accumulation in *Arabidopsis*. *J. Plant Res.* **2011**, *124*, 193–200.
423. Bhargava, A.; Mansfield, S.D.; Hall, H.C.; Douglas, C.J.; Ellis, B.E. MYB75 functions in regulation of secondary cell wall formation in the *Arabidopsis* inflorescence stem. *Plant Physiol.* **2010**, *154*, 1428–1438.
424. Xu, Z.; Mahmood, K.; Rothstein, S.J. ROS Induces Anthocyanin Production via Late Biosynthetic Genes and Anthocyanin Deficiency Confers the Hypersensitivity to ROS-Generating Stresses in *Arabidopsis*. *Plant Cell Physiol.* **2017**, *58*, 1364–1377.
425. Lewis, D.R.; Ramirez, M.V.; Miller, N.D.; Vallabhaneni, P.; Ray, W.K.; Helm, R.F.; Winkel, B.S.; Muday, G.K. Auxin and ethylene induce flavonol accumulation through distinct transcriptional networks. *Plant Physiol.* **2011**, *156*, 144–164.
426. Piskurewicz, U.; Jikumaru, Y.; Kinoshita, N.; Nambara, E.; Kamiya, Y.; Lopez-Molina, L. The gibberellic acid signaling repressor RGL2 inhibits *Arabidopsis* seed germination by stimulating abscisic acid synthesis and ABI5 activity. *Plant Cell* **2008**, *20*, 2729–2745.
427. Finkelstein, R.R.; Lynch, T.J. The *Arabidopsis* abscisic acid response gene ABI5 encodes a basic leucine zipper transcription factor. *Plant Cell* **2000**, *12*, 599–609.

428. Yu, L.H.; Wu, J.; Zhang, Z.S.; Miao, Z.Q.; Zhao, P.X.; Wang, Z.; Xiang, C.B. *Arabidopsis* MADS-box transcription factor AGL21 acts as environmental surveillance of seed germination by regulating *ABI5* expression. *Mol. Plant* **2017**, *10*, 834–845.
429. Chang, G.; Wang, C.; Kong, X.; Chen, Q.; Yang, Y.; Hu, X. AFP2 as the novel regulator breaks high-temperature-induced seeds secondary dormancy through *ABI5* and *SOM* in *Arabidopsis thaliana*. *Biochem. Biophys. Res. Commun.* **2018**, *501*, 232–238.
430. Dekkers, B.J.; Schuurmans, J.A.; Smeekens, S.C. Interaction between sugar and abscisic acid signalling during early seedling development in *Arabidopsis*. *Plant Mol. Biol.* **2008**, *67*, 151–167.
431. Reeves, W.M.; Lynch, T.J.; Mobin, R.; Finkelstein, R.R. Direct targets of the transcription factors ABA-Insensitive (ABI) 4 and ABI5 reveal synergistic action by ABI4 and several bZIP ABA response factors. *Plant Mol. Biol.* **2011**, *75*, 347–363.
432. Suzuki, M.; Wang, H.H.Y.; McCarty, D.R. Repression of the LEAFY COTYLEDON 1/B3 regulatory network in plant embryo development by *VP1/ABSCISIC ACID INSENSITIVE 3-LIKE B3* genes. *Plant Physiol.* **2007**, *143*, 902–911.
433. Qüesta, J.I.; Song, J.; Geraldo, N.; An, H.; Dean, C. *Arabidopsis* transcriptional repressor VAL1 triggers Polycomb silencing at *FLC* during vernalization. *Science* **2016**, *353*, 485–488.
434. Chen, N.; Veerappan, V.; Abdelmageed, H.; Kang, M.; Allen, R.D. HSI2/VAL1 silences AGL15 to regulate the developmental transition from seed maturation to vegetative growth in *Arabidopsis*. *Plant Cell* **2018**, doi:10.1105/tpc.17.00655.
435. Schneider, A.; Aghamirzaie, D.; Elmarakeby, H.; Poudel, A.N.; Koo, A.J.; Heath, L.S.; Grene, R.; Collakova, E. Potential targets of VIVIPAROUS1/ABI3-LIKE1 (VAL1) repression in developing *Arabidopsis thaliana* embryos. *Plant J.* **2016**, *85*, 305–319.
436. Tsukagoshi, H.; Morikami, A.; Nakamura, K. Two B3 domain transcriptional repressors prevent sugar-inducible expression of seed maturation genes in *Arabidopsis* seedlings. *Proc. Natl. Acad. Sci. USA* **2007**, *104*, 2543–2547.
437. Jia, H.; Suzuki, M.; McCarty, D.R. Regulation of the seed to seedling developmental phase transition by the LAFL and VAL transcription factor networks. *Wiley Interdiscip. Rev. Dev. Biol.* **2014**, *3*, 135–145.
438. Sun, X.; Li, Y.; Cai, H.; Bai, X.; Ji, W.; Ding, X.; Zhu, Y. The *Arabidopsis* AtbZIP1 transcription factor is a positive regulator of plant tolerance to salt, osmotic and drought stresses. *J. Plant Res.* **2012**, *125*, 429–438.
439. Liang, M.; Li, H.; Zhou, F.; Li, H.; Liu, J.; Hao, Y.; Wang, Y.; Han, S. Subcellular distribution of NTL transcription factors in *Arabidopsis thaliana*. *Traffic* **2015**, *16*, 1062–1074.
440. Chung, M.S.; Lee, S.; Min, J.H.; Huang, P.; Ju, H.W.; Kim, C.S. Regulation of *Arabidopsis thaliana* plasma membrane glucose-responsive regulator (AtPGR) expression by *A. thaliana* storekeeper-like transcription factor, AtSTKL, modulates glucose response in Arabidopsis. *Plant Physiol. Biochem.* **2016**, *104*, 155–164.
441. Aghdasi, M.; Smeekens, S.; Schluepman, H. Microarray analysis of gene expression patterns in *Arabidopsis* seedlings under trehalose, sucrose and sorbitol treatment. *Int. J. Plant Prod.* **2008**, *2*, 309–320.
442. Peng, H.; Zhao, J.; Neff, M.M. ATAF2 integrates *Arabidopsis* brassinosteroid inactivation and seedling photomorphogenesis. *Development* **2015**, *142*, 4129–4138.
443. Huh, S.U.; Lee, S.B.; Kim, H.H.; Paek, K.H. ATAF2, a NAC transcription factor, binds to the promoter and regulates *NIT2* gene expression involved in auxin biosynthesis. *Mol. Cells* **2012**, *34*, 305–313.
444. Takasaki, H.; Maruyama, K.; Takahashi, F.; Fujita, M.; Yoshida, T.; Nakashima, K.; Myouga, K.; Toyooka, K.; Yamaguchi-Shinozaki, K.; Shinozaki, K. SNAC-As, stress-responsive NAC transcription factors, mediate ABA-inducible leaf senescence. *Plant J.* **2015**, *84*, 1114–1123.
445. Nakano, T.; Suzuki, K.; Ohtsuki, N.; Tsujimoto, Y.; Fujimura, T.; Shinshi, H. Identification of genes of the plant-specific transcription-factor families cooperatively regulated by ethylene and jasmonate in *Arabidopsis thaliana*. *J. Plant res.* **2006**, *119*, 407–413.
446. Delessert, C.; Kazan, K.; Wilson, I.W.; Straeten, D.V.D.; Manners, J.; Dennis, E.S.; Dolferus, R. The transcription factor ATAF2 represses the expression of pathogenesis-related genes in *Arabidopsis*. *Plant J.* **2005**, *43*, 745–757.
447. Bi, Y.M.; Zhang, Y.; Signorelli, T.; Zhao, R.; Zhu, T.; Rothstein, S. Genetic analysis of *Arabidopsis* GATA transcription factor gene family reveals a nitrate-inducible member important for chlorophyll synthesis and glucose sensitivity. *Plant J.* **2005**, *44*, 680–692.
448. Richter, R.; Behringer, C.; Müller, I.K.; Schwechheimer, C. The GATA-type transcription factors GNC and GNL/CGA1 repress gibberellin signaling downstream from DELLA proteins and PHYTOCHROME-INTERACTING FACTORS. *Genes Dev.* **2010**, *24*, 2093–2104.
449. Mara, C.D.; Irish, V.F. Two GATA transcription factors are downstream effectors of floral homeotic gene action in *Arabidopsis*. *Plant Physiol.* **2008**, *147*, 707–718.

450. Richter, R.; Behringer, C.; Zourelidou, M.; Schwechheimer, C. Convergence of auxin and gibberellin signaling on the regulation of the GATA transcription factors GNC and GNL in *Arabidopsis thaliana*. *Proc. Natl. Acad. Sci. USA* **2013**, *110*, 13192–13197.
451. Chiang, Y.H.; Zubo, Y.O.; Tapken, W.; Kim, H.J.; Lavanway, A.M.; Howard, L.; Pilon, M.; Kieber, J.J.; Schaller, G.E. Functional characterization of the GATA transcription factors GNC and CGA1 reveals their key role in chloroplast development, growth, and division in *Arabidopsis*. *Plant Physiol.* **2012**, *160*, 332–348.
452. Gangappa, S.N.; Chattopadhyay, S. MYC2 differentially regulates GATA-box conaining promoters during seedling development in *Arabidopsis*. *Plant Signal. Behav.* **2013**, *8*, e25679.
453. An, D.; Kim, H.; Ju, S.; Go, Y.S.; Kim, H.U.; Suh, M.C. Expression of *Camelina* WRINKLED1 isoforms rescue the seed phenotype of the *Arabidopsis wri1* mutant and increase the triacylglycerol content in tobacco leaves. *Front. Plant Sci.* **2017**, *8*, 34.
454. Lee, H.G.; Kim, H.; Suh, M.C.; Kim, H.U.; Seo, P.J. The MYB96 transcription factor regulates triacylglycerol accumulation by activating *DGAT1* and *PDAT1* expression in *Arabidopsis* seeds. *Plant Cell Physiol*. **2018**, doi:10.1093/pcp/pcy073.
455. Kang, N.K.; Kim, E.K.; Kim, Y.U.; Lee, B.; Jeong, W.J.; Jeong, B.R.; Chang, Y.K. Increased lipid production by heterologous expression of AtWRI1 transcription factor in *Nannochloropsis salina*. *Biotechnol. Biofuels* **2017**, *10*, 231.
456. Zhai, Z.; Liu, H.; Shanklin, J. Phosphorylation of WRINKLED1 by KIN10 results in its proteasomal degradation, providing a link between energy homeostasis and lipid biosynthesis. *Plant Cell* **2017**, doi:10.1105/tpc.17.00019.
457. Durrett, T.P.; Weise, S.E.; Benning, C. Increasing the energy density of vegetative tissues by diverting carbon from starch to oil biosynthesis in transgenic *Arabidopsis*. *Plant Biotechnol. J.* **2011**, *9*, 874–883.
458. Baud, S.; Wuillème, S.; To, A.; Rochat, C.; Lepiniec, L. Role of WRINKLED1 in the transcriptional regulation of glycolytic and fatty acid biosynthetic genes in *Arabidopsis*. *Plant J.* **2009**, *60*, 933–947.
459. Santos-Mendoza, M.; Dubreucq, B.; Baud, S.; Parcy, F.; Caboche, M.; Lepiniec, L. Deciphering gene regulatory networks that control seed development and maturation in *Arabidopsis*. *Plant J.* **2008**, *54*, 608–620.
460. Min, J.H.; Ju, H.W.; Yoon, D.; Lee, K.H.; Lee, S.; Kim, C.S. *Arabidopsis* basic Helix-Loop-Helix 34 (bHLH34) is involved in glucose signaling through binding to a GAGA *cis*-element. *Front. Plant Sci.* **2017**, *8*, 2100.
461. Wang, C.; Yao, X.; Yu, D.; Liang, G. Fe-deficiency-induced expression of *bHLH104* enhances Fe-deficiency tolerance of *Arabidopsis thaliana*. *Planta* **2017**, *246*, 421–431.
462. Li, X.; Zhang, H.; Ai, Q.; Liang, G.; Yu, D. Two bHLH transcription factors, bHLH34 and bHLH104, regulate iron homeostasis in *Arabidopsis thaliana*. *Plant Physiol.* **2016**, *170*, 2478–2493.
463. Tripathi, P.; Rabara, R.C.; Reese, R.N.; Miller, M.A.; Rohila, J.S.; Subramanian, S.; Shen, Q.J.; Morandi, D.; Bücking, H.; Shulaev, V.; et al. A toolbox of genes, proteins, metabolites and promoters for improving drought tolerance in soybean includes the metabolite coumestrol and stomatal development genes. *BMC Genom.* **2016**, *17*, 102.
464. Pandey, G.K.; Grant, J.J.; Cheong, Y.H.; Kim, B.G.; Li, L.; Luan, S. ABR1, an APETALA2-domain transcription factor that functions as a repressor of ABA response in *Arabidopsis*. *Plant Physiol.* **2005**, *139*, 1185–1193.
465. Serra, T.S.; Figueiredo, D.D.; Cordeiro, A.M.; Almeida, D.M.; Lourenço, T.; Abreu, I.A.; Sebastián, A.; Fernandes, L.; Contreras-Moreira, B.; Oliveira, M.M.; et al. OsRMC, a negative regulator of salt stress response in rice, is regulated by two AP2/ERF transcription factors. *Plant Mol. Biol.* **2013**, *82*, 439–455.
466. Chow, C.N.; Zheng, H.Q.; Wu, N.Y.; Chien, C.H.; Huang, H.D.; Lee, T.Y.; Chiang-Hsieh, Y.F.; Hou, P.F.; Yang, T.Y.; Chang, W.C. PlantPAN 2.0: An update of plant promoter analysis navigator for reconstructing transcriptional regulatory networks in plants. *Nucleic Acids Res.* **2015**, *44*, D1154–D1160.

V- Régulation post-transcriptionnelle : rôle des PUF

Ce dernier chapitre de l'analyse bibliographique traite du rôle des protéines PUF dans la régulation post-transcriptionnelle d'une multitude de gènes dans le règne animal tels *Caenorhabditis elegans*, *Drosophila melanogaster*, et *Saccharomyces cerevisiae*… Mais, l'intérêt de ce type de protéines chez les végétaux a fait l'objet de très peu d'études, alors que la régulation post-transcriptionnelle est un mécanisme très puissant permettant à la cellule de répondre très rapidement et efficacement aux changements physiologiques, par exemple le changement du statut carboné, engendré par la survenue des modifications environnementales ou autres. Les protéines PUF sont une des familles protéiques impliquées dans le métabolisme des ARNs, qui reconnaissent des motifs spécifiques, notamment au niveau de la séquence 3'UTR et ainsi affectent la localisation, la stabilité et la traduction de l'ARNm cible.

The PUF Protein Family: Overview on PUF RNA Targets, Biological Functions, and Post Transcriptional Regulation

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Abstract: Post-transcriptional regulation of gene expression plays a crucial role in many processes. In cells, it is mediated by diverse RNA-binding proteins. These proteins can influence mRNA stability, translation, and localization. The PUF protein family (Pumilio and FBF) is composed of RNA-binding proteins highly conserved among most eukaryotic organisms. Previous investigations indicated that they could be involved in many processes by binding corresponding motifs in the 3'UTR or by interacting with other proteins. To date, most of the investigations on PUF proteins have been focused on *Caenorhabditis elegans*, *Drosophila melanogaster*, and *Saccharomyces cerevisiae*, while only a few have been conducted on *Arabidopsis thaliana*. The present article provides an overview of the PUF protein family. It addresses their RNA-binding motifs, biological functions, and post-transcriptional control mechanisms in *Caenorhabditis elegans*, *Drosophila melanogaster*, *Saccharomyces cerevisiae*, and *Arabidopsis thaliana*. These items of knowledge open onto new investigations into the relevance of PUF proteins in specific plant developmental processes.

Keywords: PUF protein; post-transcriptional; regulation; plant; RNA-binding motifs

1. Introduction

In most eukaryotic organisms, gene expression is commonly regulated at the transcriptional and posttranscriptional levels; this is considered as a powerful strategy for these organisms to flexibly adapt their growth and development to environmental inputs. Extensive investigations have reported that RNA-binding proteins (RBPs) regulate many aspects of RNA processing, such as RNA splicing, polyadenylation, capping, modification, transport, localization, translation, and stability, called RNA metabolism [1–5]. The resolution of protein structures and the functional characterization of RBPs have shown that these proteins possess several conserved motifs and domains such as RNA-recognition motifs (RRMs), zinc fingers, K homology (KH) domains, DEAD/DEAH boxes (highly conserved motif (Asp-Glu-Ala-Asp) in RNA helicases), Pumilio/FBF (*Caenorhabditis elegans* Pumilio-*fem-3* binding factor, PUF) domains, and pentatricopeptide-repeat (PPR) domains [6].

The Pumilio RNA-binding protein family—the PUF family—is a large family of RBPs found in all eukaryotes; the number of PUF gene copies in each model organism is highly variable. The PUF family is mainly involved in post-transcriptional control by binding to specific regulatory *cis*-elements of their mRNA targets. Through this interaction they govern RNA decay and translational repression [7]. They also act by promoting ribosome stalling and facilitating the recruitment of microRNAs (miRNAs) and chromosomal instability [8–11]. Therefore, PUF protein influences the expression level of their target gene dramatically through the post-transcriptional level. For example, Puf6p can inhibit Asymmetric Synthesis of HO (*ASH1*) mRNA translation in yeast. The experiment from Gu et al. showed that the *ASH1* in *puf6* mutant had a higher expression level than in the wild type [12]. Suh et al. indicated that FBF, a PUF protein in *Caenorhabditis elegans*, can represses *gld-1* expression through interact with *gld-1* mRNA. GLD-1 level increased approximately sixfold in *fbf* mutant than in wild type [13].

The present article provides a rapid overview of PUF proteins, especially their binding motifs, biological functions, and regulation mechanisms, which seem to be conserved among eukaryotes. Given that our knowledge of the functional roles of RBPs in plants is lagging far behind our understanding of their roles in

other organisms, this article ends by briefly underlying the interest of investigating the role of the PUF family in certain key mechanisms of plant functioning.

2. RNA-Binding Target of PUF Proteins

Drosophila melanogaster Pumilio (DmPUM) and *Caenorhabditis elegans* Pumilio-*fem-3* binding factor (FBF) are the two founding members of the PUF protein family [14]. These canonical PUF proteins contain an extensively conserved RNA-binding domain (the Pumilio homology domain, PUM-HD), composed of eight consecutive α-helical PUF repeats that adopt a crescent-shaped structure [1,14–18]. The crystal structure of PUM-HD revealed that each of the eight PUF repeats specifically recognizes a single nucleotide in its target RNA, and can thereby bind to as many as eight consecutive nucleotides, and this binding model is conserved [7,19]. PUF proteins initially appeared to bind RNAs containing a 5'-UGU-3' triplet (Figure 1), and were thought to act cooperatively with other proteins [14,19–24]. For instance, DmPUM binds to the Nanos response element (NRE) that harbors motifs A (5′-GUUGU-3′) and B (5′-AUUGUA-3′) in the 3'UTR of *hunchback* (*hb*) mRNA [25–27]. Each motif contains the core UGU triplet and interacts with one Pumilio protein in a cooperative manner [28]. In *Caenorhabditis elegans*, FBF-1 and FBF-2 (*C. elegans fem-3 mRNA-binding factors 1 and 2*, two nearly identical proteins collectively called FBF) bind to the same core RNA-binding sites that possess the UGU trinucleotide and an AU pair located 3 nucleotides downstream (5′-UGUDHHAUA-3′; D, A or G or T; and H, A or C or T) [29]. The binding activity of FBF-2 and other *C. elegans* PUMs (PUF6 and PUF11) is enhanced by an additional binding pocket for cysteine located upstream [30]. In *Saccharomyces cerevisiae*, Puf3p, which localized in mitochondria, binds the RNA sequence 5′-UGUANAUA-3′, while yeast Puf4p and Puf5p recognize 5′-UGUR-3′ (R, purine)-containing sites [31,32]. The experiment also indicated that yeast Puf4p and Puf5p mainly function in nucleolus [33]. To be functional, PUF1p (Jsn1p) and the closely related protein PUF2p bind RNAs containing 5′-UAAU-3′ rather than the more common motif 5′-UGUR-3′. This difference is assigned to their "non-canonical" features consisting of fewer PUF-repeats [34]. In Murine, PUM2, which contains a C-terminal RNA-binding domain related to the *Drosophila Pumilio* homology domain (PUM-HD), can bind to the consensus sequence 5′-UGUANAUARNNNNBBBBSCCS-3′ (N, any base; R, A or G; B, C or G or T; and S, G or C) [35]. According to many authors [7,19,36], the binding model of each PUF repeat to an RNA base could be similar. However, PUF proteins can recognize RNA sequences beyond the PUM-HD scaffold and also interact with non-cognate sequences, underlying the higher complexity and adaptability of their binding activity [37–39]. To support this point, other studies showed that PUF proteins bind to CDSs or 5'UTRs. They bind to *paralytic* (*para*) in the CDS region of its mRNA, which encodes the Drosophila voltage-gated sodium channel paralytic [40]. In *Cryptococcus neoformans*, Pum1, an ortholog of both *S. cerevisiae* Puf3p and *Drosophila melanogaster* Pumilio, can only bind to the consensus binding element 5′-UGUACAUA-3′ in the 5'UTR of its own mRNA to participate to the regulation of hyphal morphogenesis [41].

In plants, few investigations have been led to discover PUF-binding sites and thereby their role in plant growth and development. The experimental results from Tam et al. indicated that AtPum2, an Arabidopsis PUF protein, binds the RNA of *Drosophila* Nanos Response Element I (NRE1) 5′-UGUAUAUA-3′ located in its 3'UTR [7]. They also showed that APUM1 to APUM22 can shuttle between nucleus and cytoplasm through the exportin1 mediated pathway. However, APUM23 and APUM24 localized in nucleus [7]. Through three-hybrid assays, Francischini and Quaggio showed that among the 25 PUF members identified in Arabidopsis, APUM1 to APUM6 can specifically bind to the Nanos response element sequence, which is also recognized by Drosophila Pumilio proteins [42]. They also identified an APUM-binding consensus sequence through three-hybrid screening assay in Arabidopsis RNA library, i.e., a 5′-UGUR-3′ tetranucleotide sequence reported to be present in all targets of the PUF family [1]. However, the "non-canonical" Arabidopsis PUM23 (APUM23) binding sequence is 10 nucleotides long, contains a 5′-UUGA-3′ core sequence, and has a preferred cytosine at nucleotide position 8 [43]. These investigations showed that the consensus PUF-binding motif may be ubiquitous among eukaryotes, but no study in plants has reported a PUF motif in other regions than the 3'UTR.

3. Putative Biological Functions of PUF proteins

Many studies demonstrated that individual PUF proteins can recognize hundreds of unique transcripts, suggesting that this family of proteins can regulate many aspects of eukaryote mechanisms, including stem cell control, developmental patterning, neuron functioning, and organelle biogenesis (Table 1). Up to now, the most

extensive investigations about PUF proteins have focused on *Caenorhabditis elegans*, *Drosophila melanogaster*, and *Saccharomyces cerevisiae*, and only few reports are available about plants.

Based on the biological functions analyzed so far, PUF proteins significantly control diverse processes in these species. In Drosophila, Pumilio was identified initially from its requirement for embryonic development through regulating *Hunchback* (an important morphogen gene), in collaboration with the zinc finger protein Nanos [70]. Other processes such as stem cell proliferation, motor neuron function, and memory formation are under the control of Pumilio [70]. In *Caenorhabditis elegans*, FBFs control gametogenesis by mediating the sperm/oocyte switch, while PUF8 displays several functions, including the sperm-oocyte switch during normal development and its antagonistic effects on germline stem cell proliferation [14]. The latter depends on the genetic context, in that PUF8 and MEX3 (a KH-type RNA-binding protein) redundantly promote germline stem cell proliferation in *Caenorhabditis elegans* [52]. PUF8 also acts as a repressor of germline stem cell proliferation in temperature-sensitive *glp-1*(*ar202*) gain-of-function mutants whose GLP-1 activity is high [71]. Two groups of PUF/RNA-binding proteins, PUF-3/11 and PUF-5/6/7, play different roles in *Caenorhabditis elegans* oogenesis. All of them are involved in oocyte formation, but PUF-3/11 limits oocyte growth while PUF-5/6/7 promotes oocyte organization and formation [72]. Salvetti et al. identified a homologous protein of *Drosophila Pumilio* in *Dugesia japonica*, named *DjPum*. It is expressed in planarian stem cells and involved in the formation of the regenerative blastema [73]. Moreover, these same authors showed that *DjPum* is essential for neoblast maintenance.

The yeast PUF protein Mpt5p regulates the stability of *HO* mRNA by stimulating removal of its poly(A) tail [74]. *HO* is involved in mating-type switching in yeast: it introduces double-stranded DNA breaks that initiate recombination [75]. The PUF3 protein plays a key role because it can bind and regulate more than 100 mRNAs that encode proteins with mitochondrial functions [76]. A bioinformatics method showed that *hmt1*, a protein arginine *N*-methyltransferase, and *dut1*, which encodes a dUTP pyro-phosphatase, were predicted as putative mRNA targets of PUF4p in yeast [33]. PUF5p is a broad RNA regulator in *S. cerevisiae* that binds to more than 1000 RNA targets; it makes up around 16% of the yeast transcriptome. These RNAs regulate many aspects of *S. cerevisiae* development such as embryonic cell cycle, cell wall integrity, or chromatin structure [77]. Nop9, an *S. cerevisiae* PUF protein, recognizes sequences and structural features of 20S pre-rRNA near the nuclease cleavage site. It also associates with the SSU processome/90S pre-ribosome through protein–protein interactions before its 20S pre-rRNA target site is transcribed [78]. Mpt5p (also called Puf5p or Uth4p) promotes temperature tolerance and increased replicative life span in *S. cerevisiae* through an unknown mechanism thought to be partly involved in the cell wall integrity (CWI) pathway. mpt5Δ mutants also have a short life span; this defect is suppressed when CWI signaling is activated [79].

Table 1. Biological functions, binding motifs, and target mRNA of some of the most described PUF proteins in different living organisms.

Organisms	PUF Family Member	Target mRNA	Binding Motif	Biological Function	References
Caenorhabditis elegans	**FBF**	***Gld-1*, *Fem3***	**5′-UGUGCCAUA-3′, 5′-UGUGUCAUU-3′**	**Maintenance of stem cell proliferation; the hermaphroditic switch between spermatogenesis and oogenesis; adaptation in the AWC chemosensory neuron.**	**[29,48,49]**
	PUF-5	***HIS3* (a reporter gene), *obr-3*, *cpi-2*, *srm-6*, *fog-1*, *srz-10*, *C17H11***	**5′-CYCUGUAYYYUGU-3′**	**Oocyte maturation; nuclear enlargement; yolk uptake; early embryogenesis**	**[49,50]**
	PUF-6	***HIS3* (a reporter gene)**	**5′-CYCUGUAYYYUGU-3′**	**Primordial germ cell development**	**[49,50]**
	PUF-7	***HIS3* (a reporter gene)**	**5′-CYCUGUAYYYUGU-3′**	**Primordial germ cell development**	**[49,50]**
	PUF-8	**Unknown**	**Unknown**	**Hermaphrodite spermoocyte switch; Germ-Line Proliferation**	**[49,51,52]**
	PUF-9	**Unknown**	**Unknown**	**Differentiation of epidermal stem cells at the larval-to-adult transition**	**[49,53]**
Cryptococcus neoformans	**PUM1**	***Znf2***	**5′-UGUACAUA-3′**	**Hyphal morphogenesis of sexual development**	**[41]**
Drosophila melanogaster	**PUMILIO**	***hbNRE*; *hunchback*; *cyclin B*; *eIF4E*; *Bicoid*; *para***	**Nanos response element**	**Anterior patterning system; mitotic arrest of primordial germ cells; maintenance of germline stem cells; primordial follicle pool; gonadogenesis; oogenesis; neuronal function; sodium current in motoneurons**	**[15,21,40,54–58]**
Saccharomyces cerevisiae	**MPT5**	***HO***	**Nanos response element**	**Mating-type switching; Lifespan**	**[23,59]**
	PUF4	***HO***	**Nanos response element**	**Lifespan**	**[1,59,60]**
	PUF3	***COX17***	**5′-UGUAUAUAU-3′**	**Mitochondrial biogenesis and motility; thermotolerance; hyperosmotic stress resistance**	**[32,59,61]**

	PUF2	**Unknown**	**5′-UAAUAAUUW-3′**	**Binds mRNAs encoding membrane-associated proteins**	**[59,62]**
	PUF1/JSN1	**Unknown**	**Unknown**	**A high copy suppressor of certain tubulin mutations**	**[59,63]**
	PUF6	***ASH1***	**5′-UUGU-3′ motif**	**Mating-type switching; protein/peptide accumulation**	**[12,59]**
Xenopus	**XPum2**	***Xenopus cyclin B1***	**5′-UGUAAAUA-3′**	**Oocyte maturation**	**[22,25,64]**
Arabidopsis thaliana	**APUM1-6**	***FASCIATA-2, CLAVATA-1* and *ZWILLE/PINHEAD***	**5′UGUANAUA**	**shoot meristem organization, stem cell maintenance and maintenance of cellular organization of apical meristems**	**[42]**
	APUM5	**CMV tripartite RNA 3′UTR regions**	**5′-UGUAAUA-3′; 5′-UGUAGUA-3′; 5′-UGUACAUAAUA-3′**	**Defensive repressor of *Cucumber mosaic virus* (CMV) infection**	**[65]**
	APUM5	***RAB18 COR15 RD22 DREB2A***	**5′-UGUA-3′**	**Abiotic stress response**	**[66]**
	APUM9 and APUM11	**Unknown**	**Unknown**	**Seed dormancy**	**[67]**
	APUM23	**Unknown**	**Unknown**	**Leaf development and organ polarity; Processing and/or degradation of 35S pre-rRNA and rRNA maturation by-products**	**[4,68]**
	APUM24	**7S pre-rRNA; *ITS2***	**Unknown**	**rRNA processing and early embryogenesis**	**[69]**

Certain reports reveal the pathways in which PUF proteins are involved in other species. *Peronophythora litchi PIM90* encodes a putative PUF protein; its expression is relatively lower during cyst germination and plant infection, but it is highly expressed during asexual and sexual development [80]. In *Plasmodium falciparum*, *PfPUF1* plays an important role in the differentiation and maintenance of gametocytes, especially female gametocytes [81]. In the *PfPUF1*-disrupted lines, gametocytes appeared normal before stage III but subsequently exhibited a sharp decline in gametocytemia. In *Cryptococcus*, *Pum1* is auto-repressive during growth, controls its own morphotype expression, and positively stabilizes the expression of *ZNF2* (a filamentation regulator) to achieve the filamentous morphotype required for sexual development [41]. In humans, the two Pumilio proteins PUM1 and PUM2 were identified as positive regulators of Retinoic acid-inducible gene I (RIG-I) signaling, which plays a pivotal role in innate immunity [82]. Overexpression of PUM1 and PUM2 increased IFN-β (an important factor in RIG-I signaling) promoter activity induced by Newcastle disease virus (NDV), while the opposite effect was reported when these Pum proteins were knocked down [82].

PUF proteins may also act as post-transcriptional repressors through a conserved mechanism in Plant. APUM5 is associated with both biotic and abiotic stress responses [66]. APUM5-overexpressing plants showed hypersensitive phenotypes under salt and drought treatment during germination at the seedling stage and vegetative stage. Further results indicated that the APUM5-Pumilio homology domain (PHD) protein bound to the 3'UTR of many salt and drought stress-responsive genes containing putative Pumilio RNA-binding motifs in their 3'UTR [66]. AtPUM23 regulates leaf morphogenesis by regulating the expression of KANADI (*KAN*) genes. KANADI genes are members of the GARP family, key regulators of abaxial identity [68]. Moreover, PUF proteins have also been predicted to participate in many mechanisms in Arabidopsis, such as responses to nutrients, light, iron deficiency, ABA (Abscisic acid) signaling, and osmotic stress [7]. For example, APUM23, a nucleolar constitutively PUF-domain protein expressed at higher levels in metabolically active tissues, was upregulated in the presence of glucose or sucrose. APUM23 loss of function plants showed slow growth, with serrated and scrunched leaves, and an abnormal venation pattern via rRNA processing [4]. A transcriptome analysis in Arabidopsis revealed that several PUF members, in particular APUM9 and APUM11, showed higher transcript levels in reduced dormancy 5 mutant during seed imbibition. This study indicated that PUF proteins might also be involved in seed dormancy in plants [63]. Some studies showed that APUM-1 to APUM-6 may be involved in Arabidopsis growth and development in the early stage through binging to the RNA of their target genes such as *CLAVATA-1*, *WUSCHEL*, *FASCIATA-2*, and *PINHEAD/ZWILLE,* which are involved in the regulation of meristem growth and stem cell maintenance [42,83]. PUF protein APUM24 was also recently described as expressed in tissues undergoing rapid proliferation and cell division [65]. Moreover, APUM24 is required for timely removal of rRNA byproducts for rapid cell division and early embryogenesis in Arabidopsis. APUM24 loss of function plants displayed defects in cell patterning.

4. PUF Proteins Control Post-Transcriptional Processes through Different Mechanisms

PUF proteins exert their post-transcriptional action through various mechanisms such as activation of mRNA translation, repression of mRNA translation, and localization of mRNA [58,84,85]. One PUF repression mechanism probably correlates with shortening of the poly(A) tail of target mRNAs though deadenylation and repression awaits further research [1] (Figure 2). In yeast, PUF6p inhibits the initiation of *ASH1* mRNA translation via interactions with Fun12p during its transport; this repression can be relieved by CK2 phosphorylation in the N-terminal region of PUF6p when the mRNA reaches the bud tip [86]. PUF6p can also form a protein–RNA complex with She2p and repress translation by interacting with translation initiation factors and preventing ribosome transit[12]. Mpt5p, a yeast PUF protein, regulates *HO* mRNA and triggers shortening its poly(A) tail. A yeast PUF protein physically binds Pop2p (a component of the Ccr4p–Pop2p–Not deadenylase complex) required for PUF repression activity. Simultaneously, the PUF protein recruits deadenylase Ccr4p and Dcp1p and Dhh1p, which are involved in mRNA regulation. The PUF-Pop2p interaction is conserved in yeast, worms, and humans [60].

In *Caenorhabditis elegans*, FBF regulates the activation of *gld-1* (*defective in germline development-1*). A possible mechanism of that regulation is linked to cytoplasmic polyadenylation, i.e., extension of the mRNA poly(A) tail by cytoplasmic poly(A) polymerase [13]. FBF interacts with gld-1 mRNA and with the cytoplasmic polyadenylase, which it recruits [87]. However, it is also involved in another mechanism. In fact, FBF can bind the 3'UTR of EGL-4, a cGMP-dependent protein kinase, and may localize translation near the sensory cilia and cell body. Furthermore, the photoconvertible stony coral protein Kaede was used as a reporter gene in that

experiment. The cell biology analysis showed that the subcellular distribution of newly synthesized Kaede dramatically changed in the *fbf-1* mutant. This result suggests that the binding of FBF may direct the subcellular localization of EGL-4 translation and enhance its translation [88]. In humans, Nop9 is a PUF-like protein. It recognizes sequences and structural features of 20S pre-rRNA near Nob1, the cleavage site of the nuclease and thus reduces Nob1 cleavage efficiency [78]. Nob1 cleavage is the final processing step in the production of mature 18S small subunit ribosomal RNA.

5. Conclusions

Post-transcriptional regulation is an essential component of gene expression regulation. Numerous studies conducted over several decades have unveiled and characterized many factors involved in post-transcriptional regulation, such as micro-RNAs, poly(A)-binding proteins (PABPs), small nuclear RNAs (snRNAs), or RNA-binding proteins (RBPs). PUF family RNA-binding proteins are determining post-transcriptional regulators present throughout eukaryotes. PUF proteins influence many aspects of different metabolic pathways, and the expression of PUF genes is regulated by many endogenous signals [25,48,89,90]. This article provides an overview of PUF proteins, i.e., their RNA targets, biological functions, and regulation mechanisms. These findings may lead us to discover more information and functions about plant PUF proteins, as current knowledge about the regulation of PUF gene expression and their role in plant biology is scarce. Most studies on plant PUF proteins have only focused on *Arabidopsis thaliana*, in which 26 PUF family members have been reported [7,42]. The relevance of PUF proteins in specific plant developmental processes such as branching, rhizogenesis, flowering, that are well known to be finely and flexibly controlled by endogenous and exogenous stimuli, still remains to be investigated. For example, the 3'UTR of some branching related genes in Arabidopsis, such as *MORE AXILLARY BRANCHES 2* (*AtMAX2*) and *SMAX1-LIKE 6* (*SMXL6*), contained the putative binding sites of PUF protein. In addition, the putative PUF binding sites also were found in the 3'UTR of *Flower Locus T* (*FT*) and *TERMINAL FLOWER 1* (*TFL1*), which are related to flowering in Arabidopsis. The 3'UTR of *RETARDED ROOT GROWTH* (RRG), a rhizogenesis related gene, harbors many putative PUF binding sites. Therefore, some plant developmental processes may be controlled by PUF protein at the post-transcriptional level. The detail mechanism of these developmental processes needs to be studied deeply in the future.

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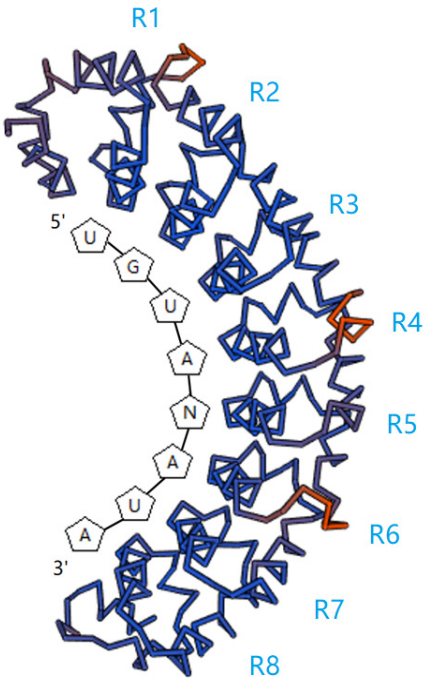


Figure 1. Predictive stick models of the APUM2 (*Arabidopsis Thaliana* Pumilio 2, AT2G29190) PUM-HD (Pumilio homology domain) bound to its target motif. The analysis result based on the research of Francischini and Quaggio [42]. They showed that the PUM-HD of APUM2 bound to the core nucleotides of 5′-UGUANAUA-3′. The each repeat of PUM-HD bound to corresponding nucleotide through Van der Waals force. The protein structure was generated by SWISS-MODEL (https://swissmodel.expasy.org/) [44,45,46,47]

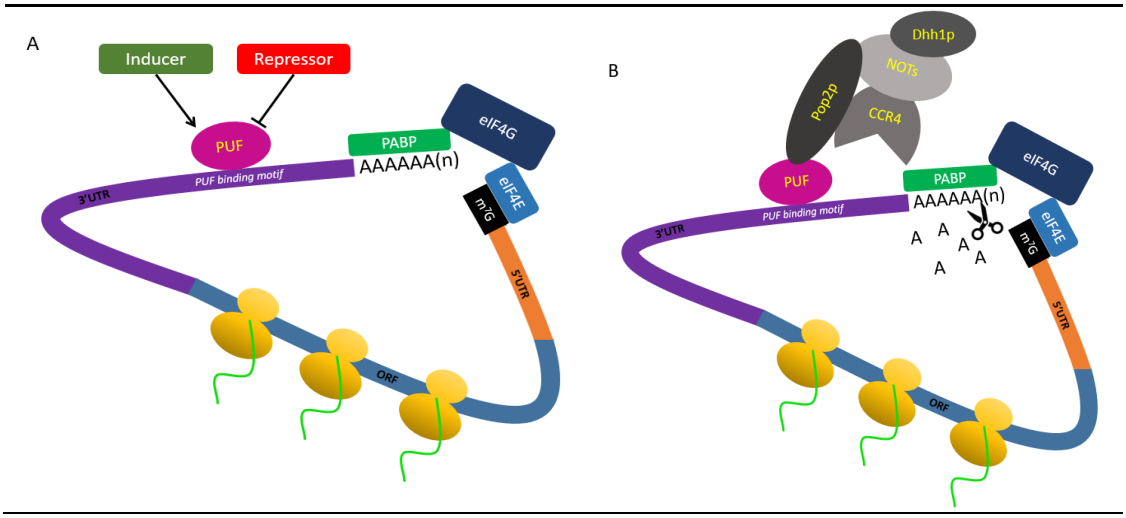


Figure 2. The common model of PUF protein influences mRNA stability. (**A**) Some genes regulate the expression or binding efficiency of PUF proteins in nucleus and/or in cytoplasm; (**B**) The PUF protein can bind to the PUF binding motif, which is located in the 3'UTR of target gene, and recruit the CCR4-POP2-NOT complex through interacting with Pop2 (the subunit of CCR4-POP2-NOT complex). The CCR4-POP2-NOT complex acts as a deadenylase in cell. It can affect the mRNA stability by reducing the length of poly(A) tail. Meanwhile, Dhh1p (DExD/H-box ATP-dependent RNA helicase), which can interact with CCR4-POP2-NOT complex, acts on the cap to activate decapping and inhibit translation [60].

References

1. Wickens, M.; Bernstein, D.S.; Kimble, J.; Parker, R. A PUF family portrait: 3′ UTR regulation as a way of life. *Trends Genet.* **2002**, *18*, 150–157.
2. Glisovic, T.; Bachorik, J.L.; Yong, J.; Dreyfuss, G. RNA-binding proteins and post-transcriptional gene regulation. *FEBS Lett.* **2008**, *582*, 1977–1986.
3. Keene, J.D. RNA regulons: Coordination of post-transcriptional events. *Nat. Rev. Genet.* **2007**, *8*, 533–543.
4. Abbasi, N.; Kim, H.B.; Park, N.I.; Kim, H.S.; Kim, Y.K.; Park, Y.I.; Choi, S.B. APUM23, a nucleolar PUF domain protein, is involved in pre-ribosomal RNA processing and normal growth patterning in Arabidopsis. *Plant J.* **2010**, *64*, 960–976.
5. Ray, D.; Kazan, H.; Cook, K.B.; Weirauch, M.T.; Najafabadi, H.S.; Li, X.; Gueroussov, S.; Albu, M.; Zheng, H.; Yang, A.; et al. A compendium of RNA-binding motifs for decoding gene regulation. *Nature* **2013**, *499*, 172–177.
6. Wu, Z.; Zhu, D.; Lin, X.; Miao, J.; Gu, L.; Deng, X.; Yang, Q.; Sun, K.; Zhu, D.; Cao, X.; et al. RNA-binding proteins At RZ-1B and At RZ-1C play a critical role in regulation of pre-mRNA splicing and gene expression during Arabidopsis development. *Plant Cell* **2016**, *28*, 55–73.
7. Tam, P.P.; Barrette-Ng, I.H.; Simon, D.M.; Tam, M.W.; Ang, A.L.; Muench, D.G. The PUF family of RNA-binding proteins in plants: Phylogeny, structural modeling, activity and subcellular localization. *BMC Plant Biol.* **2010**, *10*, 44.
8. Friend, K.; Campbell, Z.T.; Cooke, A.; Kroll-Conner, P.; Wickens, M.P.; Kimble, J. A conserved PUF–Ago–eEF1A complex attenuates translation elongation. *Nat. Struct. Mol. Biol.* **2012**, *19*, 176–183.
9. Van Etten, J.; Schagat, T.L.; Hrit, J.; Weidmann, C.A.; Brumbaugh, J.; Coon, J.J.; Goldstrohm, A.C. Human Pumilio proteins recruit multiple deadenylases to efficiently repress messenger RNAs. *J. Biol. Chem.* **2012**, *287*, 36370–36383.
10. Miles, W.O.; Tschöp, K.; Herr, A.; Ji, J.Y.; Dyson, N.J. Pumilio facilitates miRNA regulation of the E2F3 oncogene. *Genes Dev.* **2012**, *26*, 356–368.
11. Lee, S.; Kopp, F.; Chang, T.C.; Sataluri, A.; Chen, B.; Sivakumar, S.; Yu, H.; Xie, Y.; Mendell, J.T. Noncoding RNA NORAD regulates genomic stability by sequestering Pumilio proteins. *Cell* **2016**, *164*, 69–80.
12. Gu, W.; Deng, Y.; Zenklusen, D.; Singer, R.H. A new yeast PUF family protein, PUF6p, represses ASH1 mRNA translation and is required for its localization. *Genes Dev.* **2004**, *18*, 1452–1465.
13. Suh, N.; Crittenden, S.L.; Goldstrohm, A.; Hook, B.; Thompson, B.; Wickens, M.; Kimble, J. FBF and its dual control of gld-1 expression in the *Caenorhabditis elegans* germline. *Genetics* **2009**, *181*, 1249–1260.
14. Zhang, B.; Gallegos, M.; Puoti, A.; Durkin, E.; Fields, S.; Kimble, J.; Wickens, M.P. A conserved RNA-binding protein that regulates sexual fates in the *Caenorhabditis elegans* hermaphrodite germ line. *Nature* **1997**, *390*, 477–484.
15. Barker, D.D.; Wang, C.; Moore, J.; Dickinson, L.K.; Lehmann, R. Pumilio is essential for function but not for distribution of the Drosophila abdominal determinant Nanos. *Genes Dev.* **1992**, *6*, 2312–2326.
16. Zamore, P.D.; Williamson, J.R.; Lehmann, R. The Pumilio protein binds RNA through a conserved domain that defines a new class of RNA-binding proteins. *RNA* **1997**, *3*, 1421–1433.
17. Wang, X.; Zamore, P.D.; Hall, T.M.T. Crystal structure of a Pumilio homology domain. *Mol. Cell* **2001**, *7*, 855–865.
18. Hall, T.M.T. De-coding and re-coding RNA recognition by PUF and PPR repeat proteins. *Curr. Opin. Struct. Biol.* **2016**, *36*, 116–121.
19. Wang, X.; McLachlan, J.; Zamore, P.D.; Hall, T.M.T. Modular recognition of RNA by a human pumilio-homology domain. *Cell* **2002**, *110*, 501–512.
20. Ahringer, J.; Kimble, J. Control of the sperm-oocyte switch in *Caenorhabditis elegans* hermaphrodites by the fem-3 3′ untranslated region. *Nature* **1991**, *349*, 346–348.
21. Sonoda, J.; Wharton, R.P. Recruitment of Nanos to hunchback mRNA by Pumilio. *Genes Dev.* **1999**, *13*, 2704–2712.
22. Nakahata, S.; Katsu, Y.; Mita, K.; Inoue, K.; Nagahama, Y.; Yamashita, M. Biochemical identification of Xenopus Pumilio as a sequence-specific cyclin B1 mRNA-binding protein that physically interacts with a Nanos homolog, Xcat-2, and a cytoplasmic polyadenylation element-binding protein. *J. Biol. Chem.* **2001**, *276*, 20945–20953.
23. Tadauchi, T.; Matsumoto, K.; Herskowitz, I.; Irie, K. Post-transcriptional regulation through the HO 3′ UTR by Mpt5, a yeast homolog of Pumilio and FBF. *EMBO J.* **2001**, *20*, 552–561.
24. Crittenden, S.L.; Bernstein, D.S.; Bachorik, J.L.; Thompson, B.E.; Gallegos, M.; Petcherski, A.G.; Moulder, G.; Barstead, R.; Wickens, M.; Kimble, J. A conserved RNA-binding protein controls germline stem cells in *Caenorhabditis elegans*. *Nature* **2002**, *417*, 660–663.
25. Spassov, D.; Jurecic, R. The PUF Family of RNA-binding Proteins: Does Evolutionarily Conserved Structure Equal Conserved Function? *IUBMB Life* **2003**, *55*, 359–366.

26. Galgano, A.; Forrer, M.; Jaskiewicz, L.; Kanitz, A.; Zavolan, M.; Gerber, A.P. Comparative analysis of mRNA targets for human PUF-family proteins suggests extensive interaction with the miRNA regulatory system. *PLoS ONE* **2008**, *3*, e3164.
27. Zamore, P.D.; Bartel, D.P.; Lehmann, R.; Williamson, J.R. The PUMILIO-RNA Interaction: A single RNA-binding domain monomer recognizes a bipartite target sequence. *Biochemistry* **1999**, *38*, 596–604.
28. Gupta, Y.K.; Lee, T.H.; Edwards, T.A.; Escalante, C.R.; Kadyrova, L.Y.; Wharton, R.P.; Aggarwal, A.K. Co-occupancy of two Pumilio molecules on a single hunchback NRE. *RNA* **2009**, *15*, 1029–1035.
29. Bernstein, D.; Hook, B.; Hajarnavis, A.; Opperman, L.; Wickens, M. Binding specificity and mRNA targets of a *Caenorhabditis elegans* PUF protein, FBF-1. *RNA* **2005**, *11*, 447–458.
30. Qiu, C.; Kershner, A.; Wang, Y.; Holley, C.P.; Wilinski, D.; Keles, S.; Kimble, J.; Wickens, M.; Hall, T.M. Divergence of Pumilio/fem-3 mRNA binding factor (PUF) protein specificity through variations in an RNA-binding pocket. *J. Biol. Chem.* **2012**, *287*, 6949–6957.
31. Valley, C.T.; Porter, D.F.; Qiu, C.; Campbell, Z.T.; Hall, T.M.T.; Wickens, M. Patterns and plasticity in RNA-protein interactions enable recruitment of multiple proteins through a single site. *Proc. Natl. Acad. Sci. USA* **2012**, *109*, 6054–6059.
32. García-Rodríguez, L.J.; Gay, A.C.; Pon, L.A. PUF3p, a Pumilio family RNA binding protein, localizes to mitochondria and regulates mitochondrial biogenesis and motility in budding yeast. *J. Cell Biol.* **2007**, *176*, 197–207.
33. Gerber, A.P.; Herschlag, D.; Brown, P.O. Extensive association of functionally and cytotopically related mRNAs with Puf family RNA-binding proteins in yeast. *PLoS Biol.* **2004**, *2*, e79.
34. Porter, D.F.; Koh, Y.Y.; VanVeller, B.; Raines, R.T.; Wickens, M. Target selection by natural and redesigned PUF proteins. *Proc. Natl. Acad. Sci. USA* **2015**, *112*, 15868–15873.
35. White, E.K.; Moore-Jarrett, T.; Ruley, H.E. PUM2, a novel murine PUF protein, and its consensus RNA-binding site. *RNA* **2001**, *7*, 1855–1866.
36. Lu, G.; Dolgner, S.J.; Hall, T.M.T. Understanding and engineering RNA sequence specificity of PUF proteins. *Curr. Opin. Struct. Biol.* **2009**, *19*, 110–115.
37. Cheong, C.G.; Hall, T.M.T. Engineering RNA sequence specificity of Pumilio repeats. *Proc. Natl. Acad. Sci. USA* **2006**, *103*, 13635–13639.
38. Gupta, Y.K.; Nair, D.T.; Wharton, R.P.; Aggarwal, A.K. Structures of human Pumilio with noncognate RNAs reveal molecular mechanisms for binding promiscuity. *Structure* **2008**, *16*, 549–557.
39. Miller, M.T.; Higgin, J.J.; Hall, T.M.T. Basis of altered RNA-binding specificity by PUF proteins revealed by crystal structures of yeast Puf4p. *Nat. Struct. Mol. Biol.* **2008**, *15*, 397–402.
40. Muraro, N.I.; Weston, A.J.; Gerber, A.P.; Luschnig, S.; Moffat, K.G.; Baines, R.A. Pumilio binds para mRNA and requires Nanos and Brat to regulate sodium current in Drosophila motoneurons. *J. Neurosci.* **2008**, *28*, 2099–2109.
41. Kaur, J.N.; Panepinto, J.C. Morphotype-specific effector functions of Cryptococcus neoformans PUM1. *Sci. Rep.* **2016**, *6*, 23638.
42. Francischini, C.W.; Quaggio, R.B. Molecular characterization of Arabidopsis thaliana PUF proteins–binding specificity and target candidates. *FEBS J.* **2009**, *276*, 5456–5470.
43. Zhang, C.; Muench, D.G. A nucleolar PUF RNA-binding protein with specificity for a unique RNA sequence. *J. Biol. Chem.* **2015**, *290*, 30108–30118.
44. Biasini M, Bienert S, Waterhouse A, Arnold K, Studer G, Schmidt T, Kiefer F, Cassarino TG, Bertoni M, Bordoli L, Schwede T (2014). SWISS-MODEL: modelling protein tertiary and quaternary structure using evolutionary information. *Nucleic Acids Research 2014* (1 July 2014) 42 (W1): W252-W258
45. Kiefer F, Arnold K, Künzli M, Bordoli L, Schwede T (2009). The SWISS-MODEL Repository and associated resources. *Nucleic Acids Res*. 37, D387-D392.
46. Arnold K, Bordoli L, Kopp J, and Schwede T (2006). The SWISS-MODEL Workspace: A web-based environment for protein structure homology modelling. *Bioinformatics*.,22,195-201.
47. Guex, N., Peitsch, M.C. Schwede, T. (2009). Automated comparative protein structure modeling with SWISS-MODEL and Swiss-PdbViewer: A historical perspective. *Electrophoresis*, 30(S1), S162-S173.
48. Kraemer, B.; Crittenden, S.; Gallegos, M.; Moulder, G.; Barstead, R.; Kimble, J.; Wickens, M. NANOS-3 and FBF proteins physically interact to control the sperm–oocyte switch in *Caenorhabditis elegans*. *Curr. Biol.* **1999**, *9*, 1009–1018.
49. Stein, L.; Sternberg, P.; Durbin, R.; Thierry-Mieg, J.; Spieth, J. WormBase: Network access to the genome and biology of *Caenorhabditis elegans*. *Nucleic Acids Res.* **2001**, *29*, 82–86.

50. Stumpf, C.R.; Kimble, J.; Wickens, M. A *Caenorhabditis elegans* PUF protein family with distinct RNA binding specificity. *RNA* **2008**, *14*, 1550–1557.
51. Bachorik, J.L.; Kimble, J. Redundant control of the *Caenorhabditis elegans* sperm/oocyte switch by PUF-8 and FBF-1, two distinct PUF RNA-binding proteins. *Proc. Natl. Acad. Sci. USA* **2005**, *102*, 10893–10897.
52. Ariz, M.; Mainpal, R.; Subramaniam, K. *Caenorhabditis elegans* RNA-binding proteins PUF-8 and MEX-3 function redundantly to promote germline stem cell mitosis. *Dev. Biol.* **2009**, *326*, 295–304.
53. Nolde, M.J.; Saka, N.; Reinert, K.L.; Slack, F.J. The *Caenorhabditis elegans* pumilio homolog, puf-9, is required for the 3′ UTR-mediated repression of the let-7 microRNA target gene, hbl-1. *Dev. Biol.* **2007**, *305*, 551–563.
54. Forbes, A.; Lehmann, R. Nanos and Pumilio have critical roles in the development and function of Drosophila germline stem cells. *Development* **1998**, *125*, 679–690.
55. Asaoka-Taguchi, M.; Yamada, M.; Nakamura, A.; Hanyu, K.; Kobayashi, S. Maternal Pumilio acts together with Nanos in germline development in Drosophila embryos. *Nat. Cell Biol.* **1999**, *1*, 431–437.
56. Parisi, M.; Lin, H. The Drosophila pumilio gene encodes two functional protein isoforms that play multiple roles in germline development, gonadogenesis, oogenesis and embryogenesis. *Genetics* **1999**, *153*, 235–250.
57. Mak, W.; Fang, C.; Holden, T.; Dratver, M.B.; Lin, H. An important role of Pumilio 1 in regulating the development of the mammalian female germline 1. *Biol. Reprod.* **2016**, *94*, 134.
58. Quenault, T.; Lithgow, T.; Traven, A. PUF proteins: Repression, activation and mRNA localization. *Trends Cell Biol.* **2011**, *21*, 104–112.
59. Cherry, J.M.; Hong, E.L.; Amundsen, C.; Balakrishnan, R.; Binkley, G.; Chan, E.T.; Christie, K.R.; Costanzo, M.C.; Dwight, S.S.; Engel, S.R.; et al. Saccharomyces genome database: The genomics resource of budding yeast. *Nucleic Acids Res.* **2011**, *40*, D700–D705.
60. Goldstrohm, A.C.; Hook, B.A.; Seay, D.J.; Wickens, M. PUF proteins bind Pop2p to regulate messenger RNAs. *Nat. Struct. Mol. Biol.* **2006**, *13*, 533–539.
61. Olivas, W.; Parker, R. The Puf3 protein is a transcript-specific regulator of mRNA degradation in yeast. *EMBO J.* **2000**, *19*, 6602–6611.
62. Yosefzon, Y.; Koh, Y.Y.; Chritton, J.J.; Lande, A.; Leibovich, L.; Barziv, L.; Petzold, C.; Yakhini, Z.; Mandel-Gutfreund, Y.; Wickens, M.; et al. Divergent RNA binding specificity of yeast Puf2p. *RNA* **2011**, *17*, 1479–1488.
63. Machin, N.A.; Lee, J.M.; Barnes, G. Microtubule stability in budding yeast: Characterization and dosage suppression of a benomyl-dependent tubulin mutant. *Mol. Biol. Cell* **1995**, *6*, 1241–1259.
64. Jalal Kiani, S.; Taheri, T.; Rafati, S.; Samimi-Rad, K. PUF proteins: Cellular functions and potential applications. *Curr. Protein Pept. Sci.* **2017**, *18*, 250–261.
65. Huh, S.U.; Kim, M.J.; Paek, K.H. Arabidopsis Pumilio protein APUM5 suppresses cucumber mosaic virus infection via direct binding of viral RNAs. *Proc. Natl. Acad. Sci. USA* **2013**, *110*, 779–784.
66. Huh, S.U.; Paek, K.H. APUM5, encoding a Pumilio RNA binding protein, negatively regulates abiotic stress responsive gene expression. *BMC Plant Biol.* **2014**, *14*, 75.
67. Xiang, Y.; Nakabayashi, K.; Ding, J.; He, F.; Bentsink, L.; Soppe, W.J. Reduced Dormancy5 encodes a protein phosphatase 2C that is required for seed dormancy in Arabidopsis. *Plant Cell* **2014**, *26*, 4362–4375.
68. Huang, T.; Kerstetter, R.A.; Irish, V.F. APUM23, a PUF family protein, functions in leaf development and organ polarity in Arabidopsis. *J. Exp. Bot.* **2014**, *65*, 1181–1191.
69. Shanmugam, T.; Abbasi, N.; Kim, H.S.; Kim, H.B.; Park, N.I.; Park, G.T.; Oh, S.A.; Park, S.K.; Muench, D.G.; Choi, Y.; et al. An arabidopsis divergent Pumilio protein, APUM24, Is essential for embryogenesis and required for faithful pre-rRNA processing. *Plant J.* **2017**, *92*, 1092–1105, doi:10.1111/tpj.13745.
70. Weidmann, C.A.; Goldstrohm, A.C. Drosophila Pumilio protein contains multiple autonomous repression domains that regulate mRNAs independently of Nanos and brain tumor. *Mol. Cell. Biol.* **2012**, *32*, 527–540.
71. Racher, H.; Hansen, D. PUF-8, a Pumilio homolog, inhibits the proliferative fate in the *Caenorhabditis elegans* germline. *G3 Genes Genomes Genet.* **2012**, *2*, 1197–1205.
72. Hubstenberger, A.; Cameron, C.; Shtofman, R.; Gutman, S.; Evans, T.C. A network of PUF proteins and Ras signaling promote mRNA repression and oogenesis in *Caenorhabditis elegans*. *Dev. Biol.* **2012**, *366*, 218–231.
73. Salvetti, A.; Rossi, L.; Lena, A.; Batistoni, R.; Deri, P.; Rainaldi, G.; Locci, M.T.; Evangelista, M.; Gremigni, V. DjPum, a homologue of Drosophila Pumilio, is essential to planarian stem cell maintenance. *Development* **2005**, *132*, 1863–1874.
74. Goldstrohm, A.C.; Seay, D.J.; Hook, B.A.; Wickens, M. PUF protein-mediated deadenylation is catalyzed by Ccr4p. *J. Biol. Chem.* **2007**, *282*, 109–114.
75. Herskowitz, I. Life cycle of the budding yeast *Saccharomyces cerevisiae*. *Microbiol. Rev.* **1988**, *52*, 536–553.

76. Zhu, D.; Stumpf, C.R.; Krahn, J.M.; Wickens, M.; Hall, T.M.T. A 5′ cytosine binding pocket in Puf3p specifies regulation of mitochondrial mRNAs. *Proc. Natl. Acad. Sci. USA* **2009**, *106*, 20192–20197.
77. Wilinski, D.; Qiu, C.; Lapointe, C.P.; Nevil, M.; Campbell, Z.T.; Hall, T.M.T.; Wickens, M. RNA regulatory networks diversified through curvature of the PUF protein scaffold. *Nat. Commun.* **2015**, *6*, 8213.
78. Zhang, J.; McCann, K.L.; Qiu, C.; Gonzalez, L.E.; Baserga, S.J.; Hall, T.M.T. Nop9 is a PUF-like protein that prevents premature cleavage to correctly process pre-18S rRNA. *Nat. Commun.* **2016**, *7*, 13085.
79. Stewart, M.S.; Krause, S.A.; McGhie, J.; Gray, J.V. Mpt5p, a stress tolerance-and lifespan-promoting PUF protein in *Saccharomyces cerevisiae*, acts upstream of the cell wall integrity pathway. *Eukaryot. Cell* **2007**, *6*, 262–270.
80. Jiang, L.; Ye, W.; Situ, J.; Chen, Y.; Yang, X.; Kong, G.; Liu, Y.; Tinashe, R.J.; Xi, P.; Wang, Y.; et al. A PUF RNA-binding protein encoding gene *PlM90* regulates the sexual and asexual life stages of the litchi downy blight pathogen *Peronophythora litchii*. *Fungal Genet. Biol.* **2017**, *98*, 39–45.
81. Shrestha, S.; Li, X.; Ning, G.; Miao, J.; Cui, L. The RNA-binding protein Puf1 functions in the maintenance of gametocytes in *Plasmodium falciparum*. *J. Cell Sci.* **2016**, *129*, 3144–3152.
82. Narita, R.; Takahasi, K.; Murakami, E.; Hirano, E.; Yamamoto, S.P.; Yoneyama, M.; Kato, H.; Fujita, T. A novel function of human Pumilio proteins in cytoplasmic sensing of viral infection. *PLoS Pathog.* **2014**, *10*, e1004417.
83. Reichel, M.; Liao, Y.; Rettel, M.; Ragan, C.; Evers, M.; Alleaume, A.M.; Horos, R.; Hentze, M.W.; Preiss, T.; Millar, A.A. In planta determination of the mRNA-binding proteome of Arabidopsis etiolated seedlings. *Plant Cell* **2016**, *28*, 2435–3452.
84. Cooke, A.; Prigge, A.; Opperman, L.; Wickens, M. Targeted translational regulation using the PUF protein family scaffold. *Proc. Natl. Acad. Sci. USA* **2011**, *108*, 15870–15875.
85. Abbasi, N.; Park, Y.I.; Choi, S.B. Pumilio Puf domain RNA-binding proteins in Arabidopsis. *Plant Signal. Behav.* **2011**, *6*, 364–368.
86. Deng, Y.; Singer, R.H.; Gu, W. Translation of ASH1 mRNA is repressed by PUF6p–Fun12p/eIF5B interaction and released by CK2 phosphorylation. *Genes Dev.* **2008**, *22*, 1037–1050.
87. Luitjens, C.; Gallegos, M.; Kraemer, B.; Kimble, J.; Wickens, M. CPEB proteins control two key steps in spermatogenesis in *C. elegans*. *Genes Dev.* **2000**, *14*, 2596–2609.
88. Kaye, J.A.; Rose, N.C.; Goldsworthy, B.; Goga, A.; Noelle, D.L. A 3′ UTR pumilio-binding element directs translational activation in olfactory sensory neurons. *Neuron* **2009**, *61*, 57–70.
89. Lee, M.H.; Hook, B.; Pan, G.; Kershner, A.M.; Merritt, C.; Seydoux, G.; Thomson, J.A.; Wickens, M.; Kimble, J. Conserved regulation of MAP kinase expression by PUF RNA-binding proteins. *PLoS Genet.* **2007**, *3*, e233.
90. Moore, F.L.; Jaruzelska, J.; Fox, M.S.; Urano, J.; Firpo, M.T.; Turek, P.J.; Dorfman, D.M.; Pera, R.A. Human Pumilio-2 is expressed in embryonic stem cells and germ cells and interacts with DAZ (Deleted in AZoospermia) and DAZ-like proteins. *Proc. Natl. Acad. Sci. USA* **2003**, *100*, 538–543.

VI –Problématique

L'étude bibliographique a mis en évidence l'importance de la ramification dans le fonctionnement de la plante et la complexité de sa régulation, en faisant intervenir des facteurs endogènes (hormones, nutriments) et exogènes (lumière). De plus, il est connu que ces facteurs endogènes (hormones, nutriments) interagissent de manière antagoniste ou synergique pour réguler une variété de processus physiologiques tout au long du cycle de vie de la plante (Sakr *et al*., 2018). Toutefois, très peu de données sont disponibles quant à leurs interactions dans le contrôle du débourrement. Il est également admis que les signaux émanant de ces facteurs doivent inévitablement être intégrés localement au niveau du bourgeon, pour déterminer sa réponse finale (dormant ou non-dormant). Un des candidats pour cette fonction intégratrice est le facteur de transcription *BRANCHED1*, qui appartient à la famille TCP (TEOSINTE BRANCHED1 (TB1), CYCLOIDEA (CYC), PROLIFERATING CELL NUCLEAR ANTIGEN FACTOR1 (PCF1), and PCF2)), spécifique des plantes et connue pour une diversité de processus biologiques. Cependant, les mécanismes moléculaires impliqués dans la régulation de *RhBRC1* par ces facteurs endogènes restent encore fragmentaires. Pour contribuer à l'identification de ces mécanismes, ce projet de thèse a été construit autour de deux parties :

1) La première partie montre le rôle du métabolisme primaire (la glycolyse/cycle de Krebs et OPPP) dans la régulation du débourrement et l'expression de *RhBRC1,* en réponse à l'effet combiné de l'auxine et du saccharose (deux acteurs majeurs de la ramification). Ces deux voies (la glycolyse/cycle de Krebs et OPPP) agissent en synergie sur l'expression de *RhBRC1*. De plus, le promoteur de *RhBRC1* constitue le site d'intégration des signaux émanant de ces deux voies du métabolisme primaire, en impliquant deux régions promotrices distinctes. Ce travail ouvre des perspectives très diversifiées notamment en termes d'identification des facteurs de transcription impliqués dans cette régulation et les mécanismes associés à leur régulation.
2) La deuxième partie s'applique à démontrer le rôle de la région 3'UTR du gène *RhBRC1* dans sa régulation par les sucres et par l'effet combiné du saccharose et de l'auxine. Cette région 3'UTR s'est avérée capable d'intégrer les mécanismes de régulation post-transcriptionnelle du gène *RhBRC1* liés au métabolisme primaire, avec une forte sensibilité pour la voie OPPP. Enfin, une protéine de la famille PUF, *Rh*PUF4, a été caractérisée comme potentielle acteur de cette régulation, notamment dans la transduction du signal de la voie OPPP.

L’ensemble de ces données a été obtenu sur la plante modèle, le rosier, en s’appuyant sur une stratégie pluridisciplinaire, intégrant des approches de biotechnologies, de pharmacologie, métabolomique e et transcriptomique. De plus, il s’agit d’une étude multi-échelle, avec des résultats issus de plantes décapitées, de bourgeons isolés et de cals génétiquement transformés. Les résultats obtenus seront ensuite intégrés à ceux de la littérature afin de mieux comprendre le rôle de l’effet combiné du sucre et de l’auxine lors des processus et mécanismes régulant le débourrement.

RESULTS

Bud outgrowth and *RhBRC1* expression are antagonistically regulated by auxin and sugar through glycolysis/tricarboxylic acid cycle and oxidative pentose phosphate pathways

Ming Wang et al.

Abstract

Shoot branching is a central process during plant growth and development that influences many important agronomic traits. BRANCHED1 (BRC1/TB1/FC1), belonging to a TCP transcription factor family, is consensually considered as one of the axillary bud-located hub for an array of cues including auxin and sugar. This study unveils the physiological and molecular mechanisms underpinning the combined effects of auxin and sugar on bud outgrowth. We showed that glycolysis/TCA cycle (tricarboxylic acid cycle) and OPPP (oxidative pentose phosphate pathway) are important modulators of the antagonistic effect of auxin and sucrose on both *RhBRC1* expression and bud outgrowth. Both processes were necessary for a successful bud outgrowth. Using the stably transformed Rosa calli with the promoter sequence of *RhBRC1* (*pRhBRC1*) appears as a converging point of the combined effect of auxin and sugar. In addition, OPPP and glycolysis/TCA-cycle act cooperatively and respectively through (-1973bp to 1611bp) and (-1611bp to -632bp) promoter regions to regulate *RhBRC1* expression. EMSA (electrophoretic mobility shift assay) results suggest a possible feedback regulation of sugar metabolism by BRC1. These findings underline the prevailing role of sugar metabolism and pRhBRC1 promoter regulation in the antagonistic effect of auxin and sucrose in shoot branching.

Key words

Bud outgrowth; RhBRC1; sucrose; auxin; glycolysis/tricarboxylic acid cycle; oxidative pentose phosphate pathways

Introduction

Shoot branching is a particularly significant trait in agriculture and horticulture sectors, which determines light capture efficiency, crop productivity, plant disease resistance and visual quality of ornamental plants (Lemerle *et al*., 1996; Zhao *et al*., 2006; Simon *et al*., 2011; Ta *et al*., 1987; Boumaza *et al*., 2009&2010; Garbez *et al*., 2015). Shoot branching depends on the induction of axillary buds along the stem to grow into branches, or to remain dormant, allowing plants to finely tune the degree of shoot development to resource availability. The transcriptional regulator, *BRANCHED1* (*BRC1*)/*TEOSINTE BRNACHED* (*TB1*), is one of the major genes in controlling shoot branching (Aguilar-Martínez *et al*., 2007; Seale *et al*., 2017). It is expressed inside the buds where it locally promotes bud growth arrest in many species (reviewed in Rameau *et al*. 2015, Martín-Fontecha *et al*., 2017; Wang *et al*., 2019). *Branched1* (*brc1*) or its homologue gene knock out mutants exhibited more branching numbers or tiller numbers (Doebley *et al*., 1997; Wang *et al*., 1999; Takeda *et al*., 2003; Aguilar-Martínez *et al*., 2007; Dun *et al*., 2009). In Arabidopsis, most *AtBRC1*-driven genetic programs, including cell division, ribosomal protein genes activation and abscisic acid (ABA) accumulation and signaling, largely overlapped with those repressed in dormant buds (Gonzalez-Grandio *et al*., 2013&2017). *BRC1* expression responds to diverse shoot branching-influencing endogenous (hormones, sugars) and exogenous (light) factors, supporting its role as one important hub for the convergence of their related-signaling pathways within buds (Rameau *et al*., 2015; Martín-Fontecha, *et al*., 2018; Wang *et al*., 2019), while it is still unknown how these pathways are integrated to regulate *BRC1* expression.

Bud growth is a complex process in plant, which has long been considered to be driven by hormones and/or carbohydrates (Philips, 1975; Van den Ende, 2014). The classical hormone hypothesis relies on that auxin, produced in young leaves at the apical shoot meristem (Ljung *et al*., 2001) and moved down in the polar auxin transport stream (PATS), restricts the growth of axillary bud along the stem (Sachs and Thimann, 1964; Morris, 1977; Cline, 1994; Li and Bangerth, 1999; Balla *et al*., 2011). Auxin cannot enter the buds and operates outside it through two non-mutually exclusive models, referred as to “auxin canalization model” and “second messenger model” (Aguilar-Martinez *et al*., 2007; Domagalska and Leyser, 2011, Dun *et al*. 2012). Auxin can lead to upregulation of *BRC1* transcription (Aguilar-Martínez *et al*., 2007), through the action of two antagonistic actors, CK (Cytokinin) and SL (Strigolactone), that both act directly in axillary buds (reviewed in Rameau *et al.,* 2015, Wang *et al*., 2019). In stem, auxin inhibits CK biosynthesis (Dun *et al*., 2009; Müller and Leyser, 2011; Brewer *et al*., 2013),

whose elevated level in axillary buds resulted in a *BRC1* downregulation and branching activation (Braun *et al*., 2012). SL biosynthesis is stimulated by auxin (Sorefan *et al*., 2003, Foo *et al*., 2005; Johnson *et al*., 2006; Zou *et al*., 2006; Arite *et al*., 2007&2009; Hayward *et al*., 2009) and operates by promoting *BRC1* expression and consequently, bud growth arrest (Gomez-Roldan *et al*., 2008; Brewer *et al*., 2009; Aguilar-Martínez *et al*., 2007; Dun *et al*., 2012; Brewer *et al*., 2015; Revel *et al*., 2015). Downstream SL, *DWARF 53* (*D53*)/ *Strigolactone more axillary like* (*SMXL6, 7* and *8*) and *SQUAMOSA PROMOTER BINDING PROTEIN-LIKE* (*SPL*) have been identified, at least in monocots, as components of SL core signaling pathway mediated *TB1*/*BRC1* upregulation (Jiao *et al*., 2010; Lu *et al*., 2013; Liu *et al*., 2017; Song *et al*., 2017). In addition, CK and SL can also regulate bud growth through *BRC1*-independent pathway (Minakuchi *et al*., 2010; Guan *et al*., 2012; Seale *et al*., 2017; Waldie and Leyser, 2018).

The nutritional hypothesis states that access to sugar assimilates is the prevailing factor regulating axillary bud growth (Phillips, 1975; Van den Ende, 2014) and decapitation (removal of the active growing apical part of plant) allows available carbon resources to be reallocated to the axillary buds, acting as sink organs (Snow, 1929; Skoog and Thimann, 1934). In pea, Mason *et al*. (2014) demonstrated that sucrose is an early signal for bud growth initiation after apex decapitation that enters bud prior the earliest signs of its outgrowth and of auxin depletion at the vicinity of bud. This resource reallocation constitutes the main source of carbon and energy to meet the strong metabolic activity of growing bud as reported in peach tree (Maurel *et al*., 2004a&2004b), walnut tree (Decourteix *et al*., 2008; Alves *et al*., 2007; Bonhomme *et al*., 2010), rose (Girault *et al*., 2010; Henry *et al*., 2011; Rabot *et al*., 2012) and pea (Fichtner *et al*., 2017). Accordingly, restriction of the sugar supply to bud by defoliation (Mitchell, 1953; Kebrom *et al*., 2010; Mason *et al*., 2014) or the failure of bud to compete efficiently for sugars (Fletcher and Dale, 1974; Kebrom *et al*., 2010&2012; Kebrom and Brutnell, 2015; Kebrom and Mullet, 2016) lead to delay or arrest of bud outgrowth. This sugar deprivation could be triggered by unfavorable endogenous and exogenous factors and coupled to growth arrest (Kebrom and Mullet, 2016; Tarancón *et al*., 2017; Martín-Fontecha *et al*., 2018; Wang *et al*., 2018). Sugar also plays a signal role as supported by the promotive effect of non-metabolizable analogues of sucrose (palatinose and lactulose) and fructose (psicose) on bud outgrowth (Rabot *et al*., 2012; Barbier *et al*., 2015; Fichtner *et al*., 2017) and by the tight correlation between bud outgrowth and trehalose-6-phosphate (T6P), one major sugar-signaling mediator (Fichtner *et al*., 2017). T6P is prevalent for carbohydrate utilization and growth in Arabidopsis (Schluepmann *et al*., 2003) that negatively regulates SnRK1 (sucrose non-fermenting-1-related protein kinase 1)

activity, a central sensor of overall energy homeostasis (Baena-Gonzalez *et al*., 2007), together with TOR (target of rapamycin) kinase (Xiong *et al*., 2013).

Sugar availability to bud also regulates *BRC1* expression in *Sorghum bicolor* (Kebrom *et al*., 2010; Kebrom and Mullet, 2015), *Pisum sativum* (Mason *et al*., 2014) and in *Rosa sp*. (Barbier *et al*., 2015). Others branching-related genes including *MAX2* gene, encoding a F-box protein of SL signaling in wheat (Kebrom *et al*., 2010; Barbier *et al*., 2015) and *IPT3*, encoding a CK biosynthesis protein in *Rosa sp*. (Barbier *et al*., 2015) are sugar-responsive genes. The finding that exogenous sucrose supply through petiole of intact plant mimics plant decapitation, since promoting bud growth and repressing *BRC1* expression, supports a possible interaction between hormonal (auxin) and nutritional (sugar) hypotheses in the regulation of bud growth (Mason *et al*., 2014).

Many reports indicated that the activity of sugar metabolism plays an important role in an array of growth processes, such as flowering process, fruit ripening, starch accumulation and leaf growth (Morris and Arthur, 1985; Holaday *et al*., 1992; Schaffer and Petreikov, 1997; Christiaens *et al*., 2016; Cañas *et al*., 2017). Bud growing is considered as a highly carbohydrate and energy consuming processes (Jana and Shekhawat, 2011; Polyn *et al*., 2015; Fan *et al*., 2017) that including cell proliferation, elongation and neo-organogenesis activity (Shimizu and Mori, 1998; Mori and Shimizu, 1998; Girault *et al*., 2008; Serrano-Mislata *et al*., 2015). This situation sharply stands out from very limited metabolic activity and cell division of dormant buds (Shimizu and Mori, 1998; Mori and Shimizu, 1998; Ruttink *et al*., 2007) and exogenous auxin hampers sugar absorption by buds (Henry *et al*., 2011). Glycolysis and the tricarboxylic acid cycle (TCA-cycle) are the major route of sugar catabolism, providing energy and carbon materials for sustained growth and many other developmental processes. It is also the converging control point for a variety of stimuli, such as nutrient limitation, osmotic stress, drought, cold/freezing (Plaxton, 1996; Fernie *et al*., 2002; Fernie *et al*., 2004). A potential role of glycolysis in bud outgrowth would be in line with bud growth inhibition in response to the glycolysis inhibitor 2-DOG (2-deoxyglucose, Wick *et al*., 1957; Rabot *et al*., 2012; Xiong *et al*., 2013). Oxidative pentose phosphate pathway (OPPP) is another major metabolic pathway connected to glycolysis that plays a pivotal role for maintaining carbon homoeostasis, providing reducing power, precursors for nucleotide, hormones and amino acid biosynthesis, and mitigating the oxidative stress (Pugin *et al*., 1997; Kruger and von Schaewen, 2003; Stincone *et al*., 2015). The involvement of OPPP in bud outgrowth is still unclear, even if the *pgl3-1,* a plastidial 6-phosphoglucolactonase antisense mutant in arabidopsis, exhibited reduced growth phenotype, comparatively to wild type (Bussell *et al*., 2013). The aim of this study is to

provide insight into the link between the regulation of primary sugar metabolism (glycolysis/TCA cycle and OPPP), *RhBRC1* expression and bud growth, in response to the combined effect of auxin and sucrose, two main inputs driving bud outgrowth. We performed a comprehensive characterization of the combined effect of auxin and sucrose on these two sugar metabolism pathways, and then we investigated their involvement in the regulation of bud outgrowth and *RhBRC1* expression. We demonstrate that glycolysis/TCA-cycle and OPPP are both regulated antagonistically by auxin and sucrose within buds and are both required for a successful bud outgrowth and the concomitant repression of *RhBRC1* expression. By studying different truncated *RhBRC1* promoters-contained Rosa calli, we gained valuable insights into the hub role of *RhBRC1* promoter in glycolysis/TCA-cycle and OPPP pathways-emanating signals. Two distinct regions (-1973bp to -1611bp and -1611bp to -632bp) of *RhBRC1* promoter were identified to be central in this differential regulation process.

Results

Sucrose and auxin regulate bud outgrowth an *RhBRC1* expression antagonistically

Based on previous data indicating that sucrose stimulates bud outgrowth while auxin inhibits it (Mason *et al*., 2014; Barbier *et al*., 2015), we firstly investigated whether both bud outgrowth and *RhBRC1* expression could be modulated by the combined effect of auxin and sucrose in *Rosa sp.*. In order to better control the levels of these two antagonistic regulators of bud growth, *in-vitro* cultured buds were used (Figure S1A, Chatfield *et al*., 2000; Rabot *et al*., 2012; Barbier *et al*., 2015; Waldie and Leyser, 2018). These buds were supplied with either sucrose alone (10, 50 or 100mM) or with both 1µM NAA (1-naphthaleneacetic acid, a synthetic plant hormone of the auxin family) and the same sucrose gradient concentration. This sucrose range concentration was lower than that reported in the phloem sap, ranging from 100 to 900mM (Ohshima *et al*., 1990; Nadwodnik and Lohaus, 2008; Jensen *et al*., 2013), and matched with that previously used to characterize sucrose-dependent promotion of bud outgrowth in *Rosa sp*. (Barbier *et al*., 2015). The time-course of bud outgrowth was monitored during 120h (Figure 1B) and comprised a 48h-lag phase (no visible growth) followed by a sustained growth phase, at the end of which bud length reached 0.22, 0.32 and 0.47 cm under sucrose concentration of 10, 50 and 100mM, respectively. Addition of 1µM NAA to the sucrose-containing medium led to a total inhibition of 10mM and 50mM sucrose-fed bud growth and to only partial reduction for 100mM sucrose-fed bud growth. Buds co-treated with 1µM NAA + 100mM sucrose almost reached the same length (0.25 cm at 120h) as those supplied with 10mM sucrose, which was twice lower than 100mM sucrose-fed buds. Buds grown on 100mM mannitol, an osmotic control, with or without 1µM NAA, did not display any outgrowth (Figure S1B). All these results confirm that bud outgrowth was under the antagonistic effect of auxin and sucrose.

RhBRC1 expression was then monitored on bud samples at 10 and 24h, a time prior the onset of rapid growth phase (Figure 1C, Figure S1B). *RhBRC1* transcript level progressively decreased as sucrose concentration increased from 10 to 100mM, and reached its lowest level in 100mM sucrose-fed buds (2.5 fold lower when compared to 10mM sucrose for 24h, Figure 1C). The opposite trends was found in response to auxin feeding only for 24h (Figure S1C). In this case, the highest level of *RhBRC1* expression occurred in buds supplied with 1µM NAA + 10mM sucrose, with a value twice of that of buds treated with 1µM NAA + 100mM sucrose for 24h (Figure 1C). Buds supplied with 1µM NAA + 10mM sucrose exhibited the highest level of *RhBRC1* and no outgrowth (dormant buds), while those supplied either with 1µM NAA + 100mM sucrose or with 10mM sucrose displayed the same level of *RhBRC1* and a moderate

outgrowth (they reached 0.25 cm length within 120h instead of 0.47cm for 100mM sucrose) (Figure 1B). The expression pattern of *RhHB40*, a homologue of *AtHB40* (a HD-ZIP transcription factor) which was transcriptionally and directly controlled by *AtBRC1* (Gonzalez-Grandio *et al*., 2017), was also investigated in the same treated buds to evaluate whether this changes in *BRC1* level could be translated into the regulation of BRC1-downstream regulated genes (Figure S2). Likewise *RhBRC1*, *RhHB40* exhibited an early responsiveness to sucrose (sucrose-mediated *RhHB40* downregulation in concentration manner) and to the combined effect of NAA and sucrose (auxin-dependent upregulation of *RhHB40* was counteracted by increased sucrose concentration). Buds co-treated with 1µM NAA + 50mM sucrose, which did not exhibit any growth, displayed a slight downregulation of both *RhBRC1* and *RhHB40* (Figure 1C, Figure S2), that may not be sufficient to promote bud arrest. In order to investigate the molecular mechanism behind the combined effect of auxin and sucrose, we focused on two auxin treatments leading to complete (1µM NAA + 10mM sucrose) or partial (1µM NAA + 100mM sucrose) reduction of bud growth and on their respective control (10mM sucrose or 100mM sucrose) (Figure 1).

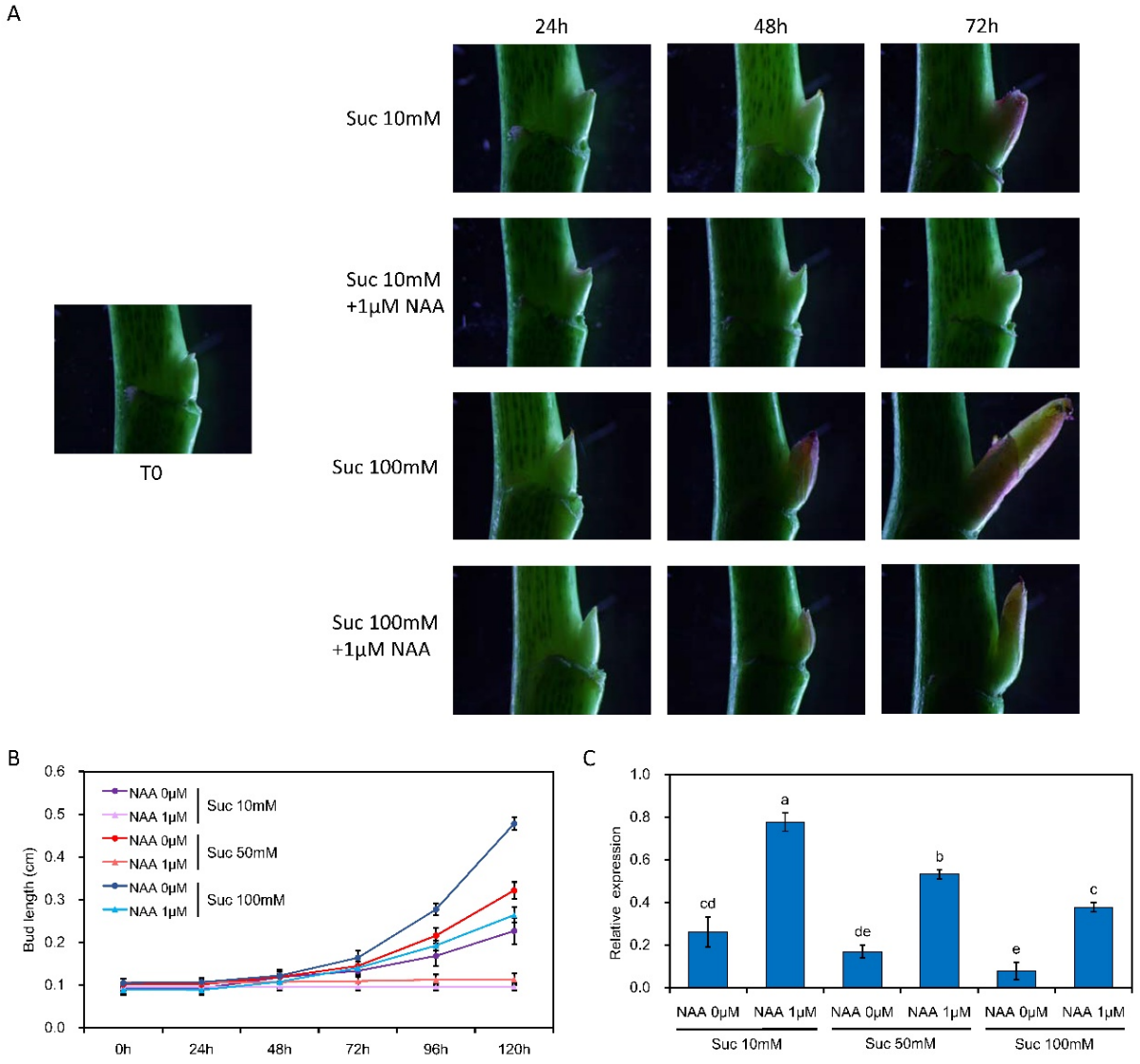


Figure 1. Bud outgrowth and transcript levels of *RhBRC1* are under the combined effects of auxin and sucrose. A, The picture of the bud under different treatment within 72h; B, Time-course of bud outgrowth during 120h, in media supplied with sucrose alone (Suc) or sucrose and NAA (NAA and Suc). C, Transcription level of *RhBRC1* in buds supplied for 24h with sucrose alone (Suc) or with sucrose and auxin (Suc and NAA). Data are mean ± SE of three biological repetitions. NAA (1-naphthaleneacetic acid). The letters indicate significant differences between the diverse treatments with $P < 0.05$.

Glycolysis/TCA-cycle and OPPP are controlled by the combined effect of sucrose and auxin

In order to check whether sucrose and auxin could affect glycolysis/TCA cycle and OPPP, a transcriptomic approach and qRTP-PCR were carried out on buds placed on sucrose alone (10 or 100mM) or with 1µM auxin for 24h. We showed that at leat the expression of eight genes encoding enzymes-related to primary sugar metabolism responded antagonistically to auxin and sucrose (Figure 2, Figure S3B). Addition of 1µM NAA resulted in downregulation of transcript level for three main glycolysis- [hexokinase (HXK), 6-phosphofructokinase (FK) and pyruvate kinase (PK)] and two TCA cycle-related enzymes [2-oxoglutarate dehydrogenase (OGDH), malate dehydrogenase (MDH)] within the first 24h. Most of these transcripts, except those for MDH and OGDH, were more expressed in bud fed with 100mM than with 10mM sucrose. The inhibitory effect of auxin was once again stronger (twice less) with low (10mM) than with elevated (100mM) sucrose concentration (Figure 2A). Metabolite profiling carried out on buds at 24 and 48h after sucrose and auxin application revealed that the amounts of seven compound (glucose-6-P, fructose-6-P, pyruvate, 2-oxoglutarate, succinate, fumarate, malate) were affected antagonistically by auxin and sucrose only at 48h (Figure 2A; Figure S3A&B). NAA consistently resulted in a significant reduction of their level in 10mM sucrose-fed buds, relative to those supplied with 100mM sucrose. The level of five products (glucose 6-P, fructose 6-P, pyruvate, 2-oxoglutarate and malate) correlated well with the transcript level changes of genes encoding their respective enzymes (HXK, FRK, PK, OGDH and MDH) in response to the combined effect of auxin and sucrose (Figure 2A). Such repression of glycolytic/TCA activity in dormant buds (1µM auxin + 10mM sucrose) resulted in a two-fold drop of the ratio ATP to ADP, relative to those incubated on 1mM auxin + 100mM sucrose (Figure 2B).

In addition, increasing sucrose concentration in the incubation medium led to an upregulation of the expression of transcripts for two main OPPP enzymes: glucose-6-phosphate 1-dehydrogenase (G6PD) and 6-phosphogluconate dehydrogenase (PGD) (Figure 2A), which are the two main enzymes producing NADPH in OPPP (Figure 2, Figure 3SA). The transcript level of these two OPPP enzymes were also highly inhibited in response to auxin, and this auxin effect was once again stronger with low (10mM) than with elevated (100mM) sucrose concentration (Figure 2A). This situation is consistent with a reduced (at least three times) ratio of NADPH to $NADP^+$ in dormant buds (1µM auxin + 10mM sucrose), compared to active buds (1µM auxin + 100mM sucrose) (Figure 2C). Moreover, the contents of ribulose-5-phosphate and ribose 5-phosphate, two intermediates of OPPP, were consistently lower (at least twice) in

buds incubated on 1µM NAA + 10mM sucrose than to 1µM NAA + 100mM sucrose for 48h (Figure 2A).

Auxin-mediated downregulation of primary sugar metabolism (glycolysis/TCA-cycle and OPPP) also occurred in the decapitated plant within the first 24h (Figure 3), before the beginning of sustained bud outgrowth (Girault *et al*., 2008, Figure 4). Dormant buds (under apical dominance) exhibited conjointly a high transcription level of *RhBRC1* and a lower transcription level of transcripts coding HXK, FRK, PK, OGDH and MDH, G6PD and 6-6PGD, the enzymes related-respectively to glycolysis/TCA-cycle and OPPP, comparatively to active buds (released from apical dominance). In addition, dormant buds (*in-vitro* and *in planta*) exhibited highest expression than active buds for two sugar starvation markers (*RhSTP1*, a H^+-monosaccharide cotransporter; *RhASN1*, an asparagine synthetase) (Cordoba *et al*., 2014; Nunes *et al*., 2013) (Figure 3). These findings highlight for the first time that glycolysis/TCA-cycle and OPPP-dependent sugar metabolism is a main target of the opposite effect of auxin and sugar and could have a central role in the control of bud growth ability and transcript level of *RhBRC1*.

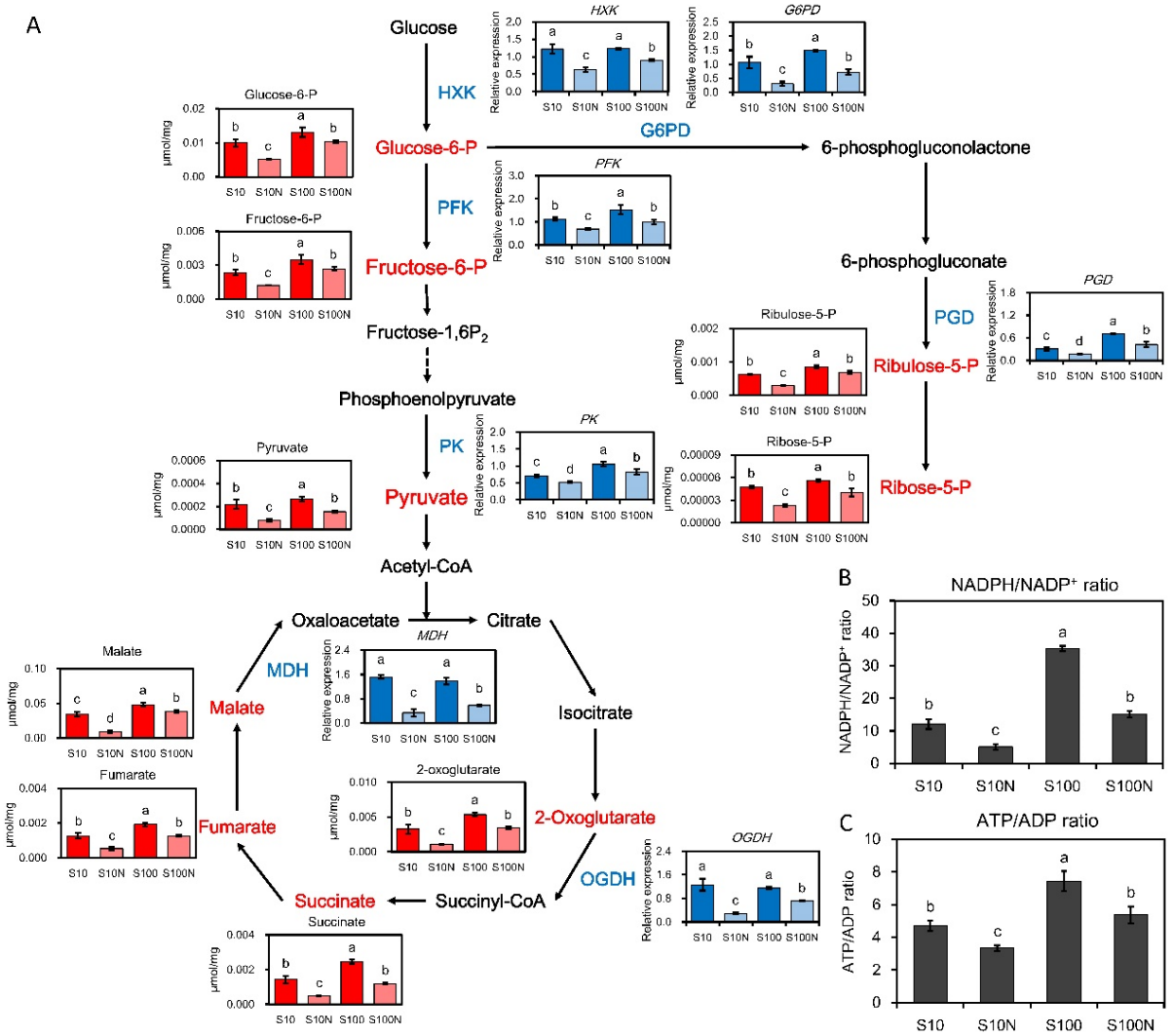


Figure 2. Compound levels and transcription levels of some key genes related to glycolysis/TCA-cycle and OPPP are modulated under the interacting effect of auxin and sucrose. The red column in bar graph correspond to metabolomic data. The blue column related bar graph means the transcription level identified by qRT-PCR. *HXK*, hexokinase; *PFK*, 6-phosphofructokinase; *PK*, pyruvate kinase; *OGDH*, 2-oxoglutarate dehydrogenase, *MDH*, malate dehydrogenase; *G6PD*, glucose-6-phosphate 1-dehydrogenase; *PGD*, 6-phosphogluconate dehydrogenase; S10, sucrose 10mM; S10N, 10mM sucrose + 1μM NAA; S100, sucrose 100mM; S100N, sucrose 100mM + 1μM NAA. Light color means the treatment with auxin. Data of qRT-PCR are mean ± SE of three biological replicates.

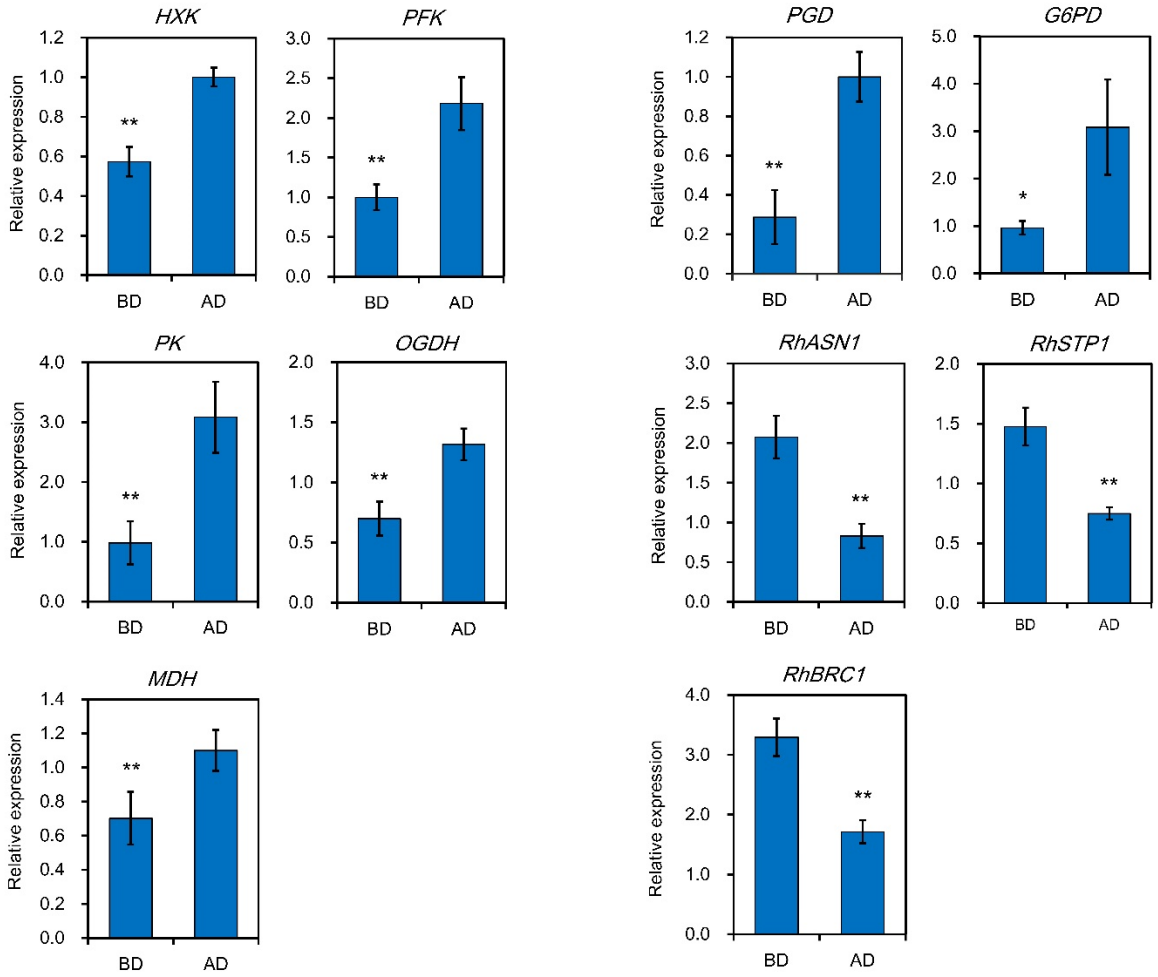


Figure 3. Transcription levels of the glycolysis/TCA-cycle and OPPP-related enzymes and *RhASN1*, *RhSTP1*, *RhBRC1* in the buds before decapitation (BD) or after decapitation (AD). *HXK*, hexokinase; *PFK*, 6-phosphofructokinase; *PK*, pyruvate kinase; *OGDH*, 2-oxoglutarate dehydrogenase; *MDH*, malate dehydrogenase; *G6PD*, glucose-6-phosphate 1-dehydrogenase; *PGD*, 6-phosphogluconate dehydrogenase, *RhASN1* : *Rosa hybrida* asparagine synthetase 1; *RhSTP1* : *Rosa hybrida* sugar transporter protein 1.

Both glycolysis/TCA-cycle and OPPP are involved in the regulation of bud outgrowth and *RhBRC1* expression

Our results showed that bud outgrowth and sugar metabolism through glycolysis/TCA-cycle and OPPP responded antagonistically to sucrose and auxin, arising the question whether these two pathways are both required for bud outgrowth. We first tested the individual effect of 2-deoxyglucose (2-DOG, an inhibitor of glycolysis activity, Wick *et al*., 1957; Xiong *et al*., 2013) and 6-aminonicotinamide (6-AN, an OPPP inhibitor, Lange and Proft, 1970; Hothersall *et al*., 1998; Lejay *et al*., 2008) on these processes in decapitated plant (Figure 4). Exogenous supply of either 2-DOG or 6-AN, through the cut petiole of the topmost node (bud below the decapitation point) of decapitated plants, resulted in significant reduction of bud outgrowth (from 20 to 70 %) in a dose dependent manner over time of 120h, compared to control (Figure 4B&C). These findings indicate that the outgrowth of buds within plants could be linked to the metabolic activity of both glycolysis/TCA-cycle and OPPP. As 2-DOG and 6-AN target GPI and G6PD activities respectively, branching number was compared in their respective loss-of-function Arabidopsis mutant (at*gpi* and *atg6pd*) relatively to wild type (WT) and loss-of-function *brc1* mutant. In comparison to WT, *atgpi* and *atg6pd* exhibited a lower branches percentage (74% and 63% respectively) than *col-0* (Figure 4D&E), by contrast to elevated branches number of *atbrc1* mutant (145% more than wild type).

We then studied the effects of 2-DOG and 6-AN on the growth of *in vitro*-cultured buds supplied with low (10mM) and elevated (100mM) sucrose concentration (Figure 5), as we previously carried out with auxin. When 5mM 2-DOG (a glycolysis effector) was added to sucrose-containing medium, bud outgrowth was significantly reduced (70% of the control) under 100mM sucrose, but completely inhibited under 10mM sucrose (Figure 5A). The same inhibitory trends, depending on sucrose concentration, were exhibited by buds co-treated with 10mM 6-AN and sucrose (Figure 5B). Under these conditions, 10mM 6-AN resulted in total and partial (60%) growth arrest for buds placed on 10mM and 100mM respectively (Figure 5B). *RhBRC1* abundance was also monitored in 10 and 100mM sucrose-fed *in vitro* cultured buds treated with 2-DOG and 6-AN (Figure 5B&D). Overall, these two negative effectors of primary sugar metabolism upregulated the transcript level of *RhBRC1*, more strongly with 10mM than with 100mM sucrose, supporting that *RhBRC1* level was also under the control of both glycolysis/TCA-cycle and OPPP activities. Similar pattern was also found for *RhHB40* (a marker of transcriptional activity of *RhBRC1*) under the same experimental conditions (Figure S5A&B).

To go further in understanding the role of these two sugar pathways, different concentrations of 6-Phosphogluconate (6-PG, an direct intermediate of OPPP) and glycerol (feeding glycolysis at the level of triose (pyruvate)) were tested on both the growth of *in-vitro* cultured buds and their *RhBRC1* transcript level (Figure 4A). Glycerol supply leaded to the accumulation of glycerol-3-P, a compound of fueling glycolysis downstream steps while inhibiting glucose-6-phosphate isomerase (GPI), which provides glucose-6P, the initial substrate of OPPP (Figure 4A; Aubert *et al*., 1994; Lejay *et al*., 2008). Buds supplied with different concentrations of either glycerol (from 1mM and 30mM) or 6-PG (0.1mM and 1mM) exhibited very weak growth within 120h and their length during this time-course remained very close (from 0.12cm to 0.17cm) to that of those incubated on mannitol (0.11cm dormant buds, Figure 5E&G). These findings thus indicate neither glycolysis/TCA alone no OPPP alone is able to promote bud outgrowth but both pathways (glycolysis/TCA-cycle and OPPP) are required for that. Such buds exhibited a reduced transcript level of *RhBRC1* as glycerol (from 1 to 30mM) or 6-PG (from 0.1 to 1mM) concentration increased but this *RhBRC1* level remained at least twice higher (even if with 30mM glycerol and 1mM 6-PG) than that of those fed with 10mM sucrose (moderately active buds, Figure 5G&H). Interestingly, bud outgrowth and *RhBRC1* transcript level are more responsive to the co-presence of glycerol and 6-PG in incubation medium. Indeed, buds co-supplied with 30mM glycerol and 1mM 6-PG exhibited a significant growth (0.5cm within the first 120h) and lowest level of *RhBRC1* (almost 5-fold), relatively to those measured with 30mM glycerol or 1mM 6-PG alone (their length hardly reached 0.17cm). Similarly, and toward a lower extend, buds co-incubated on 10mM glycerol and 0.1mM 6-PG displayed higher ability to grow out, together with lower level of *RhBRC1*, when compared to those treated either with 10mM glycerol or 0.1mM 6-PG (Figure 5E&F). Similar trends were found with RhBH40 (Figure S5C&D). These findings clearly support a tight link between sugar metabolism (glycolysis/TCA-cycle and OPPP activity) and *RhBRC1* transcript level, in a way suggesting that these two pathways act cooperatively to control *RhBRC1* transcription and the growth ability of bud.

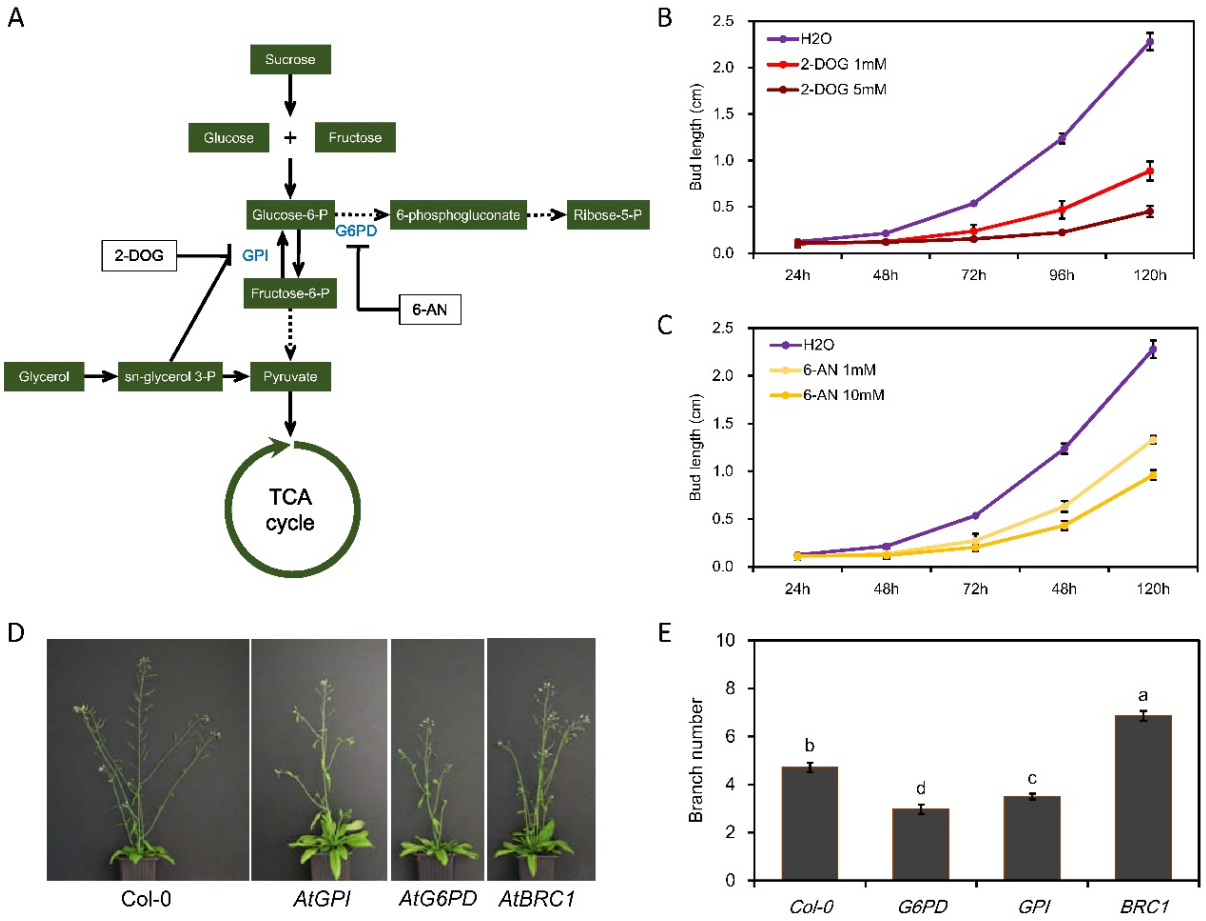


Figure 4. Different sugar metabolism inhibitors reduced bud outgrowth, in a dose dependent manner, at the plant scale. A, Sugar metabolism (glycolysis/TCA-cycle and OPPP)-related targets of different effectors; B, Time-course of bud outgrowth of decapitated plants treated with the different concentration of 2-DOG, an effector of glycolysis; C, Time-course of bud outgrowth of decapitated plants treated with the different concentration of 6-AN, an effector of OPPP (Oxidative Pentose Phosphate Pathway); D&E, the phenotype and branching numbers of each *Arabidopsis* mutant respectively. 2-DOG : 2-deoxyglucose ; 6-AN : 6-aminonicotinamide, TCA : Tricarboxylic acid cycle. Data are mean ± SE of three biological replicates, each replicate contains 15 buds.

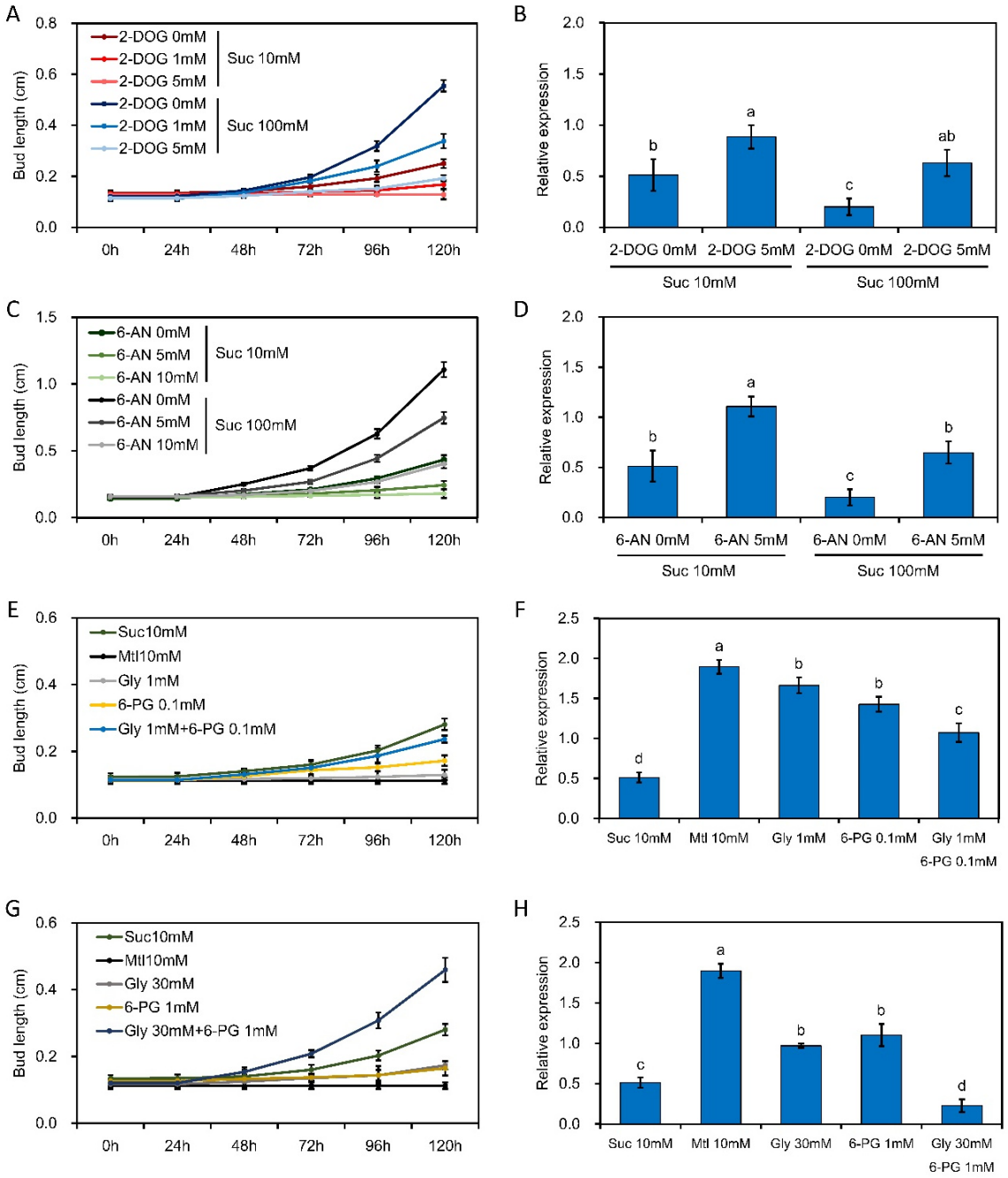


Figure 5. Both glycolysis/TCA-cycle and OPPP are necessary for *in vitro* cultured bud outgrowth. A&C, length of buds incubated on 10mM or 100mM sucrose with different concentrations of 2-DOG or 6-AN; B&D, *RhBRC1* transcript level in buds incubated on 10mM or 100mM sucrose with 5mM 2-DOG or 5mM 6-AN; E and F respectively length buds and transcript levels of *RhBRC1* in buds incubated on mannitol (10mM), sucrose (10mM), glycerol (1mM), 6-phosphogluconate alone (0,1mM) or on glycerol and 6-phosphogluconate (Gly 1mM/ 6-PG 0,1mM); G and H, respectively length buds and transcript levels of *RhBRC1* in buds incubated on mannitol (10mM), sucrose (10mM), glycerol (30mM), 6-phosphogluconate alone (1mM) or on glycerol and 6-phosphogluconate (Gly 30mM/ 6-PG 1mM). Data are mean ± SE of three biological replicates; each replicate contains 15 buds for time-kinetics of buds and 40 buds for qRT-PCR.

Promoter activity is a node of control for the opposite effect of auxin and sucrose

In order to give a first an insight into the mechanism involved in primary sugar metabolism dependent *RhBRC1* regulation, the 1973bp of *RhBRC1* promoter region was analyzed using PlantPAN (Chang *et al*., 2008; Chow *et al*., 2015 and 2018) and PlantTFDB database (Jin et al., 2016) to identify putative sugar related *cis*-elements. The common predicted results (similar score >0.9 in PlantPAN database and q-value <0.05 in PlantTFDB database) were selected and 18 motifs were identified and are mainly limited to the region between 1611bp and 632bp (Figure 6A). Among them, there is one E2F transcription factors (involved in TOR signaling pathway, Xiong *et al*., 2013) binding site (E2FCONSENSUS) located at -1082bp and one NAC (NAM, ATAF1/2, CUC2) transcription factor binding site at -1104bp. NAC transcription factors are plant-specific which are found in a wide range of land plants (Olsen *et al*., 2005). Other sugar-related motifs such as G-box, W-box, bZIP transcription factor binding sites were also present. Based on this, three different 5' deletions fragments of *RhBRC1* promoter : 1973bp (putative full RhBRC1 promoter), 1611bp (containing most of sugar-related *cis*-elements) and 632bp (corresponding to transcription start site, TSS) were fused to the GFP coding sequence in expression vectors that were stably transformed into *Rosa* callus (Figure 6A). Investigating the individual effect of sucrose and mannitol (as osmotic control) on the full promoter of *RhBRC1* (1976bp) reveals that sucrose addition to the incubation medium led to a reduced GFP transcript level in a concentration dependent manner, while no significant effect was found with mannitol (Figure S7A&B). The same fluorescence intensity trend was found when it was assessing through the relative transcription level of GFP or through a mean of thirty spots of fluorescence intensity randomly chosen on the callus for each treatment (Figure S7B). This latter approach was then selected to assess the intensity of GFP of transformed callus exposed to different treatments.

Based on this, we firstly investigated the combined effect of auxin and sucrose on 35S-GFP transformed Rosa callus that accordingly show no alteration of GFP intensity (Figure S8). This is not the case for BRC1 promoter that is responsive to sucrose and auxin (Figure 6). Sucrose effect was only restricted to 1973bp and 1611bp-transformed Rosa callus, while the 632bp-transformed ones did not exhibit any response to sucrose (Figure 6B). Regarding auxin, the intensity of GFP increased when these transformed callus were exposed to rising auxin (NAA) concentration (Figure 6C) and was as well limited to 1973bp and 1611bp-transformed Rosa callus. The promoter region of *RhBRC1* was likely involved in the opposite effect of sucrose and NAA (Figure 6D) since co-treatment with auxin and sucrose (1µM NAA + 10mM sucrose

and 1µM NAA + 100mM sucrose) led to a higher fluorescence intensity than their respective controls (10mM and 100mM sucrose respectively). Globally, the highest level of fluorescence was exhibited by 1µM NAA + 10mM sucrose-treated callus, which was twice higher than with 1µM NAA + 100mM sucrose. In addition, fluorescence level of callus expressing GFP with the 632bp-promoter sequence remained almost unchanged under these different conditions (Figure 6D). We then checked whether sucrose and auxin-dependent BRC1 regulation in callus could be linked to their antagonistic action on glycolysis/TCA-cycle and OPPP, as it is the case in vegetative buds (Figure 2). The transcript level for the seven-sucrose metabolism-related enzymes (HXK, FRK, PK, OGDH, MDH, G6PD, PGD) were investigated in different transformed callus after 8H incubation. Except MDH, the transcript level of all these enzymes were antagonistically responsive to sucrose and auxin (Figure S9), supporting that this effect on sugar metabolism occurred in both buds and callus. The callus system is thus a powerful tool to dissect the molecular mechanism behind this regulation.

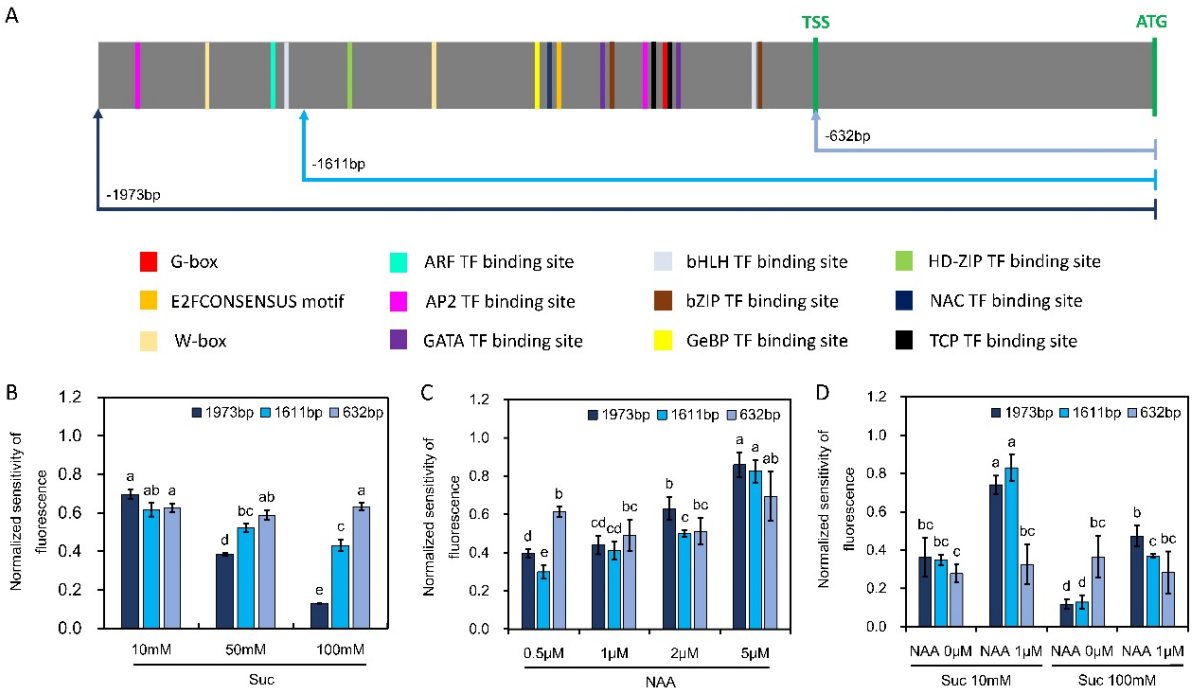


Figure 6. Sucrose and auxin (NAA) modulated antagonistically the activity of *RhBRC1* promoter regions. A, Schema of different parts and putative sugar-related *cis*-elements of *RhBRC1* promoter; B,C&D, Fluorescence level of 1973bp, 1611bp and 632bp upstream ATG- contained calli in response to sucrose concentrations, NAA concentration and combination of sucrose and auxin concentration respectively. Suc, sucrose; NAA, 1-naphthaleneacetic acid; TSS, transcription start site. Data are mean ± SE of three measurements, each measurement contained six calli. The letters indicate significant differences between the different treatments with $P < 0.05$.

Involvement of glycolysis/TCA-cycle and OPPP in the regulation of *RhBRC1* promoter activity

Regarding 2-DOG treatment, different *pRhBRC1*-transformed callus were initially placed on 100mM sucrose (as sole carbon source). The 1973bp and 1611bp-contained callus, displayed almost the same fluorescence intensity, that increased in response to rising concentration of 2-DOG, being four-fold higher with 5mM than with 0.5mM (Figure 7A). The callus transformed with 632bp construct remained insensitive to 2-DOG. Glycerol or pyruvate supply, used as sole carbon source, resulted in decreased fluorescence intensity (3.5 and 4.5 fold respectively) for the 1973bp and 1611bp-constructs, in a concentration dependent manner, supporting that 1611bp of *pRhBRC1* were sufficient to respond to a potentially glycolysis-drived signal (Figure 7B&C). Like for vegetative bud, 6-AN was tested on the stably transformed Rosa callus. When the 1973bp, 1611bp and 632bp-transformed callus fed with 100mM sucrose (as sole carbon source) were exposed to 6-AN, only those contained 1973bp promoter region exhibited elevated inflorescence intensity (4.3 fold) as 6-AN concentration increased (Figure 7D). Only the 1973bp construct led to a progressive reduction of fluorescence intensity, which was inversely correlated with 6-PG concentration, an intermediate of OPPP (Figure 7E). Similar data were found when these different transformed callus were co-treated with 1mM 2-DOG (a blocker of glycolysis) and a concentration range of Glucose-6P (from 0 to 5mM). In this case, while fluorescence intensity of callus transformed with 1611 and 632bp constructs remained unchanged, those transformed with the 1973bp construct had their fluorescence intensity decreased to reach the lowest level in response to 1mM 2-DOG + 5mM Glucose-6P (Figure 7F). These findings support the importance of promoter region located between 1973bp and 1611bp in OPPP signaling pathway-dependent transcriptional regulation of *RhBRC1*.

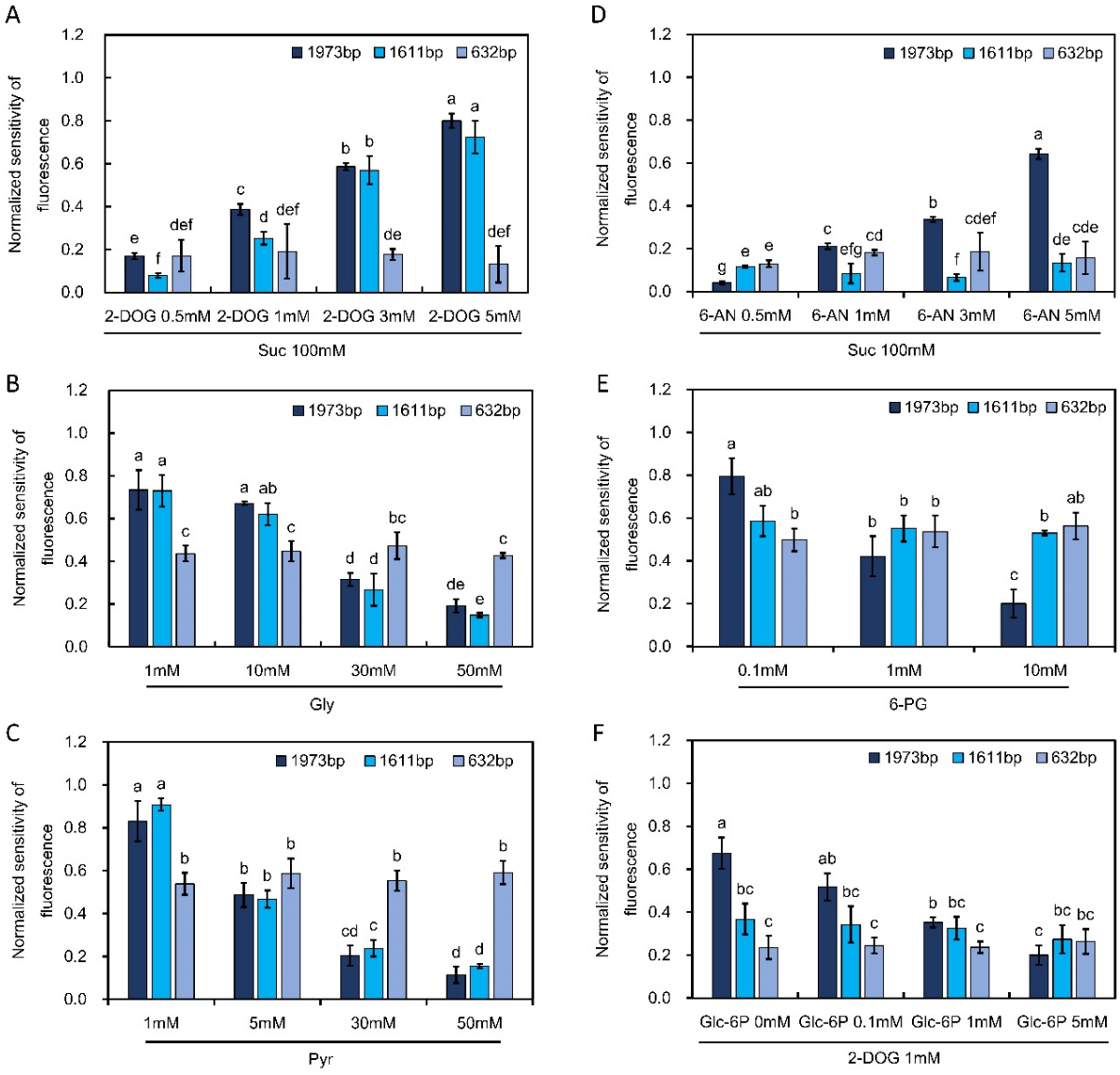


Figure 7. Glycolysis/TCA-cycle and OPPP control the activity of *RhBRC1* promoter in calli. A, B and C: Fluorescence level of 1973bp, 1611bp and 632bp contained calli under 100mM sucrose and different concentrations of 2-DOG, glycerol and pyruvate respectively. D, E and F: Fluorescence level of 1973bp, 1611bp and 632bp contained calli under different concentrations of 6-AN, 6-PG and both 2-DOG and Glc-6P respectively. Suc, sucrose. Gly, glycerol; Pyr, pyruvate; 6-PG: 6-phosphogluconate; Glc-6P, glucose 6-phosphate; 2-DOG, 2 deoxyglucose; 6-AN, 6-aminonicotinamide. Data are mean ± SE of three measurements, each measurement contained six calli. The letters indicate significant differences between the different treatments with $P < 0.05$.

RhBRC1 binds to the promoter region of glycolysis/TCA cycle and OPPP related genes

Glycolysis/TCA-cycle and OPPP negatively regulate the transcriptional activity of *RhBRC1* promoter and many biological processes are underpinning the control of BRC1 (Poza-Carrión *et al*., 2007; González-Grandío *et al*., 2017). Based on this, we carried out electrophoretic mobility shift assay (EMSA) experiments using RhBRC1 recombinant to check whether RhBRC1 (class II TB1/CYC-TCP) would be able to bind to the promoter of genes encoding some enzymes-related to glycolysis and OPPP. RhBRC1 is able to interact to the putative TCP consensus motif (KHGGGAC), as reported by Davière *et al*., 2014, (Figure S6A, table S3). Moreover, competition experiments with cold DNA probes showed that this binding activity requires an intact TCP-binding element (Figure S6A, table S3). To extent this result to the promoter of glycolysis/TCA cycle and OPPP related genes, we next selected TCP-binding related motifs within the 2 kb promoters of *HXK*, *FRK*, *PK*, *OGDH*, *MDH*, *G6PD*, *PGD*, whose respective expression is subjected to regulation by the antagonistic effect of auxin and sucrose, (Figure S6B). The putative TCP consensus motif (KHGGGAC) (Davière *et al*., 2014) was found in the promoter region of two glycolysis-related enzymes (*FRK*, *PK*) and two OPPP-(*G6PD*, *PGD*). Among them, only *G6PD* contains two TCP consensus motif and the other ones carry on one motif copy (Figure S6B). The EMSA has shown that RhBRC1 protein is able to specifically bind to the selected promoter regions of these four enzymes, including the two motifs of *G6PD* (Figure 8), highlighting a possible direct effect of the RhBRC1 activity upon some glycolysis/TCA cycle and OPPP metabolism.

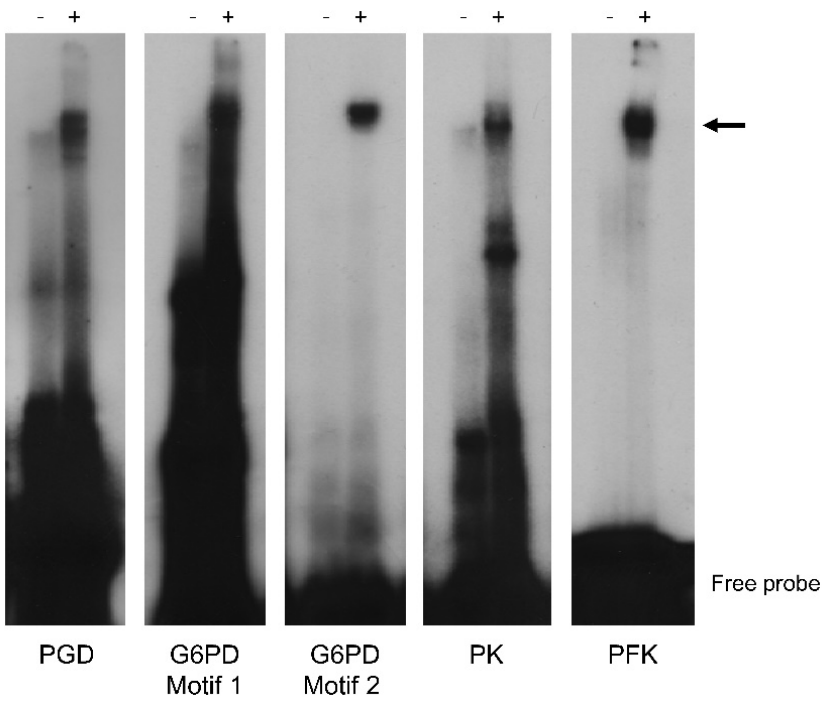


Figure 8. RhBRC1 protein binds to the promoter region of some sucrose metabolism related enzymes. PGD, 6-phosphogluconate dehydrogenase; G6PD, glucose-6-phosphate 1-dehydrogenase; PK, pyruvate kinase; PFK, 6-phosphofructokinase. Arrow indicates the bound DNA shift bands associated with RhBRC1.

Discussion

Sugar metabolism responded antagonistically to auxin and sucrose in vegetative bud

Growing vegetative bud is an active sink organ relying on its capacity to import and to metabolize sugars (Maurel *et al*., 2004; Shimizu and Mori, 1998; Mori and Shimizu, 1998; Ruttink *et al*., 2007, Rabot *et al*., 2012&2014; Savvides *et al*., 2017). Collectively, our results demonstrate that sugar metabolic activity within bud responds antagonistically to exogenous supply of auxin and sucrose, long before the onset of sustained growth, accompanied with significant modifications in the levels of several metabolites (Figure 1, 2&3A, Figure S3B). Five glycolysis/TCA-cycle (*HXK*, *FRK*, *PK*, *OGDH*, *MDH*) and two OPPP (*G6PD*, *PGD*) related-genes were repressed by auxin while they were promoted by sucrose in *in vitro*-cultured buds (Figure 2A). Consequently, dormant buds (1µM auxin and 10mM sucrose) exhibited a downregulation of these seven enzymes-encoding genes related to glycolysis/TCA-cycle and OPPP and of their respective metabolites (glucose-6P, fructose-6P, pyruvate, ribulose-5P and ribose-5P; Figure 2A&3), when compared to moderately (1µM auxin and 100mM sucrose) or to highly active buds (100mM sucrose alone) (Figure 2A). In whole plant, these seven genes were also repressed in dormant buds (under apical dominance), relatively to active buds (without apical dominance) (Figure 3), underlying a tight relationship between sugar metabolism activity and dormancy status of bud. These findings also highlight the occurrence of a complex regulatory network governing the coordination of primary sugar metabolism with the growing ability of bud. Bud outgrowth arrest is reported to be linked to the low sugar metabolic activity (Kebrom and Mullet, 2015&2016; Tarancón *et al*., 2017; Martín-Fontecha *et al*., 2018), while lateral shoots number is correlated with increased soluble sugars contents in transgenic Arabidopsis plants overexpressing cyanobacterial fructose-1,6-bisphosphatase-II in the cytosol (AcF) (Otori *et al*., 2017). In agreement with these results, dormant buds displayed a sugar-limitation status as is evidenced by the elevated transcript level of *RhSTP1* (sugar transporter protein 1) and *RhASN1* (asparagine synthetase 1) (Figure 3, Figure S4), two main sugar-starvation markers (Cordoba *et al*., 2014; Confraria *et al*., 2013; Dröge-Laser and Weiste, 2018), coupled with a lower ratio ATP to ADP (Figure 2C). High expression of *ASN1* and low expression of PFP (pyrophosphate-fructose-6-phosphate-1-phosphotransferase), a sucrose-inducible gene, were reported in dormant buds of defoliated sorghum (Kebrom and Mullet, 2015). This low availability of sugar and energy in dormant buds could trigger SnRK1 activity, the main metabolic and energy sensor kinase, resulting in transcriptional and metabolic

reprogramming behind the arrest of bud growth activity (Crozet *et al*., 2014; Tomé *et al*., 2014; Tarancon *et al*., 2017).

Previous studies report a complex crosstalk between sugar and auxin (see Sakr et al., 2018 for review). Here, auxin and sucrose target antagonistically primary sugar metabolism by regulating several glycolysis/TCA-cycle and OPPP related enzymes, which have positively been linked to growth activity in different biological systems. For instance, HXK1 plays a central role in sugar-dependent stimulation of Arabidopsis root meristem through a TOR kinase signaling pathway (Xiong et al., 2013) and in coordination of sugar metabolic activity and maize growth (Zhao et al., 2015). PFK and PK contribute to carbohydrate provision for vascular development (Prado et al., 2014; Guerriero et al., 2014) and to rapid cell growth in mammals respectively (Moon et al., 2005; Christofk et al., 2008). Main enzymes of OPPP, such as G6PD which determines the full rate of OPPP pathway (Landi *et al*., 2016; Espisoto, 2016), responded in the opposite way to the combined effect of auxin and sucrose. Relative to the moderately growing buds (1µM auxin + 100mM sucrose), dormant buds (1µM auxin + 10mM sucrose) harbored a reduced transcript level of G6PD and PGD, two NADPH-producing enzymes, which was consistently coupled with a low level of both Ribulose-5P and Ribose-5P contents (Figure 2A) and a reduced NADPH to $NADP^+$ ratio (Figure 2C).

RhBRC1 **promoter is a hub site for the combined effect of auxin and sugar**

BRC1 expression is sensitive to exogenous (light quality) end endogenous (hormones and nutrients) factors (Aguilar-Martínez *et al*., 2007; Rameau *et al*., 2015; Wang *et al*., 2019) but nothing is known how these factors could be integrated to regulate *BRC1*. Auxin and sucrose affected *RhBRC1* expression in the opposite way in both *in vitro*-cultured bud, as well as in p*RhBRC1*-transformed Rosa callus, and we showed that the -1973bp to -632bp promoter sequence was essential for these effects (Figure 1C, Figure 6D). The only available data related to transcriptional regulation of BR1 promoter was reported for that of rice *TEOSINTE BRANCHED1* (*OsTB1*, the homologue gene of *BRC1* in *Oryza sativa*) in relation with SL-dependent *OsTB1* regulation, more likely through *IPA1* (*Ideal Plant Architecture 1*), a key regulator of the plant architecture in rice. *IPA1* encodes a SPL transcription factor that repressed by D53 in strigolactone signaling in rice (Song *et al*., 2017). IPA1 can bind to *OsTB1* promoter directly and influence its expression (Lu *et al*., 2013). Furthermore, D53 homologue gene, SMXL6, 7 and 8 probably have a conserved function that affect *BRC1* expression through a *BRC1* promoter binding of a SPL transcription factor in Arabidopsis (Kerr and Beveridge, 2017; Lantzouni *et al*., 2017). The above conclusion suggested that SL, a branching related hormone

located downstream of auxin, can regulate *BRC1/TB1* transcription though their promoter region. Our findings expand this importance of *RhBRC1* promoter to the antagonistic effect of hormones and sugars. Additional studies are required to gain insight into the molecular regulatory mechanism but the presence of G-box, W-box and TCP, E2Fa, NAC transcription factor responsive *cis*-elements in the region of pRhBRC1 upstream -632bp (Figure 6A) open the way to address their role in next future. For example, the G-box corresponds to bZIP transcription factor (Sibéril *et al*., 2001) and many bZIP transcription factors (bZIP1, bZIP11, bZIP63, ABI5) are reported to be involved in sugar signaling (León and Sheen, 2003; Smeekens *et al*., 2010; Kang *et al*., 2010; Ma *et al*., 2011; Frank *et al*., 2018). C*is*-element of ATAF1, a NAC transcription factor, which can be phosphorylated by SnRK1 and regulates the expression of many genes, were also identified on *RhBRC1* promoter (Puranik *et al*., 2012; Kleinow *et al*., 2009). Interestingly, the two TCP transcription factor responsive *cis*-elements are also found in -850bp and -938bp of *RhBRC1* promoter region and EMSA results indicate that RhBRC1 can bind them, suggesting RhBRC1 could take part to this regulatory molecular network upstream its promoter (Figure S6). The exact role of these transcription factors in auxin and sugar-mediated downregulation of *RhBRC1* will be a major task to fully decipher regulatory mechanisms.

Glycolysis/TCA-cycle and OPPP are important modulators for bud outgrowth in response to the combined effect of auxin and sucrose

Metabolites derived from sugar metabolism downstream of hexokinase played an important role in plant growth and development (Doiron *et al*., 1996; Moore *et al*., 2003; Schluepmann *et al*., 2003; Wahl *et al*., 2013; Garapati *et al*., 2015; Janse van Rensburg and Van den End, 2018). In dormant buds, exogenous supply of auxin in the presence of low sugar concentration (10mM sucrose) represses both glycolysis/TCA-cycle and OPPP activity (Figure 2), and these two pathways are required for promoting bud outgrowth since their individual inhibition is sufficient to impair significantly this process (Figure 4&5). Glycolytic activity-dependent bud outgrowth fits well with the inhibitory effect of 2-DOG, an negative effector of GPI activity (Wick *et al*., 1957; Xiong *et al*., 2013), in both decapitated plants (buds released from apical dominance) and in *in vitro*-cultured buds (Figure 4&5). Moreover, Arabidopsis *gpi* mutant exhibited a lower branches number (74%), than wild type (Figure 4D&E), by contrast to elevated branches number of *atbrc1* mutants (145% more than wild type). GPI plays a central role in a variety of plant processes, including cell growth, photosynthetic capacity, CK biosynthesis (Yu *et al*., 2000; Kunz *et al*., 2014; Bahaji *et al*., 2013&2018). Strongly supporting the role of OPPP, a

significant reduction of bud outgrowth was triggered by exogenous application of 6-AN, a specific effector of G6PD, the main OPPP enzyme (Lange and Proft, 1970; Hothersall *et al*., 1998; Lejay *et al*., 2008), in both decapitated plants and *in vitro*-cultured buds (Figure 4&5). The tight link between OPPP and bud outgrowth was further evidenced by a lower branches percentage (63%) exhibited by *atg6pd*, an Arabidopsis loss-of-function mutant of G6PD, compared to wild type. Thirdly, buds fed with glycerol (glycolysis substrate) or 6-PG (OPPP substrate) exhibited much lower outgrowth activity (0.13 to 0.17cm length) than those co-fed with glycerol and 6-PG (0.24 to 0.46cm length) (Figure 5). This means that the activation of one of these two pathways is unable to promote significantly bud outgrowth while this later is operative when both glycolysis/TCA-cycle and OPPP are active. Successful bud outgrowth relies on primary processes including cell proliferation, cell elongation and neo-organogenesis (Mayer *et al*., 1998; Clark, 2001; Girault *et al*., 2008), which could imply a cooperative action of glycolysis/TCA cycle and OPPP. One possible assumption is that cell proliferation, which is a highly energy-consuming process, would be more sensitive to glycolytic/TCA-cycle activity-dependent energy status (Lunt *et al*., 2011; Reboredo-Rodríguez *et al*., 2018). As provider of reducing power (NADPH) for anabolism and oxidative stress metabolism, OPPP would rather contribute to organ elongation. In accordance with this, oxidation of NADPH by plasma membrane NADPH oxidases (RBOH1: RESPIRATORY BURST OXIDASE HOMOLOG 1) leads to the production of superoxide ($O_2^{\bullet-}$, reactive oxygen species) (Van Gestelen *et al*., 1997; Tsukagoshi *et al*., 2010; Suzuki *et al*., 2011), which is crucial for root elongation (Foreman *et al*., 2003; Dunand et al., 2007). By inhibiting glycolysis and OPPP (Figure 2), exogenous auxin could prevent both cell proliferation and elongation, two common processes of bud outgrowth, and this auxin effect is attenuated by high sugar availability.

Glycolysis/TCA-cycle and OPPP emanating signals regulate cooperatively *RhBRC1* expression via two different regions of its promoter

RhBRC1 expression was negatively correlated with glycolysis/TCA-cycle and OPPP-originating signals, because the highest transcript level of *RhBRC1* was related to low glycolytic/TCA-cycle and OPPP activity in dormant buds in whole plant (non-decapitated plant) and *in vitro*-cultured buds (10mM sucrose + 1µM auxin; Figure 1 and Figure S2). This link between *RhBRC1* expression and sugar-metabolism activity was confirmed in transformed Rosa callus. Indeed, these later exhibited in response to 10mM sucrose + 1µM auxin (unfavorable conditions of bud outgrowth) a downregulation of glycolysis/TCA-cycle and OPPP coupled with high BRC1 promoter activity (high fluorescence GFP), relatively to

100mM sucrose + 1µM auxin (promoting conditions of bud outgrowth). Consistently, *RhBRC1* expression is elevated in response to 2-DOG (a glycolysis inhibitor) and 6-AN (an OPPP inhibitor) *in vitro* cultured-buds (Figure 5), and in *pRhBRC1*-transformed Rosa callus (Figure 7). The reduction of promoter activity of *RhBRC1* in response to glycerol or pyruvate treatment further supported glycolysis-dependent *RhBRC1* regulation while the effect of 6-PG and the combined treatment of 2-DOG and Glc-6P were in line with the OPPP-mediated downregulation of *RhBRC1* expression. Promoter analysis and dissection revealed that two distinct regions of p*RhBRC1* corresponding to 1973bp-1611bp and 1611bp-632bp were involved in the integrated glycolysis- and OPPP-dependent control of *RhBRC1* expression (Figure 6&7). The glycolysis-responsive region of *RhBRC1* bears several *cis*-responsive elements to many transcriptions factor families, among them NAC2, E2Fa and some members in bZIP family that would be potential candidates in this signaling pathway. Although there are very few genes reported to be regulated through OPPP-mediated mechanism (Esposito, 2016), expression of nitrate assimilation genes in the nucleus of roots cells is promoted by a signal emanating from OPPP activity in the plastid (Bussell *et al*., 2013). Additional investigations would be required to understand how OPPP could be an important transducer in plant branching regulation. The OPPP-dependent signal could be produced by, i) one of the carbon metabolites generated through or by the OPPP activity, including 6-PG (Figure 5, De Jong *et al*., 2014); or ii) its reducing power (production of NADPH) that may be involved in redox regulation of bud outgrowth and *RhBRC1* transcription. In consistence with this, sugar-induced bud outgrowth operates through the activity of ascorbate-glutathione cycle that influences redox status of cells (Takahashi *et al*., 2014; Kebrom and Mullet, 2015). More recently, Heino *et al*. (2019) identified a H_2O_2-related transcriptional regulatory network composed of fifteen transcription factors. Chen et al. (2016) demonstrated that apoplast hydrogen peroxide (H_2O_2) can stimulate *BRC1* expression and repress the lateral bud outgrowth in tomato, which is confirmed by high BRC1 level in the two silencing mutants of two important genes involved in H_2O_2 production in tomato (RBOH1: RESPIRATORY BURST OXIDASE HOMOLOG 1 and WFI1: WHITEFLY INDUCED 1). BRC1 is involved in the regulation of an array of processes, such as inhibition of cell mitotic activity, DNA replication, maintaining ABA signaling (Martín-Trillo and Cubas, 2010; Danisman *et al*., 2012; González-Grandío *et al*., 2013; Zhang and Liu, 2018). Buds entering dormancy show a down-regulation of cell metabolism-related genes, whose promoters are significantly, enriched in TCP transcription factor-binding sites (Tatematsu *et al*., 2005; Martín-Fontecha *et al*., 2018). More interestingly, two glycolysis (PFK and PK) and two OPPP (PGD and G6PD) genes contain the putative TCP consensus motif

(KHGGGAC) that are all recognized by *RhBRC1* (Figure 8), assuming a negative feedback regulation of RhBRC1 on primary sugar metabolism. Therefore, high level of *RhBRC1* in dormant buds could contribute to the auxin-dependent primary sugar metabolism repression and to the maintenance of unfavorable sugar-and-energy-status for bud outgrowth, while increasing sugar availability downregulates BRC1 expression and in turn sustains high metabolic activity, required for bud outgrowth.

In conclusion, growing vegetative bud involves a high metabolic activity that drives its sink strength and its capacity to compete for nutrients. We demonstrate here that primary sugar metabolism, glycolysis/TCA cycle and OPPP, is one major target of the crosstalk between auxin and sugar and take a central role in the network regulatory mechanism of bud outgrowth, more likely through a transcriptional regulation of *RhBRC1* (Figure 9). Auxin cannot enter bud to regulate bud outgrowth, and acts through two hormones CK and SL (Ferguson and Beveridge, 2009; Müller and Leyser, 2011; Brewer *et al*., 2009; Wang *et al*., 2019). Understanding how these two branching-related hormones affect primary sugar metabolism of vegetative bud alone or in the presence of sugar will pave the way to improve further our understanding on the coordination of primary sugar metabolism with the growing ability of bud.

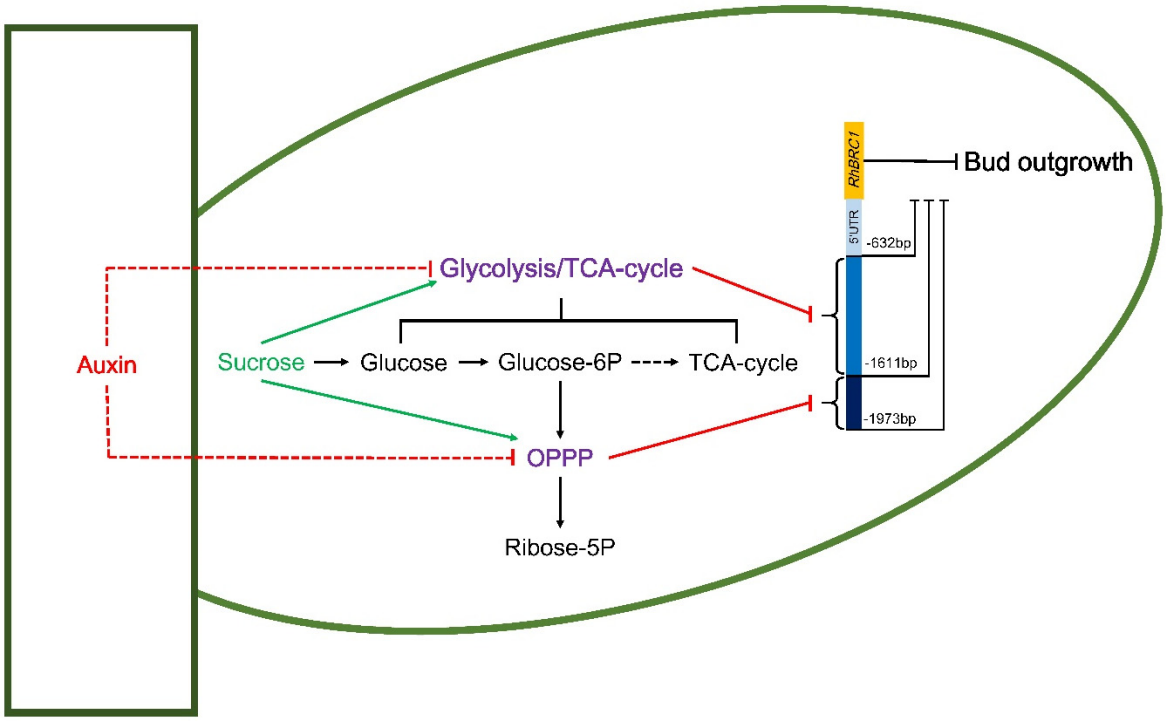


Figure 9. Auxin inhibits bud outgrowth through regulating sucrose metabolism in bud. Auxin inhibits glycolysis/TCA-cycle, but sucrose can stimulate it. Both of glycolysis/TCA-cycle and OPPP can influence the *RhBRC1* transcription through its promoter region. Dashed line means the effect of auxin.

Materials and methods

Plant culture and *in vitro* cultivation of axillary buds analysis

For the experiments on *Rosa hybrida* L., cuttings from cloned mother plants, grown in a greenhouse where the temperature was maintained around 22°C. Extra light was supplied by high-pressure sodium vapor lamps below 200Wm^{-2} and water and mineral nutrients were provided by-irrigation for 10 min day^{-1}. At the bud floral visible stage (BFV stage), one pool of plants was decapitated at the median part and used for pharmacological approaches and the other pool of plant served to harvest on single-axis plants nodes from the median part of the stem which used for many studies (Girault *et al*., 2010, Barbier *et al*., 2015, Figure S1A). Once harvested, 1.5-cm stem segments were grown *in vitro* on classical solid MS medium (Duchefa) (1% gelose, aubygel), supplemented with indicated compounds for different treatments in a growth chamber with a 16h day length at a temperature of 23/20°C (day/night). Once harvested, 1.5-cm stem segments were grown *in vitro* on classical solid MS medium (Duchefa) (1% gelose, aubygel).

RNA extraction and qRTPCR

Total RNA was extracted from the treated vegetative buds (50 buds for each extraction) or stably transformed Rosa callus (40 mg) using an RNA NucleoSpin kit (Macherey-Nagel) according to manufacturer's recommendations with small modifications (Barbier *et al*., 2015). Genomic DNA was removed by incubating RNA with DNase (Biolabs, Inc) for 10 min at 37°C (1µl of DNase for 10µg of RNA). The reaction was stopped by adding EDTA at a final concentration of 5mM followed by 10min at 75°C. The absence of contamination by genomic DNA was assessed by PCR using a specific primer designed against an intron region of the *RhGAPDH* gene (Girault *et al*., 2010; Henry *et al*., 2011). cDNA were obtained by reverse transcription performed on 1µg of RNA using SuperScript III Reverse Transcriptase (Invitrogen, Inc).

Quantitative real-time RT-PCR (qRT-PCR) was performed with SYBR Green Supermix (Biorad, Inc) using cDNA as a template, with the following program: 2 min at 50°C, 10 min at 95°C, then 40 cycles of 15 s at 95°C and 60 s at 60 °C. Specific sets of primers were selected according to their melting curves. Fluorescence detection was performed using a Chromo4 Real-time PCR detector (Biorad, Inc). Quantification of relative gene expression was determined using *RhUBC* expression as an internal control (Chua *et al*., 2011; Jain *et al*., 2006). The qRT-PCR primers were designed by Promer Premier 6 software (Table S2).

RNA-seq library construction and sequencing

In this experiment, three independent biological replicates were produced. For each biological repetition and each point, RNA samples were obtained by pooling RNA from more than 50 plants. The one node-cutting buds were collected on plants at bud floral visible stage (BFV stage). Total RNA was extracted using RNA NucleoSpin kit (Macherey-Nagel) according to manufacturer's recommendations with small modifications (Barbier *et al*., 2015). RNA-seq libraries were performed by following the manufacturer's recommendations (TruSeq-Stranded-mRNA-SamplePrep-Guide-15031047D-protocol, Illumina®, California, U.S.A). The RNA-seq samples have been sequenced in paired-end (PE) with a sizing of 260bp and a read length of 75 bases. Twelve samples per lane of NextSeq500 using individual bar-coded adapters and giving approximately 20 million of PE reads per sample are generated. All steps of the experiment, from growth conditions to bioinformatic analyses, were managed in CATdb database (Gagnot *et al*., 2007). To facilitate comparisons, each sample followed the same steps from trimming to count. RNA-Seq preprocessing includes trimming library adapters and performing quality controls. The raw data (fastq) were trimmed with Trimmomatic (Bolger *et al*., 2014) tool and ribosome sequences were removed with tool sortMeRNA (Kopylova *et al*., 2012). The genomic mapper STAR (Dobin *et al*., 2013) was used to align reads against the *Rosa chinensis* genome (Saint-Oyant *et al*., 2018). The abundance of each gene was calculated with STAR and counts only paired-end reads for which reads map unambiguously one gene, removing multi-hits. The sequence of genome and annotation files used come from GDR database (Jung *et al*., 2007; Saint-Oyant *et al*., 2018). Dispersion was estimated by the edge R method (Robinson *et al*., 2010) in the statistical software 'R' (Version 2.15.0, R Development Core Team (2005)). Expression differences were compared between stressed and unstressed plants using likelihood ratio test and *p*-values were adjusted by the Benjamini-Hochberg procedure to control False Discovery Rate (FDR). A gene was declared differentially expressed if its adjusted *p*-value < 0.05. FPKMs were calculated for visual analysis only, and were obtained by dividing normalized counts by gene length. Expression differences were compared by using likelihood ratio test and *p*-values were adjusted by the Benjamini-Hochberg procedure to control FDR.

Metabolomics analysis

The frozen samples (50mg) were re-suspended in 1ml of frozen (-20°C) Water:Acetonitrile:Isopropanol (v/v/v, 2:3:3) containing Ribitol at 4µg.mL^{-1} and extracted for 10min at 4°C with shaking at 1400 rpm in an Eppendorf Thermomixer. Insoluble material was

removed by centrifugation at 20000 *g* for 5 min. Fifty µL were collected and dried overnight at 35 °C in a speed-vac and stored at -80°C. Three blank tubes underwent the same steps as the samples. A quality control was made by pooling an equal volume of each condition. Samples from -80°C freezer were warmed 15 min before opening and dried again in a speed-vac for 1.5 hour at 35 °C before adding 10 µl of 20 mg.mL^{-1} methoxyamine in pyridine to the samples and the reaction was performed for 90 min at 28°C under continuous shaking in an Eppendorf thermomixer. Ninety µL of N-methyl-N-trimethylsilyl-trifluoroacetamide (MSTFA) (Aldrich 394866-10 x 1 mL) were then added and the reaction continued for 30 min at 37°C. After cooling, 45 µL were transferred into an Agilent vial for injection. One µL of sample was injected in splitless and split (1:30) modes on an Agilent 7890A gas chromatograph coupled to an Agilent 5977B mass spectrometer. The column was an Rxi-5SilMS from Restek. The liner (Restek # 20994) was changed before each series of 24 samples analysis. Oven temperature ramp started at 70°C for 7 min then 10°C·min^{-1} to 330°C for 5 min (run length 38 min). Helium constant flow was 0.7 mL.min^{-1}. Temperatures were the following: injector: 250°C, transfer line: 290°C, source: 250°C and quadripole 150°C. Five scans per second were acquired spanning a 50 to 600 Da range. Instrument was tuned with PFTBA with the 69 m/z and 219 m/z of equal intensities. Samples were randomized. Four different quality controls were injected at the beginning and the end of the analysis for monitoring of the derivatization stability. An injection in split mode with a 1:30 ratio was systematically performed with the following conditions: 70°C for 2 min then 30°C·min^{-1} to 330 °C for 5 min. Helium constant flow 1 mL·min^{-1}. Raw Agilent datafiles were converted in NetCDF format and analyzed with AMDIS (Meyer *et al*., 2010). Peak areas were also determined with the Targetlynx software (Waters) after conversion of the NetCDF file in masslynx format. AMDIS, Target Lynx in splitless and split 30 modes were compiled in one single Excel File for comparison. After blank mean substraction peak areas were normalized to ribitol and fresh weight.

Promoter cloning and reporter vector construction

For promoter analysis, 1973 bp upstream sequences from initiation codon were selected to do the promoter analysis. The PlantTFDB (http://planttfdb.cbi.pku.edu.cn/) and PlantPAN (http://plantpan2.itps.ncku.edu.tw/) database were used to analyze the promoter region (Jin *et al*., 2017; Chang *et al*., 2008; Chow *et al*., 2015). To isolate the predicted promoter region of *RhBRC1* (from position -1973 to initiation codon), genomic DNA was extracted from *Rosa hybrida* 'Old blush' leaves, using a NucleoSpin Plant II kit (Machery-Nagel Inc., Düren, Germany). A primer pair (PrBRC1Ps: 5' CACCAACTCAAAATGGGGAATGCG 3' and

PrBRC1Pas: 5' TAGTACCGGTGCTAATAGCGTTTG 3') was designed to facilitate directional cloning of the promoter. The 4-base-pair sequence (CACC) necessary for directional cloning in pENTR was added at the 5' end of the forward primer. PCR amplification was carried out by initial denaturation at 98°C for 30 s followed by 35 cycles of 98°C denaturation for 30 s, 60°C annealing for 30 s, and 72°C elongation for 2 min, and with a final extension of 72°C for 10 min. The 20 µL reaction mixture for the PCR consisted of an aliquot of 35 ng DNA template, 0.2 mM each of dNTP, 0.4 unit of Phusion DNA polymerase and 10 pmol of each primers. PCR products were separated in 1% (w/v) agarose gel and purified using the Wizard SV Gel and PCR Clean-Up System kit (Promega, USA). The 5' deletions of the *RhBRC1* promoter region at different positions -1973, -1611, and -632 were generated by PCR using different forward primers PrPBRC1-1F, PrPBRC1-2F, PrPBRC1-5UTR and a single reverse primer PrPBRC1-R respectively (Table S1). The PCR products were gel purified as mentioned above.

Target sequence transformation

The PCR products of *RhBRC1* promoter regions were sub-cloned into an entry vector using a pENTR Directional TOPO Cloning Kit (Invitrogen). The ligation product was transferred into *Escherichia coli* strain One Shot TOP10 Competent cells by thermal shock 30 s at 42°C. Positive clones were selected on solid LB medium supplemented with kanamycin (50 $mg.L^{-1}$). Bacteria plasmids were extracted using a NucleoSpin plasmid extraction kit (Macherey-Nagel, Germany) and confirmed by sequencing using two different primers (M13F: 5'-GTAAAACGACGGCCAG-3' and M13R: 5'-CAGGAAACAGCTATGAC-3'). From positive entry vectors, promoters were then cloned into pKGWFS7 destination vector (Karimi *et al.*, 2002) using an LR Clonase II kit (Invitrogen). The ligation product was transferred into *Escherichia coli* strain One Shot TOP10 Competent cells by thermal shock 30s at 42°C. Positive clones were selected on solid LB medium supplemented with spectinomycin (100 $mg{\cdot}L^{-1}$). Bacteria plasmidswere extracted using a NucleoSpin plasmid extraction kit (Macherey-Nagel Germany) and confirmed by sequencing using GFP-R 5'-CACGAACTCCAGCAGGAC-3' primers for pKGWFS7. The different constructions of promoter region were introduced by electroporation into *Agrobacterium tumefaciens* EHA105 (pBBR1-MCS-5).

Rose transformation

In vitro propagated shoots of *Rosa* were used as starting material. They were repeatedly sub-cultured every 6 weeks on Shoot multiplication medium (Hamama *et al*., 2015) that consisted

on (Murashige and Skoog [MS] salts and vitamins with 0.1 $g \cdot L^{-1}$ Fe-EDDHA, 30 $g \cdot L^{-1}$ sucrose, 0.1 $g \cdot L^{-1}$ myo-inositol, 4.44 μM 6-benzyladenine), solidified by 3 $g \cdot L^{-1}$ Phytagel. Young leaves were injured by several cuts and inoculated by *Agrobacterium* which had been suspended in re-suspension medium until DO_{600}=1 for 5 min. The inoculated leaves were blot drayed on sterile paper and transferred in the callus induction medium (Ibrahim *et al*., 2000) supplemented with cefotaxime (500 $mg \cdot L^{-1}$) and kanamycin (100 $mg \cdot L^{-1}$). Leaf discs were sub-cultured every 6 weeks on the same medium until the callus formed. The genomic DNA was extracted from the selected callus. Then PCR amplification was done to confirm that target fragment was transformed into callus steadily.

Callus treatments and GFP fluorescence analysis

The transformed callus were transferred onto basic medium (Murashige and Skoog [MS] salts and vitamins, pH 8.8) with different treatments for 8 h under light at 22℃ (the previous observation results showed that 8-hour-treatment is the best observation time, because the fluorescence at 2, 4 and 6 h was not strong enough and the fluorescence declined after 24 h). The fluorescence level of the transformed calli was analyzed by the fluorescence microscope. Quantification of the fluorescence level was performed on 2D images using ImageJ software. Integrated density of grey was determined on the 30 spots (selected randomly) for each sample. Each condition contained six calli and was replicated three times.

Adenylate measurements

The bud sample were frozen in liquid nitrogen and kept at −80 °C until extraction. Frozen buds ground in liquid nitrogen. An aliquot of frozen powder was taken with a liquid nitrogen pre-cooled spatula, precisely weighed (great care was taken to keep seed powder frozen at all stages) and transferred in a 1.5 ml microtube containing 600 μl of methanol/chloroform (1:1) which was immediately vortexed and incubated on ice for 10 min. After vortexing, 200 μl of H_2O was added; the microtube tube was vortexed again and centrifuged (10 min, 14 000 g, 4 °C). The upper phase was withdrawn and transferred into a microtube which was stored at −80 °C for HPLC analysis as described in Raveneau *et al*., 2017, with a modified elution gradient: step 1 (0–4 min) at 17 mM KOH; step 2 (4–26 min) with a concave isocratic gradient (Dionex GP50 pump, Curve 8) from 17 mM to 100 mM; step 3 (26–46 min) at 100 mM; step 4 (46–50 min), linear gradient (100–17 mM); step 5 (50–60 min), 17 mM KOH.

Electrophoretic mobility shift assays (EMSA)

The MBP-RhBRC1-6xHis recombinant protein was expressed in the Rosetta 2 (DE3) pLysS (Novagen) E. coli strain by induction with 0.5 mM IPTG for 4 h at 20°C, purified by binding onto a HisTrap HP column (GE Healthcare Life Sciences) and eluted with imidazole. Elution buffer was replaced by EMSA buffer (15mM HEPES-KOH pH 7.5; 40 mM KCl; 0.1 mM dithiothreitol; 10% glycerol) by filtration through a Sephadex-G25 HiTrap column (GE Healthcare Life Sciences). Oligonucleotide probes were end-filled labeled with the Klenow enzyme (Fermentas) in the presence of ^{32}P-dCTP. The sequence of the oligonucleotides is indicated in Supplemental Information (Table S3). The EMSA reaction was performed with 1ng of ^{32}P-labeled probe, 2µg of poly(dI-dC) and 100ng of RhBRC1 protein and incubated at room temperature for 20 min. The binding reactions were analyzed by electrophoresis on 6% native acrylamide gel in 0.5 x TBE buffer. After drying, the gel was autoradiographed at -80°C overnight.

References

Aguilar-Martínez, J. A., Poza-Carrión, C., & Cubas, P. (2007). Arabidopsis BRANCHED1 acts as an integrator of branching signals within axillary buds. The Plant Cell, 19(2), 458-472.

Aguilera-Alvarado, G. P., & Sánchez-Nieto, S. (2017). Plant hexokinases are multifaceted proteins. Plant and Cell Physiology, 58(7), 1151-1160.

Anoman, A. D., Flores-Tornero, M., Rosa-Telléz, S., Muñoz-Bertomeu, J., Segura, J., & Ros, R. (2016). The specific role of plastidial glycolysis in photosynthetic and heterotrophic cells under scrutiny through the study of glyceraldehyde-3-phosphate dehydrogenase. Plant signaling & behavior, 11(3), e1128614.

Arite, T., Iwata, H., Ohshima, K., Maekawa, M., Nakajima, M., Kojima, M., ... & Kyozuka, J. (2007). DWARF10, an RMS1/MAX4/DAD1 ortholog, controls lateral bud outgrowth in rice. The Plant Journal, 51(6), 1019-1029.

Arite, T., Umehara, M., Ishikawa, S., Hanada, A., Maekawa, M., Yamaguchi, S., & Kyozuka, J. (2009). d14, a strigolactone-insensitive mutant of rice, shows an accelerated outgrowth of tillers. Plant and Cell Physiology, 50(8), 1416-1424.

Aubert, S., Gout, E., Bligny, R., & Douce, R. (1994). Multiple effects of glycerol on plant cell metabolism. Phosphorus-31 nuclear magnetic resonance studies. Journal of Biological Chemistry, 269(34), 21420-21427.

Baena-González, E.; Rolland, F.; Thevelein, J.M.; Sheen, J. A central integrator of transcription networks in plant stress and energy signalling. Nature 2007, 448, 938–942.

Bahaji, A., Almagro, G., Ezquer, I., Gámez-Arcas, S., Sánchez-López, Á. M., Muñoz, F. J., ... & Doležal, K. (2018). Plastidial Phosphoglucose Isomerase Is an Important Determinant of Seed Yield through Its Involvement in Gibberellin-Mediated Reproductive Development and Storage Reserve Biosynthesis in Arabidopsis. The Plant Cell, 30(9), 2082-2098.

Bahaji, A., Sánchez-López, Á. M., De Diego, N., Muñoz, F. J., Baroja-Fernández, E., Li, J., ... & Humplík, J. F. (2015). Plastidic phosphoglucose isomerase is an important determinant of starch accumulation in mesophyll cells, growth, photosynthetic capacity, and biosynthesis of plastidic cytokinins in Arabidopsis. PLoS One, 10(3), e0119641.

Balla, J., Kalousek, P., Reinöhl, V., Friml, J., and Procházka, S. (2011). Competitive canalization of PIN-dependent auxin flow from axillary buds controls pea bud outgrowth. The Plant Journal, 65(4), 571-577.

Barbier, F., Péron, T., Lecerf, M., Perez-Garcia, M. D., Barrière, Q., Rolčík, J., ... & Roman, H. (2015). Sucrose is an early modulator of the key hormonal mechanisms controlling bud outgrowth in Rosa hybrida. Journal of experimental botany, 66(9), 2569-2582.

Beveridge, C. A., & Kyozuka, J. (2010). New genes in the strigolactone-related shoot branching pathway. Current opinion in plant biology, 13(1), 34-39.

Boumaza, R., Demotes-Mainard, S., Huché-Thellier, L. and Guérin, V. (2009). Visual characterization of the esthetic quality of the rosebush. Journal of Sensory Studies, 24, 774-796.

Boumaza, R., Huché-Thélier, L., Demotes-Mainard, S., Le Coz, E., Leduc, N., Pelleschi-Travier, S., et al. (2010). Sensory profiles and preference analysis in ornamental horticulture: the case of the rosebush. Food quality and preference, 21(8), 987-997.

Braun, N., de Saint Germain, A., Pillot, J. P., Boutet-Mercey, S., Dalmais, M., Antoniadi, I., et al. (2012). The pea TCP transcription factor PsBRC1 acts downstream of strigolactones to control shoot branching. Plant Physiology, 158(1), 225-238.

Brewer, P. B., Dun, E. A., Ferguson, B. J., Rameau, C., & Beveridge, C. A. (2009). Strigolactone acts downstream of auxin to regulate bud outgrowth in pea and Arabidopsis. Plant Physiology, 150(1), 482-493.

Brewer, P. B., Dun, E. A., Gui, R., Mason, M., & Beveridge, C. A. (2015). Strigolactone inhibition of branching independent of polar auxin transport. Plant physiology, pp-00014.

Brewer, P. B., Koltai, H., & Beveridge, C. A. (2013). Diverse roles of strigolactones in plant development. Molecular plant, 6(1), 18-28.

Broeckx, T.; Hulsmans, S.; Rolland, F. The plant energy sensor: Evolutionary conservation and divergence of SnRK1 structure, regulation, and function. J. Exp. Bot. 2016, 67, 6215–6252.

Broyer, T. C., & Hoagland, D. R. (1943). Metabolic activities of roots and their bearing on the relation of upward movement of salts and water in plants. American Journal of Botany, 30(4), 261-273.

Bussell, J. D., Keech, O., Fenske, R., & Smith, S. M. (2013). Requirement for the plastidial oxidative pentose phosphate pathway for nitrate assimilation in Arabidopsis. The Plant Journal, 75(4), 578-591.

Cañas, R. A., Yesbergenova-Cuny, Z., Simons, M., Chardon, F., Armengaud, P., Quilleré, I., ... & Brulé, L. (2017). Exploiting the genetic diversity of maize using a combined metabolomic, enzyme activity profiling, and metabolic modeling approach to link leaf physiology to kernel yield. The Plant Cell, 29(5), 919-943.

Chalfie, M., Tu, Y., Euskirchen, G., Ward, W. W., & Prasher, D. C. (1994). Green fluorescent protein as a marker for gene expression. Science, 263(5148), 802-805.

Chapman, E. J., & Estelle, M. (2009). Mechanism of auxin-regulated gene expression in plants. Annual review of genetics, 43, 265-285.

Chatfield, S. P., Capron, R., Severino, A., Penttila, P. A., Alfred, S., Nahal, H., & Provart, N. J. (2013). Incipient stem cell niche conversion in tissue culture: using a systems approach to probe early events in WUSCHELand preference, 21(8), 98lateral root primordia into shoot meristems. The Plant Journal, 73(5), 798-813.

Chen, P. W., Chiang, C. M., Tseng, T. H., & Yu, S. M. (2006). Interaction between rice MYBGA and the gibberellin response element controls tissue-specific sugar sensitivity of α-amylase genes. The Plant Cell, 18(9), 2326-2340.

Chen, X. J., Xia, X. J., Guo, X., Zhou, Y. H., Shi, K., Zhou, J., & Yu, J. Q. (2016). Apoplastic H2O2 plays a critical role in axillary bud outgrowth by altering auxin and cytokinin homeostasis in tomato plants. New Phytologist, 211(4), 1266-1278.

Chevalier, F., Perazza, D., Laporte, F., Le Hénanff, G., Hornitschek, P., Bonneville, J. M., ... & Vachon, G. (2008). GeBP and GeBP-like proteins are noncanonical leucine-zipper transcription factors that regulate cytokinin response in Arabidopsis. Plant physiology, 146(3), 1142-1154.

Chiou, T. J., & Bush, D. R. (1998). Sucrose is a signal molecule in assimilate partitioning. Proceedings of the National Academy of Sciences, 95(8), 4784-4788.

Chivasa, S., Tomé, D. F., & Slabas, A. R. (2013). UDP-glucose pyrophosphorylase is a novel plant cell death regulator. Journal of proteome research, 12(4), 1743-1753.

Cho, Y. H., Yoo, S. D., & Sheen, J. (2006). Regulatory functions of nuclear hexokinase1 complex in glucose signaling. Cell, 127(3), 579-589.

Chow, C. N., Zheng, H. Q., Wu, N. Y., Chien, C. H., Huang, H. D., Lee, T. Y., ... & Chang, W. C. (2015). PlantPAN 2.0: an update of plant promoter analysis navigator for reconstructing transcriptional regulatory networks in plants. Nucleic acids research, 44(D1), D1154-D1160.

Chresta, C. M., Davies, B. R., Hickson, I., Harding, T., Cosulich, S., Critchlow, S. E., ... & James, D. (2009). AZD8055 is a potent, selective, and orally bioavailable ATP-competitive mammalian target of rapamycin kinase inhibitor with in vitro and in vivo antitumor activity. Cancer research, 0008-5472.

Christiaens, A., De Keyser, E., Pauwels, E., De Riek, J., Gobin, B., & Van Labeke, M. C. (2016). Suboptimal light conditions influence source-sink metabolism during flowering. Frontiers in Plant Science, 7, 249.

Christofk, H. R., Vander Heiden, M. G., Harris, M. H., Ramanathan, A., Gerszten, R. E., Wei, R., ... & Cantley, L. C. (2008). The M2 splice isoform of pyruvate kinase is important for cancer metabolism and tumour growth. Nature, 452(7184), 230.

Clark, S. E. (2001). Cell signalling at the shoot meristem. Nature Reviews Molecular Cell Biology, 2(4), 276.

Cline, M. G. (1994). The role of hormones in apical dominance. New approaches to an old problem in plant development. Physiologia plantarum, 90(1), 230-237.

Cline, M. G., Thangavelu, M., & Dong-Il, K. (2006). A possible role of cytokinin in mediating long-distance nitrogen signaling in the promotion of sylleptic branching in hybrid poplar. Journal of plant physiology, 163(6), 684-688.

Coello, P.; Hey, S.J.; Halford, N.G. The sucrose non-fermenting-1-related (SnRK) family of protein kinases: Potential for manipulation to improve stress tolerance and increase yield. J. Exp. Bot. 2010, 62, 883–893.

Confraria, A., Martinho, C. S. D. S., Elias, A., Rubio-Somoza, I., & Baena-González, E. (2013). miRNAs mediate SnRK1-dependent energy signaling in Arabidopsis. Frontiers in plant science, 4, 197.

Cordoba, E., Aceves-Zamudio, D. L., Hernández-Bernal, A. F., Ramos-Vega, M., & León, P. (2014). Sugar regulation of SUGAR TRANSPORTER PROTEIN 1 (STP1) expression in Arabidopsis thaliana. Journal of experimental botany, 66(1), 147-159.

Corot, A., Roman, H., Douillet, O., Autret, H., Perez-Garcia, M. D., Citerne, S., ... & Demotes-Mainard, S. (2017). Cytokinins and abscisic acid act antagonistically in the regulation of the bud outgrowth pattern by light intensity. Frontiers in plant science, 8, 1724.

Crozet, P., Margalha, L., Confraria, A., Rodrigues, A., Martinho, C., Adamo, M., ... & Baena-González, E. (2014). Mechanisms of regulation of SNF1/AMPK/SnRK1 protein kinases. Frontiers in plant science, 5, 190.

Danisman, S., Van der Wal, F., Dhondt, S., Waites, R., de Folter, S., Bimbo, A., ... & Angenent, G. C. (2012). Arabidopsis class I and class II TCP transcription factors regulate jasmonic acid metabolism and leaf development antagonistically. Plant physiology, 159(4), 1511-1523.

Davière, J. M., Wild, M., Regnault, T., Baumberger, N., Eisler, H., Genschik, P., & Achard, P. (2014). Class I TCP-DELLA interactions in inflorescence shoot apex determine plant height. Current Biology, 24(16), 1923-1928.

De Jong, F., Thodey, K., Lejay, L. V., & Bevan, M. W. (2014). Glucose elevates NITRATE TRANSPORTER2. 1 protein levels and nitrate transport activity independently of its HEXOKINASE1-mediated stimulation of NITRATE TRANSPORTER2. 1 expression. Plant Physiology, 164(1), 308-320.

de Jong, M., George, G., Ongaro, V., Williamson, L., Willetts, B., Ljung, K., ... & Leyser, O. (2014). Auxin and strigolactone signaling are required for modulation of Arabidopsis shoot branching by nitrogen supply. Plant physiology, 166(1), 384-395.

Decourteix, M., Alves, G., Bonhomme, M., Peuch, M., Baaziz, K. B., Brunel, N., ... & Sakr, S. (2008). Sucrose (JrSUT1) and hexose (JrHT1 and JrHT2) transporters in walnut xylem parenchyma cells: their potential role in early events of growth resumption. Tree physiology, 28(2), 215-224.

Delatte, T. L., Sedijani, P., Kondou, Y., Matsui, M., de Jong, G. J., Somsen, G. W., ... & Schluepmann, H. (2011). Growth arrest by trehalose-6-phosphate: an astonishing case of primary metabolite control over growth by way of the SnRK1 signaling pathway. Plant Physiology, pp-111.

Deprost, D., Yao, L., Sormani, R., Moreau, M., Leterreux, G., Nicolaï, M., ... & Meyer, C. (2007). The Arabidopsis TOR kinase links plant growth, yield, stress resistance and mRNA translation. EMBO reports, 8(9), 864-870.

Devitt, M. L., & Stafstrom, J. P. (1995). Cell cycle regulation during growth-dormancy cycles in pea axillary buds. Plant molecular biology, 29(2), 255-265.

Dharmasiri, N., Dharmasiri, S., & Estelle, M. (2005). The F-box protein TIR1 is an auxin receptor. Nature, 435(7041), 441.

Dierck, R., De Keyser, E., De Riek, J., Dhooghe, E., Van Huylenbroeck, J., Prinsen, E., & Van Der Straeten, D. (2016). Change in Auxin and Cytokinin Levels Coincides with Altered Expression of Branching Genes during Axillary Bud Outgrowth in Chrysanthemum. PloS one, 11(8), e0161732.

Dietrich, K., Weltmeier, F., Ehlert, A., Weiste, C., Stahl, M., Harter, K., & Dröge-Laser, W. (2011). Heterodimers of the Arabidopsis transcription factors bZIP1 and bZIP53 reprogram amino acid metabolism during low energy stress. The Plant Cell, tpc-110.

Dobrenel, T., Marchive, C., Azzopardi, M., Clément, G., Moreau, M., Sormani, R., ... & Meyer, C. (2013). Sugar metabolism and the plant target of rapamycin kinase: a sweet operaTOR?. Frontiers in plant science, 4, 93.

Dobrenel, T., Marchive, C., Sormani, R., Moreau, M., Mozzo, M., Montané, M. H., ... & Meyer, C. (2011). Regulation of plant growth and metabolism by the TOR kinase. Biochemical Society Transactions. 39, 477–481.

Doebley, J., Stec, A., & Hubbard, L. (1997). The evolution of apical dominance in maize. Nature, 386(6624), 485.

Domagalska, M. A., & Leyser, O. (2011). Signal integration in the control of shoot branching. Nature Reviews Molecular Cell Biology, 12(4), 211.

Dröge-Laser, W., & Weiste, C. (2018). The C/S1 bZIP network: a regulatory hub orchestrating plant energy homeostasis. Trends in plant science, 23(5), 422-433.

Dun E. A, de Saint Germain A, Rameau C, Beveridge CA (2012) Antagonistic action of strigolactone and cytokinin in bud outgrowth control. Plant Physiol 158: 487–498

Dun, E. A., Brewer, P. B., and Beveridge, C. A. (2009). Strigolactones: discovery of the elusive shoot branching hormone. Trends in plant science, 14(7), 364-372.

Dunand, C., Crèvecoeur, M., & Penel, C. (2007). Distribution of superoxide and hydrogen peroxide in Arabidopsis root and their influence on root development: possible interaction with peroxidases. New Phytologist, 174(2), 332-341.

Durand, M., Mainson, D., Porcheron, B., Maurousset, L., Lemoine, R., & Pourtau, N. (2018). Carbon source–sink relationship in Arabidopsis thaliana: the role of sucrose transporters. Planta, 247(3), 587-611.

Elliott, A. R., Campbell, J. A., Dugdale, B., Brettell, R. I. S., & Grof, C. P. L. (1999). Green-fluorescent protein facilitates rapid in vivo detection of genetically transformed plant cells. Plant Cell Reports, 18(9), 707-714.

Esposito, S. (2016). Nitrogen assimilation, abiotic stress and glucose 6-phosphate dehydrogenase: the full circle of reductants. Plants, 5(2), 24.

Fan, K., Shen, H., Bibi, N., Li, F., Yuan, S., Wang, M., & Wang, X. (2015). Molecular evolution and species-specific expansion of the NAP members in plants. Journal of integrative plant biology, 57(8), 673-687.

Fan, K., Wang, M., Miao, Y., Ni, M., Bibi, N., Yuan, S., ... & Wang, X. (2014). Molecular evolution and expansion analysis of the NAC transcription factor in Zea mays. PLoS One, 9(11), e111837.

Fan, Z., Cai, Z., Shan, J., & Yang, J. (2017). Letter to the editor: bud position and carbohydrate play a more significant role than light condition in the developmental transition between rhizome buds and aerial shoot buds of Oryza longistaminata. Plant and Cell Physiology, 58(8), 1281-1282.

Ferguson, B. J., & Beveridge, C. A. (2009). Roles for auxin, cytokinin, and strigolactone in regulating shoot branching. Plant physiology, 149(4), 1929-1944.

Fernie, A. R., Carrari, F., & Sweetlove, L. J. (2004). Respiratory metabolism: glycolysis, the TCA cycle and mitochondrial electron transport. Current opinion in plant biology, 7(3), 254-261.

Fernie, A. R., Roscher, A., Ratcliffe, R. G., & Kruger, N. J. (2001). Fructose 2, 6-bisphosphate activates pyrophosphate: fructose-6-phosphate 1-phosphotransferase and increases triose phosphate to hexose phosphate cycling in heterotrophic cells. Planta, 212(2), 250-263.

Fernie, A. R., Tauberger, E., Lytovchenko, A., Roessner, U., Willmitzer, L., & Trethewey, R. N. (2002). Antisense repression of cytosolic phosphoglucomutase in potato (*Solanum tuberosum*) results in severe growth retardation, reduction in tuber number and altered carbon metabolism. Planta, 214(4), 510-520.

Fernie, A. R., Willmitzer, L., & Trethewey, R. N. (2002). Sucrose to starch: a transition in molecular plant physiology. Trends in plant science, 7(1), 35-41.

Fichtner, F., Barbier, F. F., Feil, R., Watanabe, M., Annunziata, M. G., Chabikwa, T. G., ... & Lunn, J. E. (2017). Trehalose 6-phosphate is involved in triggering axillary bud outgrowth in garden pea (pisum sativum L.). The Plant Journal, 92(4), 611-623.

Fletcher, G. M., & Dale, J. E. (1974). Growth of tiller buds in barley: effects of shade treatment and mineral nutrition. Annals of Botany, 38(1), 63-76.

Foo, E., Bullier, E., Goussot, M., Foucher, F., Rameau, C., and Beveridge, C. A. (2005). The branching gene RAMOSUS1 mediates interactions among two novel signals and auxin in pea. The Plant Cell, 17(2), 464-474.

Foreman, J., Demidchik, V., Bothwell, J. H., Mylona, P., Miedema, H., Torres, M. A., ... & Davies, J. M. (2003). Reactive oxygen species produced by NADPH oxidase regulate plant cell growth. Nature, 422(6930), 442.

Frank, A., Matiolli, C. C., Viana, A. J., Hearn, T. J., Kusakina, J., Belbin, F. E., ... & Cragg-Barber, K. (2018). Circadian entrainment in Arabidopsis by the sugar-responsive transcription factor bZIP63. Current Biology, 28(16), 2597-2606.

Gakière, B., Hao, J., de Bont, L., Pétriacq, P., Nunes-Nesi, A., & Fernie, A. R. (2018). NAD+ Biosynthesis and Signaling in Plants. Critical Reviews in Plant Sciences, 37(4), 259-307.

Garapati, P., Feil, R., John, E. L., Van Dijck, P., Balazadeh, S., & Mueller-Roeber, B. (2015). Transcription factor ATAF1 integrates carbon starvation responses with trehalose metabolism. Plant physiology, pp-00917.

Garbez, M., Galopin, G., Sigogne, M., Favre, P., Demotes-Mainard, S. and Symoneaux, R. (2015). Assessing the visual aspect of rotating virtual rose bushes by a labeled sorting task. Food Quality and Preference, 40, Part B, 287-295.

Gibson, S. I. (2005). Control of plant development and gene expression by sugar signaling. Current opinion in plant biology, 8(1), 93-102.

Girault, T., Abidi, F., Sigogne, M., PELLESCHI-TRAVIER, S. A. N. D. R. I. N. E., Boumaza, R., Sakr, S., and Leduc, N. (2010). Sugars are under light control during bud burst in Rosa sp. Plant, cell and environment, 33(8), 1339-1350.

Godt, D. E., & Roitsch, T. (1997). Regulation and tissue-specific distribution of mRNAs for three extracellular invertase isoenzymes of tomato suggests an important function in establishing and maintaining sink metabolism. Plant physiology, 115(1), 273-282.

Gomez-Roldan, V., Fermas, S., Brewer, P. B., Puech-Pagès, V., Dun, E. A., Pillot, J. P., ... & Bouwmeester, H. (2008). Strigolactone inhibition of shoot branching. Nature, 455(7210), 189.

González-Grandío, E., Pajoro, A., Franco-Zorrilla, J. M., Tarancón, C., Immink, R. G., & Cubas, P. (2017). Abscisic acid signaling is controlled by a BRANCHED1/HD-ZIP I cascade in Arabidopsis axillary buds. Proceedings of the National Academy of Sciences, 114(2), E245-E254.

González-Grandío, E., Poza-Carrión, C., Sorzano, C. O. S., & Cubas, P. (2013). BRANCHED1 promotes axillary bud dormancy in response to shade in Arabidopsis. The Plant Cell, tpc-112.

González-Grandío, E., Poza-Carrión, C., Sorzano, C. O. S., & Cubas, P. (2013). BRANCHED1 promotes axillary bud dormancy in response to shade in Arabidopsis. The Plant Cell, 25(3), 834-850.

Grandjean, O., Vernoux, T., Laufs, P., Belcram, K., Mizukami, Y., & Traas, J. (2004). In vivo analysis of cell division, cell growth, and differentiation at the shoot apical meristem in Arabidopsis. The Plant Cell, 16(1), 74-87.

Granot, D.; Kelly, G.; Stein, O.; David-Schwartz, R. Substantial roles of hexokinase and fructokinase in the effects of sugars on Plant Physiol. and development. J. Exp. Bot. 2013, 65, 809–819.

Guerriero, G., Giorno, F., Folgado, R., Printz, B., Baric, S., & Hausman, J. F. (2014). Callose and cellulose synthase gene expression analysis from the tight cluster to the full bloom stage and during early fruit development in Malus× domestica. Journal of plant research, 127(1), 173-183.

Hanson, J., Hanssen, M., Wiese, A., Hendriks, M. M., & Smeekens, S. (2008). The sucrose regulated transcription factor bZIP11 affects amino acid metabolism by regulating the expression of ASPARAGINE SYNTHETASE1 and PROLINE DEHYDROGENASE2. The Plant Journal, 53(6), 935-949.

Harthill, J.E.; Meek, S.E.; Morrice, N.; Peggie, M.W.; Borch, J.; Wong, B.H.; MacKintosh, C. Phosphorylation and 14tor3 binding of Arabidopsis trehalose-phosphate synthase 5 in response to 2-deoxyglucose. Plant J. 2006, 47, 211–223.

Hayward, A., Stirnberg, P., Beveridge, C., and Leyser, O. (2009). Interactions between auxin and strigolactone in shoot branching control. Plant physiology, 151(1), 400-412.

Hei, S., Liu, Z., Huang, A., & She, X. (2018). The regulator of G-protein signalling protein mediates D-glucose-induced stomatal closure via triggering hydrogen peroxide and nitric oxide production in Arabidopsis. Functional Plant Biology, 45(5), 509-518.

Heitman, J., Movva, N. R., & Hall, M. N. (1991). Targets for cell cycle arrest by the immunosuppressant rapamycin in yeast. Science, 253(5022), 905-909.

Henry, C., Rabot, A., Laloi, M., Mortreau, E., Sigogne, M., Leduc, N., . et al. (2011). Regulation of RhSUC2, a sucrose transporter, is correlated with the light control of bud burst in Rosa sp. Plant, cell and environment, 34(10), 1776-1789.

Hernandez-Garcia, C. M., Bouchard, R. A., Rushton, P. J., Jones, M. L., Chen, X., Timko, M. P., & Finer, J. J. (2010). High level transgenic expression of soybean (Glycine max) GmERF and Gmubi gene promoters isolated by a novel promoter analysis pipeline. BMC plant biology, 10(1), 237.

Hey, S. J., Byrne, E., & Halford, N. G. (2009). The interface between metabolic and stress signalling. Annals of Botany, 105(2), 197-203.

Hieno, A., Naznin, H. A., Inaba-Hasegawa, K., Yokogawa, T., Hayami, N., Nomoto, M., ... & Matsui, M. (2019). Transcriptome analysis and identification of a transcriptional regulatory network in the response to H2O2. Plant physiology, pp-01426.

Hofmann, M., & Roitsch, T. (2000). The hexokinase inhibitor glucosamine exerts a concentration dependent dual effect on protein kinase activity in vitro. Journal of Plant Physiology, 157(1), 13-16.

Holaday, A. S., Martindale, W., Alred, R., Brooks, A. L., & Leegood, R. C. (1992). Changes in activities of enzymes of carbon metabolism in leaves during exposure of plants to low temperature. Plant Physiology, 98(3), 1105-1114.

Horacio, P., & Martinez-Noel, G. (2013). Sucrose signaling in plants: a world yet to be explored. Plant signaling & behavior, 8(3), e23316.

Hothersall, J. S., Gordge, M., & Noronha-Dutra, A. A. (1998). Inhibition of NADPH supply by 6-aminonicotinamide: effect on glutathione, nitric oxide and superoxide in J774 cells. FEBS letters, 434(1-2), 97-100.

Huner, N. P., Öquist, G., & Sarhan, F. (1998). Energy balance and acclimation to light and cold. Trends in plant science, 3(6), 224-230.

Hwang, Y. S., Karrer, E. E., Thomas, B. R., Chen, L., & Rodriguez, R. L. (1998). Three cis-elements required for rice α-amylase Amy3D expression during sugar starvation. Plant molecular biology, 36(3), 331-341.

Ikeuchi, M., Sugimoto, K., & Iwase, A. (2013). Plant callus: mechanisms of induction and repression. The Plant Cell, tpc-113.

Jana, S., & Shekhawat, G. S. (2011). Plant growth regulators, adenine sulfate and carbohydrates regulate organogenesis and in vitro flowering of Anethum graveolens. Acta Physiologiae Plantarum, 33(2), 305-311.
Jang, J. C., & Sheen, J. (1994). Sugar sensing in higher plants. The Plant Cell, 6(11), 1665-1679.
Jang, J. C., León, P., Zhou, L., & Sheen, J. (1997). Hexokinase as a sugar sensor in higher plants. The Plant Cell, 9(1), 5-19.
Janse van Rensburg, H. C., & Van den Ende, W. (2018). UDP-Glucose: A Potential Signaling Molecule in Plants?. Frontiers in plant science, 8, 2230.
Jensen, K. H., Savage, J. A., & Holbrook, N. M. (2013). Optimal concentration for sugar transport in plants. Journal of the Royal Society Interface, 10(83), 20130055.
Jiang, H. and Egli, D. B. (1993). Shade Induced Changes in Flower and Pod Number and Flower and Fruit Abscission in Soybean. Agronomy Journal, 85, 221-225.
Jiang, L., Liu, X., Xiong, G., Liu, H., Chen, F., Wang, L., ... & Yi, W. (2013). DWARF 53 acts as a repressor of strigolactone signalling in rice. Nature, 504(7480), 401.
Jiao, Y., Wang, Y., Xue, D., Wang, J., Yan, M., Liu, G., et al. (2010). Regulation of OsSPL14 by OsmiR156 defines ideal plant architecture in rice. Nature genetics, 42(6), 541.
Jin JP, Tian F, Yang DC, Meng YQ, Kong L, Luo JC and Gao G. (2017). PlantTFDB 4.0: toward a central hub for transcription factors and regulatory interactions in plants. Nucleic Acids Research, 45(D1):D1040-D1045.
Johnson, X., Brcich, T., Dun, E. A., Goussot, M., Haurogné, K., Beveridge, C. A., et al. (2006). Branching genes are conserved across species. Genes controlling a novel signal in pea are coregulated by other long-distance signals. Plant physiology, 142(3), 1014-1026.
Jossier, M., Bouly, J. P., Meimoun, P., Arjmand, A., Lessard, P., Hawley, S., ... & Thomas, M. (2009). SnRK1 (SNF1-related kinase 1) has a central role in sugar and ABA signalling in Arabidopsis thaliana. The Plant Journal, 59(2), 316-328.
Kalousek P, Buchtova D, Balla J, Reinoehl V, Prochazka S (2010) Cytokinins and polar transport of auxin in axillary pea buds. Acta Univ Agric Silvic Mendel Brun 58: 79–87
Kang, S. G., Price, J., Lin, P. C., Hong, J. C., & Jang, J. C. (2010). The Arabidopsis bZIP1 transcription factor is involved in sugar signaling, protein networking, and DNA binding. Molecular plant, 3(2), 361-373.
Kang, S. G., Price, J., Lin, P. C., Hong, J. C., & Jang, J. C. (2010). The Arabidopsis bZIP1 transcription factor is involved in sugar signaling, protein networking, and DNA binding. Molecular plant, 3(2), 361-373.
Karve, A., & Moore, B. D. (2009). Function of Arabidopsis hexokinase-like1 as a negative regulator of plant growth. Journal of experimental botany, 60(14), 4137-4149.
Karve, A., Xia, X., & Moore, B. D. (2012). Arabidopsis Hexokinase-Like1 and Hexokinase1 form a critical node in mediating plant glucose and ethylene responses. Plant physiology, 158, 1965–1975..
Kebrom, T. H., & Mullet, J. E. (2016). Transcriptome profiling of tiller buds provides new insights into PhyB regulation of tillering and indeterminate growth in sorghum. Plant physiology, pp-00014.
Kebrom, T. H., and Mullet, J. E. (2015). Photosynthetic leaf area modulates tiller bud outgrowth in sorghum. Plant, cell and environment, 38(8), 1471-1478.
Kebrom, T. H., Brutnell, T. P., and Finlayson, S. A. (2010). Suppression of sorghum axillary bud outgrowth by shade, phyB and defoliation signalling pathways. Plant, cell and environment, 33(1), 48-58.
Kebrom, T. H., Burson, B. L., and Finlayson, S. A. (2006). Phytochrome B represses Teosinte Branched1 expression and induces sorghum axillary bud outgrowth in response to light signals. Plant Physiology, 140(3), 1109-1117.
Kebrom, T., Chandler, P., Swain, S., King, R., Richards, R., and Spielmeyer, W. (2012). Inhibition of tiller bud outgrowth in the tin mutant of wheat is associated with precocious internode development. Plant Physiology, pp-112.
Kerr, S. C., & Beveridge, C. A. (2017). IPA1: a direct target of SL signaling. Cell research, 27(10), 1191.
Keurentjes, J. J., Fu, J., De Vos, C. R., Lommen, A., Hall, R. D., Bino, R. J., ... & Koornneef, M. (2006). The genetics of plant metabolism. Nature genetics, 38(7), 842.
Kitomi, Y., Ito, H., Hobo, T., Aya, K., Kitano, H., & Inukai, Y. (2011). The auxin responsive AP2/ERF transcription factor CROWN ROOTLESS5 is involved in crown root initiation in rice through the induction of OsRR1, a type-A response regulator of cytokinin signaling. The Plant Journal, 67(3), 472-484.

Kleinow, T., Himbert, S., Krenz, B., Jeske, H., & Koncz, C. (2009). NAC domain transcription factor ATAF1 interacts with SNF1-related kinases and silencing of its subfamily causes severe developmental defects in Arabidopsis. Plant Science, 177(4), 360-370.

Klopotek, Y., Franken, P., Klaering, H. P., Fischer, K., Hause, B., Hajirezaei, M. R., & Druege, U. (2016). A higher sink competitiveness of the rooting zone and invertases are involved in dark stimulation of adventitious root formation in Petunia hybrida cuttings. Plant Science, 243, 10-22.

Koch, K. (2004). Sucrose metabolism: regulatory mechanisms and pivotal roles in sugar sensing and plant development. Current opinion in plant biology, 7(3), 235-246.

Köhler, R. H., Zipfel, W. R., Webb, W. W., & Hanson, M. R. (1997). The green fluorescent protein as a marker to visualize plant mitochondria in vivo. The plant journal, 11(3), 613-621.

Kravchenko, A., Citerne, S., Jéhanno, I., Bersimbaev, R. I., Veit, B., Meyer, C., & Leprince, A. S. (2015). Mutations in the Arabidopsis Lst8 and Raptor genes encoding partners of the TOR complex, or inhibition of TOR activity decrease abscisic acid (ABA) synthesis. Biochemical and biophysical research communications, 467(4), 992-997.

Kruger, N. J., & von Schaewen, A. (2003). The oxidative pentose phosphate pathway: structure and organisation. Current opinion in plant biology, 6(3), 236-246.

Kunz, H. H., Zamani-Nour, S., Häusler, R. E., Ludewig, K., Schroeder, J. I., Malinova, I., ... & Gierth, M. (2014). Loss of cytosolic phosphoglucose isomerase affects carbohydrate metabolism in leaves and is essential for fertility of Arabidopsis. Plant physiology, 166(2), 753-765.

Kunz, S., Gardeström, P., Pesquet, E., & Kleczkowski, L. A. (2015). Hexokinase 1 is required for glucose-induced repression of bZIP63, At5g22920, and BT2 in Arabidopsis. Frontiers in plant science, 6, 525.

Kuroda, H., Masuda, T., Fusada, N., Ohta, H., & Takamiya, K. I. (2001). Cytokinin–induced Transcriptional Activation of NADPH–protochlorophyllide Oxidoreductase Gene in Cucumber. Journal of Plant Research, 114(1), 1-7.

Landi, S., Nurcato, R., De Lillo, A., Lentini, M., Grillo, S., & Esposito, S. (2016). Glucose-6-phosphate dehydrogenase plays a central role in the response of tomato (Solanum lycopersicum) plants to short and long-term drought. Plant Physiology and Biochemistry, 105, 79-89.

Lange, K., & Proft, E. R. (1970). Inhibition of the 6-phosphogluconate dehydrogenase in the rat kidney by 6-aminonicotinamide. Naunyn-Schmiedebergs Archiv für Pharmakologie, 267(2), 177-180.

Lantzouni, O., Klermund, C., & Schwechheimer, C. (2017). Largely additive effects of gibberellin and strigolactone on gene expression in Arabidopsis thaliana seedlings. The Plant Journal, 92(5), 924-938.

Lastdrager, J., Hanson, J., & Smeekens, S. (2014). Sugar signals and the control of plant growth and development. Journal of experimental botany, 65(3), 799-807.

Le Moigne, M. A., Guérin, V., Furet, P. M., Billard, V., Lebrec, A., Spíchal, L., ... & Vian, A. (2018). Asparagine and sugars are both required to sustain secondary axis elongation after bud outgrowth in Rosa hybrida. Journal of plant physiology, 222, 17-27.

LeClere, S., Schmelz, E. A., & Chourey, P. S. (2010). Sugar levels regulate tryptophan-dependent auxin biosynthesis in developing maize kernels. Plant Physiology, 153(1), 306-318.

Lee, H. C., Kim, J. S., Jang, W., & Kim, S. Y. (2010). High NADPH/NADP+ ratio improves thymidine production by a metabolically engineered Escherichia coli strain. Journal of biotechnology, 149(1-2), 24-32.

Lee, Y. C., Lu, C. A., Casaretto, J., & Yu, S. M. (2003). An ABA-responsive bZIP protein, OsBZ8, mediates sugar repression of α-amylase gene expression. Physiologia Plantarum, 119(1), 78-86.

Lejay, L., Wirth, J., Pervent, M., Cross, J. M. F., Tillard, P., & Gojon, A. (2008). Oxidative pentose phosphate pathway-dependent sugar sensing as a mechanism for regulation of root ion transporters by photosynthesis. Plant physiology, 146(4), 2036-2053.

Lemerle, D., Verbeek, B., Cousens, R. d., and Coombes, N.E. (1996). The potential for selecting wheat varieties strongly competitive against weeds. Weed Research, 36, 505–513.

Lemoine, R., La Camera, S., Atanassova, R., Dédaldéchamp, F., Allario, T., Pourtau, N., ... & Faucher, M. (2013). Source-to-sink transport of sugar and regulation by environmental factors. Frontiers in plant science, 4, 272.

León, P., & Sheen, J. (2003). Sugar and hormone connections. Trends in plant science, 8(3), 110-116.

Leyser, O. (2009). The control of shoot branching: an example of plant information processing. Plant, cell and environment, 32(6), 694-703.

Li, C. J., and Bangerth, F. (1999). Autoinhibition of indoleacetic acid transport in the shoots of two-branched pea (Pisum sativum) plants and its relationship to correlative dominance. Physiologia Plantarum, 106(4), 415-420.

Li, L., & Sheen, J. (2016). Dynamic and diverse sugar signaling. Current opinion in plant biology, 33, 116-125.
Li, W., Ma, M., Feng, Y., Li, H., Wang, Y., Ma, Y., ... & Guo, H. (2015). EIN2-directed translational regulation of ethylene signaling in Arabidopsis. Cell, 163(3), 670-683.
Lilley, J. L. S., Gee, C. W., Sairanen, I., Ljung, K., & Nemhauser, J. L. (2012). An endogenous carbon-sensing pathway triggers increased auxin flux and hypocotyl elongation. Plant Physiology, 160(4), 2261-2270.
Li-Marchetti, C., Le Bras, C., Chastellier, A., Relion, D., Morel, P., Sakr, S., ... & Crespel, L. (2017). 3D phenotyping and QTL analysis of a complex character: rose bush architecture. Tree Genetics & Genomes, 13(5), 112.
Lin, X. Y., Ye, Y. Q., Fan, S. K., Jin, C. W., & Zheng, S. J. (2016). Increased sucrose accumulation regulates iron-deficiency responses by promoting auxin signaling in Arabidopsis plants. Plant physiology, 170(2), 907-920.
Liu, J., Cheng, X., Liu, P., and Sun, J. (2017). miR156-targeted SBP-Box transcription factors interact with DWARF53 to regulate TEOSINTE BRANCHED1 and BARREN STALK1 expression in bread wheat. Plant physiology, 174(3), 1931-1948.
Liu, Y. J., Wang, G. L., Ma, J., Xu, Z. S., Wang, F., & Xiong, A. S. (2018). Transcript profiling of sucrose synthase genes involved in sucrose metabolism among four carrot (Daucus carota L.) cultivars reveals distinct patterns. BMC plant biology, 18(1), 8.
Liu, Y., & Bassham, D. C. (2010). TOR is a negative regulator of autophagy in Arabidopsis thaliana. PLoS One, 5(7), e11883.
Ljung, K., Bhalerao, R. P., & Sandberg, G. (2001). Sites and homeostatic control of auxin biosynthesis in Arabidopsis during vegetative growth. The plant journal, 28(4), 465-474.
Long, J. C., Zhao, W., Rashotte, A. M., Muday, G. K., & Huber, S. C. (2002). Gravity-stimulated changes in auxin and invertase gene expression in maize pulvinal cells. Plant Physiology, 128(2), 591-602.
Lu, C. A., Lim, E. K., & Yu, S. M. (1998). Sugar response sequence in the promoter of a rice α-amylase gene serves as a transcriptional enhancer. Journal of Biological Chemistry, 273(17), 10120-10131.
Lu, Z., Yu, H., Xiong, G., Wang, J., Jiao, Y., Liu, G., ... & Fu, X. (2013). Genome-wide binding analysis of the transcription activator ideal plant architecture1 reveals a complex network regulating rice plant architecture. The Plant Cell, 25(10), 3743-3759.
Lunt, S. Y., & Vander Heiden, M. G. (2011). Aerobic glycolysis: meeting the metabolic requirements of cell proliferation. Annual review of cell and developmental biology, 27, 441-464.
Ma, J., Hanssen, M., Lundgren, K., Hernández, L., Delatte, T., Ehlert, A., ... & Smeekens, S. (2011). The sucrose-regulated Arabidopsis transcription factor bZIP11 reprograms metabolism and regulates trehalose metabolism. New Phytologist, 191(3), 733-745.
Martín-Fontecha, E. S., Tarancon, C., & Cubas, P. (2018). To grow or not to grow, a power-saving program induced in dormant buds. Current opinion in plant biology, 41, 102-109.
Martín-Trillo, M., & Cubas, P. (2010). TCP genes: a family snapshot ten years later. Trends in plant science, 15(1), 31-39.
Mason, M. G., Ross, J. J., Babst, B. A., Wienclaw, B. N., and Beveridge, C. A. (2014). Sugar demand, not auxin, is the initial regulator of apical dominance. Proceedings of the National Academy of Sciences, 111(16), 6092-6097.
Matsumura, H., Xie, Y., Shirakata, S., Inoue, T., Yoshinaga, T., Ueno, Y., ... & Kai, Y. (2002). Crystal structures of C4 form maize and quaternary complex of E. coli phosphoenolpyruvate carboxylases. Structure, 10(12), 1721-1730.
Maurel, K., Sakr, S., Gerbe, F., Guilliot, A., Bonhomme, M., Rageau, R., and Pétel, G. (2004). Sorbitol uptake is regulated by glucose through the hexokinase pathway in vegetative peach-tree buds. Journal of experimental botany, 55(398), 879-888.
Mayer, K. F., Schoof, H., Haecker, A., Lenhard, M., Jürgens, G., & Laux, T. (1998). Role of WUSCHEL in regulating stem cell fate in the Arabidopsis shoot meristem. Cell, 95(6), 805-815.
Menand, B.; Desnos, T.; Nussaume, L.; Berger, F.; Bouchez, D.; Meyer, C.; Robaglia, C. Expression and disruption of the Arabidopsis TOR (target of rapamycin) gene. Proc. Natl. Acad. Sci. USA 2002, 99, 6422–6427.
Mishra, B. S., Singh, M., Aggrawal, P., & Laxmi, A. (2009). Glucose and auxin signaling interaction in controlling Arabidopsis thaliana seedlings root growth and development. PloS one, 4(2), e4502.
Misteli, T., & Spector, D. L. (1997). Applications of the green fluorescent protein in cell biology and biotechnology. Nature biotechnology, 15(10), 961.

Mitchell, K. J. (1953). Influence of light and temperature on the growth of ryegrass (Lolium spp.) I. Pattern of vegetative development. Physiologia plantarum, 6(1), 21-46.
Moon, M. W., Kim, H. J., Oh, T. K., Shin, C. S., Lee, J. S., Kim, S. J., & Lee, J. K. (2005). Analyses of enzyme II gene mutants for sugar transport and heterologous expression of fructokinase gene in Corynebacterium glutamicum ATCC 13032. FEMS microbiology letters, 244(2), 259-266.
Moore, B., Zhou, L., Rolland, F., Hall, Q., Cheng, W. H., Liu, Y. X., ... & Sheen, J. (2003). Role of the Arabidopsis glucose sensor HXK1 in nutrient, light, and hormonal signaling. Science, 300(5617), 332-336.
Morey, S. R., Hirose, T., Hashida, Y., Miyao, A., Hirochika, H., Ohsugi, R., ... & Aoki, N. (2018). Genetic Evidence for the Role of a Rice Vacuolar Invertase as a Molecular Sink Strength Determinant. Rice, 11(1), 6.
Mori, H., Shimizu, S., & Madoka, Y. (1998). Molecular mechanisms of apical dominance from the point of view of cell cycle regulation. Plant and cell physiology, 39, S3-S3.
Moritz, B., Striegel, K., de Graaf, A. A., & Sahm, H. (2000). Kinetic properties of the glucose-6-phosphate and 6 phosphogluconate dehydrogenases from Corynebacterium glutamicum and their application for predicting pentose phosphate pathway flux in vivo. European journal of biochemistry, 267(12), 3442-3452.
Morris, D. A. (1977). Transport of exogenous auxin in two-branched dwarf pea seedlings (Pisum sativum L.). Planta, 136(1), 91-96.
Morris, D. A., & Arthur, E. D. (1985). Invertase activity, carbohydrate metabolism and cell expansion in the stem of Phaseolus vulgaris L. Journal of Experimental Botany, 36(4), 623-633.
Müller, D., and Leyser, O. (2011). Auxin, cytokinin and the control of shoot branching. Annals of Botany, 107(7), 1203-1212.
Nadwodnik, J., & Lohaus, G. (2008). Subcellular concentrations of sugar alcohols and sugars in relation to phloem translocation in Plantago major, Plantago maritima, Prunus persica, and Apium graveolens. Planta, 227(5), 1079-1089.
Nietzsche, M., Landgraf, R., Tohge, T., & Börnke, F. (2016). A protein–protein interaction network linking the energy-sensor kinase SnRK1 to multiple signaling pathways in Arabidopsis thaliana. Current Plant Biology, 5, 36-44.
Nunes, C. M., O'Hara, L., Primavesi, L., Delatte, T., Schluepmann, H., Somsen, G., ... & Paul, M. J. (2013). The trehalose 6-phosphate/SnRK1 signalling pathway primes growth recovery following relief of sink limitation. Plant physiology, pp-113.
Nuruzzaman, M., Manimekalai, R., Sharoni, A. M., Satoh, K., Kondoh, H., Ooka, H., & Kikuchi, S. (2010). Genome-wide analysis of NAC transcription factor family in rice. Gene, 465(1), 30-44.
Ohshima, T., Hayashi, H., & Chino, M. (1990). Collection and chemical composition of pure phloem sap from Zea mays L. Plant and Cell Physiology, 31(5), 735-737.
Olatunji, D., Geelen, D., & Verstraeten, I. (2017). Control of endogenous auxin levels in plant root development. International journal of molecular sciences, 18(12), 2587.
Olsen, A. N., Ernst, H. A., Leggio, L. L., & Skriver, K. (2005). NAC transcription factors: structurally distinct, functionally diverse. Trends in plant science, 10(2), 79-87.
Overmyer, K., Brosché, M., & Kangasjärvi, J. (2003). Reactive oxygen species and hormonal control of cell death. Trends in plant science, 8(7), 335-342.
Paul, M. J., Primavesi, L. F., Jhurreea, D., & Zhang, Y. (2008). Trehalose metabolism and signaling. Annu. Rev. Plant Biol., 59, 417-441.
Péron, T., Candat, A., Montiel, G., Veronesi, C., Macherel, D., Delavault, P., & Simier, P. (2017). New insights into phloem unloading and expression of sucrose transporters in vegetative sinks of the parasitic plant Phelipanche ramosa L.(Pomel). Frontiers in plant science, 7, 2048.
Phillips, I. (1975). Apical dominance. Annual Review of Plant Physiology, 26(1), 341-367.
Plaxton, W. C. (1996). The organization and regulation of plant glycolysis. Annual review of plant biology, 47(1), 185-214.
Polyn, S., Willems, A., & De Veylder, L. (2015). Cell cycle entry, maintenance, and exit during plant development. Current Opinion in Plant Biology, 23, 1-7.
Poza-Carrión, C., Aguilar-Martínez, J. A., & Cubas, P. (2007). Role of TCP gene BRANCHED1 in the control of shoot branching in Arabidopsis. Plant signaling & behavior, 2(6), 551-552.
Prado, N., de Dios Alché, J., Casado-Vela, J., Mas, S., Villalba, M., Rodríguez, R., & Batanero, E. (2014). Nanovesicles are secreted during pollen germination and pollen tube growth: a possible role in fertilization. Molecular plant, 7(3), 573-577.

Pugin, A., Frachisse, J. M., Tavernier, E., Bligny, R., Gout, E., Douce, R., & Guern, J. (1997). Early events induced by the elicitor cryptogein in tobacco cells: involvement of a plasma membrane NADPH oxidase and activation of glycolysis and the pentose phosphate pathway. The Plant Cell, 9(11), 2077-2091.
Puranik, S., Sahu, P. P., Srivastava, P. S., & Prasad, M. (2012). NAC proteins: regulation and role in stress tolerance. Trends in plant science, 17(6), 369-381.
Rabot, A., Henry, C., Baaziz, K. B., Mortreau, E., Azri, W., Lothier, J., et al. (2012). Insight into the role of sugars in bud burst under light in the rose. Plant and Cell Physiology, 53(6), 1068-1082.
Rabot, A., Portemer, V., Péron, T., Mortreau, E., Leduc, N., Hamama, L., ... & Le Gourrierec, J. (2014). Interplay of sugar, light and gibberellins in expression of Rosa hybrida vacuolar invertase 1 regulation. Plant and Cell Physiology, 55(10), 1734-1748.
Rameau, C., Bertheloot, J., Leduc, N., Andrieu, B., Foucher, F., & Sakr, S. (2015). Multiple pathways regulate shoot branching. Frontiers in plant science, 5, 741.
Rashotte, A. M., Mason, M. G., Hutchison, C. E., Ferreira, F. J., Schaller, G. E., & Kieber, J. J. (2006). A subset of Arabidopsis AP2 transcription factors mediates cytokinin responses in concert with a two-component pathway. Proceedings of the National Academy of Sciences, 103(29), 11081-11085.
Raveneau, M. P., Benamar, A., & Macherel, D. (2017). Water content, adenylate kinase, and mitochondria drive adenylate balance in dehydrating and imbibing seeds. Journal of experimental botany, 68(13), 3501-3512.
Reboredo-Rodríguez, P., González-Barreiro, C., Cancho-Grande, B., Simal-Gándara, J., Giampieri, F., Forbes-Hernández, T. Y., ... & Varela-López, A. (2018). Effect of pistachio kernel extracts in MCF-7 breast cancer cells: Inhibition of cell proliferation, induction of ros production, modulation of glycolysis and of mitochondrial respiration. Journal of functional foods, 45, 155-164.
Reitzer, L. J., Wice, B. M., & Kennell, D. (1980). The pentose cycle. Control and essential function in HeLa cell nucleic acid synthesis. Journal of Biological Chemistry, 255(12), 5616-5626.
Revel, S. M., Bart, J. J., Luo, Z., Oplaat, C., Susan, E. L., Mark, W. W., et al. (2015). Environmental control of branching in petunia. Plant physiology, pp-00486.
Richards, R. A. (2000). Selectable traits to increase crop photosynthesis and yield of grain crops. Journal of Experimental Botany, 51, 447-458.
Roessner-Tunali, U., Hegemann, B., Lytovchenko, A., Carrari, F., Bruedigam, C., Granot, D., & Fernie, A. R. (2003). Metabolic profiling of transgenic tomato plants overexpressing hexokinase reveals that the influence of hexose phosphorylation diminishes during fruit development. Plant Physiology, 133(1), 84-99.
Roitsch, T., & González, M. C. (2004). Function and regulation of plant invertases: sweet sensations. Trends in plant science, 9(12), 606-613.
Rolland, F., Baena-Gonzalez, E., & Sheen, J. (2006). Sugar sensing and signaling in plants: conserved and novel mechanisms. Annu. Rev. Plant Biol., 57, 675-709.
Roman, H., Girault, T., Barbier, F., Péron, T., Brouard, N., Pěnčík, A., ... & Le Gourrierec, J. (2016). Cytokinins are initial targets of light in the control of bud outgrowth. Plant physiology, 172(1), 489-509.
Ruan, Y. L. (2014). Sucrose metabolism: gateway to diverse carbon use and sugar signaling. Annual review of plant biology, 65, 33-67.
Rush, G. F., Gorski, J. R., Ripple, M. G., Sowinski, J., Bugelski, P., & Hewitt, W. R. (1985). Organic hydroperoxide-induced lipid peroxidation and cell death in isolated hepatocytes. Toxicology and applied pharmacology, 78(3), 473-483.
Ruttink, T., Arend, M., Morreel, K., Storme, V., Rombauts, S., Fromm, J., ... & Rohde, A. (2007). A molecular timetable for apical bud formation and dormancy induction in poplar. The Plant Cell, 19(8), 2370-2390.
Sachs, T., & Thimann, K. V. (1964). Release of lateral buds from apical dominance. Nature, 201(4922), 939-940.
Sachs, T., & Thimann, K. V. (1967). The role of auxins and cytokinins in the release of buds from dominance. American Journal of Botany, 54(1), 136-144.
Sagar, M., Chervin, C., Mila, I., Hao, Y., Roustan, J. P., Benichou, M., ... & Pech, J. C. (2013). SlARF4, an auxin response factor involved in the control of sugar metabolism during tomato fruit development. Plant physiology, 161(3), 1362-1374.
Sairanen, I., Novák, O., Pěnčík, A., Ikeda, Y., Jones, B., Sandberg, G., & Ljung, K. (2012). Soluble carbohydrates regulate auxin biosynthesis via PIF proteins in Arabidopsis. The Plant Cell, 24(12), 4907-4916.

Sakr, S., Wang, M., Dédaldéchamp, F., Perez-Garcia, M. D., Ogé, L., Hamama, L., & Atanassova, R. (2018). The Sugar-Signaling Hub: Overview of Regulators and Interaction with the Hormonal and Metabolic Network. International journal of molecular sciences, 19(9), 2506.

Salam, B. B., Malka, S. K., Zhu, X., Gong, H., Ziv, C., Teper-Bamnolker, P., ... & Eshel, D. (2017). Etiolated stem branching is a result of systemic signaling associated with sucrose level. Plant physiology, 175(2), 734-745.

Savvides, A., van Ieperen, W., Dieleman, J. A., & Marcelis, L. F. (2017). Phenotypic plasticity to altered apical bud temperature in Cucumis sativus: more leaves-smaller leaves and vice versa. Plant, cell & environment, 40(1), 69-79.

Schaffer, A. A., & Petreikov, M. (1997). Sucrose-to-starch metabolism in tomato fruit undergoing transient starch accumulation. Plant Physiology, 113(3), 739-746.

Schepetilnikov, M., Dimitrova, M., Mancera-Martínez, E., Geldreich, A., Keller, M., & Ryabova, L. A. (2013). TOR and S6K1 promote translation reinitiation of uORF-containing mRNAs via phosphorylation of eIF3h. The EMBO journal, 32(8), 1087-1102.

Schluepmann, H., Pellny, T., van Dijken, A., Smeekens, S., & Paul, M. (2003). Trehalose 6-phosphate is indispensable for carbohydrate utilization and growth in Arabidopsis thaliana. Proceedings of the National Academy of Sciences, 100(11), 6849-6854.

Seale, M., Bennett, T., & Leyser, O. (2017). BRC1 expression regulates bud activation potential, but is not necessary or sufficient for bud growth inhibition in Arabidopsis. Development, dev-145649.

Serrano-Mislata, A., Schiessl, K., & Sablowski, R. (2015). Active control of cell size generates spatial detail during plant organogenesis. Current Biology, 25(22), 2991-2996.

Shimizu, S., & Mori, H. (1998). Analysis of cycles of dormancy and growth in pea axillary buds based on mRNA accumulation patterns of cell cycle-related genes. Plant and cell physiology, 39(3), 255-262.

Shkolnik-Inbar, D., & Bar-Zvi, D. (2010). ABI4 mediates abscisic acid and cytokinin inhibition of lateral root formation by reducing polar auxin transport in Arabidopsis. The Plant Cell, tpc-110.

Sibéril, Y., Doireau, P., & Gantet, P. (2001). Plant bZIP G-box binding factors. Modular structure and activation mechanisms. European Journal of Biochemistry, 268(22), 5655-5666.

Simon, S., Morel, K., Durand, E., Brevalle, G., Girard, T., and Lauri, P.-É. (2011). Aphids at crossroads: when branch architecture alters aphid infestation patterns in the apple tree. Trees, 26, 273–282.

Skoog, F., & Thimann, K. V. (1934). Further experiments on the inhibition of the development of lateral buds by growth hormone. Proceedings of the National Academy of Sciences, 20(8), 480-485.

Smeekens, S., Ma, J., Hanson, J., & Rolland, F. (2010). Sugar signals and molecular networks controlling plant growth. Current opinion in plant biology, 13(3), 273-278.

Snow, R. (1929). The young leaf as the inhibiting organ. New Phytologist, 28(5), 345-358.

Song, X., Lu, Z., Yu, H., Shao, G., Xiong, J., Meng, X., ... & Yao, X. F. (2017). IPA1 functions as a downstream transcription factor repressed by D53 in strigolactone signaling in rice. Cell research, 27(9), 1128.

Sorefan, K., Booker, J., Haurogné, K., Goussot, M., Bainbridge, K., Foo, E., et al. (2003). MAX4 and RMS1 are orthologous dioxygenase-like genes that regulate shoot branching in Arabidopsis and pea. Genes and development, 17(12), 1469-1474.

Soundappan, I., Bennett, T., Morffy, N., Liang, Y., Stanga, J. P., Abbas, A., ... & Nelson, D. C. (2015). SMAX1-LIKE/D53 family members enable distinct MAX2-dependent responses to strigolactones and karrikins in Arabidopsis. The Plant Cell, 27(11), 3143-3159.

Stincone, A., Prigione, A., Cramer, T., Wamelink, M., Campbell, K., Cheung, E., ... & Keller, M. A. (2015). The return of metabolism: biochemistry and physiology of the pentose phosphate pathway. Biological Reviews, 90(3), 927-963.

Stirnberg, P., van De Sande, K., & Leyser, H. O. (2002). MAX1 and MAX2 control shoot lateral branching in Arabidopsis. Development, 129(5), 1131-1141.

Sturm, A., & Tang, G. Q. (1999). The sucrose-cleaving enzymes of plants are crucial for development, growth and carbon partitioning. Trends in plant science, 4(10), 401-407.

Sugden, C.; Crawford, R.M.; Halford, N.G.; Hardie, D.G. Regulation of spinach SNF1-related (SnRK1) kinases by protein kinases and phosphatases is associated with phosphorylation of the T loop and is regulated by 5′-AMP. Plant J. 1999, 19, 433–439.

Sun, C., Palmqvist, S., Olsson, H., Borén, M., Ahlandsberg, S., & Jansson, C. (2003). A novel WRKY transcription factor, SUSIBA2, participates in sugar signaling in barley by binding to the sugar-responsive elements of the iso1 promoter. The Plant Cell, 15(9), 2076-2092.

Suzuki, N., Miller, G., Morales, J., Shulaev, V., Torres, M. A., & Mittler, R. (2011). Respiratory burst oxidases: the engines of ROS signaling. Current opinion in plant biology, 14(6), 691-699.
Ta, T. C., MacDowall, F. D. H., and Faris, M. A. (1987). Utilization of carbon from shoot photosynthesis and nodule CO2 fixation in the fixation and assimilation of nitrogen by alfalfa root nodules. Canadian journal of botany, 65(12), 2537-2541.
Takahashi, H. K., Santos, L. R., Roma, L. P., Duprez, J., Broca, C., Wojtusciszyn, A., & Jonas, J. C. (2014). Acute nutrient regulation of the mitochondrial glutathione redox state in pancreatic β-cells. Biochemical Journal, 460(3), 411-423.
Takahashi-Terada, A., Kotera, M., Ohshima, K., Furumoto, T., Matsumura, H., Kai, Y., & Izui, K. (2005). Maize Phosphoenolpyruvate Carboxylase mutations at the putative binding site for glucose 6-phosphate caused desensitization and abolished responsiveness to regulatory phosphorylation. Journal of Biological Chemistry, 280(12), 11798-11806.
Tarancón, C., González-Grandío, E., Oliveros, J. C., Nicolas, M., & Cubas, P. (2017). A conserved carbon starvation response underlies bud dormancy in woody and Herbaceous Species. Frontiers in plant science, 8, 788.
Tatematsu, K., Ward, S., Leyser, O., Kamiya, Y., & Nambara, E. (2005). Identification of cis-elements that regulate gene expression during initiation of axillary bud outgrowth in Arabidopsis. Plant Physiology, 138(2), 757-766.
Thimm, O., Bläsing, O., Gibon, Y., Nagel, A., Meyer, S., Krüger, P., ... & Stitt, M. (2004). MAPMAN: a user-driven tool to display genomics data sets onto diagrams of metabolic pathways and other biological processes. The Plant Journal, 37(6), 914-939.
Tian, H., Lv, B., Ding, T., Bai, M., & Ding, Z. (2018). Auxin-BR interaction regulates plant growth and development. Frontiers in plant science, 8, 2256.
Tomé, F., Nägele, T., Adamo, M., Garg, A., Marco-llorca, C., Nukarinen, E., ... & Tomar, M. (2014). The low energy signaling network. Frontiers in plant science, 5, 353.
Tsukagoshi, H., Busch, W., & Benfey, P. N. (2010). Transcriptional regulation of ROS controls transition from proliferation to differentiation in the root. Cell, 143(4), 606-616.
Umehara, M., Hanada, A., Magome, H., Takeda-Kamiya, N., & Yamaguchi, S. (2010). Contribution of strigolactones to the inhibition of tiller bud outgrowth under phosphate deficiency in rice. Plant and Cell Physiology, 51(7), 1118-1126.
Van Gestelen, P., Asard, H., & Caubergs, R. J. (1997). Solubilization and separation of a plant plasma membrane NADPH-O2-synthase from other NAD (P) H oxidoreductases. Plant Physiology, 115(2), 543-550.
Vanhaeren, H., Inzé, D., & Gonzalez, N. (2016). Plant growth beyond limits. Trends in plant science, 21(2), 102-109.
Verbruggen, N., & Hermans, C. (2008). Proline accumulation in plants: a review. Amino acids, 35(4), 753-759.
Wai, C. M., Zhang, J., Jones, T. C., Nagai, C., & Ming, R. (2017). Cell wall metabolism and hexose allocation contribute to biomass accumulation in high yielding extreme segregants of a Saccharum interspecific F2 population. BMC genomics, 18(1), 773.
Waldie, T., and Leyser, O. (2018). Cytokinin targets auxin transport to promote shoot branching. Plant physiology, pp-01691.
Wang, M., Le Moigne, M. A., Bertheloot, J., Crespel, L., Perez-Garcia, M. D., Ogé, L., ... & Sakr, S. (2019). BRANCHED1: a key hub of shoot branching. Frontiers in plant science, 10.
Wang, P., Li, C., Li, C., Zhao, C., Xia, H., Zhao, S., ... & Wang, X. (2015). Identification and expression dynamics of three WUSCHEL related homeobox 13 (WOX13) genes in peanut. Development genes and evolution, 225(4), 221-233.
Wang, P., Zhao, Y., Li, Z., Hsu, C. C., Liu, X., Fu, L., ... & Gao, J. (2018). Reciprocal regulation of the TOR kinase and ABA receptor balances plant growth and stress response. Molecular cell, 69(1), 100-112.
Wang, R. L., Stec, A., Hey, J., Lukens, L., and Doebley, J. (1999). The limits of selection during maize domestication. Nature, 398(6724), 236-239.
Wang, R., Okamoto, M., Xing, X., & Crawford, N. M. (2003). Microarray analysis of the nitrate response in Arabidopsis roots and shoots reveals over 1,000 rapidly responding genes and new linkages to glucose, trehalose-6-phosphate, iron, and sulfate metabolism. Plant physiology, 132(2), 556-567.
Wang, W. F., Chen, P., Lv, J., Chen, L., & Sun, Y. H. (2018). Transcriptomic analysis of topping-induced axillary shoot outgrowth in Nicotiana tabacum. Gene, 646, 169-180.

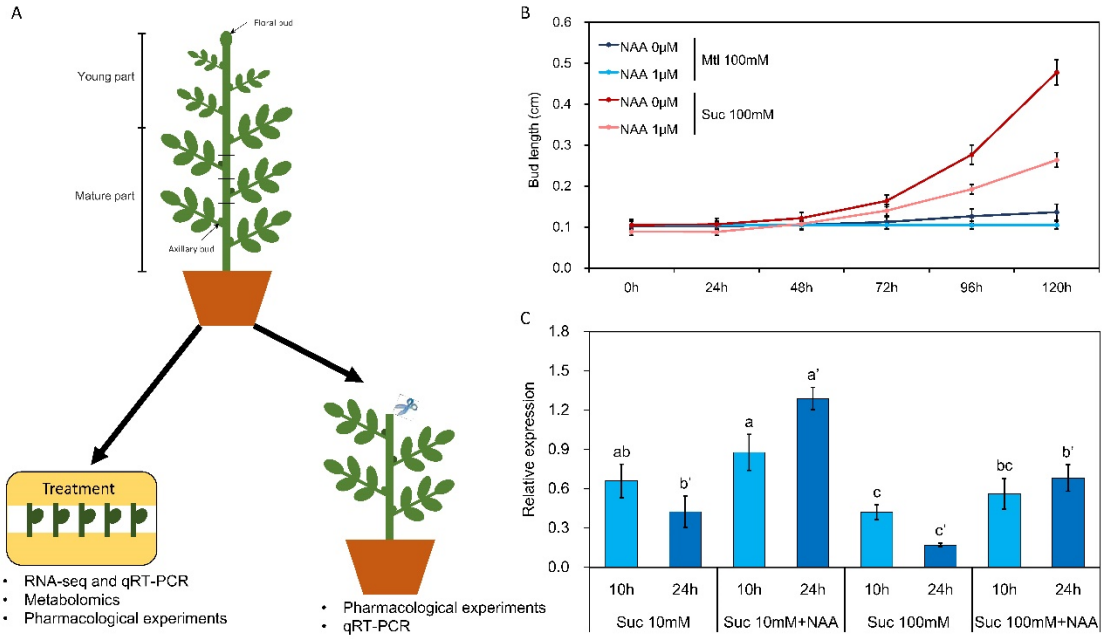
Wang, Y., Shen, W., Chan, Z., & Wu, Y. (2015). Endogenous cytokinin overproduction modulates ROS homeostasis and decreases salt stress resistance in Arabidopsis thaliana. Frontiers in plant science, 6, 1004.
Wang, Z. A., Li, Q., Ge, X. Y., Yang, C. L., Luo, X. L., Zhang, A. H., ... & Li, F. G. (2015). The mitochondrial malate dehydrogenase 1 gene GhmMDH1 is involved in plant and root growth under phosphorus deficiency conditions in cotton. Scientific reports, 5, 10343.
Wang, Z., Zhu, Y., Wang, L., Liu, X., Liu, Y., Phillips, J., & Deng, X. (2009). A WRKY transcription factor participates in dehydration tolerance in Boea hygrometrica by binding to the W-box elements of the galactinol synthase (BhGolS1) promoter. Planta, 230(6), 1155.
Watson, B. S., Bedair, M. F., Urbanczyk-Wochniak, E., Huhman, D. V., Yang, D. S., Allen, S. N., ... & Sumner, L. W. (2015). Integrated metabolomics and transcriptomics reveal enhanced specialized metabolism in Medicago truncatula root border cells. Plant physiology, 167(4), 1699-1716.
Weiste, C., & Dröge-Laser, W. (2014). The Arabidopsis transcription factor bZIP11 activates auxin-mediated transcription by recruiting the histone acetylation machinery. Nature communications, 5, 3883.
Weiste, C., Pedrotti, L., Selvanayagam, J., Muralidhara, P., Fröschel, C., Novák, O., ... & Dröge-Laser, W. (2017). The Arabidopsis bZIP11 transcription factor links low-energy signalling to auxin-mediated control of primary root growth. PLoS genetics, 13(2), e1006607.
Wick, A. N., Drury, D. R., Nakada, H. I., & Wolfe, J. B. (1957). Localization of the primary metabolic block produced by 2-deoxyglucose. J Biol Chem, 224(2), 963-969.
Wiese, A. , Elzinga, N. , Wobbes, B. , & Smeekens, S. . (2005). Sucrose-induced translational repression of plant bzip-type transcription factors. Biochemical Society Transactions, 33(1), 272-275.
Williams, S. P., Rangarajan, P., Donahue, J. L., Hess, J. E., & Gillaspy, G. E. (2014). Regulation of sucrose non-fermenting related kinase 1 genes in Arabidopsis thaliana. Frontiers in plant science, 5, 324.
Winter, H., & Huber, S. C. (2000). Regulation of sucrose metabolism in higher plants: localization and regulation of activity of key enzymes. Critical Reviews in plant sciences, 19(1), 31-67.
Wlaschin, K. F., & Hu, W. S. (2007). Engineering cell metabolism for high-density cell culture via manipulation of sugar transport. Journal of biotechnology, 131(2), 168-176.
Wullschleger, S., Loewith, R., & Hall, M. N. (2006). TOR signaling in growth and metabolism. Cell, 124(3), 471-484.
Xiao, W., Hu, S., Zhou, X., Yao, R., Luo, J., Yuan, C., ... & Liu, S. (2017). A glucuronokinase gene in Arabidopsis, AtGlcAK, is involved in drought tolerance by modulating sugar metabolism. Plant Molecular Biology Reporter, 35(2), 298-311.
Xiao, W., Sheen, J., & Jang, J. C. (2000). The role of hexokinase in plant sugar signal transduction and growth and development. Plant molecular biology, 44(4), 451-461.
Xiong, Y., & Sheen, J. (2011). Rapamycin and glucose-target of Rapamycin (TOR) signaling in plants. Journal of Biological Chemistry, jbc-M111.
Xiong, Y., & Sheen, J. (2014). The role of target of rapamycin signaling networks in plant growth and metabolism. Plant physiology, 164(2), 499-512.
Xiong, Y., McCormack, M., Li, L., Hall, Q., Xiang, C., & Sheen, J. (2013). Glucose–TOR signalling reprograms the transcriptome and activates meristems. Nature, 496(7444), 181.
Yamori, W., & Shikanai, T. (2016). Physiological functions of cyclic electron transport around photosystem I in sustaining photosynthesis and plant growth. Annual review of plant biology, 67, 81-106.
Yu, T. S., Lue, W. L., Wang, S. M., & Chen, J. (2000). Mutation of Arabidopsis plastid phosphoglucose isomerase affects leaf starch synthesis and floral initiation. Plant Physiology, 123(1), 319-326.
Yuan, T. T., Xu, H. H., Zhang, K. X., Guo, T. T., & Lu, Y. T. (2014). Glucose inhibits root meristem growth via ABA INSENSITIVE 5, which represses PIN1 accumulation and auxin activity in A rabidopsis. Plant, cell & environment, 37(6), 1338-1350.
Yue, J., Du, C., Ji, J., Xie, T., Chen, W., Chang, E., ... & Shi, S. (2018). Inhibition of α-ketoglutarate dehydrogenase activity affects adventitious root growth in poplar via changes in GABA shunt. Planta, 248(4), 963-979.
Zhang, B., & Liu, J. (2018). Molecular cloning and sequence variance analysis of the TEOSINTE BRANCHED1 (TB1) gene in bermudagrass [Cynodon dactylon (L.) Pers]. Journal of plant physiology, 229, 142-150.
Zhang, Y.; Liu, Z.; Wang, L.; Zheng, S.; Xie, J.; Bi, Y. Sucrose-induced hypocotyl elongation of Arabidopsis seedlings in darkness depends on the presence of gibberellins. J. Plant Physiol. 2010, 167, 1130–1136.
Zhao, D.L., Atlin, G.N., Bastiaans, L., and Spiertz, J.H.J. (2006). Developing selection protocols f or weed competitiveness in aerobic rice. Field Crops Research 97, 272–285.

Zhao, H., Su, T., Huo, L., Wei, H., Jiang, Y., Xu, L., & Ma, F. (2015). Unveiling the mechanism of melatonin impacts on maize seedling growth: sugar metabolism as a case. Journal of pineal research, 59(2), 255-266.

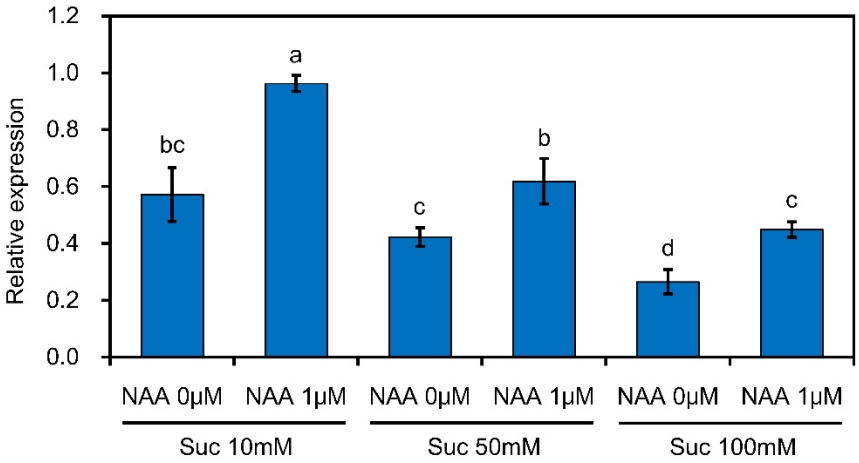
Zou, J., Zhang, S., Zhang, W., Li, G., Chen, Z., Zhai, W., ... & Zhu, L. (2006). The rice HIGHcTILLERING DWARF1 encoding an ortholog of Arabidopsis MAX3 is required for negative regulation of the outgrowth of axillary buds. The Plant Journal, 48(5), 687-698.

Zrenner, R., Salanoubat, M., Willmitzer, L., & Sonnewald, U. (1995). Evidence of the crucial role of sucrose synthase for sink strength using transgenic potato plants (Solanum tuberosum L.). The Plant Journal, 7(1), 97-107.

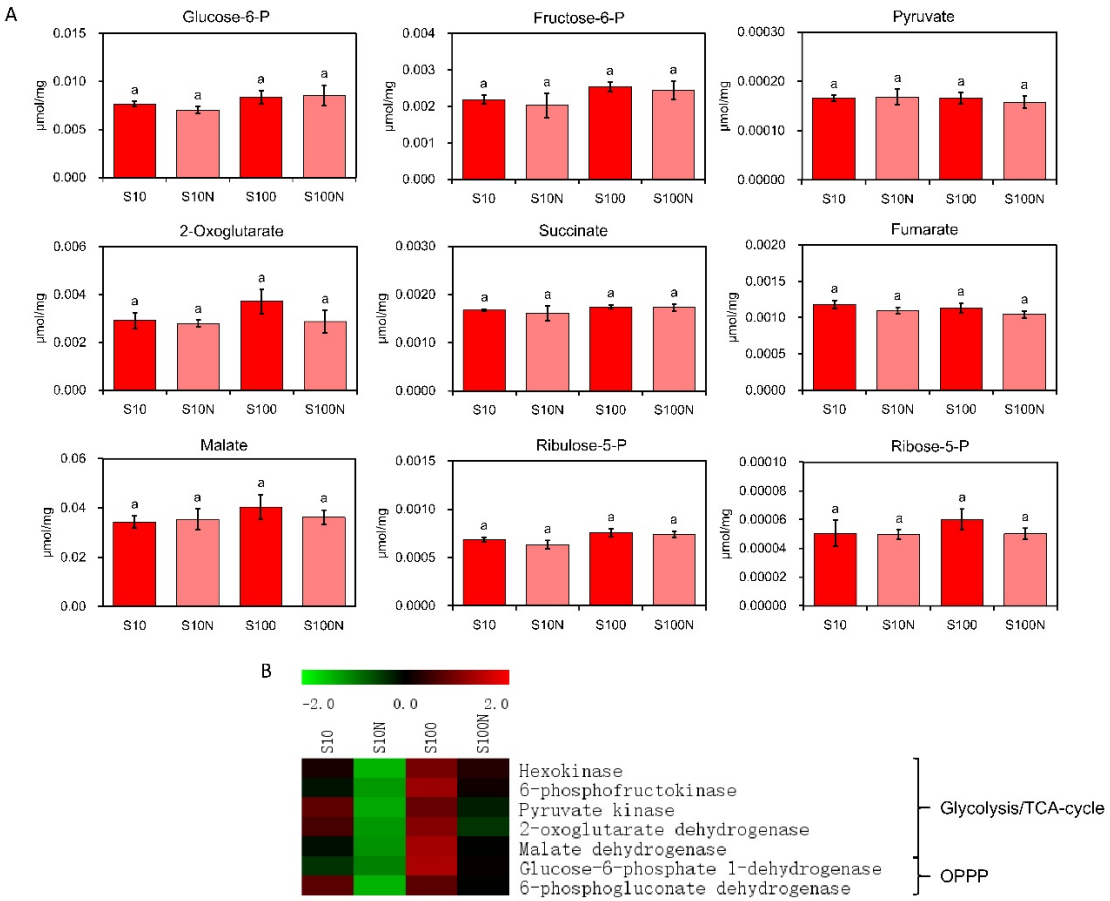
Supplemental data



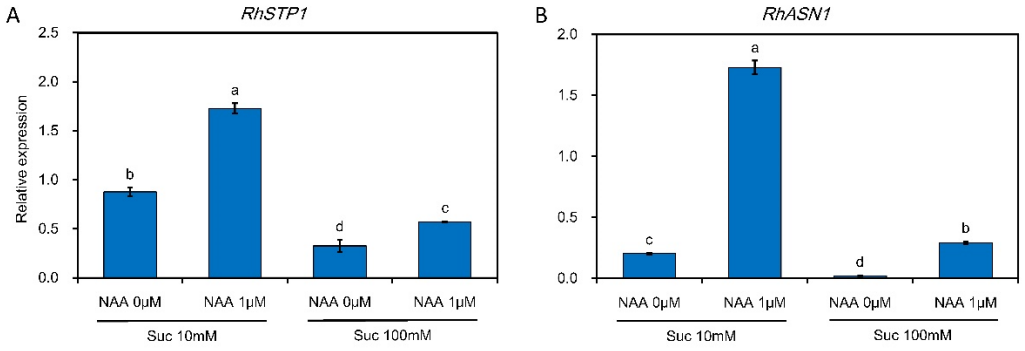
Supplementary figure 1. Bud outgrowth and transcript levels of *RhBRC1* in different treatments. A, Schematic diagram of decapitated plant (decapitation occurs above the fourth distal bud), *in vitro*-cultured buds (corresponding to the third and fourth distal buds) and experiment methods used in this study; B, Time-course of bud outgrowth during 120h with 100mM sucrose or mannitol with or without NAA (1-naphthaleneacetic acid); C, Transcription levels of *RhBRC1* in buds supplied for 10h and 24h with sucrose alone (Suc) or with sucrose and auxin (Suc and 1 μM NAA). Data are mean ± SE of three biological repetitions. .The letters indicate significant differences between the diverse treatments with $P<0.05$.



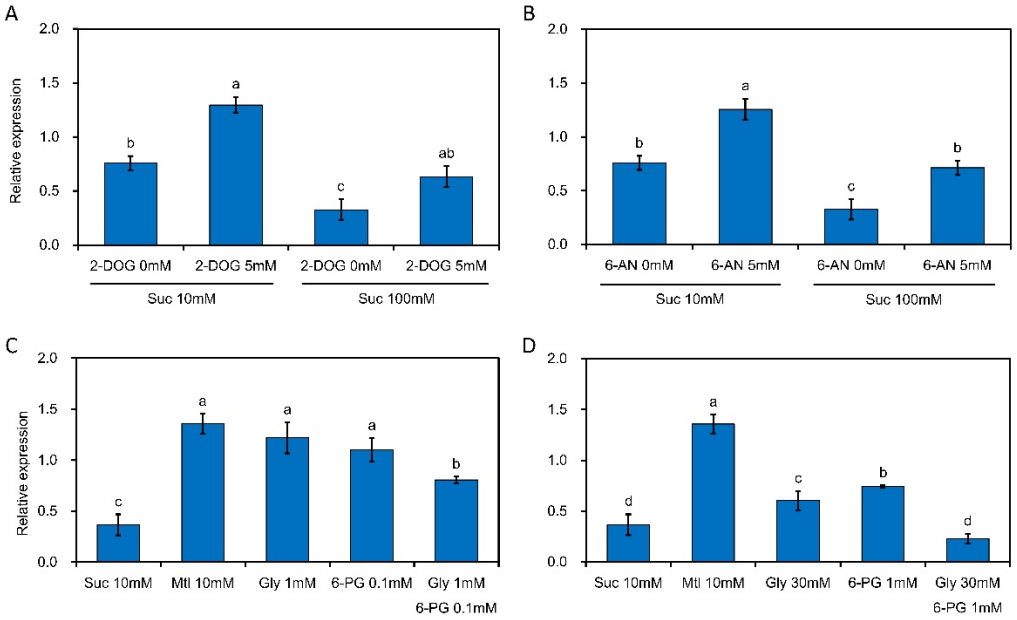
Supplementary figure 2. The transcript levels of *RhHB40* in different treatments. Data are mean ± SE of three biological repetitions. NAA (1-naphthaleneacetic acid). The letters indicate significant differences between the diverse treatments with $P<0.05$.



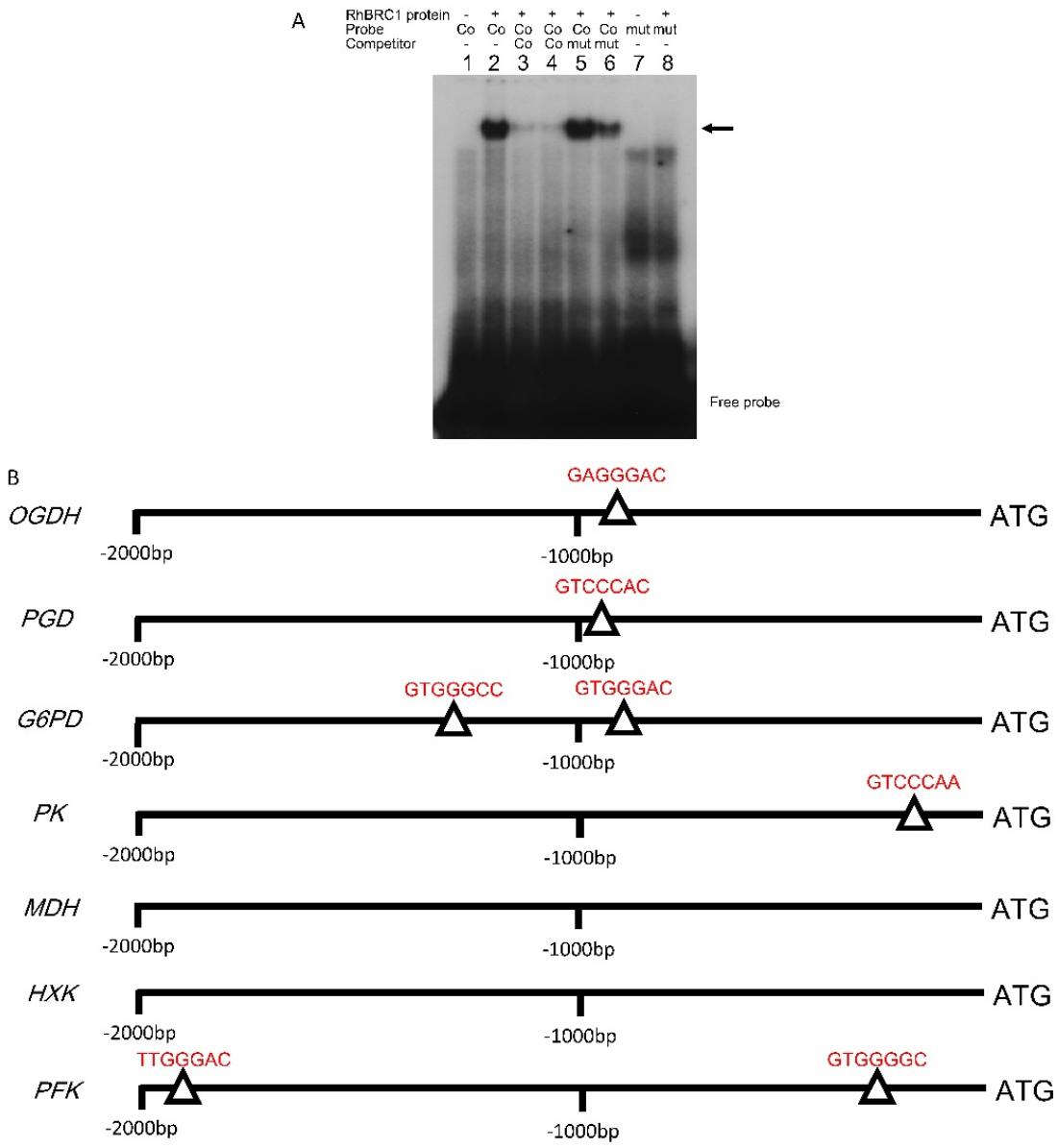
Supplementary figure 3. The changes of sugar metabolism related genes and compound within 24h. A, the changes of sugar metabolism related compounds based on metabolomics approach; B, the transcript levels of genes that encode sugar metabolism related enzymes based on RNA-seq.



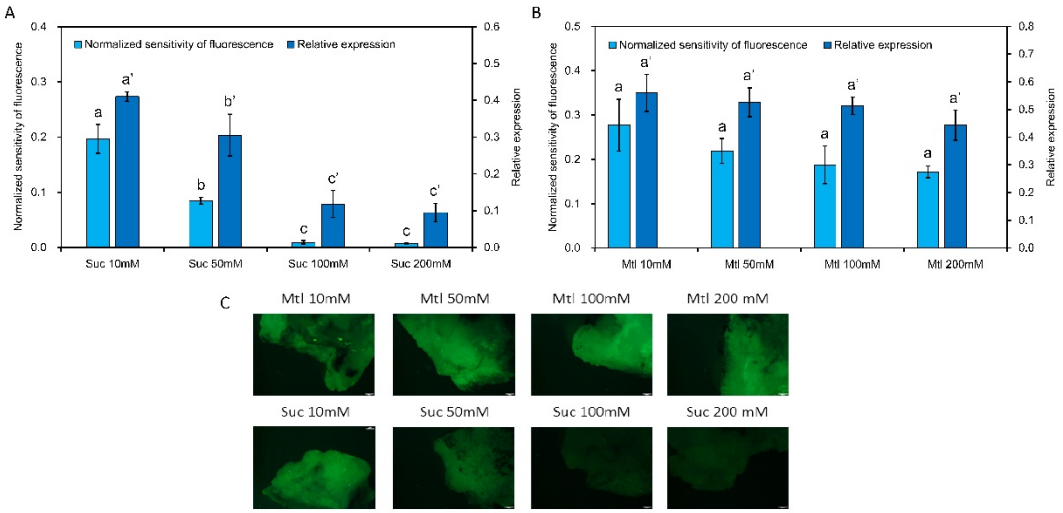
Supplementary figure 4. Antagonistic effect between sucrose and auxin on different markers of C-starvation and energy status in buds treated with 10mM and 100mM sucrose with or without auxin. A, *RhSTP1* transcription levels; B, *RhASN1* transcription levels. Data are mean ± SE of three measurements. The letters indicate significant differences between the different treatments with $P<0.05$. Suc, sucrose, Suc, sucrose; NAA, 1-naphthaleneacetic acid.



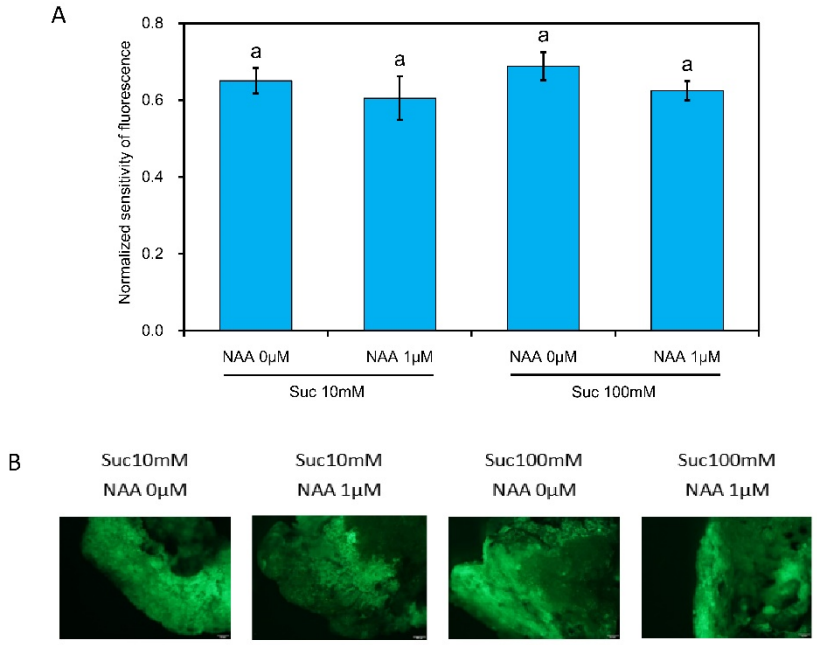
Supplementary figure 5. The transcript levels of *RhHB40* in different treatments. A&B, *RhHB40* transcript levels on 10mM or 100mM sucrose with different concentration of 2-DOG or 6-AN respectively; C&D, *RhHB40* transcript levels in buds incubated on sucrose (10mM), mannitol (10mM), glycerol (1mM or 30mM), 6-phosphogluconate alone (0,1mM or 1mM) or on glycerol and 6-phosphogluconate (Gly 1mM/6-PG 0.1mM or Gly 30mM/6-PG 1mM. Data are mean ± SE of three biological replicates; each replicate contains 15 buds for time-kinetics of buds and 40 buds for qRT-PCR.



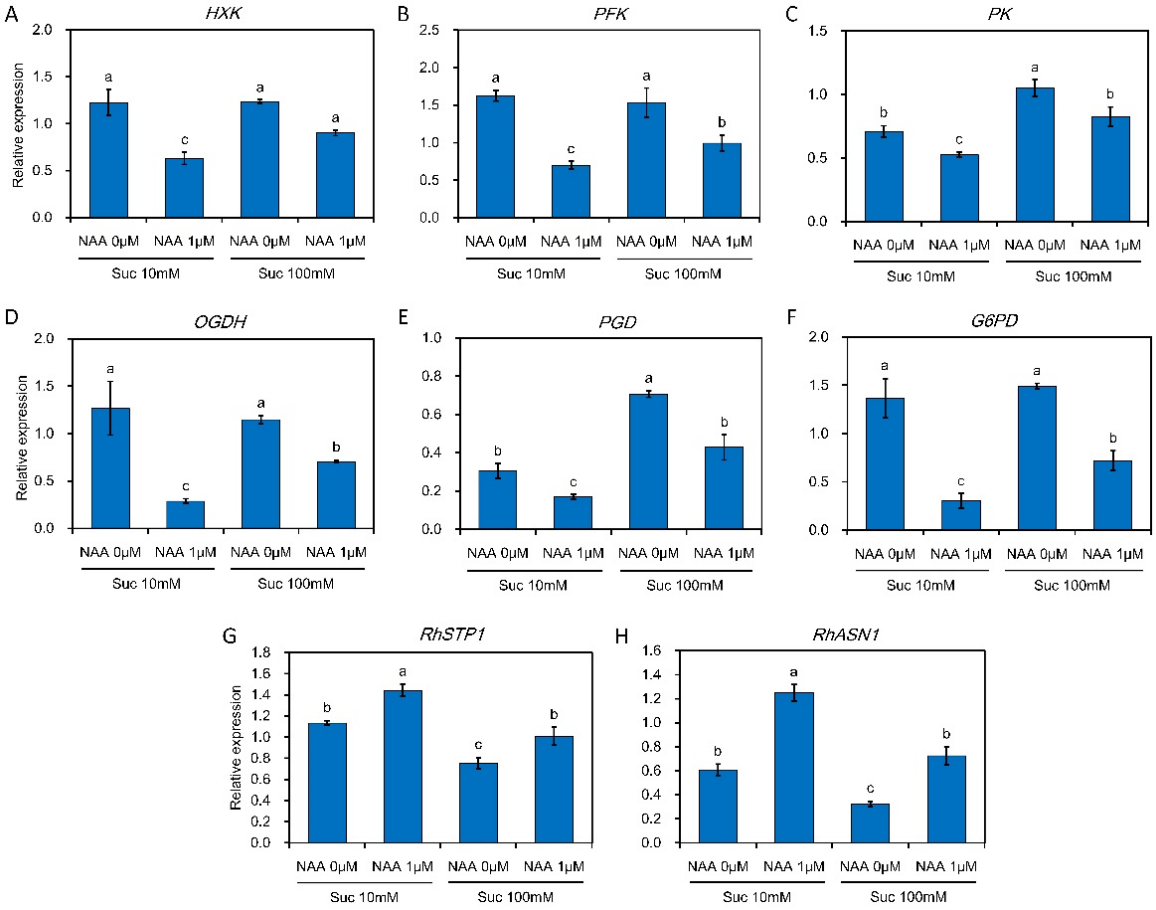
Supplementary figure 6. A- Electro Mobility Shift Assay (EMSA) using RhBRC1 protein and ^{32}P-radiolabelled oligonucleotides consensus (Co) or mutated (mut) binding sequences (table S3). + and – respectively indicate the presence or absence of the corresponding compound in the EMSA mix. Arrow indicates the bound DNA shift bands associated with RhBRC1. As indicated, 50-fold (lines 3 and 5) and 100-fold excess (lines 4 and 6) unlabelled consensus (Co) or mutated (mut) oligonucleotides were used as competitors, respectively. B- Schema of 2000bp upstream start codon of the seven sucrose metabolism related enzymes and the *cis*-elements of *RhBRC1* binding site. HXK, hexokinase; PFK, 6-phosphofructokinase; PK, pyruvate kinase; OGDH, 2-oxoglutarate dehydrogenase, MDH, malate dehydrogenase; G6PD, glucose-6-phosphate 1-dehydrogenase; PGD, 6-phosphogluconate dehydrogenase.



Supplementary figure 7. Fluorescence levels and GFP transcription levels of 1973bp *RhBRC1* promoter contained callus treated by different sucrose and mannitol concentrations. A&B, Fluorescence levels and GFP transcription levels of 1973bp *RhBRC1* promoter contained callus treated by different sucrose or mannitol concentrations, respectively; C, Fluorescence of 1973bp *RhBRC1* promoter contained callus treated by different sucrose and mannitol concentrations. Data are mean ± SE of three measurements, each measurement contained six calli. The letters indicate significant differences between the different treatments with $P<0.05$.



Supplementary figure 8. Fluorescence level of P35S contained callus treated by different conditions. A, Fluorescence level of GFP in different combinations of sucrose or NAA concentration; B, Fluorescence of GFP in different combinations of sucrose or NAA concentration. Data are mean ± SE of three measurements, each measurement contained six calli. The letters indicate significant differences between the different treatments with $P<0.05$.



Supplementary figure 9. Antagonistic effect between sucrose and auxin on sucrose metabolism related enzymens, C-starvation marker and energy status marker in calli treated with 10mM and 100mM sucrose with or without auxin. A to F, the transcript level of sucrose metabolism related enzymens; G&H, the transcript level of C-starvation marker and energy status marker (*RhSTP1* and *RhASN1*). *HXK*, hexokinase; *PFK*, 6-phosphofructokinase; *PK*, pyruvate kinase; *OGDH*, 2-oxoglutarate dehydrogenase, *G6PD*, glucose-6-phosphate 1-dehydrogenase; *PGD*, 6-phosphogluconate dehydrogenase. Data are mean ± SE of three biological replicates, each replicate contains 10 calli for qRT-PCR.

Table S1. The primers used in constructing different promoter regions

Primer name	Primer sequence (5' to 3')
PrPBRC1-1F	CACCTGTGAGCTAGTTGAGAAAACAATTG
PrPBRC1-2F	CACCTGAACAGTTTATAGTATATATTGATGAA
PrPBRC1-5UTR	CACCCTTTATGAAGAAAAGATGAGGAAAAG
PrPBRC1-R	TGTGATGTATATAGCTAATATCTGGTTG

Table S2. The qRT-PCR primers used in this study

qPrASN1	Forward	5'-CTATTCGAGCCAGCACCCC-3'
	Reverse	5'-TCTCATCAGAGCCCTCACCAG-3'
qPrSTP1	Forward	5'-TAAAGGGCGGTTGGGGATG-3'
	Reverse	5'-GGTCTTGGCTTTCTCGTGCTG-3'
qPr6PFK	Forward	5'-GTGGTTATGATTTGCTTGGACG-3'
	Reverse	5'-TCAGTGTTTGATGTCACCCCTC-3'
qPrPK	Forward	5'-TTCACCCAACCCCAACCA-3'
	Reverse	5'-CAGCGGATACTTTCCATTAGCA-3'
qPrMD	Forward	5'-GGACTCCTCCCGCTTTCG-3'
	Reverse	5'-GTGCCACTGAGCTATCACCATG-3'
qPr6PD	Forward	5'-AGAGTGCTGCTCGTATGATTGC-3'
	Reverse	5'-TTGATGCCTTTGCTGTTGTGA-3'
qPrG6PD	Forward	5'-GGCTTTACGGTTGGGACATT-3'
	Reverse	5'-TCTGAAAACCCCGACTGCTC-3'
qPrRhHB40	Forward	5'-TTCGGCAACGAGCATAAACTG-3'
	Reverse	5'-TTCTGAAACCAAACAGCCACTT-3'
qPr2OD	Forward	5'-GATGGCTGGAGGTTCATTTACA-3'
	Reverse	5'-TGCCGACTGAGGAGGGTTG-3'
qPrHXK1	Forward	5'-GTTGGGACCAAACTCAAGGA-3'
	Reverse	5'-TGGCAACTACGTCGCATAAC-3'
qPrRhSuSy	Forward	5'-GTATGAGAGTCACACCGCCT-3'
	Reverse	5'-GCTCCCGGTGAAACAATGTT-3'
qPrRhVI1	Forward	5'-CGGCCAACCTGTCTGATCCCTTA-3'
	Reverse	5'-GGGTCACGGAAATCGGTGGTTAAA-3'

Table S3. The EMSA primers used in this study

EMSAcons-F	GGGGATCTGTGGGCCCACGAG
EMSAcons-R	GGGGCTCGTGGGCCCACAGAT
EMSAcons-mut F	GGGGATCTGTGAACTCACGAG
EMSAcons-mut R	GGGGCTCGTGAGTTCACAGAT
EMSA 2OGD-a-F	GGGGGTTGGAGGGACAAGGTAGGTG
EMSA 2OGD-a-R	GGGGCACCTACCTTGTCCCTCCAAC
EMSA 6PGD-a-F	GGGGTATAGGGGGCCTTGTCTTAG
EMSA 6PGD-a-R	GGGGCTAAGACAAGGCCCCCTATA
EMSA G6P1D-a-F	GGGGGGAACTGGGCCTGGAGCAAG
EMSA G6P1D-a-R	GGGGCTTGCTCCAGGCCCAGTTCC
EMSA G6P1D-b-F	GGGGAAGAGGTGGGCCTGGACTCCT
EMSA G6P1D-b-R	GGGGAGGAGTCCAGGCCCACCTCTT
EMSA G6P1D-c-F	GGGGGCCGAGTGGGACTTTTGGTCT
EMSA G6P1D-c-R	GGGGAGACCAAAAGTCCCACTCGGC
EMSA PK-a-F	GGGGCCCGTCACGGGTCCCAAAGATC
EMSA PK-a-R	GGGGGATCTTTGGGACCCGTGACGGG
EMSA 6PFK-a-F	GGGGTTCTATTGGGACCTCCAAATC
EMSA 6PFK-a-R	GGGGGATTTGGAGGTCCCAATAGAA
EMSA 6PFK-b-F	GGGGAAACGTGGGGCATATTTGGAAG
EMSA 6PFK-b-R	GGGGCTTCCAAATATGCCCCACGTTT

3’ Untranslated region of *RhBRC1* (*Rosa hybrida BRANCHED1*) is involved in its post-transcriptional regulation in response to sugars, with a potential role of RhPUF4 (Pumilio RNA-binding protein family)

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Abstract:

Shoot branching patterns is an important phenotype during plant development. During shoot branching, *BRC1* (BRANCHED) plays a master regulator role in bud outgrowth process, and its transcript level is regulated by various exogenous and endogenous factors. However, many question are still open on the involved molecular mechanisms. Here, we investigated whether the expression of *RhBRC1* (a homologue gene of *BRC1* in *Rosa hybrioda*) could be under the post-transcriptional regulation in response to sugar a main branching-regulating factor, through its 3’UTR. The stably transformed Rosa callus with the promoter 35S (P35S)-driven GFP with either 3’UTR of *RhBRC1* (P35S::GFP::3’UTR$_{RhBRC1}$) or 3’UTR corresponding to NOS-terminator (P35S::GFP::3’UTR$_{NOS}$) were obtained and treated by various combinations of sugars, and sugar metabolism effectors. The results showed a major role of the 3’UTR of RhBRC1 in the in response to sugars, involving potentially glycolysis/TCA-cycle and OPPP (oxidative pentose phosphate pathway) emanating signals. In vegetative buds, we identified RhPUF4, a closely homologue protein of APUM2 in *Arabidopsis* belonging PUF RNA (Pumilio RNA-binding protein family) binding protein. *RhPUF4* was highly expressed in non-dormant buds at the plant scale and was upregulated by sugar availability *in vitro*-cultured buds. RhPUF4 expression was especially dependent on OPPP activity, supporting its role in OPPP-dependent posttranscriptional regulation of *RhBRC1*. These findings indicate that 3’UTR sequence could play a main role in the molecular regulatory network of *BRC1* and open new avenues to investigate new aspects of BRC1 regulation.

Key words

3’UTR; PUF; sugar, oxidative pentose phosphate pathway, glycolysis, sugar signaling

Introduction

Throughout their life cycle, plants should adjust their body to suit the various environmental conditions in which they are growing. The regulation of shoot branching is one strategy to preserve plant survival and to optimize the yield potential of agricultural, horticultural and forestry crops (Jiang and Egli, 1993; Richards, 2000). Shoot branching involves a complex regulatory network, based on systemic and local interaction of many endogenous and exogenous cues that converge into bud to modulate its ability to remain dormant or to grow into new shoot (Rameau *et al*., 2015; Wang and Jiao, 2018, Wang *et al*., 2019). *Teosinte branched1* (*TB1*)/*BRANCHED1* (*BRC1*) and their homologue genes act as an integrator of branching signals within axillary buds (Doebley *et al*., 1997; Aguilar-Martinez *et al*., 2007), although other not-yet identified master regulator could exist (Seale *et al*., 2017).

In monocots, *Teosinte branched1* (*TB1*) from *Zea mays* (Doebley *et al*., 1997) and its respective homologs in *Oryza sativa*, *OsTB1* (Takeda *et al*., 2003) and in *Sorghum bicolor*, *SbTB1* (Kebrom *et al*., 2006) were found to influence the tillers. They encode transcription factors contained a TCP domain, an approximate fifty-nine amino acid domain that allows nuclear targeting, DNA binding, and protein–protein interactions (Kosugi and Ohashi, 1997; Cubas *et al*., 1999; Kosugi and Ohashi, 2002). *TB1* and *OsTB1* are mainly expressed in axillary bud meristems, where they promote bud growth arrest (Hubbard *et al*., 2002; Takeda *et al*., 2003) and their respective knock out mutant (*tb1* and *fine culm)* exhibited an over-branching phenotype (Doebley *et al*., 1997; Wang *et al*., 1999; Takeda *et al*., 2003). Similarly, *BRANCHED1* (*BRC1*) and *BRANCHED2* (*BRC2*), closely related to *TB1*, regulate the branch process in *Arabidopsis* (Aguilar-Martínez *et al*., 2007). *BRC1* expression patterns are restricted mostly to axillary buds, anti-correlated with bud outgrowth, and *brc1* mutant phenotypes are non-pleiotropic and affect exclusively axillary bud development (Aguilar-Martínez *et al*., 2007). The *BRC1*-like genes were also identified in other plant species (for revue, see Wang *et al*., 2019).

The sugars-dependent bud growth promotion has been reported in many species including peach (Maurel *et al*., 2004), walnut tree (Bonhomme *et al*., 2009), Rosa sp. (Girault *et al*., 2010; Henry *et al*., 2011) and sorghum (Kebrom *et al*., 2010 & 2012). Exogenous supply of sugars was also necessary to sustain bud outgrowth of one-node cuttings (Henry *et al.*, 2011; Rabot *et al.*, 2012; Fichtner *et al*., 2017) and *in planta* (Mason *et al.*, 2014; Evers, 2015), while plant defoliation impaired bud growth (Kebrom *et al*., 2010). Mason *et al.* (2014) have shown in intact plant that apical dominance strongly correlates with sugar allocation to axillary bud,

revealing that apical dominance is predominantly maintained by the intense demand of shoot tip for sugars, and exogenous sucrose provision through the cut petiole stimulates bud outgrowth and mimics plant decapitation. Sucrose could act as a signaling entity, because some non-metabolizable sucrose analogues, including lactulose, are able to trigger bud outgrowth (Rabot *et al.*, 2012; Barbier *et al.*, 2015), probably via trehalose 6-P pathway in pea (Fichtner *et al*., 2017). Despite these findings, our knowledge are very fragmented regarding the molecular bases of sugar-dependent bud outgrowth promotion. The only available data suggest that sugar might be a central component of the branching regulatory network, since sucrose negatively regulates the expression level of *BRC1*(Barbier *et al.*, 2015; Mason *et al.*, 2014; Rameau *et al.*, 2015). Kebrom and Mullet (2015) demonstrate that small changes in photosynthetic leaf area affect positively the expression of *TB1* and consequently the propensity of tiller buds for outgrowth. Using Rosa sp. one-node cutting, Barbier *et al*., (2015) demonstrated that sucrose-dependent bud outgrowth stimulation could be linked to down- and up- regulation of strigolactone (SL, branching-repressing hormone) signaling genes and cytokinin (CK, branching-inducing hormone) synthesis, respectively. CK and SL, two second messengers, which are antagonistically controlled by polarized auxin transport of stem (Shimizu-Sato *et al*., 2009; Brewer *et al*., 2009), and are partly integrated within the bud by the transcription factor BRC1, (Aguilar-Martinez *et al*., 2007; Dun *et al*., 2012; Rameau *et al*., 2015; Wang *et al*., 2019).

In plants, sugar also serves as signal molecule and act through an array of signaling pathways including sucrose-, hexokinase and OPPP (oxidative pentose phosphate pathways (Kruger and von Schaewen, 2003; Smeekens *et al*., 2010; Lastdrager *et al*., 2014; Lejay *et al*., 2008; Sakr *et al*., 2018). Within this context, sugar regulates the expression of a large number of genes at different levels, including transcriptional, post-transcriptional and post-translational level (for revue, Sakr *et al*., 2018). Many regulation processes relied on the 3'UTR sequence are considered as a powerful strategy for many organisms to flexibly adjust their functioning in response to different inputs. In rice, analysis of reporter mRNA half-lives of *αAmy3* (*α-Amylase3*) demonstrated that the entire *αAmy3* 3'UTR and the two subdomains each functioned as destabilizing determinant in the turnover of mRNA in response to sugar provision, and this response was assigned to "UAUAUAUGUA" motif (Sheu *et al.*, 1994; Chan and Yu, 1998a). In maize, *Incw1*, encoding a cell-wall invertase, has two type of transcripts that differ by 3'UTR length and seemingly act as a regulatory sensor of carbon starvation (Cheng *et al*., 1999). 3'UTR may constitute a link between sink metabolism and cellular translation activity in plants, although no specific 3'UTR-related motif was identified. Nicolai *et al*. (2006) identified 224

mRNAs that most of them are post-transcriptionally repressed by sucrose starvation, allowing cell to quickly respond to a general decrease of its metabolic activity. Diverse RNA binding proteins, which regulate many aspects of RNA metabolism, such as RNA splicing, polyadenylation, capping, modification, transport, localization, translation and stability, are particularly important for a successful post-transcriptional regulation (Keen, 2007; Wang *et al*., 2018). The Pumilio RNA-binding protein family (PUF family) is a large family of RNA binding proteins found in all eukaryotes; the number of PUF gene copies highly variable in each model organism (Wickens *et al*., 2002). The PUF family takes part of post-transcriptional control by binding to specific regulatory *cis*-elements of their mRNA targets, and thereby leads to mRNA decay and translational repression (Tam *et al*., 2010). They also act by promoting ribosome stalling and facilitating the recruitment of microRNAs (miRNAs) and chromosomal instability (Friend *et al*., 2012; Van Etten *et al*., 2012; Miles *et al*., 2012; Lee *et al*., 2016).

In plants, only few investigations have been led to discover the role PUF in plant growth and development. Tam *et al*. (2010) showed that APUM2, an *Arabidopsis* PUF protein, binds the RNA of *Drosophila Nanos Response Element I* (*NRE1*) 5'-UGUAUAUA-3' located in its 3'UTR, and that APUM1 to APUM22 can shuttle between nucleus and cytoplasm through exportin1 mediated pathway, while APUM23 and APUM24 are exclusively localized in nucleus. They also indicated that PUF protein involved in many processes in plants, such as osmotic stress, sugar signaling, nutrient metabolism, drought stress, ABA signaling. Using three-hybrid screening assays, Francischini and Quaggio (2009) showed that among the 25 PUF members identified in *Arabidopsis*, APUM1 to APUM6 can specifically bind to the Nanos response element sequence, which is also recognized by *Drosophila Pumilio* proteins. They also identified an APUM binding consensus sequence *i.e.*, a UGUR tetranucleotide, which are present in all targets of the PUF family (Wickens *et al*., 2002). The "non-canonical" Arabidopsis PUM23 (APUM23) binding sequence is 10 nucleotides long, contains a 5'-UUGA-3' core sequence, and has a preferred cytosine at nucleotide position eight (Zhang and Muench, 2015). These investigations showed that the consensus PUF binding motif maybe ubiquitous among eukaryotes.

The objective of this study is to investigate whether sucrose-mediated downregulation of *RhBRC1* could involve a post-transcriptional regulation, through its 3'UTR sequence. Sequence analysis of 3'UTR of *RhBRC1* showed the presence of 6 putative PUF binding motifs (UGUR flanked downstream by an AU-rich sequence), one of them exists in the motif "UAUAUAUGUA" similar to that previously found in 3'UTR of *α-amylase 3* (Sheu *et al.*, 1994; Chan and Yu, 1998a). To gain an insight in this process the 3'UTR of *RhBRC1*-

transformed Rosa callus (P35S::GFP::3'UTR$_{RhBRC1}$) and NOS-terminator-transformed ones (P35S::GFP::3'UTR$_{NOS}$) were obtained and placed on sugars (sucrose and glucose), non-metabolizable sugars (lactulose, mannose, 3-O-methyl-glucose (3-OMG)) and effectors of glycolysis/TCA-cycle and OPPP (oxidative pentose pathway). We demonstrated that 3'UTR sequence was prevailing in sugar-mediated *RhBRC1* regulation. To go further in this regulation, twelve PUF protein members were isolated from *Rosa chinensis* genomic sequence and only *RhPUF4*, a member of PUF protein family, was more expressed in buds of decapitated plants and in sugar-fed in vitro-cultured buds, indicating that RhPUF4 is positively related to sugar-mediated bud outgrowth. More precisely, *RhPUF4* expression was mainly and positively responsive to OPPP-emanating signal. *RhPUF4* is highly close to *AtPUM2*, which is highly expressed in shoot meristem. Taken together, these results indicate that 3'UTR in RhBRC1 post-transcriptional regulation in response to sucrose and this regulation occurred in part, through OPPP-dependent up-regulation of *RhPUF4*.

Results

Sucrose and glucose influence the expression level of *RhBRC1* through its 3' UTR region

Chan and Yu. (1998a&b) have previously shown that the transcript of *α-Amylase 3* in *Oryza sativa* is sugar-repressive process, which was associated with the presence of one of these two motifs (UAUAUAUGUA and UAUAUAAUGUA) in its 3'UTR (Figure S1). Based on sugar-dependent *RhBRC1* downregulation (Barbier *et al*., 2015), we investigated whether its 3'UTR region involved in this regulation. Indeed, its 3'UTR sequence contained the same motif (UAUAUAUGUA) as that previously reported for *α-Amylase 3* and 6 PUF binding motifs, while NOS terminator (used as a control) did contain any PUF binding motifs (Figure 1). There are two and four PUF binding motifs in 3'UTR of *AtBRC1* and *OsBRC1* respectively (Figure S1). Rosa callus were transformed with two constructs, consisting on promoter 35S (P35S)-driven GFP with either 3'UTR of *RhBRC1* (P35S::GFP::3'UTR$_{RhBRC1}$) or 3'UTR corresponding to NOS-terminator (P35S::GFP::3'UTR$_{NOS}$). The transformed callus were first selected based on antibiotic resistance and the presence of 3'UTR (3'UTR$_{RhBRC1}$ and 3'UTR$_{NOS}$) was confirmed by PCR-mediated DNA amplification. The transformed callus were then transferred to the incubation medium, containing different concentrations of sucrose and glucose, ranging from 10 to 200mM and fluorescence intensity was assessed by using ImageJ software. At first, we choose 8h incubation because corresponded to the best observation time, based on the previous time kinetic from 2h to 24h (data not shown). After that, the 3'UTR$_{RhBRC1}$-transformed

callus (P35S::GFP::3'UTR$_{BRC1}$) was incubated for 8h on soluble sugar-containing medium, and the fluorescence exhibited a strong decreased intensity as sucrose concentration increased (Figure 2B). Fluorescence was highest under 10mM (low sugar concentration) and lowest in response to 100mM and 200mM sucrose and glucose respectively. Incubation on lactulose, a non metabolizable sucrose analog, decreased GFP intensity (Figure 2D). Meanwhile, the 3'UTR$_{NOS}$-related fluorescence remained almost stable in response to these sugar concentrations, supporting that 3'UTR$_{RhBRC1}$ could be a sugar sensitive sequence (Figure 2B&C). Mannitol, which used as the osmotic control, had no dramatic change of the fluorescence intensity of both 3'UTR$_{NOS}$ and 3'UTR$_{RhBRC1}$-transformed callus, except when mannitol concentration was as high as 200mM (Figure 2A). These findings support our initial assumption that the 3'UTR sequence of *RhBRC1* could mediate sugar-dependent *RhBRC1* repression, through a post-transcriptional process.

3'UTR of *RhBRC1*

CACCGCGAUGAAUAUCGAUCAGAGAGUAUAUAUGUACGUGUGUACUAAUUGCCUUCUUCUUUCUGUUU
GGAAUAAUGUAAGAUAUGUGGAAAUUAAUUAAGUAGCUUCUUAAUGAUUAUUGUGGAGUUCCCUCUAA
ACUACCAUGAUGUAUUAUAUAAAUAUUAUGUUUCCCUUAAUUUCUACCUAAUUUCCACCUUUCUCAUU

NOS-terminator

GAUCGUUCAAACAUUUGGCAAUAAAGUUUCUUAAGAUUGAAUCCUGUUGCCGGUCUUGCGAUGAUUAU
CAUAUAAUUUCUGUUGAAUUACGUUAAGCAUCUAAUAAUUAACAUCUAAUGCAUGACGUUAUUUAUGA
GAUGGGUUUUUAUGAUUAGAGUCCCGCAAUUAUACAUUUAAUACGCGAUAGAAAACAAAAUAUAGCGC
GCAAACUAGGAUAAAUUAUCGCGCGCGGUGUCAUCUAUGUUACUAGAUCGGG

Figure 1: The sequence of *RhBRC1* 3'UTR region and *NOS-terminator*. The red letter means the sugar related motif found in *α-amylase 3* in *Oryza sativa.* The underlined letter means the putative APUM2 or RhPUF4 protein binding motif. The blue letter means the the putative PUF protein binding motif.

3'UTR of *RhBRC1* was respond to glycolysis- and OPPP-emanating signals

When the 3'UTR$_{RhBRC1}$-transformed callus (P35S::GFP::3'UTR$_{BRC1}$) was incubated on mannose (non metabolizable glucose analog)-containing medium for 8h, no significant decreased in fluorescence intensity (Figure 2E) was observed, indicating a minor role of hexokinase dependent pathway. Similar data was found with 3-OMG (Figure 2F), a marker of hexokinase independent pathway (Rabot *et al*., 2012). We then checked whether the HXK-downstream pathways, glycolysis/TCA-cycle and OPPP, could involve in sugar-mediated post-transcriptional regulation of *RhBRC1* through its 3'UTR region. Effectors of glycolysis (2-deoxyglucose (2-DOG), Wick *et al*., 1957; Xiong *et al*., 2013) and of OPPP pathways (6-aminonicotinamide (6-AN), Lange and Proft, 1970; Hothersall *et al*., 1998; Lejay *et al*., 2008) and glycerol (fueling the downstream part of glycolysis and inhibiting glucose-6-phosphate isomerase to form glucose 6-phosphate required for OPPP activity, Aubert *et al*., 1994; Lejay *et al*., 2008, Figure 3A) were tested on 3'UTR$_{RhBRC1}$ and 3'UTR$_{NOS}$ -contained callus incubated either on sucrose (for 2-DOG and 6-AN) or on glycerol medium (Figure 3). Sucrose is required to produce glucose and glucose-6-phosphate (Glc-6P), the precursor for glycolysis/TCA-cycle and OPPP respectively (Figure 3A). When the 3'UTR $_{RhBRC1}$-transformed callus was co-treated with 100mM sucrose + 0.5mM 2-DOG, the fluorescence was significantly lowest and increased progressively, but not very strongly, to reach its highest level with 100mM sucrose + 5mM 2-DOG (Figure 3B). The treatment with glycerol confirmed these results because the fluorescence of 3'UTR$_{RhBRC1}$-transformed callus decreased slightly and significantly to reach its lowest level with 30mM glycerol, but increased slightly again with 50mM glycerol (Figure 3C). Under the same experimental conditions, 3'UTR$_{NOS}$- contained callus exhibited no significant changes of fluorescence intensity supporting a potential role of 3'UTR in mediating glycolysis/TCA-cycle dependent downregulation of *RhBRC1*. The treatment of 3'UTR$_{RhBRC1}$-transformed callus with different concentrations of pyruvate, derived from glycolysis, also confirmed this conclusion (Figure S2A).

In order to see whether the OPPP could lead to the post-transcriptional regulation of *RhBRC1* through its 3'UTR, the 6-AN, 6-phosphogluconate (6-PG) were tested. When 3'UTR$_{RhBRC1}$-contained callus was placed on 100mM sucrose + different concentrations of 6-AN (from 0.5 to 5mM), they exhibited an elevated fluorescence as 6-AN concentration increased. With the same sucrose concentration (100mM), the highest fluorescence corresponded to callus incubated on 5mM and the lowest one on 0.5mM 6-AN (Figure 3D). The opposite fluorescence pattern was found when 3'UTR$_{RhBRC1}$-contained callus was supplied with 6-PG, a substrate of

OPPP. The 3'UTR$_{RhBRC1}$-contained callus displayed an increased fluorescence as 6-PG concentration reduced (Figure 3E). More interestingly, when the callus was co-treated with 1mM 2-DOG and different concentrations of Glc-6P (glycolysis/TCA-cycle was blocked by 2-DOG and Glc-6P preferentially fuels OPPP), fluorescence level of 3'UTR$_{RhBRC1}$-contained callus changed significantly and consistently decreased as Glc-6P concentration increased (Figure S2B). Under the same experimental conditions, no significant changes in fluorescence level of 3'UTR$_{NOS}$-contained callus was found, supporting that this regulation was specific to 3'UTR of *RhBRC1*, that played a major role in the OPPP dependent post-transcriptional regulation of *RhBRC1*.

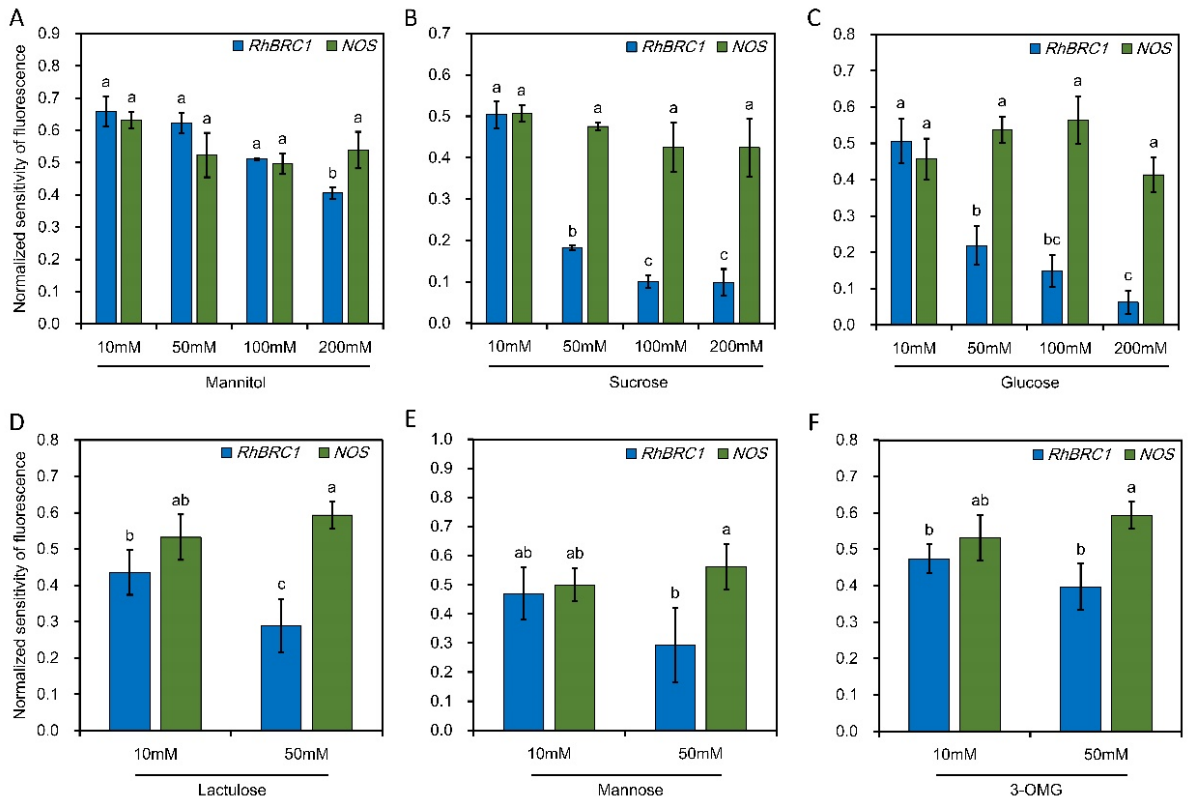

Figure 2. Fluorescence level of 3'UTR$_{RhBRC1}$-transformed callus (P35S::GFP::3'UTR$_{RhBRC1}$) compared to that of 3'UTR$_{NOS}$-transformed callus (P35S::GFP::3'UTR$_{NOS}$) under different sugar treatments. A, B&C, Fluorescence level of 3'UTR$_{RhBRC1}$- and 3'UTR$_{NOS}$- transformed callus treated with different mannitol, sucrose or glucose concentrations respectively. D, E&F, Fluorescence level of 3'UTR$_{RhBRC1}$- and 3'UTR$_{NOS}$- transformed callus treated with different lactulose, mannose and 3-OMG concentrations respectively. *RhBRC1*, 3'UTR$_{RhBRC1}$–transformed callus; *NOS*, 3'UTR$_{NOS}$-transformed callus. Data are mean ± SE of three measurements, each measurement contained six Rosa callus. The letters indicate significant differences between the different treatments with $P < 0.05$.

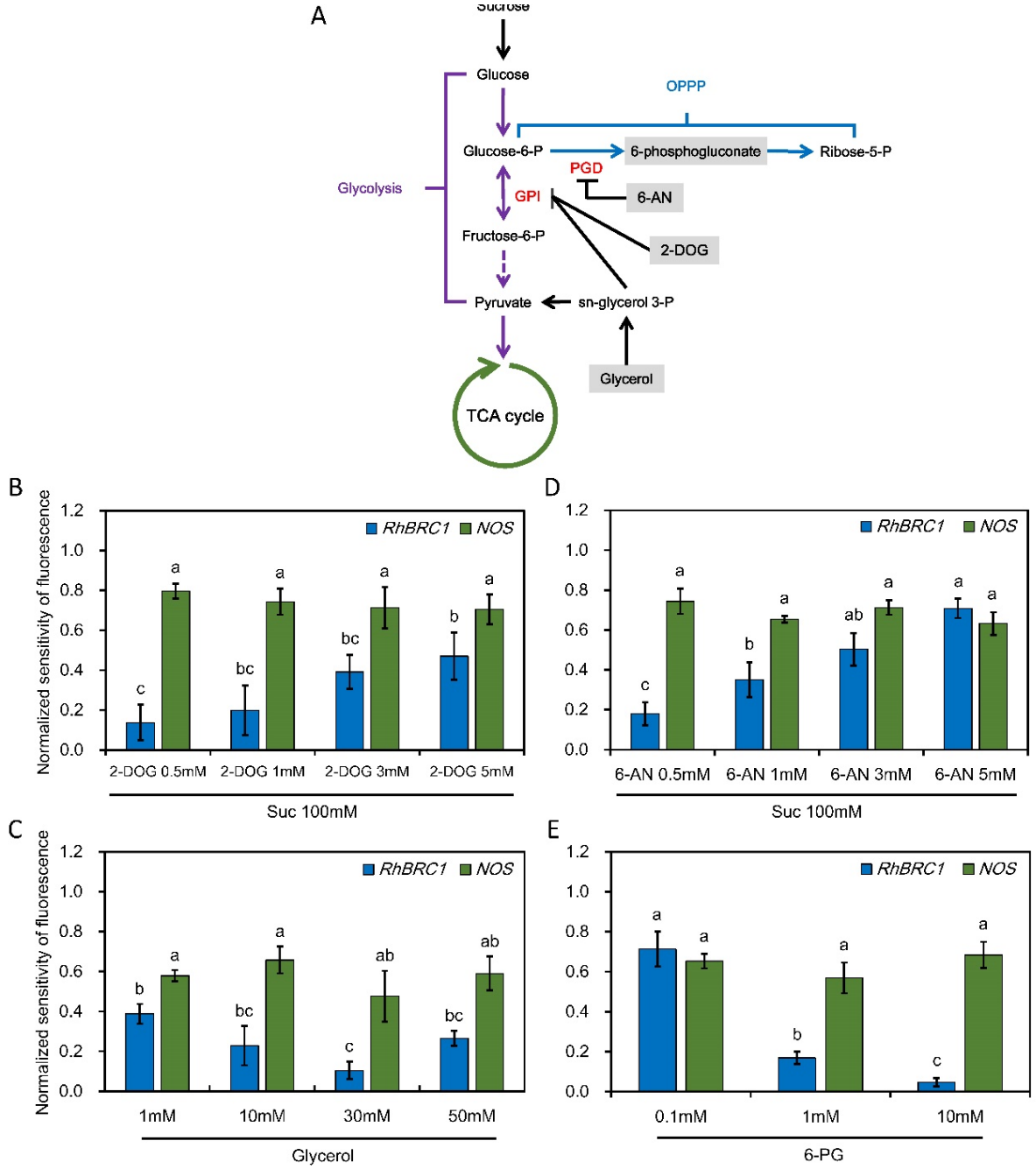

Figure 3. Both Glycolysis/TCA-cycle and OPPP participate to the post-transcriptional regulation of *RhBRC1* through its 3' UTR. A, Different effectors function at different enzymes in primary metabolism pathway; B&D, Fluorescence level of 3'UTR$_{RhBRC1}$- and 3'UTR$_{NOS}$- transformed callus in response to 100mM sucrose and different 2-DOG or 6-AN concentrations respectively; C&E, Fluorescence level of 3'UTR$_{RhBRC1}$- and 3'UTR$_{NOS}$-transformed callus in response to different glycerol or 6-AN concentrations respectively. GPI, Glucose-6-phosphate isomerase; PGD, Glucose-6-phosphate dehydrogenase; 6-PG, 6-phosphogluconate, Suc, sucrose. *RhBRC1*, 3'UTR$_{RhBRC1}$ contained callus; *NOS*, 3'UTR$_{NOS}$ contained callus. Data are mean ± SE of three measurements, each measurement contained six Rosa callus. The letters indicate significant differences between the different treatments with $P < 0.05$.

Identification of PUF family in *Rosa chinensis*

The Pumilio RNA-binding protein family (PUF family) is mainly involved in post-transcriptional control by binding to specific regulatory *cis*-elements which contained a UGUR (R, purine) flanked by a AU-riched sequence. Through this interaction, they govern RNA decay and translational repression (Tam *et al*., 2010). Based on the presence of 6 putative PUF binding motifs in 3'UTR of *RhBRC1* (Figure 1), we hypothesized that PUF protein might mediate the post-transcriptional regulation of *RhBRC1* in response to sugar. The phylogenetic analysis among the identified *RcPUF* (*Rosa chinensis* PUF) proteins was processed by MEGA7.0 software. According to previous studies, the PUF family in *Arabidopsis* have 26 members and can be grouped into five subfamilies through the phylogenetic analysis (Tam *et al*., 2010, Figure 4A). In *Rosa chinensis*, we only identified twelve PUF members which are much less than *Arabidopsis*. The PUF protein members can be categorized into four groups (Figure 4A), and their gene length varies from 2000bp to 5000bp, which is quite different within each members (Figure 4B). Moreover, of these twelve PUF members, eleven of them contain eight PUF repeats and only RC7G0558100 contains seven PUF repeats (Figure S3).

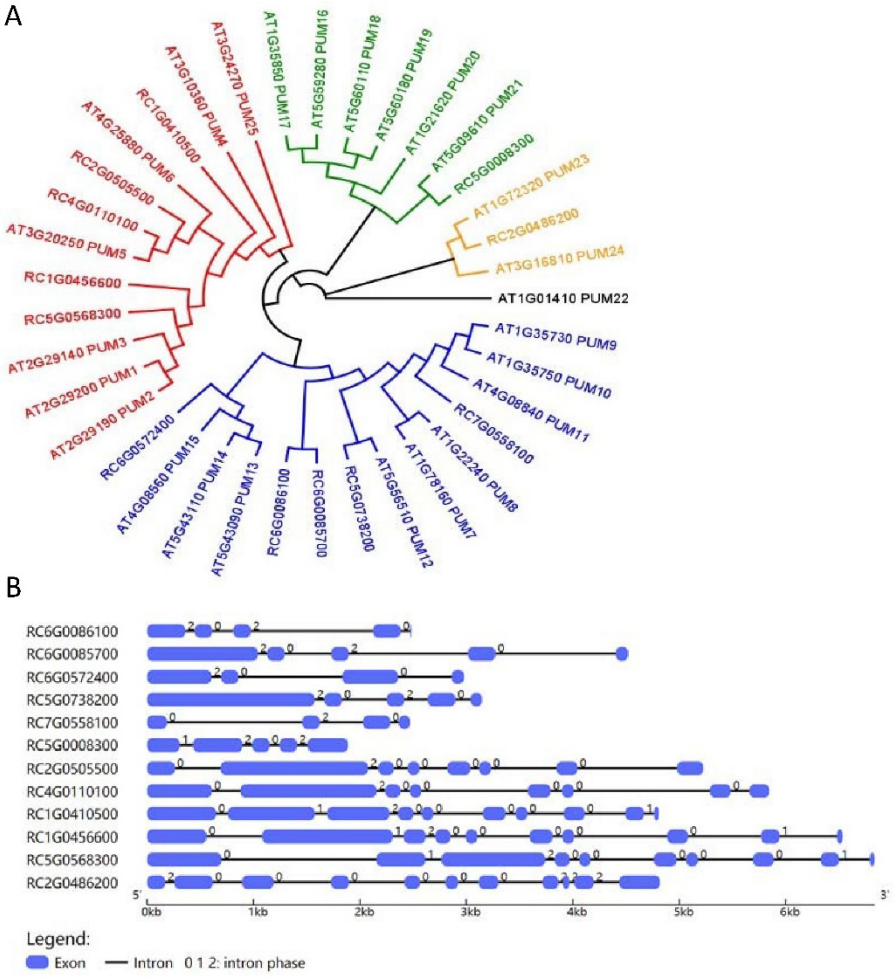

Figure 4. Identification of PUF members in *Rosa chinensis*. A, Phylogenetic tree of PUF members in *Arabidopsis thaliana* and *Rosa chinensis.* The maximum likelihood analysis in MEGA program was used for building the phylogenetic tree. The PUF sequence of *Rosa chinensis* and *Arabidopsis thaliana* were downloaded from GDR database and TAIR database respectively. B, Gene structure dynamics of PUF members in *Rosa Chinensis*. Gene structures of RCPUF members were performed by the GSDS software. C, The sequence alignment of Pumilio repeat among PUF members. Multiple alignments were generated using ClustalX program. The PUF sequence of *Rosa chinensis* were downloaded from GDR database (https://www.rosaceae.org/).

Transcription level of *RhPUF4* is under the effect of sugar

Firstly, in order to check whether PUF family proteins could be involved in sucrose-induced bud outgrowth, the expression pattern of all twelve *RhPUF*s (*Rosa hybrida PUF*) were investigated by RT-PCR in *in-vitro* cultured buds supplied with 100mM sucrose (non-dormant buds) or 100mM mannitol (dormant buds) for 24h. Using specific primer for each PUF member (Table S1), only *RhPUF4* (a homologue gene of *RC5G0568300*) showed high expression level in 100mM sucrose-fed buds, while almost no expression with 100mM mannitol was observed (Figure S4). Furthermore, *RhPUF4* expression level increased in manner that was positively correlated with sucrose concentration, supporting being a sugar inducible gene in growing bud (Figure 5C). The time course of *RhPUF4* expression within the early stage, prior the onset of rapid bud growth, showed *RhPUF4* to be early (highest level at 10h) and temporarily expressed in 100mM sucrose-fed buds (non-dormant ones), comparatively to those supplied with 100mM mannitol (dormant buds, Figure 5B). In line with this, *RhPUF4* is more expressed in non-dormant (released from apical dominance) than in dormant bud (under apical dominance) (Figure 5A). The *RhPUF4* transcription pattern was oppositely correlated with the transcription level of *RhBRC1*, because its level was lowest in the buds with high expression level of *RhBRC1* (10mM sucrose) and highest in the buds of low expression level of *RhBRC1* (250mM sucrose) (Barbier *et al*., 2015). Taken together, these findings showed that *RhPUF4* expression was early and highly expressed in non-dormant axillary buds and is negatively correlated with the expression of *RhBRC1*.

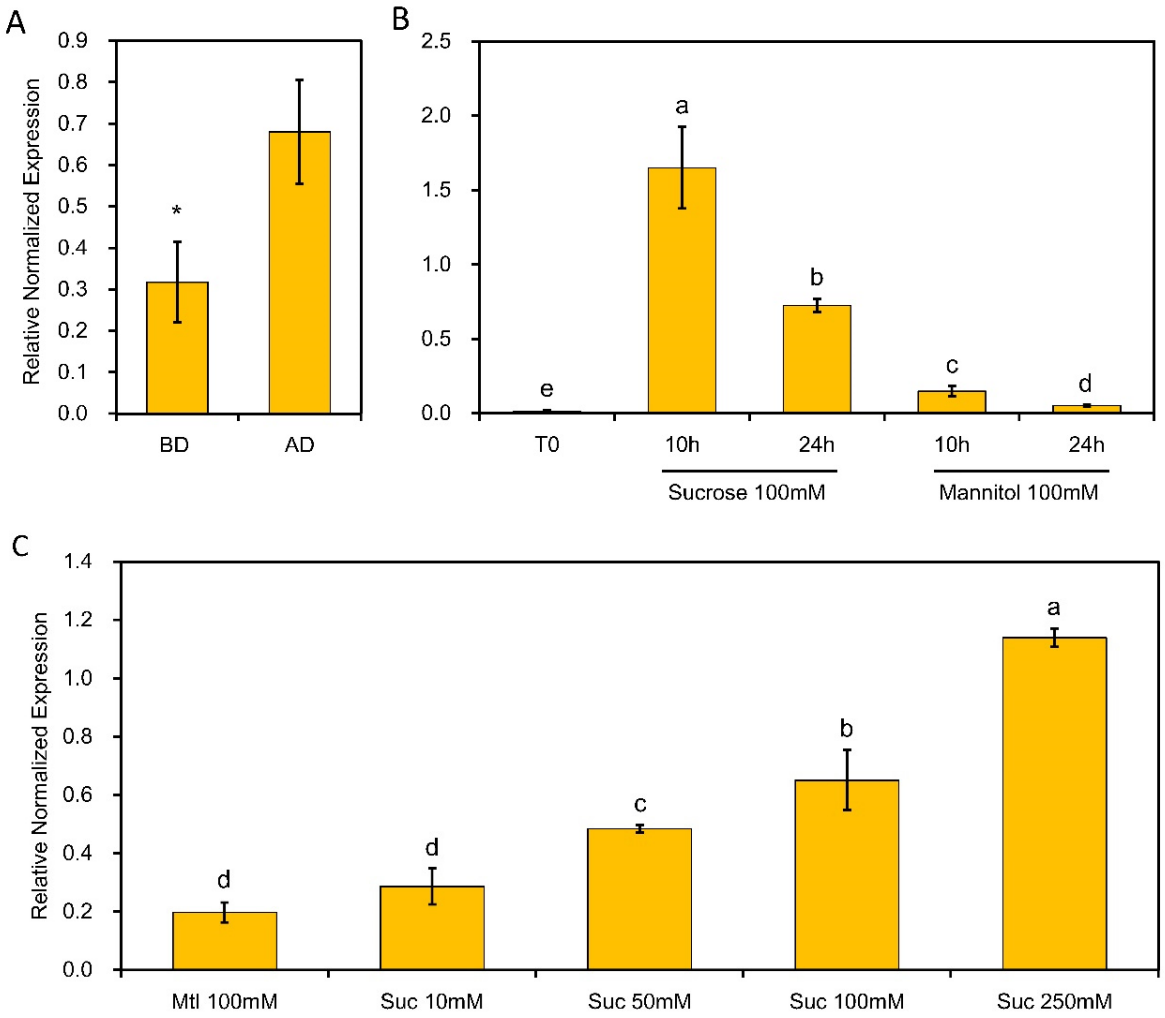

Figure 5. *RhPUF4* expression was under the control of sucrose and sucrose metabolism. A, Transcription level of *RhPUF4* in the bud before decapitation (BD) or after decapitation (AD); B, Transcription level of *RhPUF4* of *in vitro* cultured buds at 0h, 10h and 24h under 100mM of sucrose or mannitol; C, Transcription level of *RhPUF4* in buds treated with different sucrose concentrations. Mtl, mannitol; Suc, sucrose. Data are mean ± SE of three repetitions. The letters indicate significant differences between the different treatments with $P < 0.05$.

Transcript level of *RhPUF4* was more likely to be sensitive to an OPPP-emanating signal

To go further in the understanding of the relationship between *RhPUF4* and sugar-dependent post-transcriptional regulation of *RhBRC1*, we investigated its transcript level in buds treated with the glycolysis/TCA-cycle effector (2-DOG), as it was the case for the transformed Rosa callus (Figure 3B). When buds co-feed with sucrose and 2-DOG, *RhPUF4* level did not significantly change under 10mM sucrose, while unexpectedly reduced under 100mM sucrose (Figure 6A). In accordance with this, buds only supplied with glycerol or pyruvate, two compounds of glycolysis/TCA-cycle, did not exhibit significant change in *RhPUF4* transcript level (Figure 6B&C), supporting that glycolysis/TCA-cycle mediated *RhBRC1* post-transcriptional regulation would be independent of *RhPUF4*. In order to check whether *RhPUF4* regulation was dependent on OPPP-emanating signal, *RhPUF4* transcription level was investigated in buds in response directly to OPPP inhibition (sucrose-fed buds supplied with 5mM 6-AN) or to OPPP activation (buds supplied with 6-PG, a direct substrate of OPPP). The *in-vitro* cultured buds treated with 5mM 6-AN exhibited a downregulation of *RhPUF4*, which was higher with low (10mM) than with elevated (100mM) sucrose concentration (Figure 6D). Furthermore, 6-PG-treated buds displayed a concentration dependent response of *RhPUF4* transcript level. Indeed, the highest level of *RhPUF4* was found when bud was supplied with 10mM 6-PG, relatively to 0.1mM 6-PG (Figure 6F). To confirm this data, the transcript level of *RhPUF4* was assessed in 2-DOG (a blocker of glycolysis/TCA-cycle) and Glc6P-(used by OPPP) co-treated *in vitro* cultured buds. When 1mM 2-DOG-fed buds were supplied with a gradient concentration of Glc-6P (from 0 to 5mM) to activate preferentially the OPPP, the transcript level of *RhPUF4* increased in concentration dependent manner and reached its maximum under 5mM Glc-6P (Figure 6E). In addition, exogenous addition of glycerol to 6-PG treated buds did not affect the *RhPUF4* level (Figure 6G), supporting once again that transcript level of *RhPUF4* could be tightly sensitive to OPPP-dependent pathway.

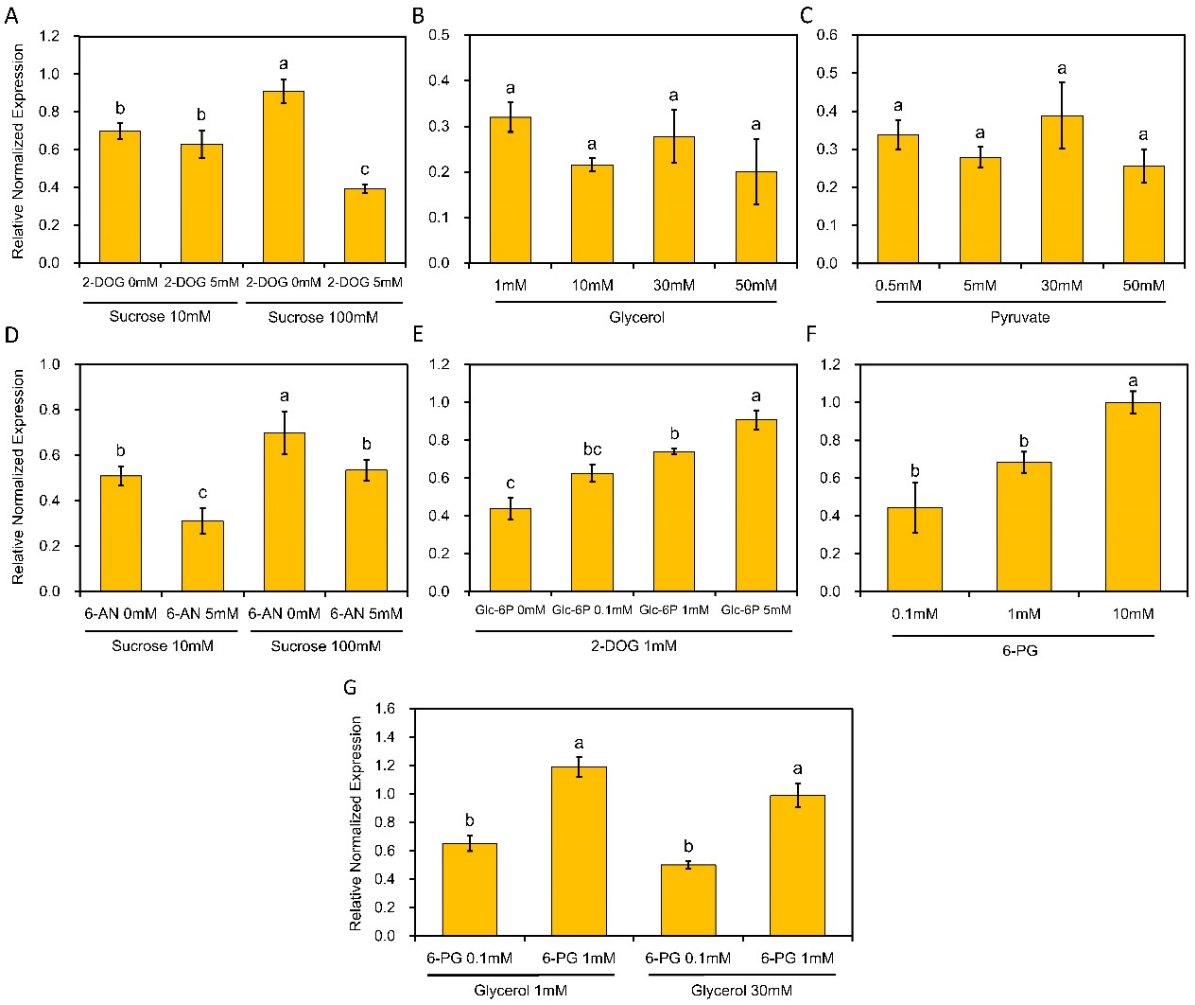

Figure 6. Transcription level of *RhPUF4* was hardly sensitive to glycolysis/TCA-cycle, but sensitive to OPPP. A&D, Transcript level of *RhPUF4* in buds treated with 10mM and 100mM sucrose with or without 5mM 2-DOG or 6-AN respectively; B&C, Transcription level of *RhPUF4* in buds treated with different concentration of glycerol or pyruvate respectively; E, Transcript level of *RhPUF4* in buds treated with 1mM 2-DOG and different concentration of Glc-6P; F, Transcript level of *RhPUF4* in buds treated with different 6-PG concentrations. G, Transcript level of *RhPUF4* in buds treated with different combination of glycerol and 6-PG. Glc-6P, glucose 6-phosphate; 6-PG, 6-phosphogluconate. Data are mean ± SE of three repetitions. The letters indicate significant differences between the different treatments with $P < 0.05$.

RhPUF4 could bind to the 3'UTR of *RhBRC1* and promote plant growth

In order to know whether RhPUF4 could real bind to the 3'UTR of *RhBRC1*, the NCBI database was used to find the homologue gene of *RhPUF4* in Arabidopsis. The Blast result showed that the *APUM2* (*AT2G29190)* is a homologue gene of *RhPUF4* with a high query cover (99%) and a low E-value (0.0). Moreover, our polygenetic tree also confirmed that *RhPUF4* was closely related to *APUM2* (Figure 4A). APUM2 is involved in cell differentiation and highly expressed in shoot meristem in Arabidopsis (Abbasi *et al*. 2011). Based on the previous reports, APUM2 has a high binding affinity to a conserved sequence, which contained a core motif of UGUR flanked with a NRKR motif (Francischini *et al*., 2009; Zhang and Muench, 2015). Moreover, UGURNRKD motif also existed in the 3'UTR of *RhBRC1* (Figure 1) and could be recognized by RhPUF4. In order to know whether RhPUF4 can also response to the same motif, we used the SWISS-MODEL database (Schwede *et al*., 2003; Biasini *et al*., 2014) to predict the tertiary structure of RhPUF4 and APUM2. The result showed that the structure of them has a high QMEAN (-1.47 and -1.45 respectively, Figure 7A&B), both of them have a conserved eight pumilio repeats (Figure 7A&B). Furthermore, the WoLF PSORT database was used to determine the subcellular localization prediction of RhPUF4 (Horton *et al*., 2007). This analysis indicated that RhPUF4 located in the nuclear and cytoplasm. Both of these results supported that RhPUF4 and APUM2 could bind to the same motif in the 3'UTR, probably based on their conserved PUF motif. In order to know the function of RhPUF4 during plant branching, the overexpressing APMU2 mutant in Arabidopsis showed a bigger plant and longer lateral buds, relatively to wild type. Moreover, the overexpressing mutants also have a thicker and longer stem than wild type (Figure 7C). In addition, the knockout mutant of APUM2 showed a wthinner and shorter stem and no bud outgrowth compared with wild type (Figure 7C).

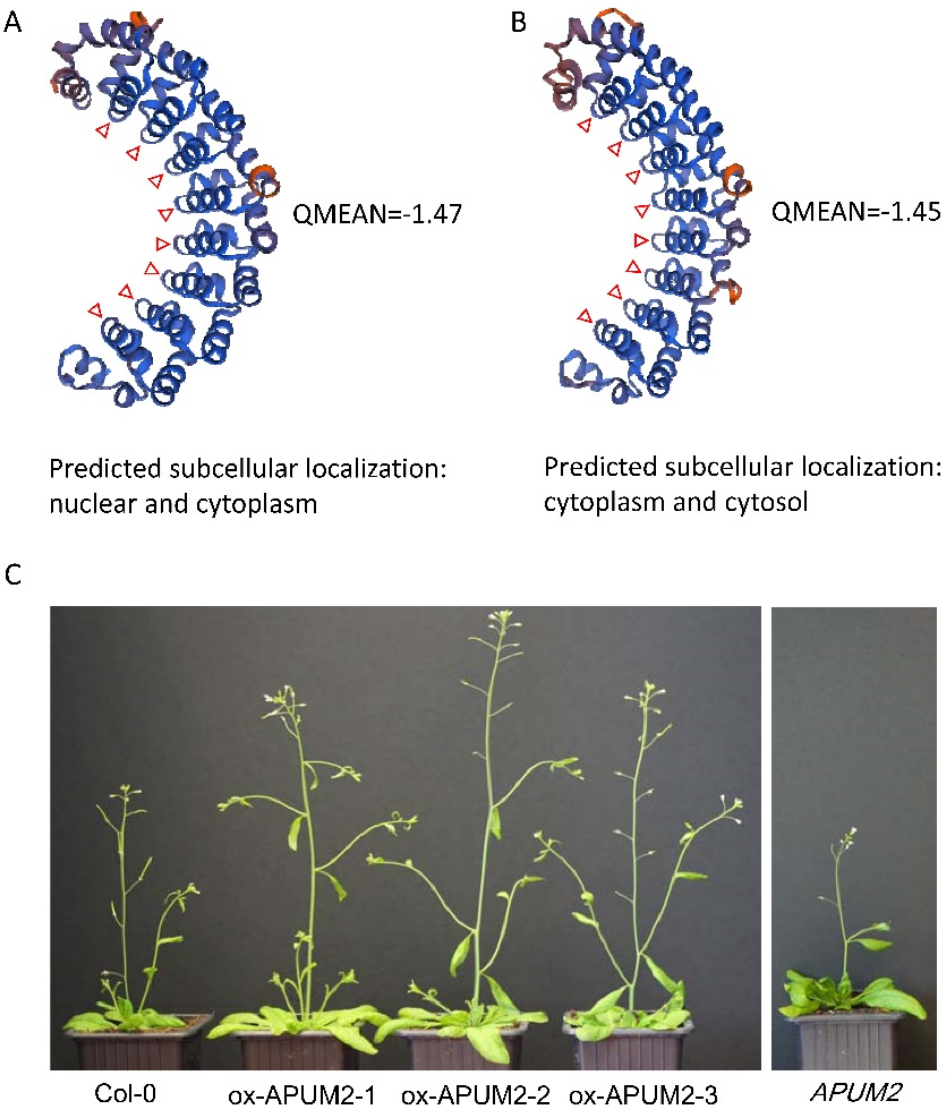

Figure 7. The RhPUF4 could promote plant growth and bind to the PUF motif. A&B, the putative tertiary structure of RhPUF4 and APUM2 respectively, based on the prediction of SWISS-MODEL database (https://swissmodel.expasy.org/); C, the phenotype of APUM2 knockout and overexpression mutants compared with wild type. The APUM2 and RhPUF4 protein sequence were downloaded from NCBI database (https://www.ncbi.nlm.nih.gov/) and GDR database (Jung *et al*., 2018; https://www.rosaceae.org/). The red triangle means pumilio repeats.

Discussion

Involvement of 3'UTR region in sugar-mediated downregulation of *RhBRC1*

BRC1 and its homologues genes played central role in shoot branching and were downregulated by sugars (Wang *et al*., 2019). We showed that one mechanism behind sucrose-dependent *RhBRC1* downregulation occurred through its 3'UTR sequence, which contained six putative PUF motifs, one of them is present in the reported sugar-related motif (UAUAUAUGUA) (Figure 1). *BRC1* was regulated at different levels, including post-transcriptional level, as evidenced by micorRNA393-dependent repression of *OsTB1* and stimulation of the tillers in rice (Li *et al*., 2016). Proteins interactions also participate in this process; because BRANCHED1 interacts with FLOWERING LOCUS T to repress the floral transition of the axillary meristems (Niwa *et al*., 2013) and TIE1 (TCP interactor containing EAR motif protein 1) can directly interact with BRC1 directly, and repress its binding efficiency (Yang *et al*., 2018). In addition, the expression of some TCP transcription factor members, the same family as BRC1, is regulated through post-transcriptional regulation (Parapunova *et al*., 2014; Liu *et al*., 2017). In *Arabidopsis*, miRNA319 can target many TCP transcription factor members, in response to ABA and CK (Liu and Chen, 2009; Zhou and Luo, 2014). 3'UTR of some genes are also under SL control. For example, miR156 targeted the 3'UTR of SL-related genes, SPL3, SPL9 and SPL15, to regulate shoot branching process (Gandikota *et al*., 2007; Schwarz *et al*., 2008; Bennett *et al*., 2016). Here, exogenous supply of sucrose or glucose can indeed reduce the fluorescence of the P35S::GFP::3'UTR$_{RhBRC1}$-transformed callus in a concentration dependent manner (Figure 2A), while no effect was observed for control (P35S::GFP::3'UTR$_{NOS}$-transformed callus) (Figure 2A). In line with this, no effect of mannitol was found in both cases of transformed callus (Figure 2A). The involvement of 3'UTR region in sugar signaling is limited to cases related to sugar abundance (Chan and Yu, 1998b; Cheng *et al*., 1999), and 3'UTR may constitute a link between organ metabolism and sugar availability in plants. The exact motif involved in sugar-mediated post-transcriptional regulation is still unknown but a role of UAUAUAUGUA sequence has been reported in sugar-posttranscriptional dependent regulation of *α-amylase 3* (Chan and Yu, 1998a). Interestingly, this motif exists 3'UTR of *RhBRC1* in Rosa, supporting to be conserved between monocots (rice) and dicots (Rosa).

Sucrose-mediated posttranscriptional regulation of RhBRC1 mainly through OPPP

3’UTR of *BRC1* is sensitive to sucrose and lactulose (its non-metabolizable analog) that both induces bud outgrowth and represses *RhBRC1* expression in Rosa buds (Barbier *et al*., 2015). In contrast to glucose, no significant decrease was exhibited by P35S::GFP::3’UTR$_{RhBRC1}$-transformed callus in response to mannose mannose, a non-metabolizable glucose analog and linked to HXK signaling pathway (Rabot *et al*., 2012), assuming a minor role of this pathway in glucose-mediated BRC1 posttranscriptional regulation. Downstream of HXK, glycolysis/TCA-cycle and OPPP are the two important sugar metabolism pathways. They provide the energy for plant development, the precursor for amino acid synthesis and the signal molecule for modulating some pathways (Koch, 2004; Gibson, 2005). Moreover, they also involve in the regulation of microRNAs, transcription factors and for crosstalk with hormonal, oxidative and defense signaling (Ruan, 2014). Here, we showed that two sucrose metabolism pathways regulate, at different extent, *RhBRC1* abundance at post-transcriptional level. The fluorescence level of P35S::GFP::3’UTR$_{RhBRC1}$-transformed callus indicated that 3’UTR of *RhBRC1* was slightly but significantly sensitive to glycolysis/TCA-cycle (Figure 3B&C). Although sucrose + 2-DOG co-treated 3’UTR$_{RhBRC1}$-contained callus displayed an increased fluorescence, in a manner that was correlated with 2-DOG concentration, this difference remained only slightly statistically significant. The same results were also found with the glycerol and pyruvate treated 3’UTR$_{RhBRC1}$-transformed callus, indicating that the glycolysis and its related TCA cycle-dependent *RhBRC1* expression could weakly be mediated through its 3’UTR. By contrast to glycolysis, the 3’ UTR of *RhBRC1* was found to be significantly responsive to OPPP (Figure 3D&E). Indeed, the fluorescence of 3’UTR$_{RhBRC1}$-transformed callus was activated and inhibited by 6-AN (OPPP blocker) and 6-PG (OPPP inducer) respectively. In accordance with this, the combination of 2-DOG (blocker of glycolysis) and Glc-6P (preferentially used by OPPP in the presence of 2-DOG) reduced fluorescence of 3’UTR$_{RhBRC1}$-contained callus. All these findings were specific to 3’UTR$_{RhBRC1}$, because no significant modification of fluorescence was found with 3’UTR$_{NOS}$-contained callus. In eukaryote cells, many factors are related to post-transcriptional regulation, such as RNA-binding protein, microRNA, protein phosphorylation, methylation (Chekulaeva and Filipowicz, 2009; Filipowicz *et al*., 2008; Keene, 2007). It has been indicated that some post-transcriptional related factors were involved in OPPP. For example, TOR kinase can mediate the upregulation of G6PD (glucose-6-phosphate dehydrogenase, one of key enzymes in OPPP) and that the activity of TOR kinase is probably under the positive regulation of NADPH, a production of OPPP (Corradetti and Guan, 2006; Liu and Bassham, 2010). Moreover, MicroRNA124 and Hsp27 in *Homo sapiens* were also reported to be involved in OPPP (Qiu *et al*., 2015; Cosentino

et al., 2011). However, there are very few reports about the link between OPPP and post-transcriptional factors in plants.

Involvement of RhPUF4 in posttranscriptional of *RhBRC1* mediated by OPPP

OPPP and glycolysis could reduce the expression of *RhBRC1* through its 3' UTR region, even if the glycolysis had a weak effect (Figure 3). However, the post-transcriptional regulation between sugar metabolism-emanating signal and 3'UTR of *RhBRC1* was still unknown. The regulatory regions within the 3'UTR can influence polyadenylation, translation efficiency, localization, and stability of the mRNA (Barrett *et al*., 2012). RNA binding proteins that can bind to those *cis*-elements are key players in controlling mRNA stability, translation and localization (Wickens *et al*., 2002) and the functional characterization of RNA-binding proteins have shown that these proteins possess several conserved motifs and domains such as RNA-recognition motifs (RRMs), zinc fingers, K homology (KH) domains, DEAD/DEAH boxes (highly conserved motif (Asp-Glu-Ala-Asp) in RNA helicases), pentatricopeptide-repeat (PPR) domains and Pumilio/FBF (Caenorhabditis elegans Pumilio-fem-3 binding factor, PUF) domains (Wang *et al*., 2018). Among the domains mentioned above, the PUF protein can bind *cis*-elements which contained a UGUR (R, purine) motif (Valley *et al*., 2012; García-Rodríguez *et al*., 2007). Sucrose-fed in vitro cultured buds exhibited high ability to grow out, coupled with a downregulation of *RhBRC1* (Barbier *et al*., 2015) and an upregulation of *RhPUF4* (Figure 5). At the plant scale, *RhPUF4* is more abundant in non-dormant buds than in dormant ones. This sucrose-mediated RhPUF4 was tightly linked to OPPP because it was reduced by 6-AN (OPPP blocker) but stimulated by 6-PG (OPPP inducer) (Figure 6D, E&F). In accordance with this, 2-DOG and Glc-6P co-treated buds exhibited an upregulation of transcript level of *RhPUF4* and the same effect was found in response to Glc-6P alone (Figure 6E). These findings indicated that the *RhPUF4* level was more likely controlled by an OPPP-emanating signal, and was stimulated when OPPP was active and bud can grow out. Given OPPP led to both *RhPUF4* stimulation and *RhBRC1* down-regulation through its 3'UTR (Figure 3&6), it is tenting to speculate that RhPUF4 may be a mediator between OPPP and 3'UTR *RhBRC1* (Figure 7). This is supported by the fact that *RhPUF4* was closely related to *APUM2* (Figure 4A), that has a high binding affinity to a conserved sequence, containing a core motif of UGUR flanked with a NRKR motif (Francischini *et al*., 2009; Zhang *et al*., 2015) that exists in 3'UTR of *RhBRC1* (Figure 1). In that condition, OPPP-mediated upregulation of *RhPUF4* can reduce mRNA stability and/or translation of *RhBRC1* by binding to its own 3'UTR.

In contrast to OPPP, the transcription level of *RhPUF4* was not regulated by glycolysis. Sucrose+2-DOG, glycerol or pyruvate treated buds exhibited no significant modification of *RhPUF4* level. It seems that the *RhPUF4* may not be mediated by glycolysis/TCA-cycle dependent signal, and arises the question about the involvement of another post-transcriptional player. One possible candidate would be a microRNA, because in *Homo sapiens*, some microRNA are regulated by glycolysis and regulate its target genes (Zhao *et al*., 2016; Tang *et al*., 2012).

Material and methods

Cloning and transformation of *RhBRC1* 3'UTR

To isolate the 3'UTR of *RhBRC1* (206 bp), genomic DNA was extracted from leaves of *Rosa hybrid* 'Old blush', using a NucleoSpin Plant II kit (Machery-Nagel Inc., Düren, Germany). A primer pair (Pr3'UTRs: 5' CACCTAACACCGCGATGAATATCGATC 3' and Pr3'UTRas: 5' AATGAGAAAGGTGGAAATTAGGTAG 3') was designed to amplify the 3'UTR sequence. The 4 base pair sequence (CACC) necessary for directional cloning in pENTR was added on the 5' end of the forward primer. PCR amplification was carried out by initial denaturation at 98°C for 30s followed by 35 cycles of 98°C denaturation for 30s, 60°C annealing for 30s, and 72°C elongation for 2 min, and with a final extension of 72°C for 10min. The 20µL reaction mixture for the PCR consisted of an aliquot of 35ng DNA template, 0.2mM each of dNTP, 0.4unit of Phusion DNA polymerase and 10pmol each of the primers. PCR products were separated in 1% (w/v) agarose gel and purified using the Wizard SV Gel and PCR Clean-Up System kit (Promega, USA). The PCR products were separated in 1% (w/v) agarose gel and purified using the Wizard SV Gel and PCR Clean-Up System kit (Promega, USA).

The PCR products of *RhBRC1* 3'UTR were sub-cloned into an entry vector using a pENTR Directional TOPO Cloning Kit (Invitrogen). The ligation product was transferred into *Escherichia coli* strain One Shot TOP10 Competent *E.coli* by thermal shock at 42°C. The plasmids of several bacteria clones were extracted using a NucleoSpin plasmid extraction kit (Macherey-Nagel, Germany) and confirmed by sequencing using two different primers (M13F: 5' GTAAAACGACGGCCAG 3' and M13R: 5' CAGGAAACAGCTATGAC 3'). From positive entry vectors, 3'UTR of *RhBRC1* was then cloned, respectively, into pKGWFS7 destination vector (Karimi *et al.*, 2002) and pGWB6 destination vector (Tsuyoshi *et al.*, 2007) using an LR Clonase II kit (Invitrogen). The ligation product was transferred into *Escherichia coli* strain One Shot TOP10 Competent *E.coli* by thermal shock at 42°C. The plasmids of several bacteria clones were extracted using a NucleoSpin plasmid extraction kit (Macherey-NagelGermany) and confirmed by sequencing using GFP-F 5' CCACCCTCGTGACCACC 3' and GFP-R 5' CACGAACTCCAGCAGGAC 3' primers for respectively pGWB6 and pKGWFS7. The 3'UTR of *RhBRC1* were introduced by electroporation in *Agrobacterium tumefaciens* EHA105 (-pBBR1-MCS-5).

Rosa callus transformation

In vitro propagated shoots of *Rosa* were used as starting material. They were repeatedly sub-cultured every 6 weeks on Shoot multiplication medium (Hamama *et al*., 2015), consisting on (Murashige and Skoog [MS] salts and vitamins with 0.1 $g \cdot L^{-1}$ Fe-EDDHA, 30 $g \cdot L^{-1}$ sucrose, 0.1 $g \cdot L^{-1}$ myo-inositol, 4.44 µM 6-benzyladenine), solidified by 3 $g \cdot L^{-1}$ Phytagel. young leaves were injured by several cuts and inoculated by *Agrobacterium* (EHA105) which had been suspended in re-suspension medium until DO_{600}=1 for 5 min. The inoculated leaves were blot drayed on sterile paper and transferred in the callus induction medium (Ibrahim *et al*., 2000) completed with cefotaxime (500 mg/L) and Kanamycine (100 mg/L). Leaf discs were sub-cultured every 6 weeks on the same medium until the callus formed. The genomic DNA was extracted from the selected callus and PCR was used to confirm that whether the target fragment was transformed into callus steadily.

Callus treatments and GFP quantification

The transformed callus were put into liquid basic medium (Murashige and Skoog [MS] salts and vitamins, pH=8.8) with different treatments for 8 hours under light in 22°C. Indeed, the kinetics of GFP fluorescence showed that 8 hours incubation was the best observation time, because the fluorescence was stronger than for 2, 4 and 6 hours while it dropped after 24 hours. GFP intensity was assessed under the fluorescence microscope and its quantification of the GFP intensity was performed on 2D images using ImageJ software. Integrated density of grey was determined on the 30 randomly selected spots on the representative part for each sample. Each condition were replicate between three and eight times.

Plant culture and *in vitro* cultivation of axillary buds analysis

For the experiments on *Rosa hybrida* L., cuttings from cloned mother plants were grown in a greenhouse where the temperature was maintained around 22°C. Nodes from the median part of the stem were harvested on single-axis plants when the floral bud was visible (BFV stage), as previously described (Girault *et al*., 2010, Rabot *et al*., 2012, Barbier *et al*., 2015). For decapitation plant, stems of plants with a terminal floral bud (0.5 cm above the fifth basal five-leaflet leaf) were removed. After 24h, the lateral bud from third and fourth basal five-leaflet leaf were collected for qRT-PCR. For *in vitro* cultured bud, 1.5-cm stem segments were transferred in vitro on classical solid MS medium with different sucrose metabolism effectors (2-DOG for glycolysis, 6-AN for OPPP) or different products in sugar metabolism pathway (Glucose 6-phosphate a precursor of glycolysis and OPPP, glycerol and pyruvate for glycolysis,

6-phosphogluconate for OPPP), in a growth chamber (Strader) with a 16h day length at a temperature of 23/20°C (day/night).

RNA extraction

Total RNAs were extracted from the *in vitro*-cultured buds using an RNA NucleoSpin kit (Macherey-Nagel) (Barbier *et al*., 2015). Genomic DNA was removed by incubating RNAs with DNase (Biolabs, Inc) for 10 min at 37°C (1 µl of DNase for 10 µg of RNA). The reaction was stopped by adding EDTA at a final concentration of 5 mM followed by 10 min at 75°C. The absence of contamination by genomic DNA was checked by PCR using a specific primer designed against an intron region of the *RhGAPDH* gene (Girault *et al*., 2010; Henry *et al*., 2011). cDNA was obtained by reverse transcription performed on 1µg of RNA using SuperScript III Reverse Transcriptase (Invitrogen, Inc).

qRT-PCR

Quantitative real-time PCR (qRT-PCR) was performed with SYBR Green Supermix (Biorad, Inc) using cDNA as a template, with the following program: 2min at 50°C, 10min at 95°C, then 40 cycles of 15 s at 95°C and 60 s at 60 °C. Specific sets of primers were selected according to their melting curves. Fluorescence detection was performed using a Chromo4 Real-time PCR detector (Biorad, Inc). Quantification of relative gene expression was determined using *RhUBC* expression as an internal control (Chua *et al*., 2011; Jain *et al*., 2006). The *RhPUF4* expression level was detected by primer qPrRhPUF4 (Forward, 5'-GCTTGCTGCCCTGAATGAT-3'; Reverse, 5'-GCAAGGCTCCAAGATACGC-3') and each PCR results corresponded to three biological repetitions.

Statistical analyses

R software was used for caring the statistical analyses. One-way ANOVA ($\alpha = 0.05$) was run to test for the effects of different conditions on bud outgrowth, gene transcription level and fluorescence level. Significant differences are indicated by different letters or asterisks directly on the figures.

References

Abbasi, N., Park, Y. I., & Choi, S. B. (2011). Pumilio Puf domain RNA-binding proteins in Arabidopsis. Plant signaling & behavior, 6(3), 364-368.

Acevedo-Hernández, G. J., León, P., & Herrera-Estrella, L. R. (2005). Sugar and ABA responsiveness of a minimal RBCS lightG. J., León, P., & Herrera‐Estrella, L. R. (2005). Sugar and ABA responsiveness of a minim

Aguilar-Martínez, J. A., Poza-Carrión, C., & Cubas, P. (2007). Arabidopsis BRANCHED1 acts as an integrator of branching signals within axillary buds. The Plant Cell, 19(2), 458-472.

Andreassi, C., & Riccio, A. (2009). To localize or not to localize: mRNA fate is in 3′ UTR ends. Trends in cell biology, 19(9), 465-474.

Aubert, S., Gout, E., Bligny, R., & Douce, R. (1994). Multiple effects of glycerol on plant cell metabolism. Phosphorus-31 nuclear magnetic resonance studies. Journal of Biological Chemistry, 269(34), 21420-21427.

Aukerman, M. J., & Sakai, H. (2003). Regulation of flowering time and floral organ identity by a microRNA and its APETALA2-like target genes. The Plant Cell, 15(11), 2730-2741.

Barbier, F., Péron, T., Lecerf, M., Perez-Garcia, M. D., Barrière, Q., Rolčík, J., ... & Roman, H. (2015). Sucrose is an early modulator of the key hormonal mechanisms controlling bud outgrowth in Rosa hybrida. Journal of experimental botany, 66(9), 2569-2582.

Barker, D. D., Wang, C., Moore, J., Dickinson, L. K., and Lehmann, R. (1992). Pumilio is essential for function but not for distribution of the Drosophila abdominal determinant Nanos. Genes and Development, 6(12a), 2312-2326.

Barrett, L. W., Fletcher, S., & Wilton, S. D. (2012). Regulation of eukaryotic gene expression by the untranslated gene regions and other non-coding elements. Cellular and molecular life sciences, 69(21), 3613-3634.

Bennett, T., Liang, Y., Seale, M., Ward, S., Müller, D., & Leyser, O. (2016). Strigolactone regulates shoot development through a core signalling pathway. Biology open, bio-021402.

Bennett, T., Sieberer, T., Willett, B., Booker, J., Luschnig, C., & Leyser, O. (2006). The Arabidopsis MAX pathway controls shoot branching by regulating auxin transport. Current Biology, 16(6), 553-563.

Biasini, M., Bienert, S., Waterhouse, A., Arnold, K., Studer, G., Schmidt, T., ... & Schwede, T. (2014). SWISS-MODEL: modelling protein tertiary and quaternary structure using evolutionary information. Nucleic acids research, 42(W1), W252-W258.

Bonhomme, M., Peuch, M., Ameglio, T., Rageau, R., Guilliot, A., Decourteix, M., ... & Lacointe, A. (2009). Carbohydrate uptake from xylem vessels and its distribution among stem tissues and buds in walnut (Juglans regia L.). Tree physiology, 30(1), 89-102.

Brewer, P. B., Dun, E. A., Ferguson, B. J., Rameau, C., & Beveridge, C. A. (2009). Strigolactone acts downstream of auxin to regulate bud outgrowth in pea and Arabidopsis. Plant Physiology, 150(1), 482-493.

Bruce Alberts; Alexander Johnson; Julian Lewis; Martin Raff; Keith Roberts; Peter Walter (2007). Molecular Biology of the Cell (Fifth ed.). Garland Science.

Chabikwa, T. G., Brewer, P. B., & Beveridge, C. A. (2019). Initial bud outgrowth occurs independent of auxin flow out of buds. Plant physiology, pp-00519.

Chan, M. T., & Yu, S. M. (1998a). The 3′ untranslated region of a rice α-amylase gene functions as a sugar-dependent mRNA stability determinant. Proceedings of the National Academy of Sciences, 95(11), 6543-6547.

Chan, M. T., & Yu, S. M. (1998b). The 3′ untranslated region of a rice α-amylase gene mediates sugar-dependent abundance of mRNA. The Plant Journal, 15(5), 685-695.

Chandler, J. W. (2016). Auxin response factors. Plant, cell & environment, 39(5), 1014-1028.

Chekulaeva, M., & Filipowicz, W. (2009). Mechanisms of miRNA-mediated post-transcriptional regulation in animal cells. Current opinion in cell biology, 21(3), 452-460.

Cheng, W. H., Taliercio, E. W., & Chourey, P. S. (1999). Sugars modulate an unusual mode of control of the cell-wall invertase gene (Incw1) through its 3′ untranslated region in a cell suspension culture of maize. Proceedings of the National Academy of Sciences, 96(18), 10512-10517.

Chiariello, N.R.; Mooney, H.A.; Williams, K. Growth, carbon allocation and cost of plant tissues. In Plant Physiological Ecology; Springer Netherlands: New York, NY, USA, 2000; pp. 327–365.

Collart, M. A., & Panasenko, O. O. (2012). The Ccr4–not complex. Gene, 492(1), 42-53.

Corradetti, M. N., & Guan, K. L. (2006). Upstream of the mammalian target of rapamycin: do all roads pass through mTOR?. Oncogene, 25(48), 6347.
Cosentino, C., Grieco, D., & Costanzo, V. (2011). ATM activates the pentose phosphate pathway promoting anti‐oxidant defence and DNA repair. The EMBO journal, 30(3), 546-555.
Cubas, P., Lauter, N., Doebley, J., and Coen, E. (1999). The TCP domain: a motif found in proteins regulating plant growth and development. The Plant Journal, 18(2), 215-222.
de Jong, M., George, G., Ongaro, V., Williamson, L., Willetts, B., Ljung, K., ... & Leyser, O. (2014). Auxin and strigolactone signaling are required for modulation of Arabidopsis shoot branching by N supply. Plant physiology, pp-114.
Dierck, R., Leus, L., Dhooghe, E., Van Huylenbroeck, J., De Riek, J., Van Der Straeten, D., & De Keyser, E. (2018). Branching gene expression during chrysanthemum axillary bud outgrowth regulated by strigolactone and auxin transport. Plant Growth Regulation, 1-14.
Doebley, J., Stec, A., and Hubbard, L. (1997). The evolution of apical dominance in maize. Nature, 386(6624), 485-488.
Eulgem, T., Rushton, P. J., Robatzek, S., & Somssich, I. E. (2000). The WRKY superfamily of plant transcription factors. Trends in plant science, 5(5), 199-206.
Evers, J. B. (2015). Sugar as a key component of the shoot branching regulation network. Plant, cell & environment, 38(8), 1455-1456.
Fernie, A. R., Carrari, F., & Sweetlove, L. J. (2004). Respiratory metabolism: glycolysis, the TCA cycle and mitochondrial electron transport. Current opinion in plant biology, 7(3), 254-261.
Fichtner, F., Barbier, F. F., Feil, R., Watanabe, M., Annunziata, M. G., Chabikwa, T. G., ... & Lunn, J. E. (2017). Trehalose 6‐phosphate is involved in triggering axillary bud outgrowth in garden pea (pisum sativum L.). The Plant Journal, 92(4), 611-623.
Filipowicz, W., Bhattacharyya, S. N., & Sonenberg, N. (2008). Mechanisms of post-transcriptional regulation by microRNAs: are the answers in sight?. Nature reviews genetics, 9(2), 102.
Francischini, C. W., & Quaggio, R. B. (2009). Molecular characterization of Arabidopsis thaliana PUF proteins–binding specificity and target candidates. The FEBS journal, 276(19), 5456-5470.
Frank, A., Matiolli, C. C., Viana, A. J., Hearn, T. J., Kusakina, J., Belbin, F. E., ... & Cragg-Barber, K. (2018). Circadian entrainment in Arabidopsis by the sugar-responsive transcription factor bZIP63. Current Biology, 28(16), 2597-2606.
Friend, K., Campbell, Z. T., Cooke, A., Kroll-Conner, P., Wickens, M. P., and Kimble, J. (2012). A conserved PUF–Ago–eEF1A complex attenuates translation elongation. Nature structural & molecular biology, 19(2), 176-183.
Gandikota, M., Birkenbihl, R. P., Höhmann, S., Cardon, G. H., Saedler, H., & Huijser, P. (2007). The miRNA156/157 recognition element in the 3translation elongation. Nature structural & molecular biology, 19(2), 176-183.y, 28(16), 2597-2606.2(4), ngs. The Plant Journal, 49(4), 683-693.
García-Rodríguez, L. J., Gay, A. C., and Pon, L. A. (2007). PUF3p, a Pumilio family RNA binding protein, localizes to mitochondria and regulates mitochondrial biogenesis and motility in budding yeast. The Journal of cell biology, 176(2), 197-207.
Gerstberger, S., Hafner, M., & Tuschl, T. (2014). A census of human RNA-binding proteins. Nature Reviews Genetics, 15(12), 829.
Gibson, S. I. (2005). Control of plant development and gene expression by sugar signaling. Current opinion in plant biology, 8(1), 93-102.
Girault, T., Abidi, F., Sigogne, M., PELLESCHI-TRAVIER, S. A. N. D. R. I. N. E., Boumaza, R., Sakr, S., and Leduc, N. (2010). Sugars are under light control during bud burst in Rosa sp. Plant, cell and environment, 33(8), 1339-1350.
Glisovic, T., Bachorik, J. L., Yong, J., & Dreyfuss, G. (2008). RNA-binding proteins and post‐transcriptional gene regulation. FEBS letters, 582(14), 1977-1986.
González Grandío, E. (2016). Genetic pathways controlling shoot branching upstream and downstream of BRANCHED1 of Arabidopsis thaliana.
Gu, W., Deng, Y., Zenklusen, D., and Singer, R. H. (2004). A new yeast PUF family protein, PUF6p, represses ASH1 mRNA translation and is required for its localization. Genes and development, 18(12), 1452-1465.
Guilfoyle, T. J., & Hagen, G. (2007). Auxin response factors. Current opinion in plant biology, 10(5), 453-460.
Guo, S., Xu, Y., Liu, H., Mao, Z., Zhang, C., Ma, Y., ... & Chong, K. (2013). The interaction between OsMADS57 and OsTB1 modulates rice tillering via DWARF14. Nature communications, 4, 1566.

Hall, T. M. T. (2016). De-coding and re-coding RNA recognition by PUF and PPR repeat proteins. Current opinion in structural biology, 36, 116-121.
Hanson, J., Hanssen, M., Wiese, A., Hendriks, M. M., & Smeekens, S. (2008). The sucrose regulated transcription factor bZIP11 affects amino acid metabolism by regulating the expression of ASPARAGINE SYNTHETASE1 and PROLINE DEHYDROGENASE2. The Plant Journal, 53(6), 935-949.
Hellmann, H. A., & Smeekens, S. (2014). Sugar sensing and signaling in plants. Frontiers in plant science, 5, 113.
Henry, C., Rabot, A., Laloi, M., Mortreau, E., Sigogne, M., Leduc, N., . *et al*. (2011). Regulation of RhSUC2, a sucrose transporter, is correlated with the light control of bud burst in Rosa sp. Plant, cell and environment, 34(10), 1776-1789.
Ho, S. L., Chao, Y. C., Tong, W. F., & Yu, S. M. (2001). Sugar coordinately and differentially regulates growth-and stress-related gene expression via a complex signal transduction network and multiple control mechanisms. Plant Physiology, 125(2), 877-890.
Horton, P., Park, K. J., Obayashi, T., Fujita, N., Harada, H., Adams-Collier, C. J., & Nakai, K. (2007). WoLF PSORT: protein localization predictor. Nucleic acids research, 35(suppl_2), W585-W587.
Hothersall, J. S., Gordge, M., & Noronha-Dutra, A. A. (1998). Inhibition of NADPH supply by 6‐aminonicotinamide: effect on glutathione, nitric oxide and superoxide in J774 cells. FEBS letters, 434(1-2), 97-100.
Hubbard, L., McSteen, P., Doebley, J., and Hake, S. (2002). Expression patterns and mutant phenotype of teosinte branched1 correlate with growth suppression in maize and teosinte. Genetics, 162(4), 1927-1935.
Jiang, H. and Egli, D. B. (1993). Shade Induced Changes in Flower and Pod Number and Flower and Fruit Abscission in Soybean. Agronomy Journal, 85, 221-225.
Jung, S., Lee, T., Cheng, C. H., Buble, K., Zheng, P., Yu, J., ... & Frank, M. (2018). 15 years of GDR: New data and functionality in the Genome Database for Rosaceae. Nucleic acids research, 47(D1), D1137-D1145.
Kang, S. G., Price, J., Lin, P. C., Hong, J. C., & Jang, J. C. (2010). The Arabidopsis bZIP1 transcription factor is involved in sugar signaling, protein networking, and DNA binding. Molecular plant, 3(2), 361-373.
Kebrom, T. H., and Mullet, J. E. (2015). Photosynthetic leaf area modulates tiller bud outgrowth in sorghum. Plant, cell and environment, 38(8), 1471-1478.
Kebrom, T. H., Brutnell, T. P., & Finlayson, S. A. (2010). Suppression of sorghum axillary bud outgrowth by shade, phyB and defoliation signalling pathways. Plant, cell & environment, 33(1), 48-58.
Kebrom, T. H., Brutnell, T. P., Hays, D. B., & Finlayson, S. A. (2010). Vegetative axillary bud dormancy induced by shade and defoliation signals in the grasses. Plant signaling & behavior, 5(3), 317-319.
Kebrom, T. H., Burson, B. L., and Finlayson, S. A. (2006). Phytochrome B represses Teosinte Branched1 expression and induces sorghum axillary bud outgrowth in response to light signals. Plant Physiology, 140(3), 1109-1117.
Kebrom, T., Chandler, P., Swain, S., King, R., Richards, R., & Spielmeyer, W. (2012). Inhibition of tiller bud outgrowth in the tin mutant of wheat is associated with precocious internode development. Plant Physiology, pp-112.
Keene, J. D. (2007). RNA regulons: coordination of post-transcriptional events. Nature Reviews Genetics, 8(7), 533.
Kertesz, S., Kerenyi, Z., Merai, Z., Bartos, I., Palfy, T., Barta, E., & Silhavy, D. (2006). Both introns and long 3owth in the tin mutant of wheat is associated with precocious internode in plants. Nucleic acids research, 34(21), 6147-6157.
Koch, K. (2004). Sucrose metabolism: regulatory mechanisms and pivotal roles in sugar sensing and plant development. Current opinion in plant biology, 7(3), 235-246.
Kosugi, S., and Ohashi, Y. (1997). PCF1 and PCF2 specifically bind to cis elements in the rice proliferating cell nuclear antigen gene. The Plant Cell, 9(9), 1607-1619.
Kosugi, S., and Ohashi, Y. (2002). DNA binding and dimerization specificity and potential targets for the TCP protein family. The Plant Journal, 30(3), 337-348.
Kotov, A. A., & Kotova, L. M. (2018). Auxin–cytokinin interactions in the regulation of correlative inhibition in two-branched pea seedlings. Journal of experimental botany, 69(12), 2967-2978.
Kruger, N. J., & von Schaewen, A. (2003). The oxidative pentose phosphate pathway: structure and organisation. Current opinion in plant biology, 6(3), 236-246.

Lange, K., & Proft, E. R. (1970). Inhibition of the 6-phosphogluconate dehydrogenase in the rat kidney by 6-aminonicotinamide. Naunyn-Schmiedebergs Archiv für Pharmakologie, 267(2), 177-180.
Lastdrager, J., Hanson, J., & Smeekens, S. (2014). Sugar signals and the control of plant growth and development. Journal of experimental botany, 65(3), 799-807.
Lee, S., Kopp, F., Chang, T. C., Sataluri, A., Chen, B., Sivakumar, S., Mendell, J. T., *et alet al*. (2016). Noncoding RNA NORAD regulates genomic stability by sequestering PUMILIO proteins. Cell, 164(1), 69-80.
Lejay, L., Wirth, J., Pervent, M., Cross, J. M. F., Tillard, P., & Gojon, A. (2008). Oxidative pentose phosphate pathway-dependent sugar sensing as a mechanism for regulation of root ion transporters by photosynthesis. Plant physiology, 146(4), 2036-2053.
Leyser, H. M., de Saint Germain, A., Waldie, T., Troadec, C., Citerne, S., Kadakia, N., ... & Estelle, M. (2018). The pea branching RMS2 gene encodes the PsAFB4/5 auxin receptor and is involved in an auxin-strigolactone regulation loop.
Leyser, O. (2003). Regulation of shoot branching by auxin. Trends in plant science, 8(11), 541-545.
Li, L., & Sheen, J. (2016). Dynamic and diverse sugar signaling. Current opinion in plant biology, 33, 116-125.
Li, X., Xia, K., Liang, Z., Chen, K., Gao, C., & Zhang, M. (2016). MicroRNA393 is involved in nitrogen-promoted rice tillering through regulation of auxin signal transduction in axillary buds. Scientific reports, 6, 32158.
Liu, J., Cheng, X., Liu, P., Li, D., Chen, T., Gu, X., & Sun, J. (2017). MicroRNA319-regulated TCPs interact with FBHs and PFT1 to activate CO transcription and control flowering time in Arabidopsis. PLoS genetics, 13(5), e1006833.
Liu, Q., & Chen, Y. Q. (2009). Insights into the mechanism of plant development: interactions of miRNAs pathway with phytohormone response. Biochemical and biophysical research communications, 384(1), 1-5.
Liu, Y., & Bassham, D. C. (2010). TOR is a negative regulator of autophagy in Arabidopsis thaliana. PLoS One, 5(7), e11883.
Lv, X., Zhang, M. S., Wu, Y. Q., Gao, X. F., Li, X. L., & Wang, W. Z. (2017). The Roles of Auxin in Regulating "Shoot Branching" of Cremastra appendiculata. Journal of Plant Growth Regulation, 36(2), 281-289.
Mason, M. G., Ross, J. J., Babst, B. A., Wienclaw, B. N., and Beveridge, C. A. (2014). Sugar demand, not auxin, is the initial regulator of apical dominance. Proceedings of the National Academy of Sciences, 111(16), 6092-6097.
Maurel, K., Leite, G. B., Bonhomme, M., Guilliot, A., Rageau, R., Pétel, G., & Sakr, S. (2004). Trophic control of bud break in peach (Prunus persica) trees: a possible role of hexoses. Tree Physiology, 24(5), 579-588.
Miles, W. O., Tschöp, K., Herr, A., Ji, J. Y., and Dyson, N. J. (2012). Pumilio facilitates miRNA regulation of the E2F3 oncogene. Genes & development, 26(4), 356-368.
Miller, J. E., & Reese, J. C. (2012). Ccr4-Not complex: the control freak of eukaryotic cells. Critical reviews in biochemistry and molecular biology, 47(4), 315-333.
Müller, D., & Leyser, O. (2011). Auxin, cytokinin and the control of shoot branching. Annals of Botany, 107(7), 1203-1212.
Nicolai, M., Roncato, M. A., Canoy, A. S., Rouquie, D., Sarda, X., Freyssinet, G., & Robaglia, C. (2006). Large-scale analysis of mRNA translation states during sucrose starvation in Arabidopsis cells identifies cell proliferation and chromatin structure as targets of translational control. Plant Physiology, 141(2), 663-673.
Nie, H., Zhao, C., Wu, G., Wu, Y., Chen, Y., & Tang, D. (2012). SR1, a Calmodulin Binding Transcription Factor, Modulates Plant Defense and Ethylene-Induced Senescence by Directly Regulating NDR1 and EIN3. Plant physiology, pp-111.
Niwa, M., Daimon, Y., Kurotani, K. I., Higo, A., Pruneda-Paz, J. L., Breton, G., ... & Araki, T. (2013). BRANCHED1 interacts with FLOWERING LOCUS T to repress the floral transition of the axillary meristems in Arabidopsis. The Plant Cell, tpc-112.
Parapunova, V., Busscher, M., Busscher-Lange, J., Lammers, M., Karlova, R., Bovy, A. G., ... & de Maagd, R. A. (2014). Identification, cloning and characterization of the tomato TCP transcription factor family. BMC plant biology, 14(1), 157.

Potuschak, T., Lechner, E., Parmentier, Y., Yanagisawa, S., Grava, S., Koncz, C., & Genschik, P. (2003). EIN3-dependent regulation of plant ethylene hormone signaling by two Arabidopsis F box proteins: EBF1 and EBF2. Cell, 115(6), 679-689.

Qiu, Z., Guo, W., Wang, Q., Chen, Z., Huang, S., Zhao, F., ... & He, X. (2015). MicroRNA-124 reduces the pentose phosphate pathway and proliferation by targeting PRPS1 and RPIA mRNAs in human colorectal cancer cells. Gastroenterology, 149(6), 1587-1598.

Rabot, A., Henry, C., Ben Baaziz, K., Mortreau, E., Azri, W., Lothier, J., ... & Le Gourrierec, J. (2012). Insight into the role of sugars in bud burst under light in the rose. Plant and Cell Physiology, 53(6), 1068-1082.

Rabot, A., Portemer, V., Péron, T., Mortreau, E., Leduc, N., Hamama, L., ... & Le Gourrierec, J. (2014). Interplay of sugar, light and gibberellins in expression of Rosa hybrida vacuolar invertase 1 regulation. Plant and Cell Physiology, 55(10), 1734-1748.

Rameau, C., Bertheloot, J., Leduc, N., Andrieu, B., Foucher, F., *et al*. (2015). Multiple pathways regulate shoot branching. Frontiers in plant science, 5, 741.

Razem, F. A., El-Kereamy, A., Abrams, S. R., & Hill, R. D. (2006). The RNA-binding protein FCA is an abscisic acid receptor. Nature, 439(7074), 290.Andreassi, C., & Riccio, A. (2009). To localize or not to localize: mRNA fate is in 3′ UTR ends. Trends in cell biology, 19(9), 465-474.

Revalska, M., & Iantcheva, A. (2018). Pi-starvation is mitigated in Medicago truncatula plants with upregulated auxin transport through auxin–strigolactone interaction. Plant Cell, Tissue and Organ Culture (PCTOC), 133(3), 405-415.

Richards, R. A. (2000). Selectable traits to increase crop photosynthesis and yield of grain crops. Journal of Experimental Botany, 51, 447-458.

Rolland, F., Baena-Gonzalez, E., & Sheen, J. (2006). Sugar sensing and signaling in plants: conserved and novel mechanisms. Annu. Rev. Plant Biol., 57, 675-709.

Ruan, Y. L. (2014). Sucrose metabolism: gateway to diverse carbon use and sugar signaling. Annual review of plant biology, 65, 33-67.

Sakr, S., Wang, M., Dédaldéchamp, F., Perez-Garcia, M. D., Ogé, L., Hamama, L., and Atanassova, R. (2018). The Sugar-Signaling Hub: Overview of Regulators and Interaction with the Hormonal and Metabolic Network. International journal of molecular sciences, 19(9), 2506.

Schwarz, S., Grande, A. V., Bujdoso, N., Saedler, H., & Huijser, P. (2008). The microRNA regulated SBP-box genes SPL9 and SPL15 control shoot maturation in Arabidopsis. Plant molecular biology, 67(1-2), 183-195.

Schwede, T., Kopp, J., Guex, N., & Peitsch, M. C. (2003). SWISS-MODEL: an automated protein homology-modeling server. Nucleic acids research, 31(13), 3381-3385.

Seale, M., Bennett, T., and Leyser, O. (2017). BRC1 expression regulates bud activation potential, but is not necessary or sufficient for bud growth inhibition in Arabidopsis. Development, dev-145649.

Sheu, J. J., Jan, S. P., Lee, H. T., & Yu, S. M. (1994). Control of transcription and mRNA turnover as mechanisms of metabolic repression of α‐amylase gene expression. The Plant Journal, 5(5), 655-664.

Shimizu-Sato, S., Tanaka, M., & Mori, H. (2009). Auxin–cytokinin interactions in the control of shoot branching. Plant molecular biology, 69(4), 429.

Shimmori, Y., Kanesaki, Y., Nozawa, M., Yoshikawa, H., & Ehira, S. (2018). Transcriptional Activation of Glycogen Catabolism and the Oxidative Pentose Phosphate Pathway by NrrA Facilitates Cell Survival Under Nitrogen Starvation in the Cyanobacterium Synechococcus sp. Strain PCC 7002. Plant and Cell Physiology, 59(6), 1225-1233.

Smeekens, S., Ma, J., Hanson, J., & Rolland, F. (2010). Sugar signals and molecular networks controlling plant growth. Current opinion in plant biology, 13(3), 273-278.

Song, S., Huang, H., Gao, H., Wang, J., Wu, D., Liu, X., ... & Xie, D. (2014). Interaction between MYC2 and ETHYLENE INSENSITIVE3 modulates antagonism between jasmonate and ethylene signaling in Arabidopsis. The Plant Cell, tpc-113.

Song, X., Lu, Z., Yu, H., Shao, G., Xiong, J., Meng, X., ... & Yao, X. F. (2017). IPA1 functions as a downstream transcription factor repressed by D53 in strigolactone signaling in rice. Cell research, 27(9), 1128.

Stincone, A., Prigione, A., Cramer, T., Wamelink, M. M., Campbell, K., Cheung, E., ... & Keller, M. A. (2015). The return of metabolism: biochemistry and physiology of the pentose phosphate pathway. Biological Reviews, 90(3), 927-963.

Stirnberg, P., van De Sande, K., & Leyser, H. O. (2002). MAX1 and MAX2 control shoot lateral branching in Arabidopsis. Development, 129(5), 1131-1141.
Sun, C., Palmqvist, S., Olsson, H., Borén, M., Ahlandsberg, S., & Jansson, C. (2003). A novel WRKY transcription factor, SUSIBA2, participates in sugar signaling in barley by binding to the sugar-responsive elements of the iso1 promoter. The Plant Cell, 15(9), 2076-2092.
Takeda, T., Suwa, Y., Suzuki, M., Kitano, H., UeguchisTanaka, M., Ashikari, M., *et al*. (2003). The OsTB1 gene negatively regulates lateral branching in rice. The Plant Journal, 33(3), 513-520.
Tam, P. P., Barrette-Ng, I. H., Simon, D. M., Tam, M. W., Ang, A. L., and Muench, D. G. (2010). The PUF family of RNA-binding proteins in plants: phylogeny, structural modeling, activity and subcellular localization. BMC plant biology, 10(1), 44.
Tang, H., Lee, M., Sharpe, O., Salamone, L., Noonan, E. J., Hoang, C. D., ... & Shrager, J. B. (2012). Oxidative stress-responsive microRNA-320 regulates glycolysis in diverse biological systems. The FASEB Journal, 26(11), 4710-4721.
Tian, L., Liu, H., Ren, L., Ku, L., Wu, L., Li, M., ... & Dou, D. (2018). MicroRNA 399 as a potential integrator of photo-response, phosphate homeostasis, and sucrose signaling under long day condition. BMC plant biology, 18(1), 290.
Tsouko, E., Khan, A. S., White, M. A., Han, J. J., Shi, Y., Merchant, F. A., ... & Frigo, D. E. (2014). Regulation of the pentose phosphate pathway by an androgen receptor–mTOR-mediated mechanism and its role in prostate cancer cell growth. Oncogenesis, 3(5), e103.
Valley, C. T., Porter, D. F., Qiu, C., Campbell, Z. T., Hall, T. M. T., and Wickens, M. (2012). Patterns and plasticity in RNA-protein interactions enable recruitment of multiple proteins through a single site. Proceedings of the National Academy of Sciences, 109(16), 6054-6059.
Van Etten, J., Schagat, T. L., Hrit, J., Weidmann, C. A., Brumbaugh, J., Coon, J. J., and Goldstrohm, A. C. (2012). Human Pumilio proteins recruit multiple deadenylases to efficiently repress messenger RNAs. Journal of Biological Chemistry, 287(43), 36370-36383.
Waldie, T., & Leyser, O. (2018). Cytokinin targets auxin transport to promote shoot branching. Plant physiology, pp-01691.
Wang, L., Wang, B., Jiang, L., Liu, X., Li, X., Lu, Z., ... & Li, J. (2015). Strigolactone signaling in Arabidopsis regulates shoot development by targeting D53-like SMXL repressor proteins for ubiquitination and degradation. The Plant Cell, tpc-15.
Wang, M., Ogé, L., Perez-Garcia, M. D., Hamama, L., & Sakr, S. (2018). The PUF Protein Family: Overview on PUF RNA targets, biological functions, and post transcriptional regulation. International journal of molecular sciences, 19(2), 410.
Wang, R. L., Stec, A., Hey, J., Lukens, L., and Doebley, J. (1999). The limits of selection during maize domestication. Nature, 398(6724), 236-239.
Wang, X., McLachlan, J., Zamore, P. D., and Hall, T. M. T. (2002). Modular recognition of RNA by a human pumilio-homology domain. Cell, 110(4), 501-512.
Wang, X., Zamore, P. D., and Hall, T. M. T. (2001). Crystal structure of a Pumilio homology domain. Molecular cell, 7(4), 855-865.
Wang, Y., & Li, J. (2011). Branching in rice. Current opinion in plant biology, 14(1), 94-99.
Wang, Y., and Jiao, Y. (2018). Axillary meristem initiation-a way to branch out. Current opinion in plant biology, 41, 61-66.
Weaver, R. J. (2007). Part V: Post-transcriptional events. Molecular Biology.
Wick, A. N., Drury, D. R., Nakada, H. I., & Wolfe, J. B. (1957). Localization of the primary metabolic block produced by 2-deoxyglucose. J Biol Chem, 224(2), 963-969.
Wickens, M., Bernstein, D. S., Kimble, J., & Parker, R. (2002). A PUF family portrait: 3′ UTR regulation as a way of life. TRENDS in Genetics, 18(3), 150-157.
Wild, M., & Achard, P. (2013). The DELLA protein RGL3 positively contributes to jasmonate/ethylene defense responses. Plant signaling & behavior, 8(4), e23891.
Xiong, Y., McCormack, M., Li, L., Hall, Q., Xiang, C., & Sheen, J. (2013). Glucose–TOR signalling reprograms the transcriptome and activates meristems. Nature, 496(7444), 181.
Xu, J., Zha, M., Li, Y., Ding, Y., Chen, L., Ding, C., & Wang, S. (2015). The interaction between nitrogen availability and auxin, cytokinin, and strigolactone in the control of shoot branching in rice (Oryza sativa L.). Plant cell reports, 34(9), 1647-1662.
Yang Y, Nicolas M, Zhang J, Yu H, Guo D, Yuan R, *et al*. (2018) The TIE1 transcriptional repressor controls shoot branching by directly repressing BRANCHED1 in Arabidopsis. PLoS Genet 14(3): e1007296.

Yang, L., Conway, S. R., & Poethig, R. S. (2011). Vegetative phase change is mediated by a leaf-derived signal that represses the transcription of miR156. Development, 138(2), 245-249.
Yang, L., Xu, M., Koo, Y., He, J., & Poethig, R. S. (2013). Sugar promotes vegetative phase change in Arabidopsis thaliana by repressing the expression of MIR156A and MIR156C. elife, 2, e00260.
Yang, Y., Nicolas, M., Zhang, J., Yu, H., Guo, D., Yuan, R., ... & Qin, G. (2018). The TIE1 transcriptional repressor controls shoot branching by directly repressing BRANCHED1 in Arabidopsis. PLoS genetics, 14(3), e1007296.
Yoine, M., Ohto, M. A., Onai, K., Mita, S., & Nakamura, K. (2006). The lba1 mutation of UPF1 RNA helicase involved in nonsenserepressing the expression of MIR156A and MIR156C. elife, 2, e00260. in rice signalling in Arabidopsis. The Plant Journal, 47(1), 49-62.
Yoo, S. D., Cho, Y. H., Tena, G., Xiong, Y., & Sheen, J. (2008). Dual control of nuclear EIN3 by bifurcate MAPK cascades in C 2 H 4 signalling. Nature, 451(7180), 789.
Yu, S., Cao, L., Zhou, C. M., Zhang, T. Q., Lian, H., Sun, Y., ... & Wang, J. W. (2013). Sugar is an endogenous cue for juvenile-to-adult phase transition in plants. elife, 2, e00269.
Yu, S., Lian, H., & Wang, J. W. (2015). Plant developmental transitions: the role of microRNAs and sugars. Current Opinion in Plant Biology, 27, 1-7.
Zažímalová, E., Petrášek, J., & Benková, E. (Eds.). (2014). Auxin and its role in plant development (pp. 2675-2688). Heidelberg: Springer.
Zeng, Y., Wu, Y., Avigne, W. T., & Koch, K. E. (1998). Differential regulation of sugar-sensitive sucrose synthases by hypoxia and anoxia indicate complementary transcriptional and posttranscriptional responses. Plant Physiology, 116(4), 1573-1583.
Zhang, B., Gallegos, M., Puoti, A., Durkin, E., Fields, S., Kimble, J., and Wickens, M. P. (1997). A conserved RNA-binding protein that regulates sexual fates in the Caenorhabditis elegans hermaphrodite germ line. Nature, 390(6659), 477-484.
Zhang, B., Pan, X., Cobb, G. P., & Anderson, T. A. (2006). Plant microRNA: a small regulatory molecule with big impact. Developmental biology, 289(1), 3-16.
Zhang, C., & Muench, D. G. (2015). A nucleolar PUF RNA-binding protein with specificity for a unique RNA sequence. Journal of Biological Chemistry, 290(50), 30108-30118.
Zhao, E., Maj, T., Kryczek, I., Li, W., Wu, K., Zhao, L., ... & Szeliga, W. (2016). Cancer mediates effector T cell dysfunction by targeting microRNAs and EZH2 via glycolysis restriction. Nature immunology, 17(1), 95.
Zhou, M., & Luo, H. (2014). Role of microRNA319 in creeping bentgrass salinity and drought stress response. Plant signaling & behavior, 9(4), 1375-91.
Zouine, M., Fu, Y., Chateigner-Boutin, A. L., Mila, I., Frasse, P., Wang, H., ... & Bouzayen, M. (2014). Characterization of the tomato ARF gene family uncovers a multi-levels post-transcriptional regulation including alternative splicing. PloS one, 9(1), e84203.

Supplemental Data

Table S1. The specific PCR primers of each RhPUF members

PrRhPUF1	Forward	5' GAGGAACATGAGTGGAGGTCT 3'
	Reverse	5' CATTTGAAGGCTAAGGGTCAG 3'
PrRhPUF2	Forward	5' TGCCCTACCAGAACGGTTTA 3'
	Reverse	5' CAGCAAGAGCCTGACAACACT 3'
PrRhPUF3	Forward	5' ATGGCTTAGGTGGGTTTGGT 3'
	Reverse	5' ACTGACAATGCCGTCTGGAA 3'
PrRhPUF4	Forward	5' CTTGAAACAGCCACTACGGA 3'
	Reverse	5' GGTCATCACAAGTCTCCAACAC 3'
PrRhPUF5	Forward	5' TCAGGTCCTCTTCTTGTCCG 3'
	Reverse	5' TCCCTTTCAGTGCCTTATTCC 3'
PrRhPUF6	Forward	5' ATGCAGCACATGCTCTGG 3'
	Reverse	5' TAAGTTGGTTCGTCAATTCGT 3'
PrRhPUF7	Forward	5' AGCGTCCAATCATGCCACTAG 3'
	Reverse	5' ATACTGGTCCTGAGCAAGAGCA 3'
PrRhPUF8	Forward	5' TAGTGGCAGTTCAGGCAATC 3'
	Reverse	5' TCCATCCGTCCCTGTTAGTC 3'
PrRhPUF9	Forward	5' TCTTGCACTAAGATGCCAATG 3'
	Reverse	5' CAGCTTATCTCGATGTCTCCC 3'
PrRhPUF10	Forward	5' ATACAAAGCCATTGCCTCAG 3'
	Reverse	5' CTTGCAGATCAATCGGTCTC 3'
PrRhPUF11	Forward	5' TGCACAATATGGTGCGAGTG 3'
	Reverse	5' CCTCTTTGAAAACAGACGCCT 3'
PrRhPUF12	Forward	5' GCAGCGATAACCAGTTAGGC 3'
	Reverse	5' TCTCTCAGCTCCAAACATATGC 3'

3'UTR of *α-amylase 3*

CGGCUCAAGCCCUAAACUGAACGGGAUAGUCAUGCUCAAACCAGUUUCUACACGGCAAGAAUUUACUGA
UUCUUAUACUUUUGCAGUCAAUUAAAUUAUGGUUUUUAUAUAUGUAAUUUUGUAUCCGAUUGUAGUUG
UAUCCGAUUGUAGCGUUCGAAUAAGUAGGCAGGCUCUCUAGCCUCUAGGUUAAUUGCGGGGCAUAUGU
AGCUUGCCAGGCAUAUGUAGCUUGCCAGUUAAUUGUGUUUGUAUCACGCAGUUUGUAACCGUUGGUGC
AAUAUAUAAUGUCAGGUUCAGG

3'UTR of *AtBRC1*

AACUGAUUUCAUUUAACAUUAAUAUCUCAAAUUAAUGAUAUAUAGUUUGGUGAGAGAGAUAUGUUAAU
CCAUCUUAUGUUUUUUUUUCUUAACAUCGUAAUUAAUCAUGUUUAUAUGAAGGCUUUUUCGUCAUUUU
AGUGUCAAAUAUUAAACCUAUGUGAAGAAAUUAAUGCAAUUUGUAUAAUAUUUUGUUUUCAUAGUUCG
AGUGGAU

3'UTR of *OsTB1*

UGUGAUCAUCCAUCCACACACGAACGAACGAACGAACGGUACGGCACUAAGAUCGAACUCCUGCAGCUA
CAUAAUUAUCCUUUGCUUCUCAAGAGUAAUAAUUCUUGACGUGUUAAUUAAUCCGGGUGUGUAUUAAU
UCCCUCUUUAUUAUUUUUUCUCGCGUUUAUCCGGAGUUGACUGUGGUGAAGACGAACUUUGGUUUGGU
CAUCGCAUGGUGUGCAUUGCAUAUAUAGCUAGCACUAUCGUCUGAUCGAUGAUUCAUCAUCAAUGGAGU
CGUCUAGUAUUAA

Figure S1. 3'UTR region of *α-amylase 3*, *AtBRC1* and *OsTB1*. The 3'UTR of them was gotten from NCBI database (www.ncbi.nlm.nih.gov). The red letter means the sugar related motif found in *α-amylase 3* in *Oryza sativa.* The underlined letter means the core PUF binding motif.

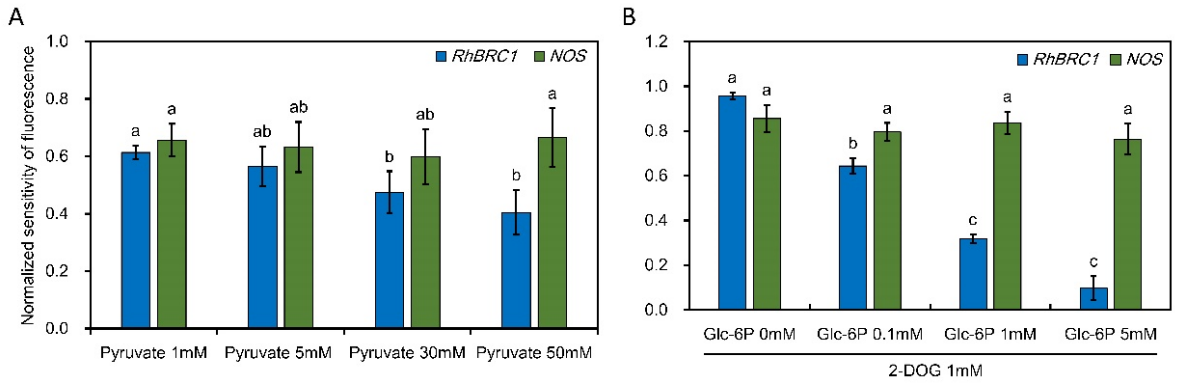

Figure S2. Fluorescence level of 3'UTR$_{RhBRC1}$-transformed callus (P35S::GFP::3'UTR$_{RhBRC1}$) is sensitive to OPPP, but slightly sensitive glycolysis/TCA-cycle. A, 3'UTR$_{RhBRC1}$-transformed callus was treated with different pyruvate concentration; B, 3'UTR$_{RhBRC1}$-transformed callus was treated with 1mM 2-DOG with different Glc-6P concentration. Glc-6P, glucose-6-phosphate. Data are mean ± SE of three measurements, each measurement contained six calli. The letters indicate significant differences between the different treatments with $P < 0.05$.

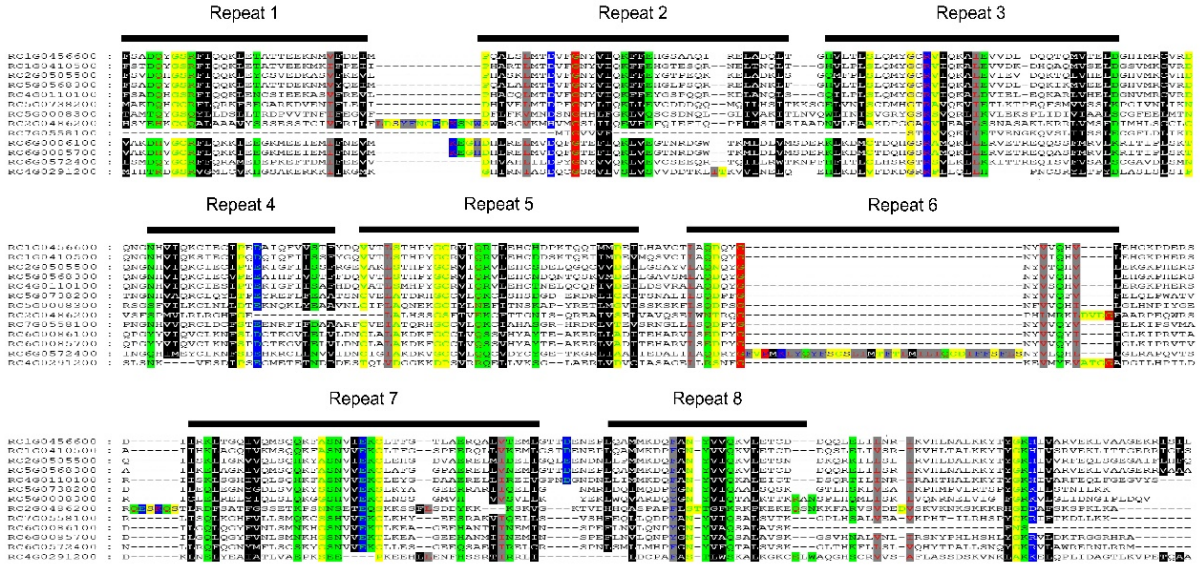

Figure S3. The sequence alignment of Pumilio repeat among PUF members in *Rosa chinensis*. Multiple alignments were generated using ClustalX program. The PUF sequence of *Rosa chinensis* were downloaded from GDR database (https://www.rosaceae.org/).

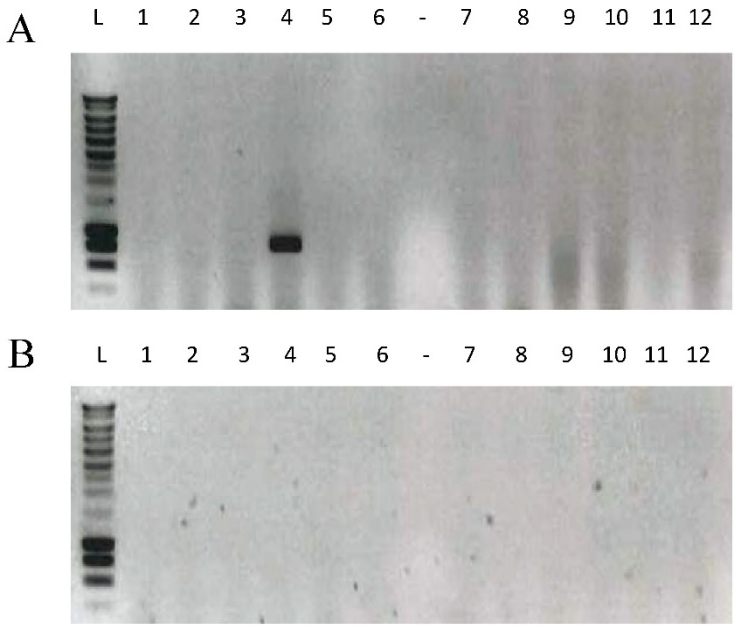

Figure S4. The expression of 12 putative RhPUF members in 100mM sucrose treated bud and 100mM mannitol treated bud. A, The expression of 12 RhPUF members in 100mM sucrose treated buds. B, The expression of 12 RhPUF members in 100mM mannitol treated buds. L, Ladder; 1, *RhPUF1*; 2, *RhPUF2*; 3, *RhPUF3*; 4, *RhPUF4*; 5, *RhPUF5*; 6, *RhPUF6*; 7, *RhPUF7*; 8, *RhPUF8*; 9, *RhPUF9*; 10, *RhPUF10*; 11, *RhPUF11*; 12, *RhPUF12*; -, negative control.

DISCUSSION AND PERSPECTIVES

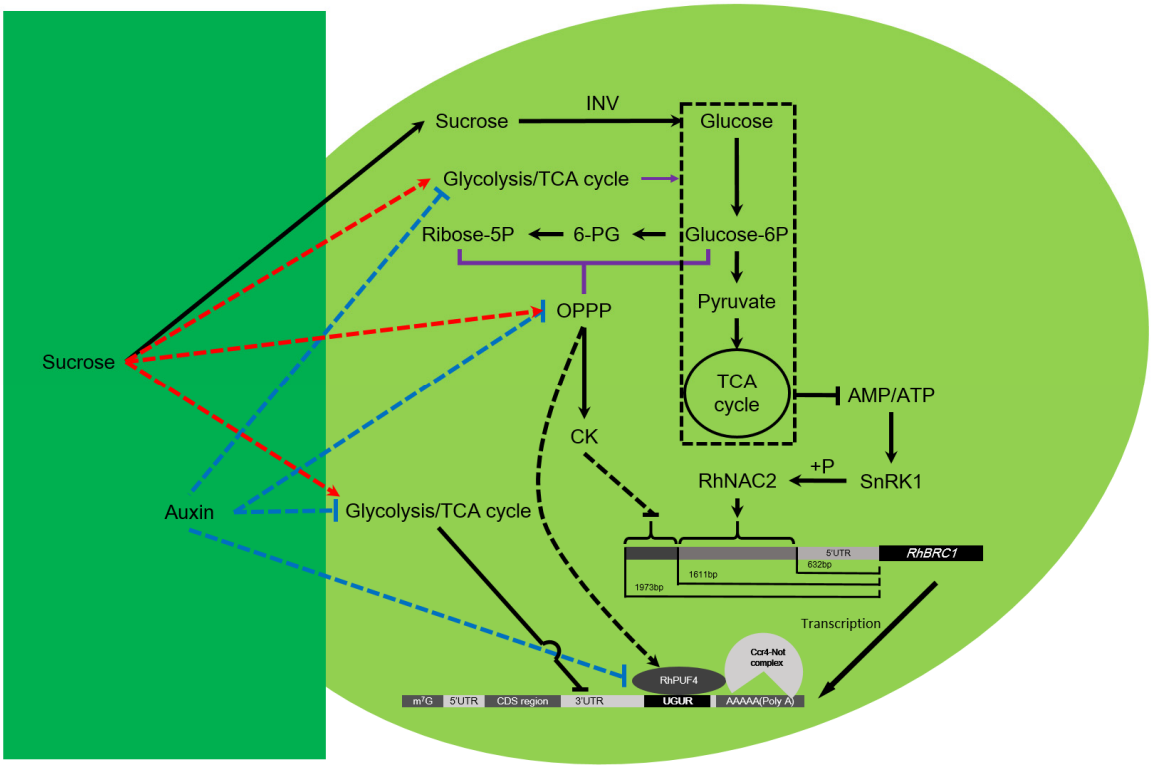

Figure 1. The overview of hypothesis in this study. Auxin can go to the bud to inhibit glycolysis/TCA cycle, but sucrose can stimulate it. The reduced glycolysis/TCA cycle leads to a high AMP/ATP ratio (low energy status). While the AMP activate the SnRK1, which might phosphorylate NAC2 transcription factor. The phosphorylated NAC2 can bind to the promoter region of RhBRC1 to influence its transcription. Meanwhile, the influenced of OPPP can lead to the change of CK level, which was reported to be a repressor of BRC1 etranscription. After transcription, RhPUF4 can bind the 3'UTR of RhBRC1 to regulate its expression. There exist some PUF binding sites in the 3'UTR of RhBRC1. PUF protein can recruit Ccr4-Not complex to the 3'UTR of target mRNA and enhance the degradation of target mRNA by cutting poly(A) tail. Moreover, the transcription of RhPUF4 is stimulated by OPPP that enhanced by sucrose and inhibited by auxin. +P, phosphorylation; 6-PG, 6-phosphogluconate; CK, cytokinin; INV, vacuolar invertase. The colorful dashed line measn the effect of sucrose or auxin.

Auxin and sucrose affect antagonistically the primary sugar metabolism and sink strength of bud

Sugar is a central factor of many essential metabolic and signaling pathways. Plants synthesize sugar from carbon dioxide and water through photosynthesis, allowing them to store energy absorbed from sunlight internally. In plants, sugar not only provides energy, but also various products for plant development, including amino acids, plant hormones and nucleotides. Moreover, some important signaling molecules, such as sucrose, glucose, trehalose 6-phosphate, UDP-glucose, and those derived from sugar metabolism downstream hexokinase played an important role in plant growth and development (Doiron *et al*., 1996; Moore *et al*., 2003; Schluepmann *et al*., 2003; Wahl *et al*., 2013; Garapati *et al*., 2015; Janse van Rensburg and Van den End, 2018, Sakr *et al*., 2018). Here, we showed that the exogenous stem auxin could inhibit the primary sugar metabolism by reducing the transcription level of many key enzymes related to glycolysis (hexokinase, 6-phosphofructokinase, pyruvate kinase), TCA cycle (2-oxoglutarate dehydrogenase and malate dehydrogenase) and OPPP (glucose-6-phosphate 1-dehydrogenase and 6-phosphogluconate dehydrogenase). This situation led to the reduction of bud ability to import and use carbohydrate necessary for its outgrowth. In line with this, Otori *et al* (2017) indicated that the overexpressing of fructose-1,6-bisphosphatase in the cytosol enhance sucrose metabolism capacity and stimulate *Arabidopsis* shoot branching. Our data also showed a tight correlation between the ability of bud to grow out and the transcription level of many key enzymes-related to glycolysis/TCA and OPPP, because they were both higher in 100mM sucrose-fed buds than in those supplied with 10mM sucrose. Accordingly, the auxin–dependent inhibition of bud outgrowth could be linked to a bud state marked by sugar starvation and energy depletion, which in accordance with the abundance of the sugar starvation markers in auxin-treated buds (*STP1* and *ASN1*, Baena-González and Sheen, 2008; Delatte *et al*., 2011; Cordoba *et al*., 2014) and with the low ATP/AMP ratio. The sugar status is thus deeply involved in the ability of bud to grow out and might affect the transcript level of *BRC1* within bud (Mason *et al*., 2014; Barbier *et al*., 2015a; Barbier *et al*., 2015b). Interestingly, auxin-dependent reduction of both bud outgrowth and sugar metabolism occurred in manner that it was anti-correlated with sucrose availability for bud growth. At low (10mM) sucrose concentration, exogenous stem auxin inhibited completely bud outgrowth and strongly sugar metabolism while this effect was significantly mitigated with elevated (100mM) sucrose concentration (in this condition, there was both a moderate bud outgrowth and sugar metabolic activity). Taken

together, these findings indicate that the primary sugar metabolism (glycolysis/TCA and OPPP) is one prevailing target of auxin and sucrose interacting effect.

The detail mechanism behind how auxin regulates the transcription level of those seven sucrose-catabolizing enzymes is still unknown. Stem-transported auxin cannot enter axillary bud and two non-mutually exclusive models have been proposed to explain the relationship between auxin and bud outgrowth. One is "the second messenger model" and another one is "the auxin canalization model". According to the second messenger model, auxin promotes strigolactones (SL, a repressor of bud growth) and represses cytokinins (CK, an inducer of bud growth) pathways, which can move into buds to exert their antagonist action on bud outgrowth (Teichmann and Muhr, 2015, Rameau *et al*., 2015). Based on the promoter bioinformatics analysis, the promoter of all the genes encoding for the seven sugar metabolism enzymes under the combined effect of auxin and sucrose contained the ARR-B transcription factor (CK related transcription factor, Yokoyama *et al*., 2007; Kieber, 2008) binding sites. Among them, both 2-oxoglutarate dehydrogenase and 6-phosphofructokinase contain three ARR-B transcription factor-binding sites; 6-phosphogluconate dehydrogenase and glucose-6-phosphate 1-dehydrogenase contain five ARR-B transcription factor-binding sites; Hexokinase, malate dehydrogenase and pyruvate kinase have seven, nine and twelve ARR-B binding sites respectively. This indicated that CK might participate to sucrose metabolism through the regulation of these main enzymes of glycolysis/TCA and OPPP. However, only promoter of 2-oxoglutarate dehydrogenase gene (TCA cycle) and glucose-6-phosphate 1-dehydrogenase gene (OPPP) contained one BES1 transcription factor (SL related transcription factor, Wang *et al*., 2013) binding site respectively. Therefore, the further experiments are needed to demonstrate whether auxin can influence sugar metabolism through CK-and SL-related transcription factors. The auxin canalization model results from the consideration that outgrowth and establishment of auxin canalization (polarized auxin transport) from an axillary bud is tightly correlated (Li and Bangerth, 1999). According to this model, the downward auxin stream in the main stem blocks the establishment of auxin canalization from axillary buds, and these axillary buds are activated when only they are able to export their own auxin (Li and Bangerth, 1999; Domagalska and Leyser, 2011). In this case, the present of auxin in dormant bud can block sugar metabolism and this effect can be released when auxin come out the bud. In this case, we cannot exclude that bud-located auxin regulate negatively sugar metabolism and this inhibitory effect would be removed when bud resumes its outgrowth and exports its own auxin on the main stem. In line with this, many AuxREs (auxin response elements, Ulmasov *et al*., 1995) exits in the promoter of the genes of seven sugar metabolism-related enzymes. At this stage of

our knowledge, these two mechanisms are plausible and additional work is needed to confirm which hypothesis could actually be of a great interest.

The transcription level and protein activity of vacuolar invertase and sucrose synthase were also involved in the antagonistic effect between sucrose and auxin. In plant, sucrose synthase is an enzyme that catalyzes sucrose into UDP-glucose and fructose, while vacuolar invertase catalyzes sucrose into glucose and fructose. They both influence the sink strength deeply (Chen *et al*., 2017; Bahuguna *et al*., 2018; Morey *et al*., 2018). Auxin and sucrose affected antagonistically the expression and activity of these two sucrose-metabolizing enzymes. More interestingly, auxin inhibited both expression and activity of vacuolar invertase, which in line with being a positive marker of bud outgrowth in Rosa sp (Girault *et al*., 2010; Rabot *et al*., 2012). This situation arises the question on the role of sucrose synthase in bud outgrowth and what would be the role of the balance between sucrose synthase and vacuolar invertase during bud outgrowth. Taken together, these findings and those from sugar metabolism support that auxin influences negatively the sink strength of buds and this effect was mitigated by elevated sucrose supply to bud.

The bud not only requires carbon skeleton to outgrowth, but also need additional nutrient factors, such as nitrate, sulphur, phosphorus, potassium, *etc*. (Barbier *et al*., 2017; Umehara *et al*., 2010; Cline, 1991; Van Cleve, 1977; Rubinstein and Nagao, 1976). Furthermore, sugar metabolism has a tight connection with them (Leigh and Wyn Jones, 1994; Jonasson *et al*., 1996; Deeken *et al*., 2002). However, the molecular mechanism whereby different nutrient factors participate to bud outgrowth is still deficient. One example from Umehara *et al* (2010) showed that strigolactones can act as endogenous inhibitors of axillary bud outgrowth due to phosphate deficiency. Potassium also can influence cell development by affecting calcium signaling and ROS signaling (Ho and Tsay, 2010).

Moreover, nitrate is a key nutrient as well as a signaling molecule that affects both metabolism and development of plants (Krouk *et al*., 2010). As previously reported, nitrate is necessary for bud outgrowth (Scheible *et al*., 1997; Vasudevan *et al*., 2004; Le Moigne *et al*., 2018; Wang *et al*., 2019). Moreover, nitrate controls numerous signaling and metabolism pathways during plant development, such as signaling pathways of calcium, auxin, cytokinin and metabolism of sugar and amino acid (Riveras *et al*., 2015; Desikan *et al*., 2002; Miyawaki *et al*., 2004; Krouk *et al*., 2010; Champigny and Foyer, 1992). In addition, there exist a tight interaction between nitrate and sugar (Lejay *et al*., 2003; Chow *et al*., 2007; Balotf *et al*., 2016; Sakr *et al*., 2018). All these information underline the complexity of the regulatory molecular

network behind the modulation of bud outgrowth and deserve to be integrated in the future research to understand how all these factors converge into to the regulation of bud growth.

Auxin and sucrose antagonistically regulate *RhBRC1* expression at the promoter level

BRC1 is highly interesting as a key regulator of multi-layered signals that govern plant architecture in response to multiple internal (hormones, nutrients) and environmental (light) signals. In bud, auxin can stimulate the expression of *BRC1*, while its expression is reduced by sucrose (Barbier *et al*., 2015a; Rameau *et al*., 2015). Here, we clearly showed that this antagonistic effect between sucrose and auxin was integrated at both promoter level of *RhBRC1*.

Indeed, the region located between 1973 and 611bp was required for integrating auxin- and sucrose-mediated upregulation and downregulation of BRC1 respectively. These findings arise the question about the molecular mechanisms behind such a regulation. At this stage of our knowledge, many hypotheses are still being plausible. As we mentioned above, the effect of auxin relied on the antagonistic action of two hormones, SL and CK, which act downstream auxin and are able to enter bud and regulate *BRC1* expression (Ferguson *et al*., 2009; Brewer *et al*., 2009; Dun *et al*., 2012). Moreover, Barbier *et al*. (2015a) showed an interaction between sucrose, CK and SL, in manner that sucrose stimulates CK synthesis and reduces SL signaling in Rosa buds. Based on this, one possible mechanism will be built up on the "exclusive hormonal hypothesis", according to which sucrose and auxin regulate indirectly *BRC1* expression through CK and SL. Therefore, the observed effect on *BRC1* expression will reflect the well-known opposite action of these two branching-related hormones. The interaction between sucrose and these two plant branching hormones has been widely reported. Previous studies showed that CK and sugars can cross-influence their metabolism and transport (Lara *et al*., 2004; Werner *et al*., 2008; Kushwah and Laxmi, 2014; Sakr *et al*., 2018). Li *et al*. (2016) reported that both mutants of *MAX1* and *MAX2*, involved in SL biosynthesis and signaling, respectively, were hyposensitive to glucose repression of seedling establishment. This suggested that this repression is under the cooperative effect of SL and glucose, probably *via* the hexokinase independent pathway. An alternative hypothesis will be linked to "the sugar-hormonal interacting hypothesis", according to which sucrose influences *BRC1* level through both hormonal (CK and SL) pathways and sugar specific pathway (irrespectively of CK and SL). This hypothesis was in line with our findings emphasizing the prevailing of primary sugar metabolism in the *BRC1* regulation (see below). *Arabidopsis* buds lacking *BRC1* expression can remain inhibited and sensitive to inhibition by SL (Seale *et al*., 2017), indicating that SL effect could also involve in a not-yet identified actor.

In eukaryotic cells, amino acids synthesis is related to sugar metabolism. Different products of glycolysis and TCA cycle provide carbon skeleton for amino acids synthesis. In Rosa sp., Le Moigne *et al*. (2018) indicated that root-derived asparagine is required for bud outgrowth not only for transferring the nitrogen to bud, but also might be acting as a signaling entity. In *Homo sapiens*, recent study demonstrated that asparagine can stimulate TOR signaling pathway by regulating mTORC1 activity and protein synthesis (Krall *et al*., 2016). In plants, TOR signaling can integrate nutrients and energy signaling to promote cell proliferation and growth (Xiong and Sheen, 2014). Moreover, in *Arabidopsis*, TOR can activate cell proliferation in shoot apexes (Li *et al*., 2017). Based on this, it will be interesting to complete our knowledge on the regulation of *BRC1*, while investigating whether *BRC1* expression could be sensitive to asparagine signaling pathway and how sucrose and asparagine act synergistically to control *BRC1* expression at both promoter level.

OPPP participates the regulation of *RhBRC1* transcription

The OPPP is a metabolic pathway parallel to glycolysis, and acts as a fundamental component of cellular metabolism. It provides precursors for nucleotide and amino acid biosynthesis, producing reducing power (NADPH) required for nitrate reduction, and defeat oxidative stress, and thereby it is important for plant development (Kruger *et al*., 2003; Pugin *et al*., 1997). Here, the transcription level of glucose-6-phosphate 1-dehydrogenase and 6-phosphogluconate dehydrogenase, the two important enzymes of OPPP, were stimulated by sucrose and decapitation, while inhibited by auxin. Moreover, in order to investigate whether the transcription level of *RhBRC1* is under the regulation of OPPP, the 6-AN (OPPP inhibitor) and 6-phosphogluconate (compound of OPPP) were used. 6-AN can stimulate the transcription of *RhBRC1*, while the feeding of 6-phosphogluconate can reduce *RhBRC1* transcription in buds. In line with this, the results from transformed callus indicated that OPPP-dependent *RhBRC1* regulation occurred through its promoter region located between 1973 and 1611bp. In plant, the OPPP can provide the precursor of CKs synthesis (Hirose *et al*., 2008; Bahaji *et al*., 2015) that can reduce *BRC1* transcription (Müller and Leyser, 2011; Dierck *et al*., 2016). Indeed, some CK related transcription factor binding sites, such as ARR-B transcription factor (Sakai *et al*., 2001; Yokoyama *et al*., 2007) and GeBP transcription factor (Chevalier *et al*., 2008), also exist in -955bp and -864bp of the promoter region of *RhBRC1* respectively. However, whether CK acts as a mediator between OPPP and *BRC1* expression is still unknown. In other words, sucrose-mediated stimulation of OPPP could lead to CK production in buds and to reduction of *BRC1* expression. This hypothesis deserves to be tested because CK and OPPP-emanating

signal implies the same region of *RhBRC1* (between 1973 and 1611) to control negatively its transcriptional activity.

NADPH is another important product of OPPP. NADPH provides the reducing equivalents for biosynthetic reactions and the oxidation-reduction involved in protecting against the toxicity of reactive oxygen species (ROS), allowing the regeneration of glutathione (GSH) (Rush *et al*., 1985). Moreover, OPPP, NADPH and ROS are closely connected in plant. Plasma membrane NADPH oxidases catalyze the production of a ROS molecule superoxide ($O_2^{\bullet-}$) from NADPH and oxygen (Suzuki *et al*., 2011). $O_2^{\bullet-}$ is crucial for root growth and root hair development (Foreman *et al*., 2003) and could be converted into another ROS molecule such as hydrogen peroxide (H_2O_2) (Dunand *et al*., 2007). H_2O_2 is important for various developmental and physiological processes such as the growth of root hairs, cellular proliferation and differentiation (Foreman *et al*., 2003; Gapper & Dolan, 2006; Kwak *et al*., 2006; Dunand *et al*., 2007; Tsukagoshi *et al*., 2010). H_2O_2 could be converted by peroxidases into another active ROS hydroxyl radical ($^{\bullet}OH$) which is essential for cell elongation because of its loosening effect on cell walls (Chen & Schopfer, 1999; Liszkay *et al*., 2004). Therefore, ROS play an integral role as signaling molecules during plant development (Baxter *et al*., 2013). In plant, previous knowledge indicated that ROS signaling is integrated with many different signaling networks, including protein kinase networks, calcium signaling, cellular metabolic networks and redox responses (Mittler *et al*., 2011), but higher level of ROS is harmful to cell (Mittler, 2017). Chen *et al*. (2016) showed that application of hydrogen peroxide (H_2O_2) on axillary bud could induce *BRC1* transcription in tomato, and then caused an inhibited bud outgrowth. In this study, preliminary data (not shown) carried out in sucrose fed-bud supplied with or without auxin showed that auxin could reduce the ROS accumulation level in bud, while it is stimulated by sucrose. Therefore, it is very interesting to find out the relationship between OPPP, ROS and *BRC1* expression. In other words, whether ROS is one possible pathway, through which OPPP may regulate *BRC1* expression.

Moreover, as mentioned before, we indicated some sugar related *cis*-elements based on the promoter analysis of *RhBRC1*, but nothing is known on OPPP related transcription factors. In the future, it will be particularly interesting to address this question.

The OPPP also regulates the level of *RhBRC1* through its 3' UTR, because 6-AN treatment led to fluorescence stimulation of 3' UTR_{BRC1}-transformed callus, while 6-phosphogluconate can inhibit it. In line with this, very low fluorescence measured in 3' UTR_{BRC1}-transformed callus in response to the combined effect of 2-DOG (effector of glycolysis) and G6P (precursor of glycolysis and OPPP), relative to control (3'UTR_{NOS}-transformed callus). More interestingly,

the 3'UTR of *RhBRC1* bore several putative PUF protein binding sites. Among twelve PUF members in *Rosa hybrida*, we found an OPPP-related PUF protein, RhPUF4, whose transcription level in buds was positively regulated by OPPP. This was evidenced by the fact that buds supplied with 6-AN (an effector of OPPP) exhibited a low transcript level of *RhPUF4*, by contrast to those fed with 6-phosphogluconate (a substrate for OPPP). In this case, two questions related to the mechanism behind OPPP-mediated upregulation of *RhPUF4* and to the ability of *RhPUF4* to bind to the 3' UTR of *RhBRC1* to regulate the mRNA stability of *RhBRC1* are still unanswered.

Glycolysis influences transcriptionally and post-transcriptionally the level of *RhBRC1*

Glycolysis is the metabolic pathway that converts glucose into pyruvate, and then pyruvate can go further into TCA cycle. Glycolysis is the link between sucrose and TCA cycle and provides energy for cell functionning. In this study, we showed that glycolysis can influence the transcription level of *RhBRC1*. When buds were treated by 2-DOG, an effector of glycolysis, the transcript level of *RhBRC1* was stimulated, indicating that *BRC1* expression would be responsive to potentially glycolysis-emanating signal. This glycolysis effect happened on both the promoter region that located within 1973 and 1611bp and 3'UTR of *RhBRC1*, even if the 3' UTR was only slightly sensitive to glycolysis. Through promoter analysis, we identified some sugar-related transcription factors binding sites in the promoter region of *RhBRC1*, such as G-box (Hwang *et al*., 1998), W-box (Sun *et al*., 2003), E2F transcription factors binding site (Xiong *et al*., 2013) and NAC transcription factors binding site (Kleinow *et al*., 2009; Puranik *et al*., 2012), *etc*. For example, the G-box corresponds to bZIP transcription factor (Sibéril *et al*., 2001) and many bZIP transcription factors are reported to involve in sugar signaling, such as bZIP1, bZIP11, bZIP63, ABI5, *etc* (León and Sheen, 2003; Smeekens *et al*., 2010; Kang *et al*., 2010; Ma *et al*., 2011; Frank *et al*., 2018). Based on our RNA-seq results, two-homologue genes of bZIP63 and ABI5 were identified to be under the regulation of the antagonistic effect between sucrose and auxin. The binding sites of E2Fa, a sugar related transcription factor, which can be phosphorylated by TOR kinase (Xiong *et al*., 2013), are also found in the promoter region of *RhBRC1*. Moreover, we found that the transcription level of *RhASN1* (*Asparagine synthase 1*), a marker of SnRK1 activity (Delatte *et al*., 2011; Nunes *et al*., 2013), is stimulated by auxin while inhibited by sucrose. It means that the activity of SnRK1 (stress and energy depletion integrator, Jossier *et al*., 2009) would be involved in the interacting effect of sucrose and auxin. Were identified on *RhBRC1* promoter two *cis*-element of ATAF1, a NAC transcription factor, which can be phosphorylated by SnRK1 and regulates the expression of

many genes (Puranik *et al*., 2012; Kleinow *et al*., 2009). All these transcription factors might act in glycolysis-dependent *RhBRC1* transcription and bud outgrowth and their exact role deserves to be investigated in the near future.

Regarding 3'UTR region, we showed that the 2-DOG can slightly stimulate the fluorescence of 3'UTR contained callus while the fluorescence can be reduced by glycerol. These findings indicated that glycolysis could also influence the transcription level of *RhBRC1* through its 3' UTR region. By contrast to OPPP, this glycolysis-dependent posttranslational regulation of *RhBRC1* could not be assigned to *RhPUF4*, expression of which in bud was insensitive to exogenous addition of both effector of glycolysis (2-DOG) and glycolysis substrates (glycerol and pyruvate). Whether some other RNA binding proteins would take part of glycolysis-mediated posttranscriptional regulation of *RhBRC1* should be addressed in the future.

RhBRC1 **could regulate the main sugar metabolism pathways**

As a TCP family transcription factor, the expression level of *BRC1* is under the control of various factors, such as sugar, plant hormones, water, light, *etc* (Aguilar-Martínez *et al*., 2007; Rameau *et al*., 2015; Wang *et al*., 2019). *BRC1* can control negatively the expression of many genes, which involved in chloroplast function, chlorophyll synthesis, amino acid and protein synthesis, chromatin structure and cell cycle division (González-Grandío *et al*., 2013). Further experiments showed that *BRC1* positively influences ABA responses genes (González-Grandío and Cubas, 2014; Nicolas and Cubas, 2016). Other TCP transcription factors participate to various metabolism pathways and regulate plant growth. Indeed, AtTCP9 and AtTCP20 participate to jasmonic acid metabolism in Arabidopsis, and AtTCP2, AtTCP3, AtTCP11 and AtTCP15 may involve in circadian clock in *Gossypium barbadens* (Giraud *et al*., 2010; Hao *et al*., 2012; Danisman *et al*., 2012&2013; González-Grandío *et al*., 2013). Despite these information, nothing is known about whether the primary sugar metabolism could be under the control of *BRC1*. To give the first information, the bioinformatics analysis of the promoter of the genes encoding for the seven sucrose metabolism-related enzymes under the control of sucrose and auxin were carried out. Five of them, including two glycolysis (6-phosphofructokinase, pyruvate kinase), one TCA cycle (2-oxoglutarate dehydrogenase) and two OPPP (6-phosphogluconate dehydrogenase, glucose-6-phosphate 1-dehydrogenase), did contain at least one TCP binding motif (KHGGGVC, Davière *et al*., 2014). Based on this, we could not exclude that *BRC1* may exert a negative feedback control of sugar metabolism and thereby strengthening the auxin-dependent downregulation of sugar metabolism in dormant bud.

To validate this hypothesis, first task will be to check whether *BRC1* could bind to the promoter region the genes encodings these five sugar metabolism-related enzymes.

References

Aguilar-Martínez, J. A., Poza-Carrión, C., & Cubas, P. (2007). Arabidopsis BRANCHED1 acts as an integrator of branching signals within axillary buds. The Plant Cell, 19(2), 458-472.

Baena-González, E., & Sheen, J. (2008). Convergent energy and stress signaling. Trends in plant science, 13(9), 474-482.

Baena-González, E., Rolland, F., Thevelein, J. M., & Sheen, J. (2007). A central integrator of transcription networks in plant stress and energy signalling. Nature, 448(7156), 938.

Bahaji, A., Sánchez-López, Á. M., De Diego, N., Muñoz, F. J., Baroja-Fernández, E., Li, J., ... & Humplík, J. F. (2015). Plastidic phosphoglucose isomerase is an important determinant of starch accumulation in mesophyll cells, growth, photosynthetic capacity, and biosynthesis of plastidic cytokinins in Arabidopsis. PLoS One, 10(3), e0119641.

Bahuguna, R. N., Tamilselvan, A., Muthurajan, R., Solis, C. A., & Jagadish, S. V. K. (2018). Mild preflowering drought priming improves stress defences, assimilation and sink strength in rice under severe terminal drought. Functional Plant Biology.

Balotf, S.; Kavoosi, G.; Kholdebarin, B. Nitrate reductase, nitrite reductase, glutamine synthetase, and glutamate synthase expression and activity in response to different nitrogen sources in nitrogen‐starved wheat seedlings. Biotechnol. Appl. Biochem. 2016, 63, 220–229.

Barbier, F. F., Dun, E. A., & Beveridge, C. A. (2017). Apical dominance. Current Biology, 27(17), R864-R865.

Barbier, F. F., Lunn, J. E., & Beveridge, C. A. (2015b). Ready, steady, go! A sugar hit starts the race to shoot branching. Current Opinion in Plant Biology, 25, 39-45.

Barbier, F., Péron, T., Lecerf, M., Perez-Garcia, M. D., Barrière, Q., Rolčík, J., ... & Roman, H. (2015a). Sucrose is an early modulator of the key hormonal mechanisms controlling bud outgrowth in Rosa hybrida. Journal of experimental botany, 66(9), 2569-2582.

Baxter, A., Mittler, R., & Suzuki, N. (2013). ROS as key players in plant stress signalling. Journal of experimental botany, 65(5), 1229-1240.

Bi, Y. M., Zhang, Y., Signorelli, T., Zhao, R., Zhu, T., & Rothstein, S. (2005). Genetic analysis of Arabidopsis GATA transcription factor gene family reveals a nitrate‐inducible member important for chlorophyll synthesis and glucose sensitivity. The Plant Journal, 44(4), 680-692.

Brewer, P. B., Dun, E. A., Ferguson, B. J., Rameau, C., & Beveridge, C. A. (2009). Strigolactone acts downstream of auxin to regulate bud outgrowth in pea and Arabidopsis. Plant Physiology, 150(1), 482-493.

Brewer, P. B., Koltai, H., & Beveridge, C. A. (2013). Diverse roles of strigolactones in plant development. Molecular plant, 6(1), 18-28.

Champigny, M. L., & Foyer, C. (1992). Nitrate activation of cytosolic protein kinases diverts photosynthetic carbon from sucrose to amino acid biosynthesis: basis for a new concept. Plant Physiology, 100(1), 7-12.

Chen, C., Yuan, Y., Zhang, C., Li, H., Ma, F., & Li, M. (2017). Sucrose phloem unloading follows an apoplastic pathway with high sucrose synthase in Actinidia fruit. Plant Science, 255, 40-50.

Chen, L., Song, Y., Li, S., Zhang, L., Zou, C., & Yu, D. (2012). The role of WRKY transcription factors in plant abiotic stresses. Biochimica et Biophysica Acta (BBA)-Gene Regulatory Mechanisms, 1819(2), 120-128.

Chen, S. X., & Schopfer, P. (1999). Hydroxyl‐radical production in physiological reactions: a novel function of peroxidase. European Journal of Biochemistry, 260(3), 726-735.

Chen, X. J., Xia, X. J., Guo, X., Zhou, Y. H., Shi, K., Zhou, J., & Yu, J. Q. (2016). Apoplastic H2O2 plays a critical role in axillary bud outgrowth by altering auxin and cytokinin homeostasis in tomato plants. New Phytologist, 211(4), 1266-1278.

Chevalier, F., Perazza, D., Laporte, F., Le Hénanff, G., Hornitschek, P., Bonneville, J. M., ... & Vachon, G. (2008). GeBP and GeBP-like proteins are noncanonical leucine-zipper transcription factors that regulate cytokinin response in Arabidopsis. Plant physiology, 146(3), 1142-1154.

Chow, F.; Capociama, F.V.; Faria, R.; Oliveira, M.C.D. Characterization of nitrate reductase activity in vitro in Gracilaria caudata J. Agardh (Rhodophyta, Gracilariales). Braz. J. Bot. 2007, 30, 123–129.

Cline, M. G. (1991). Apical dominance. The Botanical Review, 57(4), 318-358.

Cordoba, E., Aceves-Zamudio, D. L., Hernández-Bernal, A. F., Ramos-Vega, M., & León, P. (2014). Sugar regulation of SUGAR TRANSPORTER PROTEIN 1 (STP1) expression in Arabidopsis thaliana. Journal of experimental botany, 66(1), 147-159.

Danisman, S., Van der Wal, F., Dhondt, S., Waites, R., de Folter, S., Bimbo, A., ... & Angenent, G. C. (2012). Arabidopsis class I and class II TCP transcription factors regulate jasmonic acid metabolism and leaf development antagonistically. Plant physiology, pp-112.

Danisman, S., van Dijk, A. D., Bimbo, A., van der Wal, F., Hennig, L., de Folter, S., ... & Immink, R. G. (2013). Analysis of functional redundancies within the Arabidopsis TCP transcription factor family. Journal of experimental botany, 64(18), 5673-5685.

Davière, J. M., Wild, M., Regnault, T., Baumberger, N., Eisler, H., Genschik, P., & Achard, P. (2014). Class I TCP-DELLA interactions in inflorescence shoot apex determine plant height. Current Biology, 24(16), 1923-1928.

Deeken, R., Geiger, D., Fromm, J., Koroleva, O., Ache, P., Langenfeld-Heyser, R., ... & Hedrich, R. (2002). Loss of the AKT2/3 potassium channel affects sugar loading into the phloem of Arabidopsis. Planta, 216(2), 334-344.

Delatte, T. L., Sedijani, P., Kondou, Y., Matsui, M., de Jong, G. J., Somsen, G. W., ... & Schluepmann, H. (2011). Growth arrest by trehalose-6-phosphate: an astonishing case of primary metabolite control over growth by way of the SnRK1 signaling pathway. Plant Physiology, pp-111.

Desikan, R., Griffiths, R., Hancock, J., & Neill, S. (2002). A new role for an old enzyme: nitrate reductase-mediated nitric oxide generation is required for abscisic acid-induced stomatal closure in Arabidopsis thaliana. Proceedings of the National Academy of Sciences, 99(25), 16314-16318.

Dierck, R., De Keyser, E., De Riek, J., Dhooghe, E., Van Huylenbroeck, J., Prinsen, E., & Van Der Straeten, D. (2016). Change in auxin and cytokinin levels coincides with altered expression of branching genes during axillary bud outgrowth in Chrysanthemum. PloS one, 11(8), e0161732.

Doiron, B., Cuif, M. H., Chen, R., & Kahn, A. (1996). Transcriptional glucose signaling through the glucose response element is mediated by the pentose phosphate pathway. Journal of Biological Chemistry, 271(10), 5321-5324.

Domagalska, M. A., & Leyser, O. (2011). Signal integration in the control of shoot branching. Nature Reviews Molecular Cell Biology, 12(4), 211-221.

Dun, E. A., de Saint Germain, A., Rameau, C., & Beveridge, C. A. (2012). Antagonistic action of strigolactone and cytokinin in bud outgrowth control. Plant Physiology, 158(1), 487-498.

Dunand, C., Crèvecoeur, M., & Penel, C. (2007). Distribution of superoxide and hydrogen peroxide in Arabidopsis root and their influence on root development: possible interaction with peroxidases. New Phytologist, 174(2), 332-341.

Ferguson, B. J., & Beveridge, C. A. (2009). Roles for auxin, cytokinin, and strigolactone in regulating shoot branching. Plant physiology, 149(4), 1929-1944.

Foreman, J., Demidchik, V., Bothwell, J. H., Mylona, P., Miedema, H., Torres, M. A., ... & Davies, J. M. (2003). Reactive oxygen species produced by NADPH oxidase regulate plant cell growth. Nature, 422(6930), 442.

Frank, A., Matiolli, C. C., Viana, A. J., Hearn, T. J., Kusakina, J., Belbin, F. E., ... & Cragg-Barber, K. (2018). Circadian entrainment in Arabidopsis by the sugar-responsive transcription factor bZIP63. Current Biology, 28(16), 2597-2606.

Gapper, C., & Dolan, L. (2006). Control of plant development by reactive oxygen species. Plant physiology, 141(2), 341-345.

Garapati, P., Feil, R., John, E. L., Van Dijck, P., Balazadeh, S., & Mueller-Roeber, B. (2015). Transcription factor ATAF1 integrates carbon starvation responses with trehalose metabolism. Plant physiology, pp-00917.

Gibson, S. I. (2005). Control of plant development and gene expression by sugar signaling. Current opinion in plant biology, 8(1), 93-102.

Giraud, E., Ng, S., Carrie, C., Duncan, O., Low, J., Lee, C. P., ... & Whelan, J. (2010). TCP transcription factors link the regulation of genes encoding mitochondrial proteins with the circadian clock in Arabidopsis thaliana. The Plant Cell, tpc-110.

González-Grandío, E., & Cubas, P. (2014). Identification of gene functions associated to active and dormant buds in Arabidopsis. Plant signaling & behavior, 9(2), e27994.

González-Grandío, E., Poza-Carrión, C., Sorzano, C. O. S., & Cubas, P. (2013). BRANCHED1 promotes axillary bud dormancy in response to shade in Arabidopsis. The Plant Cell, tpc-112.

Guan, P., Wang, R., Nacry, P., Breton, G., Kay, S. A., Pruneda-Paz, J. L., ... & Crawford, N. M. (2014). Nitrate foraging by Arabidopsis roots is mediated by the transcription factor TCP20 through the systemic signaling pathway. Proceedings of the National Academy of Sciences, 111(42), 15267-15272.

Hao, J., Tu, L., Hu, H., Tan, J., Deng, F., Tang, W., ... & Zhang, X. (2012). GbTCP, a cotton TCP transcription factor, confers fibre elongation and root hair development by a complex regulating system. Journal of experimental botany, 63(17), 6267-6281.
Hirose, N., Takei, K., Kuroha, T., Kamada-Nobusada, T., Hayashi, H., & Sakakibara, H. (2007). Regulation of cytokinin biosynthesis, compartmentalization and translocation. Journal of Experimental Botany, 59(1), 75-83.
Ho, C. H., & Tsay, Y. F. (2010). Nitrate, ammonium, and potassium sensing and signaling. Current opinion in plant biology, 13(5), 604-610.
Hwang, Y. S., Karrer, E. E., Thomas, B. R., Chen, L., & Rodriguez, R. L. (1998). Three cis-elements required for rice α-amylase Amy3D expression during sugar starvation. Plant molecular biology, 36(3), 331-341.
Irigoyen, J. J., Einerich, D. W., & SB. R., Chen, L., & Rodriguez, R. L. (1998). Three cis-elements required for rice α-amylase Amy3D expressionin nodulated alfalfa (Medicago sativd) plants. Physiologia plantarum, 84(1), 55-60.
Janse van Rensburg, H. C., & Van den Ende, W. (2018). UDP-Glucose: A Potential Signaling Molecule in Plants?. Frontiers in plant science, 8, 2230.
Jonasson, S., Michelsen, A., Schmidt, I. K., Nielsen, E. V., & Callaghan, T. V. (1996). Microbial biomass C, N and P in two arctic soils and responses to addition of NPK fertilizer and sugar: implications for plant nutrient uptake. Oecologia, 106(4), 507-515.
Jossier, M., Bouly, J. P., Meimoun, P., Arjmand, A., Lessard, P., Hawley, S., ... & Thomas, M. (2009). SnRK1 (SNF1 ‐ related kinase 1) has a central role in sugar and ABA signalling in Arabidopsis thaliana. The Plant Journal, 59(2), 316-328.
Kang, S. G., Price, J., Lin, P. C., Hong, J. C., & Jang, J. C. (2010). The Arabidopsis bZIP1 transcription factor is involved in sugar signaling, protein networking, and DNA binding. Molecular plant, 3(2), 361-373.
Kleinow, T., Himbert, S., Krenz, B., Jeske, H., & Koncz, C. (2009). NAC domain transcription factor ATAF1 interacts with SNF1-related kinases and silencing of its subfamily causes severe developmental defects in Arabidopsis. Plant Science, 177(4), 360-370.
Koch, K. (2004). Sucrose metabolism: regulatory mechanisms and pivotal roles in sugar sensing and plant development. Current opinion in plant biology, 7(3), 235-246.
Konishi, M., & Yanagisawa, S. (2013). Arabidopsis NIN-like transcription factors have a central role in nitrate signalling. Nature Communications, 4, 1617.
Krall, A. S., Xu, S., Graeber, T. G., Braas, D., & Christofk, H. R. (2016). Asparagine promotes cancer cell proliferation through use as an amino acid exchange factor. Nature communications, 7, 11457.
Krouk, G., Crawford, N. M., Coruzzi, G. M., & Tsay, Y. F. (2010). Nitrate signaling: adaptation to fluctuating environments. Current opinion in plant biology, 13(3), 265-272.
Krouk, G., Lacombe, B., Bielach, A., Perrine-Walker, F., Malinska, K., Mounier, E., ... & Zazimalova, E. (2010). Nitrate-regulated auxin transport by NRT1. 1 defines a mechanism for nutrient sensing in plants. Developmental cell, 18(6), 927-937.
Kruger, N. J., & von Schaewen, A. (2003). The oxidative pentose phosphate pathway: structure and organisation. Current opinion in plant biology, 6(3), 236-246.
Kushwah, S.; Laxmi, A. The interaction between glucose and cytokinin signal transduction pathway in Arabidopsis thaliana. Plant Cell Environ. 2014, 37, 235–253.
Kwak, J. M., Nguyen, V., & Schroeder, J. I. (2006). The role of reactive oxygen species in hormonal responses. Plant Physiology, 141(2), 323-329.
Lara, M.E.B.; Garcia, M.C.G.; Fatima, T.; Ehneß, R.; Lee, T.K.; Proels, R.; Tanner, T.; Roitsch, T. Extracellular invertase is an essential component of cytokinin-mediated delay of senescence. Plant Cell 2004, 16, 1276–1287.
Le Moigne, M. A., Guérin, V., Furet, P. M., Billard, V., Lebrec, A., Spíchal, L., ... & Vian, A. (2018). Asparagine and sugars are both required to sustain secondary axis elongation after bud outgrowth in Rosa hybrida. Journal of plant physiology, 222, 17-27.
Leigh, R. A., & Wyn Jones, R. G. (1984). A hypothesis relating critical potassium concentrations for growth to the distribution and functions of this ion in the plant cell. New Phytologist, 97(1), 1-13.
Lejay, L.; Gansel, X.; Cerezo, M.; Tillard, P.; Müller, C.; Krapp, A.; Wirén, N.; Daniel-Vedele, F.; Gojon, A. Regulation of root ion transporters by photosynthesis: Functional importance and relation with hexokinase. Plant Cell 2003, 15, 2218–2232.
León, P., & Sheen, J. (2003). Sugar and hormone connections. Trends in plant science, 8(3), 110-116.

Li, C. J., & Bangerth, F. (1999). Autoinhibition of indoleacetic acid transport in the shoots of two branched pea (Pisum sativum) plants and its relationship to correlative dominance. Physiologia Plantarum, 106(4), 415-420.
Li, G.D.; Pan, L.N.; Jiang, K.; Takahashi, I.; Nakamura, H.; Xu, Y.W.; Asami, T.; Shen, R.F. Strigolactones are involved in sugar signaling to modulate early seedling development in Arabidopsis. Plant Biotechnol. 2016, 33, 87–97.
Li, X., Cai, W., Liu, Y., Li, H., Fu, L., Liu, Z., ... & Xiong, Y. (2017). Differential TOR activation and cell proliferation in Arabidopsis root and shoot apexes. Proceedings of the National Academy of Sciences, 201618782.
Li, X., Xia, K., Liang, Z., Chen, K., Gao, C., and Zhang, M. (2016). MicroRNA393 is involved in nitrogen-promoted rice tillering through regulation of auxin signal transduction in axillary buds. Scientific reports, 6, 32158.
Liszkay, A., van der Zalm, E., & Schopfer, P. (2004). Production of reactive oxygen intermediates (O2−, H2O2, and OH) by maize roots and their role in wall loosening and elongation growth. Plant physiology, 136(2), 3114-3123.
Ma, J., Hanssen, M., Lundgren, K., Hernández, L., Delatte, T., Ehlert, A., ... & Smeekens, S. (2011). The sucrose‐regulated Arabidopsis transcription factor bZIP11 reprograms metabolism and regulates trehalose metabolism. New Phytologist, 191(3), 733-745.
Marchive, C., Roudier, F., Castaings, L., Bréhaut, V., Blondet, E., Colot, V., ... & Krapp, A. (2013). Nuclear retention of the transcription factor NLP7 orchestrates the early response to nitrate in plants. Nature Communications, 4, 1713.
Mason, M. G., Ross, J. J., Babst, B. A., Wienclaw, B. N., & Beveridge, C. A. (2014). Sugar demand, not auxin, is the initial regulator of apical dominance. Proceedings of the National Academy of Sciences, 111(16), 6092-6097.
Mittler, R. (2017). ROS are good. Trends in plant science, 22(1), 11-19.
Mittler, R., Vanderauwera, S., Suzuki, N., Miller, G. A. D., Tognetti, V. B., Vandepoele, K., ... & Van Breusegem, F. (2011). ROS signaling: the new wave?. Trends in plant science, 16(6), 300-309.
Miyawaki, K., Matsumoto-Kitano, M., & Kakimoto, T. (2004). Expression of cytokinin biosynthetic isopentenyltransferase genes in Arabidopsis: tissue specificity and regulation by auxin, cytokinin, and nitrate. The Plant Journal, 37(1), 128-138.
Moore, B., Zhou, L., Rolland, F., Hall, Q., Cheng, W. H., Liu, Y. X., ... & Sheen, J. (2003). Role of the Arabidopsis glucose sensor HXK1 in nutrient, light, and hormonal signaling. Science, 300(5617), 332-336.
Morey, S. R., Hirose, T., Hashida, Y., Miyao, A., Hirochika, H., Ohsugi, R., ... & Aoki, N. (2018). Genetic Evidence for the Role of a Rice Vacuolar Invertase as a Molecular Sink Strength Determinant. Rice, 11(1), 6.
Müller, D., & Leyser, O. (2011). Auxin, cytokinin and the control of shoot branching. Annals of Botany, 107(7), 1203-1212.
Nicolas, M., & Cubas, P. (2016). TCP factors: new kids on the signaling block. Current opinion in plant biology, 33, 33-41.
Nunes, C. M., O'Hara, L., Primavesi, L., Delatte, T., Schluepmann, H., Somsen, G., ... & Paul, M. J. (2013). The trehalose 6-phosphate/SnRK1 signalling pathway primes growth recovery following relief of sink limitation. Plant physiology, pp-113.
Otori, K., Tamoi, M., Tanabe, N., & Shigeoka, S. (2017). Enhancements in sucrose biosynthesis capacity affect shoot branching in Arabidopsis. Bioscience, biotechnology, and biochemistry, 81(8), 1470-1477.
Pugin, A., Frachisse, J. M., Tavernier, E., Bligny, R., Gout, E., Douce, R., & Guern, J. (1997). Early events induced by the elicitor cryptogein in tobacco cells: involvement of a plasma membrane NADPH oxidase and activation of glycolysis and the pentose phosphate pathway. The Plant Cell, 9(11), 2077-2091.
Puranik, S., Sahu, P. P., Srivastava, P. S., & Prasad, M. (2012). NAC proteins: regulation and role in stress tolerance. Trends in plant science, 17(6), 369-381.
Rameau, C., Bertheloot, J., Leduc, N., Andrieu, B., Foucher, F., & Sakr, S. (2015). Multiple pathways regulate shoot branching. Frontiers in plant science, 5, 741.
Riveras, E., Alvarez, J. M., Vidal, E. A., Oses, C., Vega, A., & Gutiérrez, R. A. (2015). Ca2+ is a second messenger in the nitrate signaling pathway of Arabidopsis thaliana. Plant Physiology, pp-00961.
Rubinstein, B., & Nagao, M. A. (1976). Lateral bud outgrowth and its control by the apex. The Botanical Review, 42(1), 83-113.

Rush, G. F., Gorski, J. R., Ripple, M. G., Sowinski, J., Bugelski, P., & Hewitt, W. R. (1985). Organic hydroperoxide-induced lipid peroxidation and cell death in isolated hepatocytes. Toxicology and applied pharmacology, 78(3), 473-483.
Rushton, P. J., Somssich, I. E., Ringler, P., & Shen, Q. J. (2010). WRKY transcription factors. Trends in plant science, 15(5), 247-258.
Sakai, H., Honma, T., Aoyama, T., Sato, S., Kato, T., Tabata, S., & Oka, A. (2001). ARR1, a transcription factor for genes immediately responsive to cytokinins. Science, 294(5546), 1519-1521.
Sakr, S., Wang, M., Dédaldéchamp, F., Perez-Garcia, M. D., Ogé, L., Hamama, L., and Atanassova, R. (2018). The Sugar-Signaling Hub: Overview of Regulators and Interaction with the Hormonal and Metabolic Network. International journal of molecular sciences, 19(9), 2506.
Scheible, W. R., Lauerer, M., Schulze, E. D., Caboche, M., & Stitt, M. (1997). Accumulation of nitrate in the shoot acts as a signal to regulate shoottors and Ication in tobacco. The Plant Journal, 11(4), 671-691.
Schluepmann, H., Pellny, T., van Dijken, A., Smeekens, S., & Paul, M. (2003). Trehalose 6-phosphate is indispensable for carbohydrate utilization and growth in Arabidopsis thaliana. Proceedings of the National Academy of Sciences, 100(11), 6849-6854.
Seale, M., Bennett, T., & Leyser, O. (2017). BRC1 expression regulates bud activation potential, but is not necessary or sufficient for bud growth inhibition in Arabidopsis. Development, dev-145649.
Sible, M., Bennett, T., & Leyser, O. (2017). BRC1 expression regulates bud activation potential, but is not necessary or sufficient for bud growth inhibition in Arabidopsis. Devel
Smeekens, S., Ma, J., Hanson, J., & Rolland, F. (2010). Sugar signals and molecular networks controlling plant growth. Current opinion in plant biology, 13(3), 273-278.
Sun, C., Höglund, A. S., Olsson, H., Mangelsen, E., & Jansson, C. (2005). Antisense oligodeoxynucleotide inhibition as a potent strategy in plant biology: identification of SUSIBA2 as a transcriptional activator in plant sugar signalling. The Plant Journal, 44(1), 128-138.
Sun, C., Palmqvist, S., Olsson, H., Borén, M., Ahlandsberg, S., & Jansson, C. (2003). A novel WRKY transcription factor, SUSIBA2, participates in sugar signaling in barley by binding to the sugar-responsive elements of the iso1 promoter. The Plant Cell, 15(9), 2076-2092.
Suzuki, N., Miller, G., Morales, J., Shulaev, V., Torres, M. A., & Mittler, R. (2011). Respiratory burst oxidases: the engines of ROS signaling. Current opinion in plant biology, 14(6), 691-699.
Teichmann, T., & Muhr, M. (2015). Shaping plant architecture. Frontiers in plant science, 6, 233.
Tiwari, S. B., Hagen, G., & Guilfoyle, T. (2003). The roles of auxin response factor domains in auxin-responsive transcription. The Plant Cell, 15(2), 533-543.
To, J. P., & Kieber, J. J. (2008). Cytokinin signaling: two-components and more. Trends in plant science, 13(2), 85-92.
Tsukagoshi, H., Busch, W., & Benfey, P. N. (2010). Transcriptional regulation of ROS controls transition from proliferation to differentiation in the root. Cell, 143(4), 606-616.
Ulmasov, T., Hagen, G., & Guilfoyle, T. J. (1997). ARF1, a transcription factor that binds to auxin response elements. Science, 276(5320), 1865-1868.
Ulmasov, T., Liu, Z. B., Hagen, G., & Guilfoyle, T. J. (1995). Composite structure of auxin response elements. The Plant Cell, 7(10), 1611-1623.
Umehara, M., Hanada, A., Magome, H., Takeda-Kamiya, N., & Yamaguchi, S. (2010). Contribution of strigolactones to the inhibition of tiller bud outgrowth under phosphate deficiency in rice. Plant and Cell Physiology, 51(7), 1118-1126.
Van Cleve, K. (1977). Nitrogen, Phosphorus and Sulphur—Global Cycles. SCOPE Report 7. Forest Science, 23(4), 483-484.
Vasudevan, A., Selvaraj, N., Ganapathi, A., Kasthurirengan, S., Anbazhagan, V. R., & Manickavasagam, M. (2004). Glutamine: a suitable nitrogen source for enhanced shoot multiplication in Cucumis sativus L. Biologia Plantarum, 48(1), 125-128.
Wahl, V., Ponnu, J., Schlereth, A., Arrivault, S., Langenecker, T., Franke, A., ... & Schmid, M. (2013). Regulation of flowering by trehalose-6-phosphate signaling in Arabidopsis thaliana. Science, 339(6120), 704-707.
Wang, M., Le Moigne, M., Bertheloot, J., CRESPEL, L., Perez-Garcia, M. D., Ogé, L., ...& Sakr, S. (2019). BRANCHED1 : a key hub of shoot branching. Frontiers in plant science, (minor revision).
Wang, Y., Sun, S., Zhu, W., Jia, K., Yang, H., & Wang, X. (2013). Strigolactone/MAX2-induced degradation of brassinosteroid transcriptional effector BES1 regulates shoot branching. Developmental cell, 27(6), 681-688.

Werner, T., Motyka, V., Strnad, M., & Schmülling, T. (2001). Regulation of plant growth by cytokinin. Proceedings of the National Academy of Sciences, 98(18), 10487-10492.
Werner, T., Holst, K., Pörs, Y., Guivarc'h, A., Mustroph, A., Chriqui, D., ... & Schmülling, T. (2008). Cytokinin deficiency causes distinct changes of sink and source parameters in tobacco shoots and roots. Journal of Experimental Botany, 59(10), 2659-2672.
Xiong, Y., & Sheen, J. (2014). The role of target of rapamycin signaling networks in plant growth and metabolism. Plant physiology, 164(2), 499-512.
Xiong, Y., McCormack, M., Li, L., Hall, Q., Xiang, C., & Sheen, J. (2013). Glucose–TOR signalling reprograms the transcriptome and activates meristems. Nature, 496(7444), 181.
Yokoyama, A., Yamashino, T., Amano, Y. I., Tajima, Y., Imamura, A., Sakakibara, H., & Mizuno, T. (2007). Type-B ARR transcription factors, ARR10 and ARR12, are implicated in cytokinin-mediated regulation of protoxylem differentiation in roots of Arabidopsis thaliana. Plant and Cell Physiology, 48(1), 84-96.

REFERENCES

Barbier, F., Péron, T., Lecerf, M., Perez-Garcia, M. D., Barrière, Q., Rolčík, J., ... & Roman, H. (2015). Sucrose is an early modulator of the key hormonal mechanisms controlling bud outgrowth in Rosa hybrida. Journal of experimental botany, 66(9), 2569-2582.

Boumaza, R., DEMOTES-MAINARD, S. A. B. I. N. E., HUCHE-THELIER, L. Y. D. I. E., & Guerin, V. (2009). Visual characterization of the esthetic quality of the rosebush. Journal of Sensory Studies, 24(5), 774-796.

Boumaza, R., Huché-Thélier, L., Demotes-Mainard, S., Le Coz, E., Leduc, N., Pelleschi-Travier, S., ... & Guérin, V. (2010). Sensory profiles and preference analysis in ornamental horticulture: the case of the rosebush. Food quality and preference, 21(8), 987-997.

Corot, A., Roman, H., Douillet, O., Autret, H., Perez-Garcia, M. D., Citerne, S., ... & Demotes-Mainard, S. (2017). Cytokinins and Abscisic Acid Act Antagonistically in the Regulation of the Bud Outgrowth Pattern by Light Intensity. Frontiers in plant science, 8, 1724.

Demotes-Mainard, S., Huché-Thélier, L., Morel, P., Boumaza, R., Guérin, V., & Sakr, S. (2013). Temporary water restriction or light intensity limitation promotes branching in rose bush. Scientia Horticulturae, 150, 432-440.

Djennane, S., HIBRAND-SAINT OYANT, L. A. U. R. E. N. C. E., Kawamura, K., Lalanne, D., Laffaire, M., Thouroude, T., ... & Leduc, N. (2014). Impacts of light and temperature on shoot branching gradient and expression of strigolactone synthesis and signalling genes in rose. Plant, cell & environment, 37(3), 742-757.

Fichtner, F., Barbier, F. F., Feil, R., Watanabe, M., Annunziata, M. G., Chabikwa, T. G., ... & Lunn, J. E. (2017). Trehalose 6-phosphate is involved in triggering axillary bud outgrowth in garden pea (pisum sativum L.). The Plant Journal, 92(4), 611-623.

Fischer, A., Ramírez, H. V., & Lozano, J. (1997). Suppression of junglerice [Echinochloa colona (L.) Link] by irrigated rice cultivars in Latin America. Agronomy Journal, 89(3), 516-521.

FranceAgriMer. (2016). 2016 Publication FranceAgriMer rapport d'activité. Etabussement national des produits de l'agriculture et de la mer

Furet, P. M., Lothier, J., Demotes-Mainard, S., Travier, S., Henry, C., Guérin, V., & Vian, A. (2014). Light and nitrogen nutrition regulate apical control in Rosa hybrida L. Journal of plant physiology, 171(5), 7-13.

Girault, T., Abidi, F., Sigogne, M., PELLESCHI-TRAVIER, S. A. N. D. R. I. N. E., Boumaza, R., Sakr, S., & Leduc, N. (2010). Sugars are under light control during bud burst in Rosa sp. Plant, cell & environment, 33(8), 1339-1350.

Girault, T., Bergougnoux, V., Combes, D., VIEMONT, J. D., & Leduc, N. (2008). Light controls shoot meristem organogenic activity and leaf primordia growth during bud burst in Rosa sp. Plant, cell & environment, 31(11), 1534-1544.

Gontijo, L. M., Nechols, J. R., Margolies, D. C., & Cloyd, R. A. (2012). Plant architecture and prey distribution influence foraging behavior of the predatory mite Phytoseiulus persimilis (Acari: Phytoseiidae). Experimental and applied acarology, 56(1), 23-32.

Henry, C., Rabot, A., Laloi, M., Mortreau, E., Sigogne, M., Leduc, N., ... & PELLESCHI-TRAVIER, S. A. N. D. R. I. N. E. (2011). Regulation of RhSUC2, a sucrose transporter, is correlated with the light control of bud burst in Rosa sp. Plant, cell & environment, 34(10), 1776-1789.

Horvath, D. P., Anderson, J. V., Chao, W. S., & Foley, M. E. (2003). Knowing when to grow: signals regulating bud dormancy. Trends in plant science, 8(11), 534-540.

Huché-Thélier, L., Boumaza, R., Demotes-Mainard, S., Canet, A., Symoneaux, R., Douillet, O., & Guérin, V. (2011). Nitrogen deficiency increases basal branching and modifies visual quality of the rose bushes. Scientia horticulturae, 130(1), 325-334.

Irwin, D. L., & Aarssen, L. W. (1996, January). Testing for cost of apical dominance in vegetation: a field study of three species. In Annales Botanici Fennici (pp. 123-128). Finnish Zoological and Botanical Publishing Board.

Le Moigne, M. A., Guérin, V., Furet, P. M., Billard, V., Lebrec, A., Spíchal, L., ... & Vian, A. (2018). Asparagine and sugars are both required to sustain secondary axis elongation after bud outgrowth in Rosa hybrida. Journal of plant physiology, 222, 17-27.

Legrand, A., & Barbosa, P. (2003). Plant morphological complexity impacts foraging efficiency of adult Coccinella septempunctata L.(Coleoptera: Coccinellidae). Environmental Entomology, 32(5), 1219-1226.

Lemerle, D., Verbeek, B., Cousens, R. D., & Coombes, N. E. (1996). The potential for selecting wheat varieties strongly competitive against weeds. Weed Research, 36(6), 505-513.

Mason, M. G., Ross, J. J., Babst, B. A., Wienclaw, B. N., & Beveridge, C. A. (2014). Sugar demand, not auxin, is the initial regulator of apical dominance. Proceedings of the National Academy of Sciences, 111(16), 6092-6097.

Mor, Y., & Halevy, A. H. (1984). Dual effect of light on flowering and sprouting of rose shoots. Physiologia plantarum, 61(1), 119-124.

Rabot, A., Henry, C., Ben Baaziz, K., Mortreau, E., Azri, W., Lothier, J., ... & Le Gourrierec, J. (2012). Insight into the role of sugars in bud burst under light in the rose. Plant and Cell Physiology, 53(6), 1068-1082.

Rabot, A., Portemer, V., Péron, T., Mortreau, E., Leduc, N., Hamama, L., ... & Le Gourrierec, J. (2014). Interplay of sugar, light and gibberellins in expression of Rosa hybrida vacuolar invertase 1 regulation. Plant and Cell Physiology, 55(10), 1734-1748.

Rameau, C., Bertheloot, J., Leduc, N., Andrieu, B., Foucher, F., & Sakr, S. (2015). Multiple pathways regulate shoot branching. Frontiers in plant science, 5, 741.

Robert, C., Fournier, C., Andrieu, B., & Ney, B. (2008). Coupling a 3D virtual wheat (Triticum aestivum) plant model with a Septoria tritici epidemic model (Septo3D): a new approach to investigate plant–pathogen interactions linked to canopy architecture. Functional Plant Biology, 35(10), 997-1013.

Sakr, S., Wang, M., Dédaldéchamp, F., Perez-Garcia, M. D., Ogé, L., Hamama, L., & Atanassova, R. (2018). The Sugar-Signaling Hub: Overview of Regulators and Interaction with the Hormonal and Metabolic Network. International journal of molecular sciences, 19(9), 2506.

Valério, I. P., Carvalho, F. I. F. D., Oliveira, A. C. D., Benin, G., Souza, V. Q. D., Machado, A. D. A., ... & Fonseca, D. A. R. (2009). Seeding density in wheat genotypes as a function of tillering potential. Scientia Agricola, 66(1), 28-39.

Wang, M., Le Moigne, M., Bertheloot, J., CRESPEL, L., Perez-Garcia, M. D., Ogé, L., ...& Sakr, S. (2019). BRANCHED1 : a key hub of shoot branching. Frontiers in plant science, (minor revision).

Zhao, D. L., Atlin, G. N., Bastiaans, L., & Spiertz, J. H. J. (2006). Cultivar weed-competitiveness in aerobic rice: heritability, correlated traits, and the potential for indirect selection in weed-free environments. Crop Science, 46(1), 372-380.

UNIVERSITE ECOLOGIE
BRETAGNE GEOSCIENCES
LOIRE AGRONOMIE ALIMENTATION

AGRO CAMPUS OUEST

Titre : Réseau de régulation moléculaire de l'expression du gène *BRANCHED1* (*BRC1*) dans le bourgeon axillaire du rosier, en réponse au sucre et à l'auxine

Mots clés : BRANCHED1 (BRC1), débourrement, PUF, régulation transcriptionnelle, régulation post-transcriptionnelle

Résumé : Le débourrement du bourgeon axillaire est un processus clef au cours du développement de la plante, qui est contrôlé par des facteurs endogènes et exogènes. Au niveau du bourgeon, le facteur de transcription BRANCHED1 (*BRC1*) est l'un des principaux intégrateurs des voies de signalisations de ces facteurs. Sur la base des études précédentes, le niveau de transcription de *RhBRC1* (un gène homologue de *BRC1* chez *Rosa hybrida*) est contrôlé par le sucre et l'auxine. Cependant, les mécanismes moléculaires impliqués dans cette régulation restent à ce jour inconnus. Dans cette étude, nous avons montré que l'effet antagoniste entre le saccharose et l'auxine peut influencer le niveau de transcription de plusieurs enzymes du métabolisme de sucre, notamment la glycolyse / le cycle de Krebs et la voie oxydative des pentoses phosphates (OPPP). Cette régulation du métabolisme du sucre s'est avérée centrale dans leur effet antagoniste sur l'expression de *RhBRC1* et le débourrement des bourgeons végétatifs. Par ailleurs, la région promotrice de *RhBRC1* serait le site de convergence de l'effet antagoniste de l'auxine et de sucre, médié par la glycolyse/cycle de Krebs et l'OPPP. Deux zones du promoteur *RhBRC1* ont été identifiées pour leur implication dans cette régulation transcriptionnelle. D'autre part, cet effet antagoniste de l'auxine et du sucre implique aussi une régulation post-transcriptionnelle de *RhBRC1* à travers sa séquence 3'UTR. Une protéine de type PUF, RhPUF4, a été identifiée et les résultats obtenus isuggèrent sa capacité à se lier au 3'UTR de *RhBRC1* et régule son expression. En conclusion, l'effet antagoniste de l'auxine et de sucre, deux facteurs majeurs contrôlant la ramification chez les plantes, est en partie médié par des signaux emanant de la glycolyse et de l'OPPP et implique une régulation transcriptionnelle et post-transcriptionenle du gène intégrateur *RhBRC1*.

Title : Molecular regulatory network of *BRANCHED1* (*BRC1*) expression in axillary bud of Rosa sp. in response to sugar and auxin

Keywords : BRANCHED1 (BRC1), bud outgrowth, PUF, transcriptional regulation, post-transcriptional regulation

Abstract : Bud outgrowth is a key process for plant development, which is controlled by endogenous and exogenous cues. At the bud level, the transcription factor *BRANCHED1* (*BRC1*) is one of the main hub for the signaling pathways of these factors. Based on previous studies, the transcription level of *RhBRC1* (a homologous *BRC1* gene in *Rosa hybrida*) is controlled by sugar and auxin. However, the molecular mechanisms involved in this regulation remain unknown. Here, we have shown that the antagonistic effect of sucrose and auxin can influence the transcription level of several sugar metabolism–related enzymes, including glycolysis / TCA cycle and oxidative pathway of pentose phosphates (OPPP). This regulation of sugar metabolism has been shown to be central in their antagonistic effect on both *RhBRC1* expression and bud growth. Indeed, glycolysis/TCA cycle and OPPP promote bud outgrowth and have a negative effect on the transcription of *RhBRC1*. In addition, the promoter sequence of *RhBRC1* is the convergence site of the antagonistic effect of auxin and sugar, mediated by glycolysis / TCA cycle and OPPP. Two regions of *RhBRC1* promoter have been identified for their involvement in this transcriptional regulation. On the other hand, this antagonistic effect of auxin and sugar also involves a post-transcriptional regulation of *RhBRC1* through its 3'UTR sequence. A PUF protein, RhPUF4, has been identified and the results suggest its potential ability to bind to the *3'UTR* of RhBRC1 and to regulate its expression. In conclusion, the antagonistic effect of auxin and sugar, two major factors controlling shoot branching, is mediated by glycolysis and OPPP-emanating signals and involves transcriptional and post-transcriptional regulation of *RhBRC1*.