

Étude fonctionnelle de l'orthologue cristalline αB dans le développement musculaire et la stabilisation du sarcomère chez Drosophila melanogaster

Inga Wojtowicz

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Functional analysis of αB-crystallin's orthologue in muscle development and sarcomere stabilisation in Drosophila melanogaster

Doctoral dissertation

The thesis has been prepared at the Department of Animal Developmental Biology of Experimental Biology Institute, University of Wroclaw

and

Genetic Reproduction and Developmental Institute of Faculty of Medicine, INSERM

U1103, Clermont University,

under the supervision of

dr hab. prof. Małgorzata Daczewska

and

dr hab. Krzysztof Jagła

Wrocław, 2014

Inga Wójtowicz

Analiza funkcjonalna ortologa αB-krystaliny w rozwoju mięśni i stabilizacji sarkomerów u Drosophila melanogaster

Rozprawa doktorska

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oraz

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U1103, Clermont University,

pod kierunkiem

dr hab. prof. Małgorzaty Daczewskiej

oraz

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Abbreviations

ALP	actinin-associated LIM				
	protein				
AMP(s)	adult muscle precursor				
	cell				
ATP	adenosine triphosphate				
ATPase	adenylpyrophosphatase				
ВНК	baby hamster kidney				
BLAST	Basic Local Alignment				
	Search Tool				
BSA	bovine serum albumin				
cDNA	complementary DNA				
CI	contractility index				
CNS	central nervous system				
DNA	deoxyribonucleic acid				
DNAse	deoxyribonuclease				
Dpp	decapentaplegic				
DRM	desmin-related myopathy				
EGF	epidermal growth factor				
F-actin	filamentous actin				
FC(s)	founder cell(s)				
FCM(s)	fusion-competent				
	myoblast(s)				
FGF	fibroblast growth factor				
g	gravitational acceleration				
GFAP	glial fibrillary acidic				
	protein				
GFP	green fluorescent protein				
GTP	guanosine-5'-triphosphate				
Hsp(s)	heat shock protein(s)				
IF(s)	intermediate filament(s)				

IFM(s)	indirect flight muscle(s)				
Ig	immunoglobulin				
IP	immunoprecypitation				
kDa	kilodaltons				
М	molar				
МАРК	mitogen activated protein				
	kinase				
MDa	megadaltons				
MF(s)	microfilaments				
mM	milimolar				
MT(s)	microtubules				
NCBI	The National Center for				
	Biotechnology				
nM	nanomolar				
р	probability value				
PBS	phosphate buffered saline				
PCR	polymerase chain reaction				
PDZ	post synaptic density				
	protein				
RNA	ribonucleic acid				
RNAi	RNA interference				
SDS-PAGE	polyacrylamide gel				
	electrophoresis				
sHsp(s)	small heat shock				
	protein(s)				
TALENS	transcription activator-				
	like effector nucleases				
TBS	tris-buffered saline				
TEM	transmission electron				
	microscope				

TGF	transforming	growth	WT	wild type
	factor		μl	microliters
UAS	upstream	activating		
	sequence			

Gene symbols

act42A	actin42A	hsp22/Hspb8	heat shock protein
act5	actin5		22
act57B	actin57B	hsp23	heat shock protein
act87E	actin87E		23
ар	apterous	hsp26	heat shock protein
capZ	capping protein Z		26
col	collier	hsp27/Hspb1	heat shock protein
cryAB/αB-crystallin	αB-crystallin		27/ heat shock
dcryAB/ l(2)efl	Drosophila αB-		27kDa protein 1
	crystallin/ lethal (2)	hsp40/dHDJ1	heat shock protein
	essential of life		40
DES	desmin	hsp60	heat shock protein
dFoxo	Drosophila forkhead		60
	box O	hsp60B	heat shock protein
Dm_0	lamin Dm ₀		60B
duf	dumfounded	hsp64	heat shock protein
eve	even-skipped		64
Gal4	yeast transcription	hsp67Ba	heat shock protein
	activator protein		67Ba
	Gal4	hsp67Bb	heat shock protein
hh	hedgehog		67Bb
his3	histone3	hsp67Bc	heat shock protein
hsc-1	heat shock cognate1		67Bc
hsc-2	heat shock cognate2	hsp68	heat shock protein
hsc-3	heat shock cognate3		68
hsc-4	heat shock cognate4	hsp70	heat shock protein
hsc-5	heat shock cognate5		70
hsp20/Hspb6	heat shock protein	hsp90	heat shock protein
	20/ heat shock		90
	protein B6		

Hspb2	heat shock 27kDa			
	protein 2			
Hspb3	heat shock 27kDa			
	protein 3			
Hspb7	heat shock 27kDa			
	protein 7			
insc	inscuteable			
irreC	irregular-chiasm-C			
JNK	C-Jun N-terminal			
	protein kinase			
kirre	Kin of Irre C			
Kr	Kruppel			
l'sc	lethal of scute			
lamC	lamin C			
lb	ladybird			
lmd	lame duck			
lmnA	lamin A			
lmnB1	lamin B1			
lmnB2	lamin B2			
Mef2	Myocyte enhancer			
	factor-2			
МНС	myosin heavy chain			
MLC	myosin light chain			
rst	roughest			
SALS	sarcomere length			
	short			
slou	S59/slouch			
slp	sloppy paired			
sna	snail			
sns	sticks and stone			
tin	tinman			
Тт	tropomyosin			
Tmod	tropomodulin			

troponin troponin C troponin I troponin T twist wingless Z-band alternatively ZASP spliced PDZ motif protein

Tn

ТпС

TnI

TnT

twi

wg

Summary

The *Drosophila CG4533 (l(2)efl, dcryAB*) gene is an orthologue of vertebrate α B-*crystallin*, which encodes a small heat shock protein (sHsp). The most prominent activity of sHsps is binding proteins and protecting them from aggregation, preventing the accumulation of partially denatured or improperly folded proteins in muscle cells. α B-crystallin is also implicated in the initial phase of skeletal muscle differentiation. It was demonstrated that α B-*crystallin* plays a key role in muscle differentiation and its mutated form is involved in human desminopathies. My results revealed that *dcryAB* gene is specifically expressed in larval body wall muscles and the dCryAB expression pattern was reminiscent of the localisation of its human orthologue α B-crystallin.

Using the generated polyclonal antibodies it was found that dCryAB protein was abundantly expressed in all larval body wall muscles, it was accumulated in a perinuclear area and displayed a striated pattern at the level of M- and Z-lines. To assess the *dcryAB* role in muscle development RNAi-mediated muscle-specific gene attenuation was applied. The *dcryAB* knockdown led to formation of muscles characterised by significant defects in muscle morphology. The majority of the observed larvae exhibited defects in sarcomeric organisation, characterised by an irregular, fuzzy pattern of Z-lines in large muscle segments and smaller number of muscle nuclei. This aberrant sarcomeric pattern was often associated with muscle splitting leading to an altered muscle attachment or to the loss of the affected muscle. Ultrastuctural analyses confirmed altered sarcomeres organisation, revealing also mitochondria with barely visible mitochondrial crests and increased amount of glycogen between myofilaments. Moreover, *dcryAB* attenuation specifically in mesoderm led to impaired functionality of larval muscles and affected *Drosophila* life span, implicating *dcryAB* role in muscle development.

Presented studies also revealed that in *Drosophila* larval muscles mouse anti-vimentin antibody detected a protein which co-localised with dCryAB in the Zline and was present in the nuclear area. I believe that *Drosophila* expresses proteins that correspond to the third class of vertebrate intermediate filaments, which share a similar intracellular distribution with their vertebrate counterparts. Using co-IP approaches it was confirmed that dCryAB interacts with the vimentinlike protein like α B-crystallin interacts with desmin. Thus it is expected that the vimentin-like protein may have properties of the third class intermediate filament proteins, enclosing vimentin and desmin. Performed analyses suggest that dCryAB ensures structural integrity of somatic muscles by interacting with potential IF proteins.

In human, R120G substitution in α B-crystallin leads to the loss of its IF chaperone activity and induces aggregations of desmin in muscles, causing desmin-related myopathy (DRM). The advantage of the α B-crystallin conservation has been taken to test whether *Drosophila* mutated dCryAB displays similar properties as its vertebrate counterpart. I found that muscle-specific expression of mutated dCryAB^{R120G} caused formation of intracellular aggregates containing the vimentin-like protein as well as dCryAB^{R120G}. These symptoms led in consequence to muscle weakness, which is characteristic for patients with DRM. My studies revealed that mutated dCryAB^{R120G} mimics effects of mutation in human α B-crystallin, therefore *Drosophila* may represent a suitable model system to study DRM.

Streszczenie

Drosophila gen CG4533 (l(2)efl, dcryAB) jest ortologiem genu αB -krystaliny kręgowców. αB-krystalina jest małym białkiem szoku cieplnego, które zapobiega akumulacji częściowo zdenaturowanych lub nieprawidłowo złożonych białek, między innymi w komórkach mięśniowych. Ekspresja αB-krystaliny jest również indukowana podczas początkowej fazy różnicowania się mięśni, wskazując na jej istotną rolę w tym procesie, a także jest zaangażowana w powstawanie desminopatii u ludzi. W rozprawie doktorskiej wykazano, że ekspesja genu dcryAB obserwowana jest specyficznie w mięśniach, podobnie do swojego ludzkiego odpowiednika. Wykazano, że białko dCryAB usytuowane jest wokół jąder komórkowych, w linii M oraz na zewnętrznym obszarze linii Z. W celu oceny roli dcryAB w rozwoju mięśni, zastosowano mięśniowo specyficzną atenuację genu, przy użyciu interferencyjnego RNA. Wykazano, że obniżona ekspresja genu *dcryAB* prowadzi do nieprawidłowego rozwoju mięśni, przejawiającego się zmniejszonymi rozmiarami mięśni czy rozdzielaniem włókien mięśniowych, mniejszą liczbą jąder oraz sarkomerów. Analiza w TEM włókien mięśniowych ujawniła liczne defekty w strukturze samych sarkomerów jak również obecność mitochondriów o zaburzonej strukturze grzebieni mitochondrialnych. Na obszarze sarkoplazmy włókiem mięśniowych zaobserwowano liczne nagromadzenia glikogenu pomiędzy miofibryllami. Ponadto przeprowadzone testy behawioralne ujawniły mniejszą sprawność ruchową oraz krótszy cykl życiowy larw z wyciszonym genem dcryAB. Uzyskane wyniki wskazują na istotną rolę produktów genu dcryAB w rozwoju mięśni oraz stabilizacji sarkomerów jak również wpływu na długość cyklu życiowego Drosophila.

Przy użyciu przeciwciała przeciwko mysiej wimentynie wykazano obecność wimentyno podobnych filamentów pośrednich w mięśniach larwalnych *Drosophila*. Wykazano, że białko wimentyno podobne tworzy sieć na obszarze sarkoplazmy włókien mięśniowych. Rozmieszczenie przestrzenne białka wimentyno podobnego w mięśniach larwalnych swoją lokalizacją przypomina rozmieszczenie włókien desminowych we włóknach mięśniowych kręgowców. Przy zastosowaniu techniki koimmunoprecypitacji wykazano, że białko wimentyno podobne oddziałuje z białkiem dcryAB. Przypuszcza się, że białko

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wimentyno podobne może posiadać właściwości filamentów III klasy, obserwowanych u kręgowców.

U człowieka, substytucja R120G w αB-krystalinie powoduje utratę przez nią właściwości opiekuńczych wobec filamentów pośrednich i powstanie w komórkach agregatów zawierających między innymi desminę, co prowadzi do wywołania miopatii zależnej od desminy. W przedstawionej pracy wykorzystano konserwatywność sekwencji αB-krystaliny do sprawdzenia czy zmutowane białko dCryAB u *Drosophila* wykaże się podobnymi właściwościami co jego odpowiednik u kręgowców. Wykazano, że mięśniowo specyficzna ekspresja zmutowanego białka dCryAB^{R120G} powoduje wytworzenie się wewnątrzkomórkowych agregatów, zawierających białko wimentyno podobne, jak również dCryAB^{R120G}. U ludzi opisane symptomy prowadzą do osłabienia mięśni, co jest charakterystyczne dla pacjentów z miopatią zależną od desminy. Na podstawie otrzymanych wyników stwierdza się, że *Drosophila* może być użytecznym organizmem modelowym do badań miopatii zależnej od desminy.

1. Introduction

Drosophila melanogaster is a model organism commonly used to study development, behaviour, diseases or even evolutionary mechanisms. Thanks to the wide range of available tools to study many of the processes occurring during *Drosophila* life, it has became one of the most important models in the modern biomedical research. Many biological processes in *Drosophila* are analogous to vertebrate ones, both at the cellular and the molecular levels, but the main advantages of the fruit fly over vertebrate models are its short generation time (Fig. 1-1.), a relatively simple development and a less complex genome.

Development of the larval musculature during embryonic stages of the fruit fly is one of the processes analogous to those occurring in vertebrates. As in vertebrates, the mesoderm gives rise to three types of muscle tissues, namely: somatic muscles, also called body wall muscles which enable locomotion, visceral muscles lining the digestive tract and heart muscles building the dorsal vessel and pumping the haemolymph. *Drosophila* myogenesis progresses in two steps: embryonic and adult. During the first step, larval muscles are formed through the fusion between founder cells and fusion-competent myoblasts, whereas during the second step, adult muscle precursor cells serve to develop adult muscles either *de novo* or using larval muscle templates. The developed muscles display unique features due to information provided by identity genes, expressed in the founder cells. Finally, attached and innervated muscles become fully differentiated and functional larval muscles with a completely organised contractile apparatus.

In vertebrates, one part of the striated muscle cytoskeleton consists of an intermediate filament network, which is responsible for stabilisation of the sophisticated sarcomeric organisation, as well as linkage between the contractile apparatus and the cytoplasmic organelles. Small heat shock proteins help to stabilise the muscle cell structure by interacting with the cytoskeleton including intermediate filament components; mutations of any of these proteins can lead to muscle diseases.

Small heat shock proteins also influence the muscle development; for this reason the aim of this study is to investigate the role of αB -crystallin's orthologue

in muscle development and sarcomere stabilisation in *Drosophila melanogaster*. Surprisingly, no intermediate filament proteins have been identified in the *Drosophila* muscles to date. Studying the *Drosophila* counterpart of αB -crystallin, which is known to interact with the intermediate filament protein, is expected to provide a new insight into this issue.



Fig. 1-2. *Drosophila* **life cycle.** Images represent the developmental stages of *Drosophila*. The development time at 25°C is 8.5 days. Adult females lay up to 400 eggs (embryos), which hatch after 12–15 h. Larvae grow for about 4 days while moulting twice: into 2nd- and 3rd-instar larvae at about 24 and 48 h after hatching. Subsequently, the larvae encapsulate in the puparium and undergo a four-day metamorphosis, after which the adults emerge. After Weigmann et al. (2003).

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1.1.1. Mesoderm formation in Drosophila embryos

Mesoderm formation starts when all the cells of the internal layer of the *Drosophila* embryo express transcription factors Twist (Twi) and Snail (Sna) (Ip et al., 1992; Thisse et al., 1988) induced by a high concentration of Dorsal morphogene. The crucial role of the *twi* and *sna* genes in the mesoderm formation was established by Thisse et al. (1988), who showed that embryos lacking Twist or Snail failed to form mesoderm and died at the end of embryogenesis. Extensive genetic analyses (Baylies and Bate, 1996) and a recent genome-wide study (Sandmann et al., 2007), that Twi activated a large range of genes involved in specification of different mesodermal derivatives. One of its key targets is *tinman* (*tin*), expressed initially in the trunk mesoderm. *Tin* is crucial for mesoderm regionalization and subsequently becomes restricted to its dorsal portion, being required for dorsal fates specification.

At this point, the mesodermal anlage spreads dorsally and the process requires the function of Heartless, a Drosophila FGF receptor homologue (Carmena et al., 1998a). At the same time, unpatterned mesoderm stays under the influence of signals sent from the overlapping ectoderm. The first one, decapentaplegic (Dpp), is a member of the TGF β family and defines the dorso-ventral axis of the embryo (Fig.1.1.1-1.), whereas two other ectodermal signals: Wingless (Wg) and Hedgehog (Hh), define the antero-posterior axis (Baylies et al., 1998; Leptin and Grunewald, 1990). Dpp, expressed as a dorso-ventral gradient in ectodermal cells, maintains expression of tin in the underlying mesodermal cells and represses expression of ventrally expressed genes such as pox meso, a gene required for the proper development of the most ventral and lateral abdominal muscles and for activation of the subset of sidentity genes (Duan et al., 2007). This induction of Dpp signaling divides the mesoderm into dorsal and ventral sectors. The mesoderm partition along the antero-posterior axis also divides each mesoderm segment into two domains. These give rise to the different progenitor cells, due to expression of two segmentation genes: even-skipped (eve) and sloppy paired (slp). Consequently, progenitors of the visceral mesoderm and the fat body originate in the eve domain, whereas progenitors of the somatic muscles and the heart are produced in the *slp* domain, which is shown in Figure 1.1.1-1. (Azpiazu and Frasch, 1993; Riechmann

et al., 1997). Here, Wg signal amplifies distinctions between cells of the *eve* and *slp* domains, by maintaining a high level of Twist expression in *slp* domain cells, being a crucial element in assigning cells to the somatic myogenesis (Baylies and Bate, 1996). Finally, mesodermal cells of the dorsal part that receive Dpp and Hh from the ectoderm will form the visceral mesoderm in the *eve* domain, while cells from the ventral part will generate a part of the fat body and other mesodermal tissues. Mesodermal cells of the most dorsal part that receive Dpp and Wg signals in the *slp* domain will form the heart, whereas the remaining cells will form the somatic mesoderm (see Figure 1.1.1-1., Baylies 1998).

1.1.2. From somatic mesoderm to muscle fibre

Two waves of myogenesis occur during the *Drosophila* life cycle. During the first, embryonic wave, the body wall muscles are formed to ensure mobility of the larva. In each abdominal hemisegment, 30 different, single and multinucleated muscle fibres are formed (Fig. 1.1.2-1.). Each of them displays unique properties, such as the number of nuclei, position, orientation along antero-posterior and dorso-ventral axes, size, sites of attachment to the exoskeleton and patterns of innervation (Baylies et al., 1998). Drosophila somatic muscles are formed by the fusion between two types of cells: founder cells (FC) and fusion-competent myoblasts (FCMs) (Bate, 1990a; Richardson et al., 2008). In spite of the fact that these two types of myoblasts originate from the same competence domain, they have different properties, thanks to progressive specification taking place during successive steps of cell fate determination (Fig. 1.1.2-2.). Initially, the combination of received Wg and Dpp signals makes mesodermal cells, expressing high level of Twi, competent to start myogenic program by induction of expression of the proneural gene, lethal of scute (l'sc), in all the cells of the competent domain (Carmena et al., 1995). During initial steps of diversification (Fig. 1.1.2-2.), the competence domain subdivides into different promuscular clusters. This highly dynamic process involves a combined action of intrinsic fibroblast growth factor (FGF) and epidermal growth factor (EGF), signals which restrict expression of *l'sc* to a spatially defined subset of cells, forming promuscular clusters (Buff et al., 1998; Michelson et al., 1998). Within those clusters, cells start to express muscle

identity genes, which initiate diversification (Carmena et al., 1998), leading to the formation of distinct types of muscles. At the same time, cells from the same promuscular clusters still have potential to become either founder cells or fusioncompetent myoblasts. Subsequently, under the action of lateral inhibition process, involving Notch and MAPK pathways, only one cell in each cluster will obtain the identity of muscular progenitor, whereas remaining cells will become FCMs (Fig. 1.1.2-2.). Here, only muscle progenitor cells stay *l'sc* positive, giving rise to all FCs, whereas their surrounding cells express the gene lame duck (lmd) which is restricted to the cells fated to become FCMs (Carmena et al., 2002; Duan et al., 2001). Then, each progenitor undergoes symmetric or asymmetric division, giving rise to two FCs or one FC and one adult muscle precursor cell (AMP), which remains undifferentiated throughout embryonic embryogenesis but is required for adult muscle development during the second wave of myogenesis. This asymmetric division takes place thanks to an unequal distribution of Numb and Inscuteable (Insc) proteins, which are localised on the opposite sides of the dividing cell. In consequence, one of the cells inheriting Numb, which is able to repress Notch, becomes a FC of the larval muscle, while the second daughter cell, retaining Notch activity, becomes another FC or an AMP (Carmena et al., 1998b; Leptin and Grunewald, 1990; Ruiz Gómez and Bate, 1997). As a result of the progressive myogenic cascade, three distinct classes of myoblasts are specified, namely FCs, FCMs and AMPs.

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1.1.3. Diversification of muscle types

All larval muscles are composed of a single, multinucleated fibre originated from an individual founder cell. FCs, formed during initial steps of diversification give rise to all embryonic muscles and are thought to carry all the information needed to define unique features of individual muscles. Each FC starts to express identity genes and undergoes a series of myogenic events that direct the formation of functional muscles with unique properties (Fig. 1.2-2.). Identity genes, such as *apterous* (*ap*), *collier* (*col*), *even-skipped* (*eve*), *Kruppel* (*Kr*), *ladybird* (*lb*), *S59/slouch* (*slou*) (Tixier et al., 2010), encode developmental regulatory proteins which are expressed in different subsets of FCs. Most of them have been described in detail and their main role in the specification of muscle identities has been well understood. Their expression is determined by a negative regulation with other identity genes (Jagla et al., 2002; Knirr et al., 1999), regulatory interactions with Hox genes (Capovilla et al., 2001) and an influence of extrinsic signals like Wg (Taylor, 2006).

Acquisition of distinct muscle properties includes obtaining specific size, attachment and innervation by individual muscles. All larval muscles are composed of single but multinucleated fibres, which are derived from particular founder cell. The FC fuses with a determined number of FCMs obtained by multiple rounds of fusion, developing multinucleated myotubes (Fig. 1.1.2-2.). A large number of genes controlling different steps of myoblast fusion have been identified (Schejter and Baylies, 2010). This includes genes expressed exclusively in FCs, like dumfounded/Kin of Irre C (duf/kirre) (Ruiz Gómez et al., 2000) and *irregular-chiasm-C/roughest (irreC/rst)* (Strünkelnberg et al., 2001), but also genes expressed in FCMs, like sticks and stone (sns) (Bour et al., 2000). It has been proposed that Duf and Rst are ligands for Sns, acting here as their receptor, provoking fusion between FCs and FCMs (Baylies et al., 1998; Leptin and Grunewald, 1990). Since muscles differ in their size, they have different numbers of nuclei. This is a result of muscle type-specific regulation of the fusion process, which is dependent on the activity of identity genes (Bataille et al., 2010). Nevertheless, not only identity genes are expressed in a muscle-type specific manner. Also genes encoding cytoskeletal components or adhesion molecules are expressed differently in individual muscles, revealing their roles in acquisition of distinct muscle properties, other than muscle size. Attachment and innervation types are other unique properties of muscles, regulated by *kon-tiki* (Schnorrer et al., 2007) and *capricious* (Shishido, 1998) genes respectively, and their expression is also restricted to small muscle subsets.

1.2. Structure of Drosophila muscle fibre

Muscle cells play various roles in organisms, depending on their structure and localisation. The larval somatic musculature in *Drosophila* is responsible for locomotion, which is crucial for finding food and then a suitable place for pupation. *Drosophila* somatic muscle fibres show many similarities with vertebrate striated muscle cells, and components building contractile apparatus share a lot of homology between these two, very distant animal groups. Their similarities are observed at both, morphological and molecular levels. Organisation of insect striated muscles is remarkably regular and precise which seems to be critical for muscle development and function.

1.2.1. Unique properties and characteristics of muscle cell

Muscle tissue is mainly composed of elongated cells building a muscle. Muscle cells are specialised in changing their length that is contracting and relaxing with changing tension. Diversification process lies in the showing up in the cytoplasm of specific proteins, which take part in contraction. There are three types of muscle tissue: skeletal muscle, smooth muscle and cardiac muscle. In their structure and function the body wall muscles in *Drosophila* resemble the vertebrate skeletal muscle and, moreover, most of vertebrate muscle genes have invertebrate homologues (Sawicki, 2009).

Skeletal muscle tissue consists of long, cylindrical cells, also called fibres because of their elongated shape. Muscle cells contain a contractile apparatus, composed of myofibrils, which are tightly compacted in the whole volume of the cell. Myofibrils are the main cytoplasmic components and are built of proteins

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taking part in the contraction. These proteins form thin myofibres, arranged very regularly. Mitochondria, situated between the myofibres, provide energy needed for the generation of a contraction. Nuclei lie on the myofibrils surface, just below the cell membrane in the cytoplasmic space where other cellular organelles are also localised. Skeletal muscle cells also have a well-developed endoplasmic reticulum, which forms many compartments and channels with a characteristic arrangement. Moreover, the cell membrane also creates many big and small channels by its invagination inside the cell, which is important for performing contractions (Sawicki, 2009).

To generate contraction and ensure the proper function of the muscle cell, all its components have to be well organised and form an integrated network. This is sustained, among others, by the intermediate filaments, which are part of the cytoskeleton. Mutations in any sarcomeric or cytoskeletal components of human muscle cell very often cause various neuromuscular diseases, and thus invertebrate studies offer a possibility of improving human diseases therapies (Hooper and Thuma, 2005; Sawicki, 2009).

1.2.2. Sarcomere structure and composition

Sarcomere is the smallest functional contractile unit, building myofibril. Its structure is conserved across the animal kingdom and it is formed from highly organized macromolecular complexes consisting of thin (actin) and thick (myosin) myofilaments, together with their associated proteins (Rui et al., 2010). A single sarcomere (Fig. 1.2.2-1.) is confined by two neighboring Z-lines, also called Z-disks, which are structures made up of various structural proteins such as α -actinin, Zasp and titin (Hooper and Thuma, 2005; Lin et al., 2013; Zhang et al., 2000). The area on both sides of the Z-line, spanned by thin filaments that do not overlap thick filaments, is called I-band. The Z-line demarcates the middle of the I-band and participates in organisation and stabilisation of the thin filaments, which are cross-linked and anchored to the Z-line by α -actinin (Sparrow and Schöck, 2009). α -actinin is directly bound to the Zasp protein, the only *Drosophila* member of the cytoskeletal Alp/Enigma family, which is a group of proteins characterised by an amino-terminal PDZ domain and one or three carboxyl-terminal LIM domains.

Zasp cooperates with α -actinin in the Z-line in the maintenance and anchoring actin at the Z-line (Jani and Schock, 2007). Another Z-line protein, titin, was predicted by molecular modelling to be a component of a ternary complex of Zasp, α -actinin and titin, where Zasp and titin bind to different surfaces of α -actinin (Au et al., 2004; Leptin and Grunewald, 1990). The *Drosophila* titin (D-titin) and its smaller part kettin align and connect the thick and thin filament systems, providing elasticity to the muscle. Their N-termini are found to bind to both α -actinin and actin in the center and the periphery of the Z-line, whereas their C-termini are associated with the thick filaments. Thanks to that, they can play a role in the organisation of actin-myosin filaments into striated arrays and also in the contribution of the myofibril passive stiffness (Clark et al., 2007; Kulke et al., 2001; Leptin and Grunewald, 1990; Zhang et al., 2000). Moreover, Z-lines are also connected to the plasma membrane. Here, ends of muscle fibres are linked to the tendon matrix on the outside of the muscle via integrin junctions, forming enlarged "modified" Z-lines (Reedy and Beall, 1993).

Thin filaments (Fig. 1.2.2-1.) consist of filamentous (F)-actin associated with tropomyosin (Tm) and troponin (Tn) complex proteins. They are anchored to the Z-line and together are often referred to as the "I-Z-I" complex (Rui et al., 2010; Sparrow and Schöck, 2009). Muscle thin filaments are characterised by a diameter between 6 and 10 nm. Their main component is actin, which forms a double helix made of polymerized actin monomers. Invertebrate actin double helix repeats once every 13-15 monomers, which is every 35-40 nm (Hooper et al., 2008). The fly genome contains six actin gene loci. Particular actin proteins differ in only few amino acids, both within species and between distant species such as fly and mouse. Drosophila has four muscle-specific actins with different time points of expression. Actin 87E is expressed throughout the fly life, actin 57B is expressed in embryonic and larval muscles and actins 79B and 88F are mostly expressed in pupal and adult muscles. Moreover, other than temporal restriction of expression, the fly actins are also restricted in their spatial expression pattern (Roper et al., 2005). Other components of thin filaments are tropomyosin and troponin complexes, which are required for the proper interactions of thin filaments with myosin. Tropomyosin is a filamentous protein, formed by dimeric tropomyosin subunits, polymerised in the head-to-tail manner (Karlik and Fyrberg, 1986).

These filaments twist with the actin double helix and sterically block the myosin binding sites during relaxed state, but move away from them in the presence of Ca⁺⁺ (Hooper et al., 2008). Every tropomyosin molecule is associated with a troponin complex, which is composed of three proteins, troponin T (TnT), troponin I (TnI) and troponin C (TnC). Each subunit has different function, namely TnT binds to tropomyosin, TnI is involved in inhibition of Mg⁺⁺ ATPase activity of actomyosin and TnC binds Ca⁺⁺ removing TnI inhibition (Farah and Reinach, 1995). Altogether, actin filaments, tropomyosin and troponin complexes take part in ensuring interactions between thin and thick filaments, which is crucial for generation of muscle contraction.

Muscle thick filaments are composed of myosin and the area of sarcomere that is spanned by such filaments is known as the A-band (Fig. 1.2.2-1.). Tree pairs of molecules, the heavy chain (MHC), the essential light chain (MLC) and the regulatory chain build myosin. Heavy chains coil around each other to form a long coiled-coil tail. Hundreds of myosin tails bind to each other to form the scaffold of the thick filament. The opposite end of every heavy chain is bound to one essential light chain and one regulatory chain, forming one of the combined molecules of globular heads. Heads are connected to the tails by a short neck domain and bind to the thin filaments to generate force. The myosin molecules are oriented in the opposite directions with two peripheral regions containing protruding heads and a central region without heads. This organisation is a result of the polarisation of the myosin ends and leads to the formation of cylindrical filaments, which are fixed firmly to the M-line, situated at the centre of A-bands. Another protein, which is comprised in thick filaments, is paramyosin. This protein forms bipolar filaments, which are formed by two-chain α -helical coiled-coils. Paramyosin creates the core of the thick filament, being surrounded by myosin. It is shown that paramyosin plays a central role in determining the thick filament diameter (Hooper et al., 2008). In Drosophila indirect flight muscles (IFM) is also present characteristic protein, called flightin. It is localised in the A-band except for the H-band region (the zone of the thick filaments that is not superimposed by the thin filaments). Flightin binds to the myosin rod in the molar ratio of between 1:1 and 1:2 vv. The presence of flightin is essential for flight, for maintenance of sarcomeric integrity

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1.2.3. Myofibril assembly

In regular organisation of filaments, not only compounds they are built of are important. Also maintaining a precise organisation and the size of filaments are critical for the muscle function. It is not completely understood how filaments assemble and attain their stereotyped lengths (Bai et al., 2007). Like the sarcomere structure, the mechanism of precise myofibril assembly seems to be also conserved across animal species.

Four models of myofibril assembly have been proposed to date. The first one suggests that assembly pathways for sarcomeric thin and thick filaments arrays are remarkably independent and in the absence of one filament type, the other can still form crude networks, resembling the sarcomeric arrangement (Beall et al., 1989). Further work (Holtzer et al., 1997) confirmed that I-Z-I complexes and bipolar myosin filaments assembled independently before joining. Freefloating A-bands were detected in the absence of actin, and irregular Z-lines were observed with thin filaments attached in muscles lacking myosin. According to the second model structures called premyofibrils are formed prior to the development of mature myofibrils. Premyofibrils are characterised by interdigitating, banded patterns of I-Z-I complexes and non-muscle myosin. Subsequently, non-muscle myosin filaments are replaced by muscle myosin filaments during the premyofibril to myofibril transition, and discrete aggregates of Z-bodies grow along the premyofibrils, fusing laterally into Z-lines (LoRusso et al., 1997). The third model indicates the role of the giant protein titin during myofibrillogenesis. According to this model, the interdigitation of the I-Z-I complexes with myosin is driven by interaction of the N-terminal domain of titin with the I-Z-I complex and subsequent association of the unfolded C-terminal region with the M-line (Ehler et al., 1999). The fourth model emphasizes the role of integrin adhesion complex as the starting point for myofibrillogenesis, showing that integrins and their extracellular matrix ligands are required for sarcomere assembly and Z-line formation (Sparrow and Schöck, 2009).

More recent studies (Rui et al., 2010) verified those hypotheses and showed that sarcomere assembly was a highly coordinated process, mediated by multiple latent protein complexes and did not occur in a step-wise fashion. It was confirmed that I-Z-I proteins and myosin filaments were two independent complexes, which interacted with each other, and were responsible for the arrangement of the myofibrils. To clarify how these two complexes assembled, studies on mutant *Mhc*¹ lacking thick filaments were performed (Rui et al., 2010). They showed that homozygous *Mhc*¹ mutant muscles no longer localised in Z-lines (Fig. 1.2.3-1. A, B), indicating that I-Z-I proteins could not align into striation in the absence of MHC. Moreover, immunostaining against zipper, which corresponds to the only nonmuscle myosin, showed that zipper is strongly localised to the Z-line but not to the thick filaments and removal of MHC did not result in any obvious zipper periodic pattern (Fig. 1.2.3-1. B). This suggests that in Drosophila intermediate non-muscle myosin-containing premyofibrils do not exist during the myofibril assembly. Elimination of MHC also led to a complete disruption of the distribution of other sarcomeric components, like β -integrin (Fig. 1.2.3-1. A), titin and Zasp, whereas there was no effect on the distribution of integrin, α -actinin, zipper, kettin and Zasp at the attachment sites, suggesting that formation of muscle attachments was independent of MHC. Knocking down *Mhc* by RNAi in later stages, such as the third instar larvae, caused a loss of muscle sarcomere striation correlated with a reduction of MHC expression level, indicating that MHC played a critical role not only in the sarcomere formation but also in its maintenance. The thin filamentassociated proteins were also shown to participate in the sarcomere formation. Depletion of *TnT* or *TnI* eliminated the striation pattern, whereas knockdown of *TnC* did not lead to any significant change in MHC/actin/ α -actinin striation. Tropomyosin (Tm) is another critical component participating in the sarcomere assembly, but removal of *TnT*, *TnI* or *Tm* leads to a random distribution of all the remaining proteins, indicating the lack of loading sequence for troponinstropomyosin complex during the sarcomere assembly. The complex plays an important role in the initial sarcomere assembly by allowing stable interdigitation of thin and thick filaments and is recruited to the sarcomere as a complex (Rui et al., 2010).

I-Z-I complexes are the first identifiable structures during early myofibrillogenesis (Holtzer et al., 1997). To test if MHC assembled into thick filaments and interdigitated with thin filaments to form sarcomeres, each component of the I-Z-I complex was knocked down (Rui et al., 2010). Depletion of muscle-specific actins, act57B and act87E with incompletely depleted cytoplasmic actins, act5 and act42A caused formation of shorter and thinner striated myofibrils. This suggests that cytoplasmic actins, which are already expressed in myoblasts, may take part in formation of these shortened thin filaments. It allows speculating that the initial sarcomere assembly in muscles utilises cytoplasmic actins as building blocks (Rui et al., 2010). Attaining the stereotyped length of these filaments is not completely understood but it is known that certain capping proteins are required for the sarcomere to reach its proper size. Two ends of sarcomeric actin filaments are lined up in a regular array. The barbed ends (plus), which are cross-linked by α -actinin at the Z-line, are capped by CapZ protein. The free pointed ends (minus) are capped by other capping proteins, tropomodulin (Tmod) and sarcomere length short (SALS). The length of sarcomeric actin filaments in striated muscles is primarily regulated by modulation of the pointedend capping activity of Tmod, which limits actin assembly, suggesting that actin filaments can elongate from pointed ends (Fischer and Fowler, 2003; Mardahl-Dumesnil and Fowler, 2001). SALS protein is required for the second phase of actin filament elongation. Most likely, thanks to antagonising Tmod at the pointed ends, SALS takes part in achieving the full length of filaments. SALS is essential for attaining the final thin-filament length but is not critical for the normal organisation of other sarcomeric components (Bai et al., 2007).

Investigating the role of Z-line components showed no significant changes in the striation pattern under the α -actinin knocked-down, indicating that α -actinin was not required for the thick filament organisation (Fyrberg et al., 1998). On the other hand, it was shown that α -actinin mutant muscles contained expanded Zlines, indicating that α -actinin was required for the Z-line condensation. Attenuation of *zipper* and *Zasp* expression led to fuzzy but discernable striation, indicating that individual knockdown of these sarcomeric components did not affect the initial formation of sarcomeres. However, in later development stages of *Zasp* mutants, striation began to disappear, suggesting that Zasp was required for the sarcomere maintenance. In contrast, *kettin* mutant muscles did not show any striation pattern for any markers (Hakeda et al., 2000; Zhang et al., 2000) and it was proposed that titin/kettin acted as a third filament to regulate the sarcomere plasticity. Subsequently, it was tested if simultaneous removal of *actin* and one of the Z-line components, such as α -actinin, zipper or Zasp were associated with complete loss of striation. Altogether, these results suggest that myosin thick filaments and I-Z-I complexes assemble independently from each other, but they require each other to be properly ordered (Rui et al., 2010).

It has been also shown that zipper/Zasp/ α -actinin complexes are highly enriched at the muscle attachment sites. They act downstream of integrin, linking the muscle cytoskeleton to the cell membrane. Disruption of integrins is associated with a complete loss of myofibril striation (Volk et al., 1990) but it has been suggested that integrins are not involved in the I-Z-I complexes assembly, as association of actin and α -actinin occurs even in the absence of integrin. However, the absence of integrins blocks the interdigitation of thin and thick filaments with each other and sarcomeres cannot be formed. It has been proposed that integrins play a very important role in maintaining the tension at the cell periphery for sarcomere structural organisation and serve as anchor points for floating I-Z-I complexes (Rui et al., 2010).



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1.3. Role of intermediate filaments in muscle cell

The cytoskeleton in striated muscle cells is composed of a highly complex scaffold of microfilaments (MFs), microtubules (MTs) and intermediate filaments (IFs). Thanks to this cytoskeletal network, striated muscles are able to maintain their sophisticated sarcomeric organisation, as well as integration between contractile apparatus, nucleus and other organelles. MT and MF systems are the two principal elements of eukaryotic cells, being engaged in many basic cellular functions (Herrmann et al., 2007). Despite the fact that mutations in their proteins, like tubulin and actin, are more harmful for a cell than those in proteins of IFs, this study is particularly focused on the intermediate filament part of the cytoskeleton, as they interact with α B-crystallin (see the following chapter).

1.3.1. Characteristics and classification of intermediate filaments

Intermediate filaments are the key components, maintaining high organisation inside of the muscle cell, by interacting with various cellular structures (Capetanaki et al., 2007).

Intermediate filaments owe their name to their average diameter of approximately 10 nm, which places them between thin, 7 nm actin filaments and thick of over 20 nm microtubules. IFs are found in many cell types, including cells forming epithelial tissues, such as epidermis, those present in nerve tissue, those comprised in skeletal, smooth and cardiac muscles, as well as cultured cells, such as fibroblasts (Cooke, 1976; Eriksson et al., 2009; Goldman, 1971; Ishikawa et al., 1968; Schmitt, 1968). Thanks to the possibility of IFs isolation and purification, *in vitro* studies provided an opportunity to analyse their unique properties. It was established that IFs were insoluble under physiological conditions and could repolymerize after disassembly into subunits under conditions that would irreversibly denature many other proteins. Moreover, IFs assembly does not need nucleoside triphosphates such as ATP and GTP and thanks to that they self-assemble under very simple conditions, which is in contrast to actin and tubulin filaments (Zackroff and Goldman, 1980).

All the intermediate filaments share a common tripartite structure which consists of a highly conserved central α -helical rod domain, a variable N-terminal head domain and a C-terminal tail domain. In contrast to the conserved rod domains, the terminal C- and N- domains are the main source of enormous sequence variability among IF proteins, being responsible for the cell-specific functions of particular proteins of the family (Goldman et al., 1999). Therefore, the IFs classification is based on the similarities in their α -helical rod domain sequences, but also on the assembly properties (Eriksson et al., 2009). This classification led to distinguish: type I cytoskeletal IF proteins, including the acidic keratin proteins; type II cytoskeletal proteins including the neutral-basic keratin proteins; type III IF proteins, including GFAP, peripherin, vimentin and desmin; type IV IF proteins, including nestin, synemin and the neurofilament triplet proteins; type V IF proteins, including nuclear lamins and type VI IF proteins, including filensin and phakinin (Eriksson et al., 2009). Intermediate filaments of types I-IV are present in the cytoplasm, type V IF proteins are present in the nucleus and type VI proteins are present exclusively in eye lenses (Omary, 2009).

1.3.2. Role of IFs in muscle cells

Thanks to slight differences between various intermediate filaments, different cell types possess different types of cytoskeletal IF proteins, characterising various tissues. Epithelial cells contain mainly keratins; mesenchymal cells: vimentin; neurons: neurofilaments and muscle cells contain desmin (Franke et al., 1978). Some of the cell types express more than one IF protein and their expression is frequently regulated developmentally (Gard et al., 1979; Granger and Lazarides, 1979).

In mature muscles two IF systems exist with different functions and biochemical properties. The first one consists of nuclear lamins and the second one of type III IF proteins. Lamins form a meshwork on the inner surface of the nuclear envelope (Fig. 3.2-1.), creating the nuclear lamina (Stuurman et al., 1998). This filamentous layer provides a structural support to the nuclear membrane and participates in a chromatin organisation inside the nucleus. Three genes encoding lamins: *lmnA*, *lmnB1* and *lmnB2*, are present in the human genome, whereas the

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Drosophila genome includes only two: *lamin C* and *lamin Dm*⁰ (Schulze et al., 2009; Stuurman et al., 1998). Various types of lamins are distinguished in each of the two species: A/C (lamins A and C are alternatively spliced products from *lmnA*) and B in humans and their *Drosophila* equivalents, *lamC* and *Dm*⁰. The classification is based on their structure and expression pattern (Herrmann et al., 2007; Schulze et al., 2009). Moreover, comparison of the gene structures of lamin genes and genes encoding cytoplasmic IFs suggests that all the IF proteins derive from lamin-like progenitors (Steinert and Roop, 1988).

The second group of muscle IFs, aside from keratins (Stone et al., 2007), predominantly consists of cytoplasmic type III IF proteins, enclosing mesodermal vimentin and a muscle-specific IF protein, desmin (Capetanaki et al., 1989; Milner et al., 1996). Other intermediate filaments which are present in muscle cells, like synemin, paranemin, syncoilin and nestin, are not muscle-specific and even if they co-polymerize with type III IFs, their role remains unclear (Granger and Lazarides, 1980; Kachinsky et al., 1994; Newey et al., 2001; Price and Lazarides, 1983; Schweitzer et al., 2001). Generation of specific antibodies and the widespread use of immunofluorescence have enabled to show, that IFs form an extensive and complex network, pervading most of the cytoplasm (Franke et al., 1978; Starger et al., 1978). Even early studies showed that the most remarkable attribute of IFs was their resistance to relatively high concentrations of salt and detergents, suggesting that their role is primarily to maintain mechanical and structural integrity of the cell (Franke et al., 1978). This view got changed with the observations that mutations in genes encoding IF proteins lead to many diseases, not necessarily related to IFs structural functions. Particular attention was then paid to other properties of the IFs, pointing out their involvement in a broader spectrum of functions, such as organisation of cytoplasmic architecture, signalling, and transcription regulation; IFs are highly dynamic structures (Hyder et al., 2008; Ivaska et al., 2007; Prahlad et al., 1998). In muscle cells, desmin filaments are the most abundant intermediate filaments, playing an essential role in maintaining muscle fibre organisation. Desmin filaments (Fig. 1.3.2-1.) are attached to the sarcolemma at costameres where they stabilise the sarcolemma organisation and overlie Z-discs and M-lines, supporting myofibrils and protecting them from mechanical insult (O'Neill et al., 2002). In addition, cytoplasmic filaments are,

directly or indirectly, linked to membranous organelles, like nuclei and mitochondria. For both organelles, this association is important for keeping their proper morphology, positioning or even function (Anesti and Scorrano, 2006; Mermelstein et al., 2006; Shah et al., 2004). Moreover, cytoplasmic IFs are also believed to play a role in coordinating mechanical forces in embryonic development, growth and tissue maturation (Chen et al., 2004).



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1.3.3. IF-associated diseases

Intermediate filament proteins, together with other cytoskeleton components, form a very effective intracellular network that supports physiological functions promoting cell survival; any anomaly of these filaments either causes or predispose to a human disease (Table 1.3.3-1).

The IF-associated diseases can affect a wide range of tissues and cover the whole spectrum of genetic alterations, including missense and nonsense mutations, deletions and gene duplications (Omary, 2009). In many IF-associated diseases the histopathological and diagnostic hallmarks are characteristic cytoplasmic inclusions. It is still unclear if the formation of such inclusions protects the tissue or perpetuates the disease but their formation is a consequence of a mutation or overexpression of a particular IF (Liem and Messing, 2009; Omary et al., 2009). One such disease, in which the phenotype of inclusions is observed, is a desmin-related myopathy. As this disease is relevant to this study and is caused by mutation either in the desmin gene (*DES*) or in the α B-crystallin gene (*CryAB*), which is a member the heat shock proteins family (Goldfarb and Dalakas, 2009; Vicart et al., 1998), it will be described in the following chapter.

IF	Examples of diseases
Types I and II	
Acidic and neutral-basic	Epidermolysis bullosa simplex; epidermolytic hyperkeratosis;
keratins	Meesman corneal dystrophy; keratodermas
Type III	
Desmin	Desmin-related myopathy; dilated cardiomyopathy 1A;
	dilated cardiomyopathy with conduction system deficits;
	distal myopathy
GFAP	Alexander disease
Peripherin	Amyotrophic lateral sclerosis 1
Vimentin	Dominant cataract
Type IV	
Neurofilaments	Various Charcot-Marie-Tooth diseases; Parkinson disease;
	amyotrophic lateral sclerosis 1; neuronal IF inclusion disease
Type V	
A-type lamins	Hutchinson-Gilford progeria syndrome; dilated
	cardiomyopathy 1; restrictive dermopathy; Charcot-Marie-
	Tooth disorder type 2B1
B-type lamins	Acquired partial lypodystrophy; adult-onset leukodystrophy
Type VI	
Filensin (Bfsp1)	Autosomal-dominant cataract
Phakinin (Bsfp2)	Autosomal-dominant cataract

Diseases associated with mutations in IF proteins

Table 1.3.3-1. Diseases associated with mutations in IF proteins.Modifiedfrom Eriksson et al. (2009).

1.4. Heat shock proteins

Heat shock proteins (Hsps) are a group of proteins first discovered in *Drosophila melanogaster* after heat and chemical induction (Tissiéres et al., 1974). Subsequently, their response to heat and other stressors (cold, hypoxia, ischemia, endotoxins, heavy metals, organic solvents and reactive oxygen species) was reported in a wide variety of organisms, including bacteria, plants and animals, making it a highly conserved genetic system. Interestingly, expression of Hsps is not exclusive for the response to unfavourable conditions, and some of them are induced developmentally, whereas others are constitutively synthesised in cells, controlling protein transport, folding, unfolding, assembly, disassembly and degradation (Colinet et al., 2010; Lindquist and Craig, 1988; Mymrikov et al., 2010; Sorensen et al., 2003).

1.4.1. Classification of heat shock proteins

In Drosophila, as well as in humans, five main groups of Hsps have been distinguished. Hsps are classified into families according to their sequence homology and the approximate protein molecular mass. Namely, the Hsp90/100 family includes high-molecular-mass Hsps and in Drosophila is represented by only one gene hsp83 (Cutforth and Rubin, 1994). The complex Hsp/Hsc70 (hsp68, hsp70, hsc-1, hsc-2, hsc-3, hsc-4, hsc-5) consists of proteins with molecular mass between 68 and 73 kDa. Members of the family Hsp60 (hsp60, hsp60B, hsp64) are characterised by the molecular mass around 60 kDa, whereas size of 37 kDa is characteristic for members of the family Hsp40 (*dHDJ1*) (Kazemi-Esfarjani, 2000; Morrow and Tanguay, 2003; Timakov and Zhang, 2001). The last group of Hsps contains twelve (hsp22, hsp23, hsp26, hsp27, hsp67Ba, hsp67Bb, hsp67Bc, l(2)efl, CG14207, CG4461, CG7409, CG13133) putative small heat shock proteins (sHsps) with molecular mass between 12 and 43 kDa (Carra et al., 2010; Haass et al., 1990; Ingolia and A., 1982; Morrow and Tanguay, 2003; Sun and MacRae, 2005a). Functions of the members belonging to the first four families have been extensively studied, whereas still little is known about the function of the others (Table 1.4.1-1.), thus the objective of this study is functional analysis of *l*(*2*)*efl*, a member of the small heat shock protein family.

Family	Genes in Drosophila	Functions
sHsp	hsp22, hsp23, hsp26, hsp27, hsp67Ba, hsp67Bb, hsp67Bc, l(2)efl, CG14207, CG4461, CG7409, CG13133	Thermotolerance Protection against apoptosis
Hsp60	hsp60, hsp60B, hsp64	Involvement in spermatid individualization process Folding of nascent proteins
Hsp70	hsp68, hsp70, hsc-1, hsc-2, hsc-3, hsc-4, hsc-5	Folding of nascent proteins Thermotolerance Involvementd in clathrin-mediated endocytosis
Hsp90/100	hsp83	Ensuring proper centrosome function Maintaining of signal transduction pathways and microtubule effectors Capacitor of morphological evolution

Table 1.4.1-1. Functions of *Drosophila melanogaster* Hsps. Modified fromMorrow and Tanguay (2003).

1.4.2. Structure and function of sHsps

Within the entire group of the sHsps, protein monomers have a similar pattern, with a structure composed of a α -crystallin rod domain of ~90 residues, flanked by a hydrophobic N-terminal region and a C-terminal extension. Intriguingly, sHsps show low overall sequence conservation, except for the α crystallin domain, which owes its name to the homology to α -crystallin from the vertebrate eye lens. In this very conserved region, also called small-heat-shockprotein domain, the observed homology can exceed up to 40%, whereas N- and Ctermini vary extensively, both in sequence and in length, with average of 55 and typically <20 residues, respectively (Ingolia and A., 1982; Kim et al., 1998; Lindquist and Craig, 1988). The secondary structure of the α -crystallin domain is dominated by β -strands with limited α -helical content. β -strands, organised into a β -sheet sandwich, are responsible for dimers formation, the basic building blocks of most sHsps, which subsequently are able to assemble into large, dynamic complexes with the molecular mass of up to 1 MDa (Sun and MacRae, 2005a; Sun and MacRae, 2005b). The N-terminal extension influences higher-order oligomerisation, subunit dynamics and chaperoning, which is one of the main sHsps activity based on protection of newly made proteins from misfolding. Here, the N-terminal extension is responsible for subunit binding by attaching to one end of the α -crystallin domain, whereas the C-terminus binds to the other end stabilizing generated oligomers but also promoting solubility and chaperoning (Kim et al., 1998; Sun and MacRae, 2005b). Moreover, different members of the sHsps group are known to form homo- or hetero-complexes, whereas the knowledge about its structural organisation is still insufficient (Arrigo et al., 2007).

sHsps play a crucial role in maintaining protein homeostasis by interacting with partly unfolded, aggregate-prone proteins, by keeping them soluble and thus preventing cell damage. They are able to support folding of nascent proteins, as well as thermally and chemically denatured proteins (Fig. 1.4.2-1.) ranging from at least 4 to 100 kDa. It is thought that the mechanism of substrate binding is based on a change in the hydrophobicity profiles of several sHsps under stress conditions (Haslbeck, 2002). The binding capacity is dependent on its oligomeric state. Under physiological conditions sHsps exist in the cytoplasm in an inactive oligomeric czti 2122 tió 121 22 c21; 221 2201 2c21; 2212 2Dj t W222201 t z211; c221 25 2211 cc21 2122231; zt 2 có 21W24 H2201 21 n21222t ó o V2d 2c H3 I n21 2221 2222 V2022t 2220 1 236 t j Q 2222 2320 t z 2211 236 SXS 0 2Dztol 21tctó 2011 i Doitz22ctó 2112 I 20 221 28 201 2222.5321 201 z1 z1 21 20 201 x1 201 x1 21 20 201 x1 201 x1 20 201 x1 zt Boitrn2224 tj () 2zn 226 itz2n; c2zt 22 co) HH2 I n21 24; 22 i 226 i 222 t 22 26 i 22 27 i i 2 t W12zl 26 2nj zt 2zl 2ni 2j 2zn 22cz2z2S22 2rnj 122ni 22z222zl 22cD2czi 2z220 i t z2nj 2zt 2 221 i 22 2zzt j 3t i 31 2czt i 2zzt j 30 2zł l 2s H2zł 232 co 32 nó 2i 3nc 31 2VM2c222 i tó 2zł 2332 tó o VM2d2 2j 22i 202cct 2r2z2c2zt 2zl 22nj 22zr 22czt i 2122 t i ó 2Dj 22i 20l s crt W1r22W2t j 2rzt j c2 22 2cVØ/22a H2- HH- PS22I 2222c2i r22222I 202itj 22 Dj 2zrtj 2t 2c2 coc22Di nj 12222/LTL2 csj zl 2cm2t 2ot Wo2ozn22c22i 22Dj 22i 2czi 2cc22t j 2nzt j c2m2i 2zl 2i 212j 2i 2W2i 22 Dj co 212h n2522 22 mart j 2006/12c2 co c 221 22 nj r t W222 2nj 222 n 21 c 222 co 222 n n2222 2000 VA 20 i t 222 c 2 c H2 citi nj 12 cz21202 2j 22 22W0Co 22nn22 o 2zz2 j c2 t 2 2doi 2ccrt j S2 2I nc2 22W0Co 22nn22 2doi 2ccrt j 2t 2-D-A-2t 22Di c2 2Di n 12 22r 2Woó 2j zł2 22 W2 2n 2i 2j zr2zt j 2t i 22 z2i 2 22zr 2zt j 22s 21itl zl 2 2zt i c 12t j 2t 12j 2c22j 22bit zt 0t j 2t 12j 2c122j 22pz2l 2c2222j 2 i Zotizezeti zezeti zazeti za 12 zeti 12 ncó cheny zwoleny 12 z BL-LADR 12 zh 12 z C2 Bzzy 22



1.4.3. Involvement of sHsps in muscle development

Early studies showed that in *Drosophila shsp* genes were expressed in the absence of stress during embryogenesis and metamorphosis in a tissue-specific manner (Michaud et al., 1997; Michaud and Tanguay, 2003). In other species, like zebrafish, mouse or human, their specific pattern of expression was also established, showing their widespread importance in tissue development, that includes myogenesis (Benjamin et al., 1997; Marvin et al., 2008; Sugiyama, 2000).

In humans seven *sHsps* are expressed in cardiac and skeletal muscles. *Hspb1*, *αB-crystallin*, *Hspb6* and *Hspb8* are expressed ubiquitously, whereas *Hspb2*, Hspb3 and Hspb7 are tissue-specific. All those sHsps prevent the accumulation of partially denatured or improperly folded proteins in muscle cells, having chaperone-like activity during recovery or/and under normal conditions. Interestingly, only three of them, αB -crystallin, Hspb2 and Hspb3 are induced during the initial phase of skeletal muscle differentiation and their expression is controlled by MyoD, which is a key player in muscle differentiation, committing mesoderm cells to the skeletal lineage (Berkes and Tapscott, 2005; Mymrikov et al., 2010; Sugiyama, 2000). This fact suggests their muscle-specific function in development, which is precisely regulated by myogenic programme. The function of Hspb1 and α B-crystallin in myogenesis may be due to their cytoprotective role. which relies on myotube-specific association with actin microfilaments. It was suggested that these two sHsps were possibly involved in the initial organisation of myofibril assembly in myotubes. Moreover, Hspb1, Hspb2 and α B-crystallin are localised on Z-bands or I-bands of the skeletal and cardiac muscle myofibrils, maintaining and protecting cytoskeletal structures (Mymrikov et al., 2010; Sugiyama, 2000). Additionally, α B-crystallin stabilises IFs and prevents them from aggregating under various forms of stress but also assists them during developmental reorganisations, suggesting its engagement in muscle formation and further maintenance of its proper structure (Nicholl and Quinlan, 1994)

In the *Drosophila* genome, has been identified a gene called *lethal (2) essential for life (l(2)efl)*, which belongs to the *shsp* family and is homologous to the vertebrate αB -crystallin (Kurzik-Dumke and Lohmann, 1995). Since the function of L(2)efl protein has not been well described yet, this study is focused on analysing

its role in muscle development, sarcomere stabilisation and eventual involvement in the origin of muscle diseases.

1.4.4. DRM as a consequence of α *B*-crystallin mutation

sHsps interact with many essential cell structures and functional disruption or inappropriate association of these molecular chaperones with their substrates can foster disease. One such disease is desmin-related myopathy, a heterogeneous disorder associated with mutations of desmin or α B-crystallin.

The desmin-related myopathy (DRM) was originally described as a skeletal and cardiac myopathy, morphologically characterised by an abnormal accumulation of desmin within muscle fibres (Goebel, 1995). Early studies showed that mutation in the highly conserved carboxy-terminal end of the desmin rod domain was involved in the onset of skeletal myopathy within two American families (Goldfarb et al., 1998). However, in other studies, mutation in αB -crystallin was identified as a source of DRM phenotypes in a large French pedigree (Vicart et al., 1998). Myopathic manifestations of diseases caused by either desmin or αB crystallin mutations are identical; therefore in both cases the disorder is designated as the desmin myopathy. Consequently, systemic disorders caused by mutations in desmin, α B-crystallin or perhaps other proteins interacting with desmin and causing myopathy, are named desmin myopathy, whereas the accurate terms desminopathy and α B-crystallinopathy are used for patients with mutations in desmin and α B-crystallin, respectively. The inheritance pattern in the familial desmin myopathy is autosomal dominant or autosomal recessive, but many cases have no family history with de novo created desmin mutations. The onset of the disease depends on the inheritance and the location of the mutation, but is mostly late, which is related to the accumulation of toxic desmin aggregates inside of the cells during the life time (Goldfarb et al., 2004).

The DRM is characterised by a lower limb muscle weakness slowly spreading and involving trunk, neck flexors, facial, bulbar and respiratory muscles. Symptoms observed in skeletal muscles are often associated with cardiomyopathy, being manifested by conduction blocks and arrhythmias but also with cataract formation. In DRM patients with the missense mutation in *cryAB*, where arginine in

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codon 120 in the amino acid sequence is replaced by glycine (R120G), muscle fibres contain intracellular aggregates composed of desmin and αB-crystallin (Dalakas et al., 2000; Goldfarb and Dalakas, 2009; Goldfarb et al., 2004). The arginine in position 120 is highly conserved and mutation leads to changes in the secondary, tertiary and quaternary structure of the protein. AB-crystallin^{R120G} loses its chaperone activity *in vitro* and directly induces aggregations of type III intermediate filament proteins, like desmin in muscle fibres and vimentin in eye lenses. Deposition of those aggregates is a result of an increased binding capacity of the αB-crystallin^{R120G} and a decreased complex dissociation constant. The altered protein-protein interactions impair significantly the desmin and vimentin network, myofibril alignment, sarcomere architecture, mitochondrial architecture and function, and the ubiquitin/proteasome system. Moreover, αB-crystallin^{R120G} may also affect the cell viability because one of the functions of αB-crystallin is negative regulation of apoptosis (Bova et al., 1999; Simon et al., 2007; Wettstein et al., 2012).

Thus, the *Drosophila l(2)efl*, being homologous to αB -crystallin, may have similar functions and can be involved in muscle development and stabilisation of the structural integrity of somatic muscles.

2. Aims of the thesis

Up to date, the role of the *Drosophila* gene *lethal (2) essential of life (l(2)efl, dcryAB,* CG4533) has not been well explored. However, it is known that *dcryAB* belongs to the small heat shock proteins family, is orthologous to the human αB -*crystallin* gene and may play an important role in the *Drosophila* development. It is well established that some sHsps influence muscle development in humans as well as in *Drosophila* and therefore, the main aim of my thesis was to investigate the role of αB -*crystallin's* orthologue in *Drosophila melanogaster* muscle development and sarcomere stabilisation. I chose the third instar larva as the object of my studies, because at this stage of development *Drosophila* muscles are fully developed, functional and relatively easy to observe, making them a perfect material for examinations.

To understand the function of the *dcryAB* gene, first I wanted to describe its expression pattern in larval muscles. Knowing that dCryAB protein was abundantly expressed in all the larval body wall muscles in a very stereotypical pattern, reminiscent of the localisation of its human orthologue α B-crystallin, I attempted to check if attenuation of its expression would lead to any developmental changes. Morphological alterations and impaired function of larval muscles with decreased dCryAB level in muscle cells raised the questions: 1. could dCryAB, like its human orthologue, stabilise muscle cell structure by interacting with intermediate filaments and, 2. could its point mutation R120G lead to a disease corresponding to the desmin-related myopathy? Since it was suggested that *Drosophila* might possess a counterpart of the protein belonging to the third class of intermediate filaments, I started answering these questions by labelling its larval muscles with anti-vimentin antibody. In this way I visualised a protein which interacted with dCryAB and might be a putative IF in Drosophila muscles. Therefore, the next questions were: 1. does dCryAB ensure structural integrity of somatic muscles by interacting with IF proteins, and 2. is dCryAB involved in the pathogenesis of muscle disease corresponding to the human desmin-related myopathy?

To find answers to these questions, I used many different approaches and I hope that my thesis will contribute to our understanding of the role of *dcryAB* in muscle development and sarcomere stabilisation.

3. Material and methods

3.1. Material

3.1.1. Drosophila stocks

Fly strains were maintained at 25°C in the standard medium in the 12:12h light and dark cycling humidified incubator.

Fly strain	Source/laboratory	Catalogue number
Mef-Gal4	Bloomington Stock Center	27390
UAS-RNAi-dcryAB	Vienna Drosophila RNAi Center	40532
UAS-RNAi- dcryAB	Vienna Drosophila RNAi Center	107305
UAS- dcryAB	H. Jasper (a kind gift)	
UAS- dcryAB-GFP	K. Jagla (created for this study)	
UAS- dcryAB -GFP ^{R120G}	K. Jagla (created for this study)	
UAS-cryAB-GFP	K. Jagla (created for this study)	

3.2. Methods

3.2.1. RNA extraction and reverse transcription

To obtain *Drosophila* cDNA, total RNA was extracted from fifty 3rd instar larvae of selected lines, using a TRIzol®Reagent (Invitrogen). The remaining DNA was removed by RQ1 DNAse (Promega). To obtain human cDNA, total RNA was extracted from human fibroblasts (a kind gift from C. Barriere). 2 μ l of each RNA were used for reverse transcription, performed with the Superscript III First strand Synthesis System (Invitrogen) according to manufacturer's instructions.

3.2.2. Plasmid construction and site-directed mutagenesis

For plasmid construction two coding sequences were amplified: *dcryAB* using cDNA from WT 3rd instar larvae and *cryAB* using human cDNA via PCR. The following pairs of primers, containing Xba1 and BamH1 (Biolabs) restriction sites (underlined), were used:

- a) for *dcryAB*: forward, 5'-ATA<u>TCTAGA</u>TCCGTAGTGCCACTGATGTTC-3' with reverse, 5'- TAT<u>GGATCCCTAGGCGGTGGAGGTCTCC-3'</u>
- b) for *cryAB*: forward, 5'-ATA<u>GGATCC</u>GACATCGCCATCCACCACC-3' with reverse, 5'-ATA<u>TCTAGA</u>GAAAGGGCATCTATTTCTTGGG-3'.

To generate the point mutation R120G in amplified sequences of *dcryAB* and *cryAB*, the following pairs of primers were used (exchanged nucleotides are underlined and in bold):

for *dcryAB* mutagenesis:

- c) forward, 5'-ATATCTAGATCCGTAGTGCCACTGATGTTC-3' with reverse, 5'-AGCTGGTAGCGTC<u>C</u>GGAGAACTGGCGGG-3',
- d) forward, 5'-CCCGCCAGTTCTCCGGGACGCTACCAGCT-3' with reverse, 5'-TATGGATCCCTAGGCGGTGGAGGTCTCC-3';

for cryAB mutagenesis:

e) forward, 5'-ATAGGATCCGACATCGCCATCCACCACC-3' with reverse, 5'-GTATTTCCC<u>G</u>TGGAACTCCCT-3', f) forward, 5'-AGGGAGTTCCA<u>C</u>GGGAAATAC-3' with reverse, 5'-ATATCTAGAGAAAGGGCATCTATTTCTTGGG-3'.

PCR products amplified in reactions above were mixed in the following way: 2 μ l of the product c) with 2 μ l of the product d) and 16 μ l of water for *dcryAB*; and 2 μ l of the product e) with 2 μ l of the product f) and 16 μ l of water. Hybridization was performed in water bath by cooling down the mixtures from 99°C to 60°C. After 25 min of incubation at 60°C the mixtures were cooled down to 37°C and subsequently 2 μ l of each were amplified via PCR, by using following pairs of primers, containing Xba1 and BamH1 restriction sites (underlined):

- g) for *dcryAB:* forward, 5'-ATA<u>TCTAGA</u>TCCGTAGTGCCACTGATGTTC-3' with reverse, 5'- TAT<u>GGATCC</u>CTAGGCGGTGGAGGTCTCC-3',
- h) for *cryAB*: forward, 5'-ATA<u>GGATCC</u>GACATCGCCATCCACCACC-3' with reverse, 5'-ATA<u>TCTAGA</u>GAAAGGGCATCTATTTCTTGGG-3'.

All DNA amplifications were obtained with a high-fidelity DNA polymerase (Phusion, Biolabs) according to manufacturer's instructions. Obtained sequences were cloned into a BamH1 and Xba1 sites of pUASp-PL-Venus vector (a kind gift from Vincent Mirouse) and injected into a w¹¹⁸ embryos to produce transgenic flies, a step performed by Fly Facility platform (Clermont-Ferrand, France).

3.2.3. Semi-quantitative PCR

To compare the level of *dcryAB* expression in selected fly strains, 2 μ l of reverse transcription products (described above) were amplified via PCR, by using following pairs of primers: forward, 5'-TCCGTAGTGCCACTGATGTTC-3' with reverse, 5'- CTAGGCGGTGGAGGTCTCC-3'. After 20th, 25th and 35th cycle 5 μ l of each PCR product were taken, run on a 1% agarose gel and intensity of the bands was compared. As a control *gapdh1* was used, whose expression remains at a constant level. All the DNA amplifications were obtained with a *Taq* DNA polymerase (Invitrogen) according to manufacturer's instructions.

3.2.4. Immunofluorescence staining of Drosophila larval muscles

Third instar larvae were dissected as described previously (Budnik et al., 2006) in an ice-cold Ca²⁺-free saline buffer containing 128 mM NaCl, 2 mM KCl, 4

mM MgCl₂, 1 mM EGTA, 35 mM sucrose and 5 mM HEPES, pH 7.2 (Demontis and Perrimon, 2009). Buffer without EGTA was used for measurements of contracted muscles. Body wall muscles were fixed with 4% formaldehyde in PBS for 15 minutes and then rinsed three times for 5 minutes in PBS with 0.5% Tween20 (PBT). The material was blocked for 30 minutes in 20% horse serum in PBT at room temperature. Primary antibodies (see Material and Methods 3.2.11.) were applied over night at 4°C. After three washes adequate secondary antibodies (see Material and Methods 3.2.11.) were used for 2 hours at room temperature with or without phalloidin-TRITC (1:1000; Sigma P1951) when appropriate. Specimens labelled and mounted in Fluoromount-G antifade reagent (Southern Biotech) were analysed using a FV300 (Olympus), SP5 or SP8 (Leica) confocal microscopes. Three-dimensional models of labelled muscle fibres were constructed by using Imaris software.

3.2.5. Muscle morphology observations and muscle measurements

Muscles VL3, VL4 and SBM of abdominal segments 3 or 4 were analysed in 15-22 dissected and fixed 3rd instar larvae, as described above. Observations of muscle morphology, as well as measurements of muscle length, diameter, number and size of sarcomeres were carried out on muscles visualised with phalloidin. For counting, muscle nuclei were visualised using anti-Mef2 antibody (see Material and Methods 3.2.11.). The fibre contractility index (CI) was calculated from the following formula: CI = (size of relaxed fibres – size of contracted fibres)/size of relaxed fibres. FV300 (Olympus) confocal microscope was used for imaging and Fluoview programme (Olympus) for muscle measurements.

3.2.6. Behavioural assays

Behavioural assays were carried out on fifteen 3rd instar larvae per genotype and repeated 3 times for each individual. For all locomotor assays larvae were placed for at least 120 s on a Petri dish filled with solidified 3% agarose for acclimation before being tested. In the righting assay, larvae were placed on a Petri dish with 3% agarose in the dorsal position and the time needed to reverse to the ventral position was measured. For the journey test a 2 mm wide, 5 mm deep and 60 mm long track was made on a Petri dish containing 3% agarose. Fresh yeasts were placed behind the end line as stimuli. Larvae were placed on the test track and the time taken to crawl 50 mm distance was recorded but not longer than 420 s. Larvae which turned backward during the trial were returned to the starting line and the timing was resumed. In motility test larvae were crawling on a Petri dish with 3% agarose and the peristaltic movements were counted during 30 s.

3.2.7. Viability test

In the viability test, 200 embryos were placed on a Petri dish containing 3% agarose supplemented with grape juice and with yeast paste. Subsequently, 1st instar larvae were moved to vials with a standard medium. Individuals achieving each stage of development (3rd larval instar, pupa, imago) were counted.

3.2.8. Western Blotting

For immunoblotting, 50 dissected and frozen larvae were homogenized at 4°C in an ice-cold TSA buffer (10mM Tris pH 8,0, 140 mM NaCl and protease inhibitors from Roche). To obtain lysis, TritonX-100 and NaCl were added, up to the final concentration of 1% and 300 mM, respectively. After 30 min of incubation on ice, the lysate was centrifuged at 17000 g for 5 min at 4°C. Equal volumes of supernatant were boiled for 10 min in a loading buffer, containing 10% SDS and 10% β -mercaptoethanol, incubated on ice for 2 min and centrifuged at 2000 g for 5 min. Samples were resolved on 10% SDS-PAGE gel and transferred to a nitrocellulose membrane (Whatmann). The membrane was blocked for 1 h at room temperature with 3% non-fat milk. Western blotting was performed with rat anti-dCryAB antibody (see Material and Methods 3.2.12.). Following overnight incubation in a primary antibody solution, the membrane was washed 3x20 min in TBST (TBS + 0.5% Tween20). Subsequently, the membrane was incubated in antirat HRP-conjugated secondary antibody (see Material and Methods 3.2.12.) for 1 h at room temperature. After 3x20 min washes in TBST, signal was detected by ECL Plus (Amersham) and visualised using Amersham system on the X-ray Film (Kodak). Western blot with rabbit anti-β3-tubulin (see Material and Methods

3.2.12.) was performed as a control. The strength of signal was quantified using the ImageJ 1.47 u.

3.2.9. Co-immunoprecipitation

For co-immunoprecipitation assay, 100 dissected and frozen larvae were homogenized at 4°C in 500 µl harsher extraction buffer (HEB: 20 mM Tris-HCl [pH 7.6], 140 mM NaCl, 5 mM EDTA, 1 mM EGTA, 1% [v/v] NP-40, 0.5% [w/v] sodium deoxycholate), described previously (Perng et al., 2006) and supplemented with a protease inhibitor cocktail from Roche. 50 µl of protein G sepharose beads (Amersham Pharmacia Biotech AB) were washed 3 times with 100 µl of PBS1X and centrifuged at 2000 *g* for 5 min after each washing. After 30 min of incubation on ice, lysate was centrifuged at 17000 g for 20 min at 4°C, diluted up to a total volume of 500 µl with Ab binding & Washing buffer (Invitrogen) and preincubated for 1 h at 4°C with washed protein G sepharose to eliminate proteins that bind non-specifically to the protein G sepharose beads. The protein G sepharose beads were spun down by centrifuging at 17000 *g* for 5 min at 4°C and the supernatant was incubated for 3-4 h at 4°C with 5 µl rat anti-dCryAB antibody. Ab-protein complex was incubated with pre-cleaned beads over night at 4°C on the cradle as well as negative control containing 5% rat serum and 50 µl of washed protein G sepharose in Ab binding & Washing buffer (Invitrogen). The samples were centrifuged at 2000 *g* for 5 min at 4°C. The supernatant from IP was collected and used in the Western Blotting step as an IP efficiency control. Combined complex and negative control were washed 3 times for 5 min at 4°C with a WB washing buffer (Invitrogen). The pellet from both samples as well as the lysate before IP and the IP efficiency control were ran in Western Blot procedure described above with mouse anti-vimentin antibody (see Material and Methods 3.2.12.).

3.2.10. Immunogold

Dissected larvae (as described above) were fixed for 1.5 h at room temperature in 0.5% glutaraldehyde in PBS mixed with 4% paraformaldehyde as 1:1. Post fixation was performed after overnight incubation in 2% paraformaldehyde at 4°C. Following 3x5 min washes in PBS with 0.5% TritonX (PBT), the material was dehydrated in a graded alcohol series (35%, 50%, 75%, 85%). Subsequently, larvae were incubated in a mixture of 85% ethanol and LRwhite (London Resin Company Ltd), mixed in ratios 2:1, 1:1 and 1:2 for 1 h in each. The material was impregnated in LRwhite 2 times for 12 h at room temperature and once overnight at 4°C and subsequently embedded in LRwhite in gelatin capsules. Polymerization was performed for 24 h at 59°C and subsequently for a few days at room temperature. The capsules were removed in warm water and the material was cut using a microtome (ReihertUltracut E). Ultrathin sections were collected on a nickel mesh and blocked in 1% BSA in PBS for 30 min. Primary antibodies anti-vimentin, anti- β -actin, anti-myosin and anti-dCryAB (see Material and Methods 3.2.13.) were diluted with a buffer containing 1% BSA, 0.1% Tween20, 0.1% TritonX-100, 0.02% sodium azide in PBS (137 mmol/L NaCl, 2.7 mmol/L KCl, 10 mmol/L Na₂HPO₄ • 2H₂O, 2 mmol/L KH₂PO₄). The sections were incubated on a cradle (Stuart mini gyro-rocker SSM3) for 2 h at room temperature. After three 10 min washes in PBT, adequate secondary antibodies conjugated with gold particles were added. The secondary antibodies were diluted in the same buffer as the primary antibodies. After three washes in PBS for 10 min and 2 washes in distilled water for 2 min, the sections were contrasted in lead citrate and observed in electron microscope Zeiss EM 900.

Antigen/	Conjugated	Host	Dilution	Vendor/ Source
Antibody	moiety	species		
GFP	-	Rabbit	1:500	Biogenesis
dCryAB	-	Rat	1:500	K. Jagla
Mef2	-	Rabbit	1:1000	A. Nguyen
Kettin	-	Rat	1:25	Abcam
Vimentin	-	Mouse	1:40	Sigma
LamC28.26	-	Mouse	1:1000	DSHB
Rabbit IgG	Alexa 488	Donkey	1:300	Jackson Immuno-
				Research

3.2.11. Antibodies used in confocal labelling

Rabbit IgG	Cy5	Donkey	1:300	Jackson Immuno-
				Research
Rat IgG	Alexa 488	Donkey	1:300	Jackson Immuno-
				Research
Rat IgG	Cy5	Donkey	1:300	Jackson Immuno-
				Research
Mouse IgG	Cy3	Donkey	1:300	Jackson Immuno-
				Research

3.2.12. Antibodies used in western blot

Antigen/	Conjugated	Host	Dilution	Vendor/Source
Antibody	moiety	species		
dCryAB	-	Rat	1:2000	K. Jagla
Vimentin	-	Mouse	1:400	Sigma
β3-tubulin	-	Rabbit	1:0000	R. Renkawitz Pohl
Rat IgG	Horseradish	-	1:10000	Pierce
	peroxidase			
Mouse IgG	Horseradish	-	1:10000	Pierce
	peroxidase			
Rabbit IgG	Horseradish	-	1:10000	Pierce
	peroxidase			

3.2.13. Antibodies used in immunogold

Antigen/	Conjugated	Host	Dilution	Vendor/Source
Antibody	moiety	species		
dCryAB	-	Rat	1:500	K. Jagla
Vimentin	-	Mouse	1:50	Sigma
Myosin	-	Rat	1:1000	Invitrogen
β-actin	-	Mouse	1:10	Invitrogen
Rat IgG	18 nm gold	Goat	1:20	Jackson Immuno-
	particles			Research

Rat IgG	10 nm gold	Goat	1:100	Sigma
	particles			
Mouse IgG	10 nm gold	Goat	1:100	Jackson Immuno-
	particles			Research

3.2.14. Mitotracker

Dissected larvae (as described above) were incubated for 15 min at 37°C in 1500 nM Mitotracker®Red CMXRos (Invitrogen) diluted in an ice-cold Ca²⁺-free saline buffer. Subsequently, larvae were fixed in 4% formaldehyde for 15 min, washed in PBS three times for 10 min, mounted in Fluorescent Mounting Medium (Dakocytomation) and observed in confocal microscope FV1000 (Olympus).

3.2.15. TEM

Dissected larvae (as described above) were fixed in 2.5% glutaraldehyde in 0.1 M phosphate buffer. The material was repeatedly rinsed in the same buffer and post-fixed for 2 h in 1% OsO₄ (Sigma–Aldrich) in 0.1 M phosphate buffer. Following rinsing in phosphate buffer, the material was dehydrated first in a graded alcohol series and then in acetone, and embedded in epoxy resin Epon 812 (Sigma–Aldrich). The Epon blocks were cut on a Reichert Ultracut E ultramicrotome (Leica, Wetzlar, Germany). Ultrathin sections were contrasted with uranyl acetate and lead citrate according to the standard protocol (Reynolds, 1963) and examined in a transmission electron microscope (Zeiss EM 900; Carl Zeiss AG, Oberkochen, Germany) at an accelerating voltage of 80 kV.

3.2.16. Heat shock procedure

Third instar larvae were incubated in the water bath for 10 min at 37°C. To recover after the heat shock, larvae were incubated for 2 h at 25°C in the normal feeding conditions (Colinet et al., 2010). Subsequently, they were dissected and stained with antibodies (see section 3.2.4.) or collected to the protein extraction and western blot procedures (see section 3.2.8.).

3.2.17. Statistical analysis

Statistical analysis was carried out using the GraphPad Prism5 software. Ttest non-parametric or one-way ANOVA were used for comparisons of the lines phenotypes. The results are shown in the graphs as a standard error of mean; p<0.05 is regarded.

Name	Purpose
ImageJ 1.47u	Export and processing of microscopy data files
AdobePhotoshop CS5	Processing images
Imaris	Three-dimensional modelling
GraphPad Prism5	Statistics
Fluoview	Muscle measurements

3.2.18. Software

4. Results

4.1. *Drosophila dcryAB* gene is specifically expressed in larval body wall muscles

According to the FlyBase data base, *the Drosophila* gene l(2)efl (*CG4533*) is orthologous to the human αB -crystallin (cryAB) gene, and the amino acid alignment of their products shows 44% of identity (NCBI/BLAST). Following these assumptions, this study is based on the hypothesis that the l(2)efl product has a function similar to that of the human αB -crystallin. For this reason I propose to name it *Drosophila* αB -crystallin (dCryAB) and accordingly, to call the gene *dcryAB*.

Several Hsp genes play specific developmental functions (Haass et al., 1990). To determine a potential role of *dcryAB* in the *Drosophila* development, its expression pattern in the third instar larva was first analysed. Using the generated polyclonal antibodies it was found that dCryAB protein was abundantly expressed in all the larval body wall muscles (Fig. 4.1.1, A). Within an individual larval muscle dCryAB protein was accumulated in a perinuclear area and displayed a striated pattern at the level of M and Z-lines (Fig. 4.1.1, B-E). Three-dimensional iso-surface modelling of labelled muscles showed that the Z-line-associated dCryAB was mainly detected at the external level of Z-lines but also in the M-line (Fig. 4.1.1, F-H). Images of ultrathin sections of larval muscles, labelled with antibodies combined with gold particles, confirmed the dCryAB localisation in Z-lines (Fig. 4.1.1, I). As a control for the specificity of immunogold reaction, staining against myosin was used (Fig. 4.1.1, J), showing that even in the presence of abundant protein, the number of accessible epitopes in the ultrathin sections was relatively small but the signal was properly localised.

This first analysis showed that the dCryAB expression pattern was reminiscent of the localisation of its human orthologue α B-crystallin (Dubin et al., 1990; Golenhofen et al., 1999), suggesting that *dcryAB* might play conserved myogenic functions.

4.2. *dcryAB* attenuation leads to formation of morphologically altered muscles

To assess the role of *dcryAB* in formation of larval muscles, RNAi-mediated muscle-specific gene attenuation was applied, and the muscle morphology was analysed using phalloidin staining. Third instar larvae of two RNAi-dcryAB Drosophila lines, driven by a MefGal4 driver, were used in the analysis. Three classes of somatic muscle defects were observed: defects in sarcomere organisation, defects in muscle morphology and defects in sarcomere organisation and muscle morphology occurring together (Fig. 4.2.1, A-F). The majority of observed larvae (58% of line 40532 and 40% of line 107305) exhibited defects in sarcomeric organisation, characterised by an irregular, fuzzy pattern of Z-lines in large muscle segments (Fig. 4.2.1, D, E). This aberrant sarcomeric pattern was often associated with muscle splitting (37% of line 40532 and 40% of line 107305) leading to an altered muscle attachment or to the loss of the affected muscle (Fig. 4.2.1, D-F). Finally, in some isolated cases (about 5% in line 40532 and 20% in line 107305) muscle splitting was detected independently of sarcomeric alterations (Fig. 4.2.1, B-C, F). To confirm that RNAi-mediated muscle-specific *dcryAB* gene attenuation was efficient, Drosophila muscles were labelled with specific antidCryAB antibodies and phalloidin (Fig. 4.2.1, G, H). The localisation pattern of dCryAB in RNAi-dcryAB lines was significantly affected compared to the one described in the WT. The level of dCryAB decreased considerably, with preserved expression level of F-actin. Western blot analysis of the muscle lysate also showed a reduced content of dCryAB protein in RNAi-dcryAB line, compared to the WT, without observed reduction of β 3-tubulin expression.

Considering that each of the larval muscles displays specific properties including size, shape, number of sarcomeres and number of nuclei (Bate, 1990b), changes in any of those attributes in *dcryAB* knockdown context can give an insight into its myogenic functions. Thus, several muscle parameters were measured in larvae with muscle-targeted *dcryAB* RNAi. The measurements focused on three distinct muscles: VL3, VL4 and SBM. In all the analysed cases, muscle-specific attenuation of *dcryAB*, compared to the wild type, led to the formation of significantly shorter (VL3: 17 and 29%; VL4: 19 and 27%; SBM: 11 and 15%; in

line 40532 and 107305, respectively, Fig. 4.2.2, A) and thinner muscles (VL3: 22 and 47%; VL4: 19 and 37%; SBM: 7 and 34%; in line 40532 and 107305, respectively, Fig. 4.2.2, B). The number of sarcomeres in the muscle fibres was also reduced (VL3: 10 and 7%; VL4: 11 and 5%; SBM: 12 and 17%; in line 40532 and 107305, respectively, Fig. 4.2.2, C) indicating that the sarcomere assembly could be affected. However, except the fuzzy pattern areas (see Fig. 4.2.1, D), even when the size of sarcomeres was affected compared to the control muscles (VL3: 6 and 24% shorter; VL4: 8 and 23% shorter; SBM: 1 and 5% longer; in line 40532 and 107305, respectively), the observed differences were statistically insignificant (Fig. 4.2.2, D). In some of the RNAi-*dcryAB* line muscles, a smaller number of nuclei was observed (VL3: 19 and 0%; VL4: 20 and 20%; SBM: 20 and 0%; in line 40532 and 107305, respectively, Fig. 4.2.2, E), indicating that embryonic function of dCryAB might be directly or indirectly involved in promoting myoblast fusion events.

4.3. *dcryAB* attenuation specifically in mesoderm leads to impaired function of larval muscles and affects *Drosophila* life span

To test whether described morphological alterations affected the motility of larvae, three behavioural assays were carried out. In the righting assay the time needed for each larva to revert from the dorsal-"wrong" position to the ventral-"right" position was measured. In this test, *dcryAB*-attenuated individuals of two RNAi-mediated lines needed over twice and five times longer, respectively, to revert to the right position (Fig. 4.3.1, A). In the journey test, the speed of larvae crawling has been measured and it has been registered that *dcryAB*-RNAi larvae move slower and needded about 30% and 500% more time to go through the appointed, 5 cm distance (Fig. 4.3.1, B). In the motility test the number of peristaltic movements of crawling larvae was counted, and during 30 seconds the number of peristaltic movements executed by *dcryAB*-RNAi larvae was by over 20 and 50% smaller comparing to the control (Fig. 4.3.1, C). To confirm the contraction disturbance of muscles in tested larvae, the contractility index was calculated by comparing the length of relaxed (by EDTA) and contracted muscle fibres. Muscles of RNAi-*dcryAB* individuals had a significantly lower contractility index (VL3: 2.5 and 2.1; VL4: 3 and 2.5; SBM: 5.9 and 5.2 times lower, in line 40532

and 107305, respectively), suggesting that muscles did not contract properly (Fig. 4.3.1, D). Altogether, results of behavioural assays and contractility test indicate that *dcryAB* knockdown affects muscle contraction and induces motility defects.

It was also assessed weather *dcryAB* had an influence on survival and life span. The viability tests revealed that *dcryAB*-RNAi flies were characterised by a markedly higher mortality rate, compared to the control, at every stage of development, namely: embryo (by 30 and 31% higher), larva (by 22 and 24% higher) and pupa (by 26 and 27% higher), in line 40532 and 107305, respectively (Fig. 4.3.1, E). The life span of the surviving adult *dcryAB*-RNAi flies was also significantly shorter (up to three weeks). Thus, the muscle *dcryAB* expression is involved in control of life span and acts downstream of JNK/dFoxo pathway (Wang et al., 2005).

4.4. dCryAB co-localises with putative intermediate filaments in larval muscles

As previously described (see section 4.1.), dCryAB localises in Z-lines, Mlines and around nuclei. Moreover, three-dimensional images show that the Z lineassociated dCryAB localises mainly at the surface of sarcomeres, just beyond the muscle membrane. This sarcomeric dCryAB localisation is reminiscent of that of its vertebrate orthologue, α B-crystallin and suggests that dCryAB might co-localise with intermediate filaments that are known to link sarcomeres with sarcolemma. As the existence of intermediate filaments in *Drosophila* with homology to vimentin had already been suggested by Walter and Biessmann (1984) and dCryAB was detected at extensions of Z-lines, which is an expected location of intermediate filaments (Konieczny et al., 2008), it was decided to test whether an intermediate filament protein could be detected in *Drosophila* muscles, using antibodies directed against mouse vimentin.

Interestingly, in *Drosophila* larval muscles anti-vimentin antibody detects a protein which co-localises with dCryAB in the Z-line and is present in the nuclear area (Fig. 4.4.1, A-D). The visualised dots, slightly above the sarcomeric pattern of the detected protein, seem to attach to the sarcolemma (Fig. 4.4.1, C). In this study, the *Drosophila* protein, which is spaced at the predicted location of intermediate

filaments and has been detected by anti-vimentin antibody, will be called vimentin-like protein. As the vimentin-like position is equivalent to the position of desmin filaments in vertebrate muscles (Goldfarb and Dalakas, 2009), it is expected that the vimentin-like protein may have properties of the third class intermediate filament proteins, including vimentin. To better visualise subcellular localisation of the vimentin-like protein, three-dimensional reconstructions and iso-surface modelling were performed from confocal scans through larval muscles. They showed that the detected protein, just as dCryAB, mainly localised on the external level of the Z-line in the sarcomeres (Fig. 4.4.1, E). Immunogold staining against the vimentin-like protein confirmed its localisation in the Z-line (Fig. 4.4.1, F) but also showed that antibodies conjunct with gold particles appeared to filamentous structures (Fig. 4.5.1,C).

The vimentin-like protein as well as desmin filaments are also present in the perinuclear area. Immunocytochemistry reaction, visualised in confocal microscope, shows that the vimentin-like protein is present in the nuclear envelope area but also inside the nucleus (Fig. 4.4.2, A). To check if the vimentinlike protein was present inside the nucleus, co-staining with antibodies against histone3 was used. Confocal images (Fig. 4.4.2, B-C) show co-localisation of the vimentin-like protein and histone3, suggesting that the vimentin-like protein is indeed present inside the nucleus. Immunogold reaction against the vimentin-like protein confirmed its distribution on the external side of the nuclear envelope and inside the nucleus, being probably associated with chromatin (Fig. 4.4.2, D).

Following Walter and Biessmann (1984), it is suggested in this study that *Drosophila* expresses proteins which correspond to the third class of vertebrate intermediate filaments and that these proteins share a similar intracellular distribution with their vertebrate counterparts.

4.5. dCryAB interacts with a potential intermediate filament protein

Analysis of dCryAB amino acid alignment shows that dCryAB, like α Bcrystallin and other small heat shock proteins, contains in its sequence a conserved -crystallin rod domain. Inside this crystallin domain, dCryAB has the 77EKFEVILDVQQFS₈₉ motif which corresponds to the intermediate filament interaction domain (Fig. 4.5.1, A) of other organisms (Houck et al., 2011b). This finding suggests that dCryAB has an ability to interact with the intermediate filament protein, which potentially is the vimentin-like protein in Drosophila muscles. To verify the occurrence of possible interactions between dCryAB and the vimentin-like protein, muscle-specific gain of function of *dcryAB* fused with GFP protein was performed using UAS/GAL4 system. Indeed, in third instar larval muscles, overexpression of *dcryAB* led to formation of large cytoplasmic accumulations of dCryAB-GFP. Aggregates of dCryAB-GFP contained also the vimentin-like protein, suggesting that they interacted with each other (Fig. 4.5.1, B-D). It was shown that cytoplasmic aggregates occurred in 75% of observed UASdcryAB-GFP individuals and, at the mean time, in all visualised larvae when dCryAB-GFP aggregates were present, they contained also vimentin-like protein (Fig. 4.5.1.E). confirm detected protein-protein interactions, То COimmunoprecipitation reaction was performed using dCryAB antibodies and isolated proteins with the size around 40, 70 and 170 kDa were visualised on nitrocellulose membrane using anti-vimentin antibody. The antibody detected two bands of about 70 and 72 kDa in the protein extract from third instar larval muscles. One of these bands, corresponding to 72 kDa, was immunoprecipitated by anti-dCryAB antibody. However, the major IP-detected 170 kDa band was not seen in Western blot with anti-vimentin. This suggests that IP reaction leads to a high enrichment in 170 kDa vimentin-like protein interacting with dCryAB and/or to a formation of a highly stable protein complex of such a size. Moreover, a low intensity 40 kDa band could be detected in the IP material. The lack of this band in western blot can be explained by the enrichment resulting from the IP reaction. Described interactions are related to the fact that dCryAB is probably necessary for correct formation of vimentin-like meshwork, which was described in the sections below.

4.6. dCryAB ensures structural integrity of somatic muscles by interacting with potential IF proteins

In vertebrates, intermediate filaments form a very well organised meshwork inside muscle cells, taking part in stabilisation of their intracellular components and in positioning of organelles (Shah et al., 2004). Desmin filaments are stabilised by crystallin (Goldfarb and Dalakas, 2009), therefore I hypothesised that dCryAB maintained the stability of vimentin-like filaments in Drosophila muscle cells. To determine whether dCryAB was involved in stabilisation of structural integrity of constituent elements of somatic muscles, by interacting with IF proteins, the structure of WT larval body wall muscle cells was compared with that of *dcryAB* knocked-down ones. Confocal projections of muscle fibres, stained for the vimentin-like protein, showed that in WT muscle cells the vimentin-like protein formed a regular meshwork anchored to the sarcolemma, surrounding sarcomeres at the level of Z-bands, extending from one Z-disc to the other and finally reaching the perinuclear area (Fig. 4.6.1, A). Under RNAi *dcryAB* conditions, the vimentin-like protein looses its proper arrangement, observed as a decreased attendance of filaments around myofibrils with a fuzzy pattern occurring also around nuclei (Fig. 4.6.1, B). This fuzzy pattern can be caused by disorganisation of the filamentous formation of the vimentin-like protein, as a result of the loss of function of dCryAB. Electron microscopy observations of immunogold reaction results confirmed that in WT muscles the vimentin-like protein was organised in tight filaments (Fig. 4.6.1, C), whereas vimentin-like filaments in *dcryAB* knockeddown muscles seemed to be misarranged, forming a loose meshwork (Fig. 4.6.1, D). Considering that in vertebrates desmin intermediate filaments are linked to myonuclei and mitochondria, being responsible for their positioning and function (Capetanaki, 2002; Maloyan et al., 2005; Shah et al., 2004), it was checked if the vimentin-like protein had the same properties in Drosophila larval muscles. As expected, the disorganisation of vimentin-like filaments caused by the absence of dCryAB in muscle cells, leads to disturbance in myonuclear positioning. In WT VL3 and VL4 muscles nuclei are disposed relatively regularly along muscle fibres (Fig. 4.6.1, E). Under RNAi *dcryAB* conditions nuclei were clearly displaced to one side of the muscle fibre (Fig. 4.6.1, F), suggesting a lack of force keeping them in the

proper position. Besides, electron microscopy showed that in muscles with *dcryAB* knocked-down, interfibrillar mitochondria associated with Z-discs were swollen, comparing to the WT mitochondria (Fig. 4.6.2, A-B). They also exhibited damaged cristae (Fig. 4.6.2, A-B), suggesting that they were no longer functional. To investigate this hypothesis, I used MitoTrackerRed to follow the mitochondria pattern. The detected signal of active mitochondria in the muscles of RNAi dcryAB line appeared to be significantly reduced, indicating an impaired respiratory function of mitochondria positioned around nuclei, as well as those in the Z-line area (Fig. 4.6.2, C-D). Additionally, between myofibrils, increased deposits of glycogen were observed, supporting the respiratory disturbance in the tested muscles of RNAi dcryAB line (Fig. 4.6.2, E-F). Moreover, observed pathological changes included also misaligned Z-discs, visualised in electron microscopy images (Fig. 4.6.2, E-F). All those morphological and biochemical abnormalities suggest that dCryAB plays an important role in maintaining a properly organised vimentinlike network, and in ensuring a normal position and function of investigated muscle components.

4.7. dCryAB participates in the putative intermediate filament meshwork formation

To verify whether dCryAB was involved in the assembly of the vimentin-like meshwork, RNAi *dcryAB* larvae were exposed to heat shock conditions to provoke increased expression of *dcryAB*. *Drosophila* larvae expressing RNAi against *dcryAB* have a smaller amount of intracellular dCryAB and are characterised by a fuzzy pattern of the vimentin-like protein (see sections 4.2. and 4.5.). After 2 h of recovery from 10 min heat shock at 37°C, the dCryAB protein level in *dcryAB*-RNAi flies, as well as in WT flies, increased significantly, compared to the normal conditions (Fig. 4.7.1, D). Western blot procedure also showed that anti-dCryAB antibodies recognised an additional protein, which might correspond to another sHsp protein induced by the heat shock and not expressed in the larva in normal conditions (Fig. 4.7.1, D). Muscle immunostaining also showed an increased level of dCryAB in RNAi-*dcryAB* larvae, compared to the normal conditions (Fig. 4.7.1, A and 4.2.1, H). It was observed that in muscle cells dCryAB was restored in

sarcomeric localisation and accumulated in the cytoplasm with the vimentin-like protein. In the mean time, a recovery of the vimentin-like sharp pattern in Z-lines and in the perinuclear area was registered (Fig. 4.7.1, B-C), highlighting that dCryAB is required for the proper organisation of intermediate filament meshwork in muscle cells.

4.8. Mutated dCryAB^{R120G} mimics effects of mutations in human αBcrystallin leading to desmin-related myopathy.

Desmin-related myopathy is caused by the missense mutation R120G in α Bcrystallin. It results in intracellular aggregations of type III intermediate filaments, such as desmin and vimentin, accompanied by *aB*-crystallin. Formation of inclusion bodies in this disorder is due to misfolding of the mutated αB crystallin^{R120G} protein (Simon et al. 2007; Zobel et al. 2003). Comparison of amino acid alignment of human α B-crystallin and dCryAB shows conservation of arginine in codon 120 (Fig. 4.8.1, A). To check if the *dcryAB* R120G mutation could cause the same pathological phenotypes, a fly line expressing specifically *dcryAB*^{R120G} in its muscles was developed. The required mutation was achieved by site-directed mutagenesis where adenine from codon 124, adequate to the codon 120 in human, was replaced by guanine, resulting in exchanging arginine for glycine in the amino acid sequence of the protein (Fig. 4.8.1, B). DNA sequencing confirming the presence of desirable mutation in *dcryAB* gene was performed by GATC Biotech. It was visualised in confocal images that dCryAB^{R120G}-GFP occurred in the sarcomeres but its distribution was not as regular as that of the normal form of the protein. The mutated protein was present in some sarcomeres but lacking in sarcomeres of some muscle parts (Fig. 4.8.2, A). In the sarcomeres devoid of dCryAB^{R120G}-GFP, actin filaments were not assembled in Z-lines and seemed to not be organised in any particular order (Fig. 4.8.2, B, C). Moreover, dCryAB^{R120G}-GFP was localised ectopically in sarcomeres, meaning that dCryAB^{R120G}-GFP protein did not occur in Z-lines of some sarcomeres, being present only in the middle of the Mlines, whereas in other sarcomeres dCryAB^{R120G}-GFP appeared in Z-lines and in the edges of I-bands (Fig. 4.8.2, D, E). A Z-line shift in sarcomeres was also observed (Fig. 4.8.2, E). Ultrathin sections of larval muscle observed in TEM (Fig. 4.8.2, F)

showed misaligned and shifted Z-line indicating disturbance in its organisation. Elongated mitochondria with reduced cristae and glycogen deposits were also observed between myofibrils. In muscle fibres dCryAB^{R120G}-GFP may also form aggregates, which do not incorporate actin filaments (Fig. 4.8.3, A, B). Moreover, smaller nuclei were observed in these muscles, apart from normal-sized ones (Fig. 4.8.3, B). Compared to the control (Fig. 4.8.3, C), in a third instar larva, expressing *dcryAB*^{R120G}, a loss of proper localisation of the vimentin-like protein was observed. The vimentin-like protein showed a fuzzy sarcomeric pattern and irregular disposal inside muscle cells, accumulating among others around nuclei (Fig. 4.8.3, D, E). Moreover, dCryAB^{R120G} and the vimentin-like protein commonly form intrasarcoplasmic aggregates which accumulate together around nuclei and can even localise inside of them, which is better visualised on three-dimensional modelling images (Fig. 4.8.3, F). Muscles expressing the mutated form of dCryAB showed alterations in the shape and arrangement of nuclei. In these larval muscles, nuclei were not arranged regularly but were located randomly or/and were compacted to each other. They seemed to be smaller than nuclei of control muscles with irregular shape and varying size. 85% of tested individuals possessed delocalised dCryAB and the vimentin-like protein, always occurring together (Fig. 4.8.3, G). At the same time, 45% of larvae had deformed and displaced nuclei, which was always combined with disarrangement of the vimentin-like protein (Fig. 4.8.3, G). These results suggest that dCryAB^{R120G} does not localise like the wild type form of the protein and its sarcomeric localisation is required for normal localisation of actin filaments. Moreover, dCryAB^{R120G} and the vimentin-like protein strongly interact with each other, provoking loss of function of both proteins and muscle defects, which is similar to observations in muscles of DRM patients.

4.9. Overexpression of *dcryAB*^{R120G} leads to formation of morphologically altered muscles

Considering that the WT form of dCryAB participated in muscle formation and its attenuation led to formation of impaired muscle fibres, it was investigated if mutation R120G in dCryAB protein could also cause similar changes in larval
muscles. Thus, several muscle parameters were measured in larvae with musclespecific overexpression of *dcryAB*^{R120G}. Since in the experiments dCryAB^{R120G} was coupled with the GFP protein, in addition to the WT condition, the *Drosophila* line overexpressing the WT form of dCryAB also fused with GFP, was used as the second control for tests investigating its effect on muscle development. Measurements of three distinct muscles, VL3, VL4 and SBM, were taken. Larval muscles containing the mutated form of the dCryAB protein were significantly shorter (VL3: 25%; VL4: 24%; SBM: 4%; Fig. 4.9.1, A) and had an altered diameter (thinner: VL3: 36%; VL4: 29%; and thicker: SBM: 27%; Fig. 4.9.1, B), compared to muscles overexpressing dCryAB-GFP. The number of sarcomeres inside the muscle fibres was reduced (VL3: 22%; VL4: 21%; SBM: 0%; Fig. 4.9.1, C), with statistically insignificantly reduced length (VL3: 9%; VL4: 9%; SBM: 0%; Fig. 4.9.1, D). The differences in the measured morphological parameters of the muscle confirmed that the native dCryAB protein was necessary for the proper muscle development and for the sarcomere assembly. Moreover, muscles of the *dcryAB*^{R120G}-*GFP* line displayed a smaller number of nuclei (VL3: 19%; VL4: 20%; SBM: 20 and 10%; Fig. 4.9.1, E), indicating a reduced number of fusion events, in which dCryAB may be directly or indirectly involved.

4.10. Overexpression of *dcryAB*^{R120G} leads to impaired function of larval muscles and affects life span

Three behavioural assays were carried out in order to ascertain if the described morphological alterations affected locomotive abilities of the larvae: righting assay, journey test and motility test (for description of the tests see section 4.3). In the righting assay larvae with muscle-specific overexpression of *dcryAB*^{R120G}-*GFP* needed over four times more time to revert their body, comparing to muscles overexpressing the WT form of dCryAB fused with GFP (Fig. 4.10.1, A). In the journey test, UAS-*dcryAB*^{R120G} larvae were crawling significantly slower and took almost four times more time to go through the appointed, 5 cm distance (Fig. 4.10.1, B). In the motility test UAS-*dcryAB*^{R120G} larvae executed over 50% less peristaltic movements, comparing to the control (Fig. 4.10.1, C). The contraction disturbance of muscles in the tested fly line was confirmed by the values of the

contractility index. The muscles of the UAS-*dcryAB*^{*R120G*} individuals had a significantly lower contraction ability (VL3: 3.1; VL4: 2.3; SBM: 1.1 times lower, respectively), which explains their lower performance in behavioral assays, compared to the control (Fig. 4.10.1, D). Altogether, results of behavioral assays and contractility test indicate that the muscle-specific overexpression of *dcryAB*^{*r120G*} affects muscle contraction and induces motility defects.

The presence of *dcryAB*^{r120G} affected also the *Drosophila* survival and life span. The performed viability tests revealed that UAS-*dcryAB*^{R120G} flies showed a markedly higher mortality rate compared to the control at every stage of development, namely, embryo (by 29% higher), larva (by 31% higher) and pupa (by 29% higher) (Fig. 4.10.1, E). The life span of the surviving adult *dcryAB*-RNAi flies was also significantly shorter (up to two weeks), compared to the control flies. This indicates that muscle aggregates of the mutated form of dCryAB, together with the vimentin-like protein, may induce cell toxicity, which in turn affects life span.

4.11. Human α B-crystallin inserted to the *Drosophila* genome mimics dCryAB localisation and interaction with vimentin-like protein in larval muscle cells

To test whether human α B-crystallin (CryAB) could have the same function in *Drosophila* muscle cells as dCryAB, a fly line overexpressing human α Bcrystallin, coupled with GFP, specifically in muscles was generated. In the third instar larval muscle cells both proteins, human and *Drosophila* CryAB, occurred together in the Z-line, in the perinuclear area. α B-crystallin was present in the Mline and inside the nucleus but also in all the muscle cytoplasm (Fig. 4.11.1, A-A', C-C'). Figures 4.11.1, B-B' and C-C' show that α B-crystallin attached to the vimentinlike meshwork in Z-lines and was also present together with the vimentin-like protein inside the nucleus. The observed distribution of these three proteins suggests that dCryAB and α B-crystallin share similar subcellular localisation and thus, potentially similar functions in muscle cells, stabilising the intermediate filament network. However, further research is needed to confirm this hypothesis.

5. Discussion

Already in 1990 Haass et al. (1990) found that sHsps were present in unstressed and yet transcriptionally inactive early embryos, indicating the importance of sHsps from the very beginning of embryonic life. However, it was also shown that upon cellularisation the intensity of the sHsp27, sHsp26 and sHsp23 immuno-signal was strongly reduced and restricted to the embryo's cortex. In the next stages of embryonic development the sHsps expression increased, being again detectable in the cytoplasm of the embryonic cells, continuing to increase in the elongating germ band. Nevertheless, in fully developed embryos sHsps were strictly confined to the CNS (Haass et al., 1990). These findings directed the attention to understand the role of sHsps in human development, as well as in development of other organisms.

The main role of Hsps is to act as a chaperone by a temporary association to other polypeptides. Through this transient binding, Hsps can modulate cellular functions, for instance limiting activation of the apoptotic cascade, cell proliferation, antigen presentation or cytoskeleton organisation by influencing the ultimate function of their partners. Hsps become developmentally important already during gametogenesis, protecting male and female gametes. Dix et al. (1996) showed that male mice with disrupted Hsp70 expression lacked postmeiotic spermatids, mature sperm and were infertile, suggesting its protective role during the prophase of the first meiotic division. Another example of the Hsp importance during spermatogenesis is the role of Hsp27 in cytoskeleton dynamics of Sertoli cells which surround germ cells (Welsh et al., 1996). Here, Hsp27 colocalises with F-actin bundles helping to maintain the germ cells migration to the tubule lumen. The reported presence of Hsp27 in ovaries during normal development suggests its role also in oogenesis (Joanisse et al., 1998; Marin and Tanguay, 1996). A wide variety of studies demonstrated the Hsps expression during organogenesis. For example, Hsp26 is expressed during Drosophila development in the epithelium, proventriculus, larval brain and ventral ganglion (Marin and Tanguay, 1996), whereas Hsp90, Hsp70, Hsp25 and αB-crystallin are required for formation of mouse cartilage and bone tissues (Loones and Morange, 1998). Even up to seven sHsps (Hsp27, α B-crystallin, Hsp20, Hspb2, Hspb3, cvHsp and Hspb8) are expressed at relatively high levels during development and differentiation in mammalian heart and skeletal muscles (Davidson et al., 2002), implying their role in muscle formation. It is not known whether all these genes diverged from a common ancestor with developmental functions, however phylogenetic analysis performed in our laboratory indicates that sHsps, Hsp27, Hspb8 and α B-crystallin, involved in muscle development, have indeed a common ancestor (Fig. 5.1-1.). In human cardiac and skeletal muscles α B-crystallin, Hspb2 and Hspb3 are induced during the initial phase of skeletal muscle differentiation, controlled by MyoD, suggesting their muscle-specific function in development (Sugiyama, 2000). It was established that Hsps function as developmental buffers in different manners, most likely by preventing apoptosis or/and stabilising cytoskeleton. Nevertheless, their expression patterns vary among particular sHsps and among species.



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5.1. *dcryAB* gene plays conserved myogenic functions and dCryAB protein cellular localisation is reminiscent of its vertebrate counterpart

The Drosophila sHsp genes are clustered within the 67B region on the left arm of the third chromosome (Corces et al., 1980) except *dcrvAB* (*l(2)efl*) located on the right arm of the second chromosome at locus 59F4 (Kurzik-Dumke and Lohmann, 1995). Kurzik-Dumke and Lohmann (1995) found that *dcryAB* (*l*(*2*)*ef*) was expressed during Drosophila embryogenesis, and also during larval stages, reaching its maximum expression during the third larval instar, whereas its role remained unknown. This prompted me to try to define its function in Drosophila. It was confirmed in our laboratory that dCryAB was expressed specifically in unstressed muscles of Drosophila embryos (data not shown) as well as in larvae. Immunocytochemical analysis showed that the dCryAB protein was abundantly expressed in all the larval body wall muscles, accumulating in the perinuclear area and displaying a striated pattern at the level of M-lines and extremities of Z-lines, which was also confirmed by immunogold and iso-surface modelling analyses. The mammalian counterpart of dCryAB, α B-crystallin is expressed, among others, in unstressed pig, mouse and human lenses, heart and skeletal muscles (Brady et al., 2001; Goldfarb and Dalakas, 2009; Golenhofen et al., 1999). In eye lenses, αBcrystallin helps to maintain their transparency, whereas in muscles it acts as chaperone for desmin, vimentin and actin, helping to maintain cytoskeletal integrity. During pig (Tallot et al., 2003), rat and human (Klemenz et al., 1993) development, constant levels of α B-crystallin were observed in heart muscles. In pig (Tallot et al., 2003) and rat (Inaguma et al., 1993) skeletal muscles, αB crystallin and Hsp27 levels were found to increase from foetal to adult stage, suggesting their essential role in muscle physiology. Moreover, Ito et al. (2001) showed that during differentiation of mouse C2C12 cells the level of αB-crystallin was elevated 10-fold and α B-crystallin played a crucial role in preventing apoptotic cell death induced during the differentiation process. It seems that the role of two closely related proteins, α B-crystallin and Hsp27, is the most similar to that of dCryAB, whereas it is not completely certain if their role is displayed due to involvement in the modulation of cytoskeleton or inhibition of apoptosis. Because α B-crystallin and dCryAB are to a high extent homologous and both are localised in

Z-lines and around nuclei (Djabali et al., 1997), one could expect that they play similar roles in muscle cells.

As at the embryonic stages the body plan is formed and during the pupal stage the key metamorphosis steps occur, the higher hsps expression in embryo, larva and early pupae coincides with major developmental events, including muscle formation. To determine if dCryAB stabilised the muscle cell homeostasis buffering developmental variations, I applied RNAi-mediated muscle-specific dcryAB gene attenuation and observed muscle morphology of the third instar larvae. Obtained results show that *dcryAB* is expressed specifically in muscles and the dCryAB protein is localised around nuclei, in Z-lines and M-lines, suggesting its role in stabilisation of the structural integrity of muscle fibres. Thus, it was not surprising to observe that muscles with a attenuation of dCryAB during development displayed various morphological defects. One of them was a disturbance in the actin cytoskeleton organisation, observed in confocal microscope as a fuzzy pattern of phalloidin-stained sarcomeres, muscle splitting which in some cases led to altered muscle attachment or even to the loss of the affected muscle. DCryAB, like other sHsps, including α B-crystallin, has an actinbinding domain in its α -crystallin fragment. Association of α B-crystallin with actin filaments and its role in preventing formation of actin aggregates was already established by Bennardini et al. (1992). Mounier and Arrigo (2002) proposed that direct actin-sHsp interaction occurred to inhibit actin polymerization and to participate in the regulation of actin filament dynamics (Bennardini et al., 1992; Mounier and Arrigo, 2002). They suggested that protection of the actin cytoskeleton would be a result of an F-actin-sHsp interaction in which microfilaments would be coated by small oligomers of phosphorylated sHsps. According to this study, some sHsps would behave with the actin cytoskeleton as actin-binding proteins. Here, sHsps would be capable of either capping a microfilament or stabilizing and protecting the microfilament when organized in small, phosphorylated oligomers. Therefore, deficiency of sHsps committed in protection of actin filaments can cause their destabilisation and affect cellular processes in which they are involved, which is also true for dCryAB knockdown, leading to muscle morphology defects caused by irregular distribution of F-actin.

Assuming that each larval muscle was characterised by specific properties including size, number of sarcomeres and number of nuclei (Bate, 1990b), several muscle parameters were measured in larvae with muscle-targeted *dcryAB* knockdown. Confocal observations of muscle morphology of the third instar larva with a deficiency of dCryAB during development allowed me to notice a significant reduction of mentioned muscle parameters. The smaller muscle size is not surprising, knowing that many members of the Hsps family, like Hsp90, Hsp70, Hsp27 or α B-crystallin are known to play a vital role in the normal cell growth and development (Hartl, 1996). Andley et al. (1996) observed that α A-crystallin knockout epithelial cells of mouse lens were characterised by decreased growth. This effect could be due to a direct interaction of α A-crystallin with cell cycle regulators or to functional absence of α B-crystallin, which normally occurs in a complex with α A-crystallin. Recent results of Middleton et al. (2013) showed that in zebrafish morphant embryos expressing reduced levels of Hsp27 the size of craniofacial muscles was smaller. They suggested that Hsp27 was required for optimal growth of these muscles by influencing expression or/and assembly of cytoskeletal proteins forming myofibres (Middleton and Shelden, 2013). Considering that Hsp27 and dCryAB have a common ancestor both results seem to be consistent, emphasising the role of dCryAB in the maintenance of cytoskeletal network. Moreover, muscles in third instar larvae of Drosophila, like vertebrate striate muscles, grow by addition of sarcomere units (Rui et al., 2010). Thus, I counted sarcomeres in three different muscle fibres (VL3, VL4, SBM), to check if the smaller muscle size was due to a lower number of sarcomeres. Indeed, in all cases analysed the number of sarcomeres was slightly reduced, whereas, except the fuzzy pattern areas, their size was not affected. These results allow concluding that dCryAB plays a role in larval muscle growth, which occurs by the addition of sarcomere units. Observed lower muscle size can also be compatible with a lower number of sarcomeres. A possible hypothesis explaining this aberration is impaired myoblast fusion, which is formation of myotubes of multinucleated skeletal muscle that is essential for formation of contractile skeletal muscle tissue. In the absence of fusion, FCs differentiate in tiny and mononucleate muscles at appropriate locations and express their normal complement of genes (Rushton et al., 1995). The process of cell-cell fusion requires several distinct cellular

behaviours. Initially, FCs or myotubes and FCMs have to recognise and adhere to each other. This results in a series of cellular events that are necessary to bring the cell membranes of the two cells in close proximity to one another. Subsequently, pores are formed between the plasma membranes, and their expansion leads to fusion of the two myoblasts (Schejter and Baylies, 2010). Actin filaments participate actively in this process by forming cortical actin walls in skeletal muscle myoblast cultures (Duan and Gallagher, 2009). These results demonstrated that described actin walls underwent a dramatic reorganisation prior to "vesicle paring" and fusion pore formation. According to these findings, actin filament disorganisation can lead to disturbance of myoblast fusion. Since the smaller number of nuclei in muscles of the RNAi-dcryAB third instar larva could be a consequence of disturbed myoblast fusion, and since dCryAB may be involved in stabilisation and reorganisation of actin filaments, the smaller number of nuclei in the observed muscles and the related smaller muscle size and lower number of sarcomeres may be consequences of impaired microfilament organisation resulting from dCryAB deficiency. To verify this hypothesis it would be advisable to check if dCryAB interacts with actin filaments in cortical actin walls during early muscle differentiation and to construct flies with inactive actin binding domain inside the dCryAB rod domain and investigate if interactions between dCryAB and actin would be affected (work in progress).

Since *Drosophila* third instar larvae have fully developed locomotor behavior (Mudher et al., 2004), it was possible to perform three different behavioural assays on individuals lacking *dcryAB* expression, to assess if described muscle defects affected their motility. Obtained results revealed severe motility problems and a lower contractility index, indicating a reduced ability to perform muscle contraction. The easiest way to record motility defects is observation of unicellular organism and it has been shown by Montagna et al. (2012) that *hsp20(-) Plasmodium* sporozoites display aberrant cell motility. Observed changes in their speed are due to impaired microfilament regulation caused by the lack of Hsp20 (Montagna et al., 2012). Thus, in *Drosophila* improper muscle contraction causing impaired motility may also be provoked by dCryAB deficiency-dependent actin filament disorganisation, observed as sarcomere fuzzy pattern. On the other hand, overexpression of *dcryAB* resulted in an increased muscle mass and increased number of nuclei. Thus, it would be interesting to see if crossing flies overexpressing *dcryAB* with RNAi-*dcryAB* flies could restore the proper phenotype in terms of correct muscle size and number of nuclei, as well as the appropriate localisation of the entire set of sarcomeric proteins, allowing normal motility. Unfortunately, construction of desirable fly strains failed, and the experiment has to be repeated.

Despite of the reported importance of the sHsps in the development, it seems that their deficiency is not always lethal. Depletion of one sHsp is usually not noxious, due to a certain level of redundancy between the functions of each small heat shock protein (Morrow and Tanguay, 2012). According to many authors (Colinet et al., 2010; Hao et al., 2007; Michaud and Tanguay, 2003; Morrow et al., 2004), some of the sHsps do not play any significant role in Drosophila development under laboratory conditions. Their role is rather preventive, as flies depleted of Hsp22, Hsp23 or Hsp27 were viable but had a reduced resistance to certain types of stress and a reduced longevity. It was thus interesting to check if the proposed name of the gene: lethal (2) essential for life (Kurzik-Dumke and Lohmann, 1995), correctly suggested that its normal expression was indispensable in *Drosophila* development. Because a complete knockout of *l*(*2*)*efl* gene is not yet available and the work to create it using TALENS approach is still in progress in our laboratory, to verify this hypothesis I created conditions of attenuated *l*(2)*e*fl expression in muscles during development by muscle-specific RNAi expression against the gene product. In these circumstances I was able to obtain fertile adult flies. However, their life span was affected and I observed a higher mortality rate at every stage of development. This is consistent with results of Brady et al. (2001) who used knockout approach to show that α B-crystallin and Hspb2 were not essential for viability or reproduction of their mouse model but their disturbance could lead to apparent degeneration of some skeletal muscles. Therefore I assume that *l(2)efl* expression is also not particularly "essential for life" but this has to be confirmed by observations of the fly null mutant. Nevertheless, the *l(2)efl* has an knockdown influence on the fly longevity and muscle morphology. Because I assume that the L(2)efl protein has a similar function to the human α B-crystallin (see below, section 5.2.), I propose to call the protein drosophila- α B-crystallin (dCryAB) and the gene: *dcryAB*.

In summary, I conclude that observed sarcomere and full muscle morphology defects, like smaller muscle size, lower number of sarcomeres and nuclei, as well as larval motility defects may have the same origin, namely impaired microfilament organisation triggered by deficiency of dCryAB which is required for the proper muscle development, probably as a cytoskeleton stabiliser.

5.2. dCryAB co-localises and interacts with *Drosophila* putative intermediate filament proteins detected by anti-vimentin antibody and *dcryAB* attenuation leads to disruption of vimentin-like meshwork

The cytoskeleton in striated muscle cells is composed of a highly complex scaffold of microfilaments, microtubules and intermediate filaments. Thanks to this cytoskeletal network, striated muscles are able to maintain their sophisticated sarcomeric organisation, as well as integration between contractile apparatus, nucleus and other organelles (Herrmann et al., 2007). Intermediate filaments are the key components maintaining this precise organisation by interacting with many cellular structures (Capetanaki et al., 2007). In humans at least 65 genes, which are expressed in a tissue-specific manner, encode intermediate filament proteins (Herrmann et al., 2007). In vertebrate mature muscle cells the IF cytoskeleton is predominantly composed of desmin, muscle-specific type III IF proteins, whereas in myoblasts the main type III protein is vimentin (Capetanaki et al., 2007). A continuous cytoskeletal network maintains its integrity by interacting with small heat shock proteins, which supports the idea that sHsps may play a crucial role in maintaining the stability of cell structures.

One of the main physiological functions of sHsps is their ability to regulate the cytoskeleton dynamics (Wettstein et al., 2012). All sHsps share a similar structural pattern: a rod α -crystallin domain flanked by a variable hydrophobic Nterminal region and a C-terminal extension, where their amino acid sequence, in the corresponding regions, is similar to α -crystallin in over 40% of their length. Houck et al. (2011) described multiple sites in α B-crystallin, which modulate its interactions with desmin filaments. They demonstrated that substitution of those three sequences in α B-crystallin, situated in β 3-strand, β 8-strand and C-terminus (73DRFSVNLDVKHFS_{85, 131}LTITSSLS₁₃₈ and 155PERTIPITREE₁₆₅, respectively), could alter the interactions of α B-crystallin with desmin. It suggests that described sequences contribute to the interaction of α B-crystallin with desmin filaments (Houck et al., 2011a). Similarly, dCryAB possesses 77EKFEVILDVQQFS₈₉ motif, which corresponds to the intermediate filament interaction domain in β 3-strand of human α B-crystallin, α A-crystallin but also to *C. elegans* Hsp12.2 (Ghosh et al., 2006). Assuming that dCryAB contains an intermediate filament interaction domain, it could be well expected that the *Drosophila* cell should contain a protein partner to interact with this motif.

Except nuclear lamins, no gene encoding cytoplasmic filaments has been reported in *Drosophila* so far (Schulze et al. 2009). However, in 1981 Falkner et al. and subsequently Walter and Biessmann (1984) described two proteins (46 and 40 kDa) that appeared to form a very fine meshwork inside tissue culture cells and salivary gland cells and shared an epitope with the vertebrate intermediate filament protein vimentin (56 kDa) (Walter and Biessmann, 1984). These proteins contained antigenic determinants also found in vimentin and desmin of baby hamster kidney cells and authors suggested that the 46 kDa-sized protein was an invertebrate homologue of vimentin (Falkner et al., 1981; Walter and Biessmann, 1984). Knowing that α B-crystallin shares a high homology to dCryAB and interacts with IFs, stabilising them, I succeeded in finding putative IFs in Drosophila muscle cells, which could be a target for dCryAB. Using antibody directed to the mouse vimentin, I stained and visualised in confocal microscope a very well organised meshwork inside muscle cells, resembling the organisation of vertebrate desmin filaments. Since it was visualised with anti-vimentin antibodies, I called it vimentin-like protein. On confocal longitudinal sections of third instar larval muscle fibres, the vimentin-like protein was situated around nuclei, co-localised with actin and dCryAB in Z-lines and was associated with the sarcolemma, which was observed as a dotty pattern above the sarcomeric part of the fibre. Iso-surface modelling showed that in sarcomeres, vimentin-like protein is situated particularly on the external part of the Z-line, and immunogold assays confirmed its localisation in Z-lines and around nuclei. This suggests that the vimentin-like protein may form filaments spread between the sarcolemma and nuclei, wrapping myofibrils at the height of the Z-lines, which is consistent with the distribution of desmin filaments in vertebrate muscle cells (Goldfarb and Dalakas, 2009).

Moreover, confocal projections confirmed by electron microscopy showed that the vimentin-like protein entered nuclei. It is believed that cytoplasmic IFs play a role in coordinating mechanical forces in embryonic development, growth and maturation of tissues. Vimentin is expressed in the precursor cells and in myoblasts becoming undetectable in adult skeletal muscles. Moreover, desmin and vimentin filaments enter nuclei, possibly affecting gene activity (Capetanaki et al., 2007; Goldfarb and Dalakas, 2009; Herrmann et al., 2007). Therefore, it is possible that the vimentin-like protein in *Drosophila* can also have mechanical influence on gene activity apart from its structural role, but this function has to be verified. Nevertheless, the identical position of dCryAB and the vimentin-like protein on the extremities of Z-lines and around nuclei, as well as the presence of intermediate filament domain in the dCryAB sequence, may indicate that dCryAB interacts with the vimentin-like protein, stabilising the formed network, like α B-crystallin does with desmin and vimentin filaments (Goldfarb and Dalakas, 2009).

To verify if dCryAB interacts with the vimentin-like protein I observed third instar larval muscles overexpressing dCryAB fused with GFP protein. I visualised desirable proteins by appropriate antibodies in confocal microscope. I registered a normal distribution of dCryAB-GFP in sarcomeres but a surplus of dCryAB-GFP was clearly accumulated with the vimentin-like protein in the cytoplasm, especially around nuclei. This suggested that both proteins formed tight complexes, which was confirmed by the coIP assays. In Western blot immunoprecipitation I detected proteins with the size around 40kDa, 72kDa and 170kDa. I assume that the one with small molecular mass is the vimentin-like protein, which I detect in muscle cells. Moreover, this protein may correspond to the protein described by Falkner et al. (1981), which formed filamentous meshwork inside the *Drosophila* cells and shared the epitope with vertebrate intermediate filament proteins. Considering that the IF proteins form oligomers (Cooper, 2000) and interact with sHsps (Goldfarb and Dalakas, 2009), I suggest that detected higher mass proteins are simply two different and highly stable protein complexes formed by the vimentin-like protein subunits, possibly containing also dCryAB. Already in 1979, Kibbelaar et al. suggested possible interactions between calf eye lens actin, vimentin, and α B-crystallin (Kibbelaar et al., 1979). Bennardini et al. (1992) investigated the role of α B-crystallin in rat cardiomyocytes and found that it was bound to actin and desmin filaments in Zlines. Moreover, these interactions became even stronger during an ischemic episode, thus authors concluded that αB -crystallin could stabilise the proper conformation of various filaments protecting them from rupture by mechanical damage and from degradation by oxidative or proteolytic processes, and thus preventing aggregation. Djabali et al. (1997), studying interactions between αB crystallin and IFs, showed by co-sedimentation assay that mouse and bovine α Bcrystallin interacts with peripherin and vimentin in the temperature dependent manner, where interactions between the tested proteins were increasing with the temperature. They also showed that in cultured fibroblasts, α B-crystallin was expressed constitutively and distributed throughout the cell, with no specific subcellular localisation and did not overlap the vimentin network extending from the nuclear surface to the plasma membrane in normal growth conditions. Nevertheless, when cells were submitted to different stress conditions, αB crystallin appeared to be distributed along tracks coinciding with vimentin filaments (Djabali et al., 1997). Inconsistent with these results but consistent with mine was the report of Perng et al. (1999) who showed that Hsp27 and α Bcrystallin in cultured cells interacted with the IF network of both stressed and unstressed cells. They showed that Hsp27 associated with the full range of filament arrangements found in cells, from bundles to the very fine filament distributions, and this association was not restricted to any particular intermediate filament type, because it bound to type I and II keratins, as well as type III IFs, including vimentin and GFAP. They also found that these two sHsps formed mixed soluble complexes, suggesting that they shared at least some physiological targets and possible functions (Perng et al., 1999). All these results imply that sHsps, by interacting with IFs, help to maintain their homeostasis.

To ascertain if dCryAB was involved in maintaining structural integrity of somatic muscles by interacting with the vimentin-like protein, I checked if there were any morphological changes in muscle fibres, similar to those observed in vertebrates, when interactions between Hsps and IFs were impaired. To obtain desirable conditions I applied muscle-specific attenuation of *dcryAB* expression and observed muscle morphology of third instar larvae. Immunocytochemical reaction visualised in confocal microscope, and immunogold reaction visualised in

electron microscope revealed an altered, fuzzy and amorphous arrangement of the vimentin-like network in sarcomeres and around nuclei. Perng et al. (1999) showed that sHsps associated not only with filaments but also with the soluble fraction of intermediate filament proteins. This might help to maintain the intermediate filament protein in an assembly competent state. Moreover, IFs formed a gel in the absence of sHsps, whereas inclusion of α B-crystallin or Hsp27 prevented the gel formation but not the filament assembly. Other studies showed that implication of desmin to the human adrenal carcinoma cell line, which normally does not express any cytoplasmic IFs, led to formation of cytoplasmic aggregates with some filaments and short rod-like structures in these cells, whereas transfection of these cells with desmin and wild type α B-crystallin significantly decreased formation of cellular aggregates (Perng et al., 2004). These results suggest that *de novo* formation of the IF network involves sHsps which play a role in its further management. Thus, I assume that in wild type Drosophila muscle cells the vimentin-like meshwork is stabilised by dCryAB and the protein is involved in formation of the vimentin-like meshwork, whereas these functions are impaired by the dCryAB deficiency in cells.

Other observed morphological changes in muscle cells are related to disorganisation of cellular organelles and mechanical integration of the cell. It is well known that cytoplasmic IFs associate with the nuclear envelope and participate in shaping and positioning of nuclei. In 1994 Sarria et al. showed that human vimentin-null cultured cells or cells expressing mutant vimentin led in some cases to nuclear invaginations (Sarria et al., 1994). Shah et al. (2004) showed that in desmin-null mice nuclear shapes, as well as links to sarcomeres, were altered, indicating the role of desmin in organelles organisation (Shah et al. 2004). Also epidermis of the keratin-10-null mice was characterised by unordered spacing of enlarged nuclei (Reichelt and Magin, 2002), indicating the role of different kinds of IFs in the organelles orchestration. Gilbert et al. (2012) showed that cytoskeleton organisation affected by depletion of Hsp27 in HeLa cells also led to grave nucleus abnormalities, namely loosing the spherical shape (Gibert et al., 2012). Similarly, in my experiments, disrupting the vimentin-like network by attenuation of *dcryAB* expression led to altered positioning of nuclei, observed in confocal microscope as their irregular arrangement, being displaced to one side of

the cell. This provides evidence for the effect of the vimentin-like network on the shape and position of the nuclei. Desmin IFs also take part in stabilisation of mitochondrial morphology, their distribution in areas of high-energy demand and in their respiratory function via influencing mitochondrial membrane behaviour in muscles (Capetanaki et al., 2007; Rappaport et al., 1998). My results show that disruption of the vimentin-like network led to similar effects. Namely, mitochondrial morphology was damaged which was observed in electron microscope as swollen mitochondria with no cristae. This suggested that damaged mitochondria could be functionally impaired, which was then confirmed by Mitotracker reaction showing the presence of large numbers of respiratory inactive mitochondria in the intermyofibrilar area. Milner et al. (2000) have demonstrated that lack of desmin in cardiac and skeletal muscles led to mitochondrial swelling and degeneration of the mitochondrial matrix, as well as significant respiration impairment. The proper mitochondria distribution, number, morphology, and function was lost indicating that desmin IFs play a significant role in maintaining mitochondrial homeostasis (Milner et al., 2000). Kostareva et al. (2008) confirmed these findings by similar observations of mouse skeletal and cardiac muscles expressing desmin carrying L345P mutation, which led to desmin malformations characteristic for myopathies. Using electron microscopy they showed striking changes in mitochondria, including reduced density of cristae and significant vacuolization of the mitochondrial matrix, resulting in formation of circular membranous structures and giant mitochondria. Moreover, the motility of the tested mice was disturbed (Kostareva et al., 2008), which is consistent with results of behavioral assays of Drosophila larvae with attenuated dcryAB expression. Hnia et al. (2011) established that not only ablation of desmin filaments or its mutation leads to the collapse of organelles organisation but also absence of desmin-binding protein myotubularin can cause similar effects. Knockout or knockdown of myotubularin expression led to disruption of the myotubularin-desmin complex promoting desmin aggregation and in consequence, to abnormal mitochondrial positioning, morphology and dynamics (Hnia et al., 2011). The elevated glycogen deposits in muscle cells I observed in electron microscope might be related to the dysfunction of mitochondria. The glycogen storage was observed in different pathological cases of patients with Becker

muscular dystrophy (Rose et al., 1993) or ocular myopathy with altered mitochondria (Scelsi et al., 1984). Thus, I assume that disruption of the vimentinlike meshwork can lead to glycogen storage, caused by inability to use it by dysfunctional mitochondria. Moreover, I confirmed in electron microscope disarrangement of sarcomeres described above and observed as a fuzzy pattern of actin filaments and irregular Z-lines. This misalignment was most probably due to the lack of dCryAB causing disturbance of cytoskeleton organisation, either actin filaments (see above) or IF network. It is well known that IFs, especially desmin filaments, are responsible for supporting of myofibrils at the level of Z-line (Goldfarb and Dalakas, 2009). Desmin mutations or absence, which lead to its dysfunction are not lethal but disturb the organisation of Z-discs and costameres, affecting the integrity of the cellular IF network (Goldfarb et al., 1998; O'Neill et al., 2002). In more advanced stages, fragmented desmin filaments aggregate to form insoluble deposits, which can lead to disruption of myofibrils, breaking connections between them and impairing their binding to cellular organelles, causing myopathy (Goldfarb and Dalakas, 2009). These findings suggest that in Drosophila muscle cells the vimentin-like protein plays a role of IF proteins, including the role of desmin filaments in organisation of cellular organelles and stabilisation of myofibrils. Therefore I assume that the described conserved motif interacts with this invertebrate homologue of vimentin, which plays the role of intermediate filament protein in Drosophila muscle cells and that dCryAB, by this domain, integrates the putative intermediate filament meshwork, stabilising it.

As mentioned above, under *dcryAB* RNAi conditions I observed a lower number of nuclei in muscle cells, suggesting a smaller number of fusion events during muscle formation. The decreased number of fusion events could be caused by disturbance of either microfilament or intermediate filament network. As desmin deficiency blocks myoblast fusion (Li et al.) the impaired formation of the vimentin-like network also may have an impact on disturbed fusion process. Cytoplasmic IFs are also believed to play a role in coordinating mechanical forces in embryonic development, growth and maturation of tissues. Vimentin is expressed in precursor cells and in myoblasts and becomes undetectable in adult skeletal muscles (Capetanaki et al., 2007; Goldfarb and Dalakas, 2009; Herrmann et al., 2007). It is thus very likely that dCryAB may have an influence on muscle growth and maturation not only through interactions with actin filaments but also through orchestration of putative IF network composed of the vimentin-like protein.

Assuming that sHsps not only stabilise the formed IF network but also play a role in its de novo formation (Perng et al., 1999), I checked if the primary misfolded vimentin-like network caused by dCryAB deficiency in muscle cells during development could be restored by restoration of dCryAB expression. As sHsps are very often expressed under stress conditions (Feder and Hofmann, 1999) and their expression is temperature-dependent (Djabali et al., 1997), to induce dCryAB expression I placed *dcryAB-RNAi* third instar larvae under heat shock conditions. Subsequently, after two hours of recovery, I observed an elevated level of dCryAB protein, which was visualised in muscle fibres on confocal sections. The protein was observed in sarcomeres and around nuclei and its increased expression was confirmed by the western blot assay. Nevertheless, the most important observation was the restoring of the vimentin-like meshwork sharp pattern in Zlines and around nuclei, probably due to formation of normal interactions between the vimentin-like protein and dCryAB, confirming that dCryAB was required for its proper formation. High overexpression of dCryAB caused by heat shock led to the deposition of the protein surplus in the cytoplasmic area around the nuclei. The deposited dCryAB occurred together with the vimentin-like protein, resembling the accumulations of these two proteins in UAS-dcryAB larvae, suggesting that dCryAB could bind to the vimentin-like protein even after the muscle development had been completed. This is consistent with previous results of Djabali et al. (1997), showing that *in vivo* interaction between vimentin and α B-crystallin was clearly detected when cells were submitted to different types of stress. Moreover, when cells were subjected to heat shock treatment, authors have observed a complete rearrangement of the vimentin network and α B-crystallin positioning at the same localisation as vimentin. The recovery of the stressed cells led to redistribution of the vimentin filaments, which slowly re-extended through the cytoplasmic space (Djabali et al., 1997). Perng et al. (2004) showed that transfection of desmin protein into mouse lens cells resulted in a pronounced tendency to form aggregates, whereas cotransfection of desmin together with αB crystallin significantly reduced this tendency. Thus, I conclude that overexpression

of dCryAB protein provoked by heat shock is helpful in the vimentin-like network restoration and stabilisation.

Altogether, obtained results allow me to conclude that the vimentin-like protein is a putative *Drosophila* intermediate filament protein, taking over functions of vertebrate type III intermediate filaments. Moreover, dCryAB is required for the proper formation of the vimentin-like meshwork, and impaired interactions between them do not cause the vimentin-like protein to aggregate but cause changes in muscle morphology, sarcomeric pattern, morphology and functioning of some muscle organelles. Therefore, the primary task now is to identify the vimentin-like protein using mass spectrometry approach (work in progress). It would also be advisable to investigate the effect of loss of function of the intermediate filament domain of dCryAB on the vimentin-like meshwork. To answer this question I constructed flies containing *dcryAB* gene with inactivated intermediate filament binding domain and now the effect of this mutation needs to be verified.

5.3. Drosophila is a putative model organism to study DRM

Drosophila melanogaster is a very well studied model organism for understanding molecular mechanisms of human diseases. Many discoveries in genetics were first developed in the fly and it was shown that a big variety of basic biological, physiological and neurological properties are conserved between *D. melanogaster* and mammals. The vast majority of genes involved in all aspects of *Drosophila* development were found to be essential also for normal mammalian development (Pandey and Nichols, 2011). Moreover, *D. melanogaster* was the first major complex organism having its genome sequenced (Adams, 2000), and nearly 75% of human disease-causing genes have functional homologues in *Drosophila* (Reiter et al., 2001). Even if the compared total identity of the fly and mammal protein sequence is usually approximately 40% between homologues at the nucleotide level of the conserved functional domains, it can rise up to 80 to 90% or even higher. Thus, the fruit fly can be considered as a multi-purpose model organism, with specific advantages to each developmental stage, where the embryo is often used in fundamental developmental studies, the larva frequently serves to study developmental and physiological processes as well as some aspects of behaviour. The adult fly is used to understand functioning of the large range of fully developed organs, having their equivalents in mammals (Pandey and Nichols, 2011). Thanks to the development of a very wide range of tools to perform different genetic manipulations, *Drosophila* became a very important model organism, used to understand mechanisms of various mammalian diseases (Afsari et al., 2014; Bellen et al., 2010; Niwa and Niwa, 2011; Picchio et al., 2013). Therefore, in the light of my results it seems possible to consider *Drosophila* as a putative model of desmin-related myopathy.

In the course of some human diseases the IF network does not assemble correctly, and anomalous protein aggregates are formed inside the cells. Normally, in these pathological cases α B-crystallin can reorganise such abnormal inclusion bodies into a normal filamentous network (Koyama and Goldman, 1999). However, some mutations in α B-crystallin can lead to the loss of this chaperone activity, and up to date fifteen mutations of α B-crystallin causing markedly different features were reported (Berry et al., 2001; Chen et al., 2009; Del Bigio et al., 2011; Devi et al., 2008; Forrest et al., 2011; Inagaki et al., 2006; Liu et al., 2006a; Liu et al., 2006b; Pilotto et al., 2006; Reilich et al., 2010; Sacconi et al., 2012; Safieh et al., 2009; Selcen and Engel, 2003; Vicart et al., 1998). The WT α B-crystallin forms dimers (Bagnéris et al., 2009), and some of its mutations such as R120G (Vicart et al., 1998) or D109H are claimed to affect dimerisation of α B-crystallin (Sacconi et al., 2012). These mutations lead to the loss of α B-crystallin chaperone activity and ultimately to pathological muscle defects. Interestingly, protein sequence alignment revealed that both these residues (R120 and D109) were conserved in dCryAB, thus it was interesting to check if these particular sites had similar functions in both proteins. Therefore, by site directed mutagenesis I generated a *Drosophila* strain carrying a mutation in one of the *dcryAB* residues corresponding to the αB -crystallin^{R120G} mutation. In muscle cells of third instar larvae of Drosophila I observed in confocal microscope an irregular localisation of dCryAB^{R120G}-GFP protein in sarcomeres. Namely, dCryAB^{R120G}-GFP did not occur in sarcomeres of some muscle parts, which was associated with accumulations of actin without perceptible sarcomeric organisation. Considering that α B-crystallin stabilises actin filaments (see above), it was not surprising that in muscle parts lacking dCryAB the actin filament pattern was severely affected. Nevertheless, observation of the relatively normal sarcomeric organisation of actin filaments in muscle parts containing dCryAB^{R120G}-GFP indicates that even its mutated form is sufficient to stabilise actin filaments in Z-lines. However, a closer confocal view of sarcomeres containing dCryAB^{R120G}-GFP protein revealed its altered sarcomeric localisation compared to the wild type protein. In some groups of sarcomeres dCryAB^{R120G}-GFP did not occur in Z-lines but appeared in the middle of the M-lines, whereas in other sarcomeres it was present in Z-lines but also accumulated on the edges of the I-band. In TEM I also observed a misalignment of Z-lines, typical for humans with DRM (Goldfarb and Dalakas, 2009) but also observed in mice (Wang et al., 2001). Wang et al. (2001) showed in ultrastructural analyses that in α Bcrystallin^{R120G} transgenic mouse hearts the alignment of adjacent myofibrils at the Z-band was markedly perturbed. Golenhofen et al. (1999) studied α B-crystallin binding to pig cardiac myofibrils under normal and stress conditions. They have shown that α B-crystallin occurred in the soluble protein fraction of the cytoplasm of normal state cells, whereas during reversible damaging ischemia α B-crystallin translocated completely to the Z-line area of myofibrils. Moreover, after irreversibly damaging ischemia α B-crystallin was shifted from the Z-line to the Iband area. Authors also observed that the α B-crystallin shift to the I-band correlated with displacement of the T12 epitope of titin from the vicinity of Z-lines into I-bands. They suggested that the primary binding sites for α B-crystallin might also be located in juxtaposition to Z-lines and move into the I-bands during extreme sarcomeric stress. All these changes could be due to breakage of actin filaments at the Z-line level during overstretching and subsequent translocation of the filaments together with titin and α B-crystallin towards I-bands by residual myosin function (Golenhofen et al., 1999). Similarly, in the Drosophila larval muscles alterations of the actin filament organisation caused by overexpression of the dCryAB^{R120G}-GFP may explain shifting of α B-crystallin into the I-bands, and all these irregularities indicate that mutation R120G of dCryAB as well as α Bcrystallin leads to reducing of their chaperone-like function in relation to actin filaments.

Ultrathin sections examined in TEM allowed observing changed mitochondrial morphology and glycogen deposits in muscle fibres, and confocal

projections visualised changed mitochondrial size, features similar to those observed in larval muscles expressing RNAi against dCryAB. Therefore, observed phenotypes could be explained by the loss of α B-crystallin activity following the fact that the α B-crystallin mutation R120G alters the dynamics of α B-crystallin, causing a classical "loss of function" of the protein (Bagnéris et al., 2009). Moreover, described alterations, as well as the appearance of protein aggregates are known as typical signs observed on muscle biopsies from DRM patients (Goldfarb and Dalakas, 2009). In muscle cell of the third instar larvae of Drosophila in confocal microscope as well as on three-dimensional projections, I observed aggregates of dCryAB^{R120G-}GFP mostly containing also the vimentin-like protein. Similar cytoplasmic or perinuclear aggregates were observed by Vicart et al. (1998) in two desmin-producing cell lines: C2.7 myoblasts and BHK 21 kidney smooth muscle cells transfected with αB -crystallin^{R120G} cDNA. Both cell lines contained α B-crystallin– and desmin-labelled aggregates, which were not found in cells transfected with the wild-type αB -crystallin cDNA. Wang et al. (2001) also observed desmin and α B-crystallin-reactive aggregates in cardiomyocytes of transgenic mice carrying R120G mutation in αB -crystallin gene. Moreover, in my studies, the vimentin-like network observed in confocal microscope in muscle cells containing dCryAB^{R120G}-GFP protein lost its regularity, like it was observed in RNAi-*dcryAB* muscles. This is consistent with findings showing that expression of αB -crystallin^{R120G} led to a collapse of IF network in cells (Goldfarb et al., 1998). The muscle measurements (muscle size, number and length of sarcomeres, number of nuclei) showed that larvae expressing dCryAB^{R120G}-GFP achieved muscle parameters comparable to those of larvae expressing RNAi against *dcryAB*, which again could be explained by the loss of dCryAB function. All these observations allow concluding that the expression of *dcryAB*^{R120G}-*GFP* leads to formation of protein aggregates similar to those observed in mammalian cells in DRM. Moreover, it is very likely that the vimentin-like protein plays a role of desmin filaments in Drosophila muscle cells and the observed disturbances are the consequence of impaired vimentin-like network, caused by the lack or mutation of dCryAB.

I also noticed that in the behavioural assays the *Drosophila* larvae expressing *dcryAB*^{*R*120G} had severe motility problems, confirmed by lower

contractility index, which could be the cause of muscle weakness, being a typical symptom of the DRM (Vicart et al., 1998). The DRM is a disease caused by mutations in *desmin* or αB -crystallin genes, characterised by lower limb muscle weakness, slowly spreading and involving trunk, neck flexors, facial, bulbar and respiratory muscles. Symptoms observed in skeletal muscles are often associated with a cardiomyopathy, manifested by conduction blocks and arrhythmias but also with a cataract formation (Dalakas et al., 2000; Goldfarb and Dalakas, 2009; Goldfarb et al., 2004). Moreover, the adult flies had a shorter life span, which also is a consequence of DRM. The observed shorter life span is consistent with a recent study of Elliott et al. (2013) who found that alteration of specific interactions between α B-crystallin and desmin filaments had an impact on filament aggregation and cell viability (Elliott et al., 2013). The second explanation for the shorter life span of larvae expressing dCryAB^{R120G}-GFP may be its loss of ability to regulate apoptosis. α B-crystallin is a negative regulator of apoptosis and when its mutated form is expressed, the cell viability becomes affected (Bova et al., 1999; Simon et al., 2007; Wettstein et al., 2012). Thus, it is possible that dCryAB also functions as an apoptosis regulator and may have a similar effect to its mammalian orthologue, but this conjecture requires further investigation. A third explanation for the shorter life span may be a cellular toxicity of observed aggregates, like in other diseases which present proteins accumulations (Der Perng et al., 2006).

Apart from the DRM, sHsps have a relationship to many other disorders, and such diseases may be associated with changes to sHsps occurring either as a result of mutation, posttranslational changes or changes in the amounts of sHsps. The latter are not accompanied by a structural change in the protein *per se* and are observed in cancers and neurological diseases such as Alzheimer's, Alexander's, Creutzfeldt-Jakob, amyotrophic lateral sclerosis, Parkinson's and multiple sclerosis. In different cancer types the sHsps role varies and while some studies show that elevated expression of Hsp27 indicates good prognosis, other results show that increased sHsps indicates aggressive tumor behaviour and rather poor prognosis. Moreover, sHsps modulate metastasis and tumor progression or even drug resistance in patients undergoing cancer chemotherapy. Most of mentioned neurological diseases are associated with a tissue-specific formation of protein aggregates termed amyloids, and these protein deposits may be harmful, beneficial

or of no consequence but very often are the markers for diagnosis (Sun and MacRae, 2005a). Diseased caused by posttranslational changes are provoked by truncation, deamidation, oxidation, glycation, phosphorylation or isomerization and lead to cataract. Mutations of sHsps also lead to cataract (α A-crystallin^{R116C}, α A-crystallin^{R49C}, α B-crystallin^{R120G}), desmin-related myopathy (α B-crystallin^{R120G}), α B-crystallin^{DC13}, α B-crystallin^{DC25}), desmin-related cardiomyopathy $(\alpha B$ crystallin^{R120G}), distal hereditary motor neuropathies (Hsp25^{S135F}, Hsp25^{R127W}, Hsp25^{T151I}, Hsp25^{P182L}, Hsp22^{K141N}, Hsp22^{K141E}) and Charcot–Marie–Tooth disease (Hsp25^{S135F}, Hsp25^{R136W}, Hsp22^{K141N}). The wide range of sHsp-related diseases shows the importance of further research on the mechanism of sHsp action. Thus, I introduced the human αB -crystallin gene into the fly genome and observed in confocal microscope that its expression pattern in muscle cells was similar to the one in vertebrate cells. It was localised in the cytoplasm but was also incorporated in the vimentin-like network showing functional conservation of dCryAB and its partners. The next step would be to compare this expression to R120G mutated form of the α B-crystallin implicated in *Drosophila* larval muscles with its WT and with dCryAB^{R120G} (work in progress).

This work is the first study showing developmental importance of *Drosophila* sHsp, dCryAB. It demonstrates similarities between dCryAB and α B-crystallin role in muscle formation but also that dCryAB interacts with the putative cytoplasmic intermediate filaments, which have not been described in *Drosophila* to date. It also shows that the muscle-specific expression of dCryAB carrying pathological R120G mutation results in DRM-like muscle defects. In future, *Drosophila* could be used as a new model to study DRM, helping to understand molecular mechanisms involved in its origin but also in drug screening. Moreover, establishing that *Drosophila* possesses putative cytoplasmic IFs gives wide perspectives to study many other IFs-related diseases.

6. Conclusions and future directions

Drosophila has been established as a model organism commonly used to study a wide variety of biological processes, including some diseases related to human. This study is an attempt at assessing the role of *dcryAB* gene, which is a human orthologue of αB -crystallin, in muscle development and sarcomere stabilisation.

My studies revealed that the expression pattern of dCryAB protein was reminiscent of the αB-crystallin localisation, suggesting that *dcryAB* might play conserved myogenic roles. Indeed, dCryAB is involved in muscle formation and may be directly or indirectly involved in promoting myoblast fusion events. Its attenuation specifically in mesoderm leads to impaired function of larval muscles and affects the *Drosophila* life span. Moreover, *Drosophila* expresses proteins, which correspond to the third class of vertebrate IFs and have a similar intracellular distribution as their vertebrate counterparts. I showed that dCryAB co-localised with the putative IFs in larval muscles, interacting with them, which is related to the fact that dCryAB plays an important role in maintaining a proper organisation of the vimentin-like network, and in ensuring a normal position and function of the investigated muscle components. It is noteworthy that dCryAB also participates in the formation of the described putative intermediate filament meshwork.

Mutation of dCryAB, where the equivalent arginine of position 120 in α Bcrystallin is replaced by glycine, mimics effects of mutations in human α Bcrystallin leading to the desmin-related myopathy. dCryAB^{R120G} is delocalised, compared to the wild type form of the protein, and strongly binds to the vimentinlike protein to form aggregates in muscle fibres. Overexpression of *dcryAB^{R120G}* causes loss of function of both proteins, leading to muscle defects and affected life span, which is similar to symptoms observed in DRM patients. Implicating human α B-crystallin in the Drosophila genome leads to the expression of α B-crystallin in muscle cells. Here, α B-crystallin incorporates in dCryAB and the vimentin-like proteins, forming complexes with dCryAB as well as with the vimentin-like protein, suggesting that dCryAB shares with its human counterpart not only a

sequence homology but also its function. Thus, *Drosophila* may be a suitable model organism to study desmin-related myopathy.

Now it would be advisable to: 1) create a null mutant for *dcryAB*, to confirm its role in muscle cells; 2) confirm roles of dCryAB actin and IF binding domains by mutating them, provoking loss of their function in order to analyse specifically the requirements of those domains in muscle structure and function; 3) identify other proteins which dCryAB interacts with and which might have human orthologues; 4) identify the gene encoding the vimentin-like protein; and 5) assess the role of α B-crystallin^{R120G} in *Drosophila* muscle cells at the molecular level in order to get an insight into desmin-related myopathy. Such a complete set of analyses, started in the present study, should improve our knowledge of the mechanism of the disease.

7. References

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8. Documentation

Fig. 4.1.1. dCryAB localisation in the third instar WT larval body wall muscles. Immunocytochemical reaction, visualised in confocal microscope show that dCryAB protein is expressed in all the muscles of abdominal hemisegment of the WT *D. melanogaster* 3rd instar larva **(A)**. dCryAB is localised in Z-lines (arrows), M-lines (arrows) and perinuclear areas (arrowheads), inside of the muscle fibre **(B-E)**. Three-dimensional modelling of larval muscle fibre, previously stained with adequate antibodies and visualised in the confocal microscope, show dCryAB situated at the surface of sarcomeres **(F-H)**. Ultrathin sections, stained in the immunogold reaction and observed in TEM show dCryAB at the Z-line area (red arrowheads) in the neighbourhood of F-actin filaments, pointed by black arrowheads **(I)** and myosin filaments **(J)**. MT-mitochondrion. Scale bars: 50 μm (A), 20 μm (B-E), 5 μm (F-H), 0.4 μm (I-J).



Fig. 4.2.1. Developmental effects of *dcryAB* **knockdown in third instar larva muscles.** Normal shape of muscle fibres and correct sarcomere organisation in a wild type stereotypical abdominal hemisegment of *D. melanogaster* 3rd instar larva **(A)**. RNAi *dcryAB* knockdown leads to muscle splitting **(B-C,** arrowheads) and changing attachment sites **(D,** arrowheads) or lack of some muscles **(E,** arrowheads) Arrowheads on the image presenting WT muscles correspond to the same muscles, pointed by arrowheads on images showing Mef>RNAi *dCryAB* muscles. Some of the muscles show misarranged, pinched sarcomere pattern, pointed by asterisks **(D, E)**. Distribution of observed muscle and sarcomere defects in muscle fibres VL3 and VL4, which contours are marked by a dashed line **(G)**. The same muscles preserve expression level of F-actin **(H)**. Western Blot confirms lower level of dCryAB protein in Mef>RNAi *dcryAB* line **(I)**. Muscles on images A-E and H were stained with phalloidin. All the muscle projections were obtained in the confocal microscope. Scale bars: 50 μm (A-E, G-H).



Muscle defects in the third instar larva



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Fig. 4.2.2. Developmental effects of the *dcryAB* **knockdown on the third instar larval muscle morphology.** Diagrams A-E present results of adequate muscle measurements. Muscle measurements show that muscles with attenuated *dcryAB* expression have smaller length **(A)**, width **(B)**, number of sarcomeres **(C)**, insignificantly reduced sarcomere size **(D)** and contain lower number of nuclei **(E)**, comparing to the WT. Asterisks indicate statistical level of significance of observed differences: *p<0.1, **p<0.5, ***p<0.001.



Fig. 4.3.1. Effects of the *dcryAB* **knockdown on the third instar larva motility and life span.** Behavioural assays indicate that movement ability of Mef>RNAi *dCryAB* larvae are significantly affected. They need significantly more time to revert their body in the righting assay **(A)**, to crawl 5 cm the distance in the journey test **(B)** and execute less peristaltic movements during the time of 30 seconds **(C)**. Muscles of the RNAi *dCryAB* larvae are characterised by lower contractility index **(D)** and Mef>RNAi *dCryAB* flies show higher mortality rate **(E)**. Asterisks indicate statistical level of significance of observed differences: *p<0.1, **p<0.5, ***p<0.001.



Fig. 4.4.1. Vimentin-like protein localisation in the third instar larval muscles. Confocal scans show third instar larval muscles labeled with adequate antibodies: anti-dCryAB, anti-vimentin and phalloidin, visualising F-actin **(A-D)**. The vimentin-like protein is localised in Z-lines **(B)**, in the nuclear area and is associated to the sarcolemma (dotty pattern, pointed by arrowheads) **(C)**. The vimentin-like protein co-localises with dCryAB in Z-lines and around the nucleus **(D)**. Three-dimensional modelling of larval muscle fibres, previously stained with adequate antibodies and visualised in the confocal microscope, show the vimentin-like protein situated at the surface of sarcomeres **(E)**. Ultrathin sections, stained in the immunogold reaction and observed in TEM confirm a presence of the vimentin-like protein in the Z-line area **(F)**. N-nucleus. Scale bars: 20 μm (A-D), 10 μm (E), 0,4 μm (F), 0.1 μm (F', F").



Fig. 4.4.2. Localisation of the vimentin-like protein inside of the third instar larva muscle nucleus. Confocal scans show third instar larval muscles labeled with adequate antibodies: anti-vimentin and anti-histone 3 (H3) (A-C). The vimentin-like protein is present in the perinuclear area and inside of the nucleus (A). The vimentin-like protein co-localises with histone 3 inside of the nucleus (C). Ultrathin sections, stained in the immunogold reaction and observed in TEM show the vimentin-like protein around and inside of the nucleus, in the neigbourhood of the chromatin. Gold particles, corresponding to the vimentin-like protein are pointed by black arrowheads (D). N-nucleus, NE-nuclear envelope. Scale bars: 10 μ m (A-C), 0.1 μ m (D).



Fig. 4.5.1. Interactions of dCryAB with the vimentin-like protein in *Drosophila* third instar larval muscle cells. Schematic alignment of dCryAB protein indicates the α -crystallin rod domain containing an intermediate filament interaction domain, N- and C-termini (A). Confocal projections show accumulations of dCryAB occurring together with the vimentin-like protein (B-D). Diagram shows number of observed third instar larvae possessing in their muscles delocalised dCryAB and vimentin-like proteins (E). Western blot shows proteins with the size around 40, 72 and 170kDa labeled by anti-vimentin antibodies after co-immunoprecypitation reaction between dCryAB and vimentin-like (F). IP-immunoprecypitation, -AB-negative control, WC-whole cell lysate. N-nucleus. Scale bars: 20 µm (B-D).





F



Ε





Fig. 4.6.1. dCryAB is involved in stabilisation of structural integrity of third instar larval somatic muscles by interacting with putative IF proteins, part1. Confocal scans show anti-vimentin-like staining using imunocytochemistry method (A, B) and TEM visualisation of an immunogold procedure (C, D). Images show that in normal muscles the vimentin-like protein creates regular meshwork on extentions of Z-lines and around nuclei (A, C), whereas muscles with attenuated *dcryAB* expression have altered arrangement of the vimentin-like protein around the nucleus (arrow) and in sarcomeres (asterisk) (B, D). In muscles with *dcryAB* knockdown, visualised in the confocal microscope, nuclei position is altered (F) comparing with the control (E). N-nucleus. Scale bars, 20 μ m (A, B), 0.2 μ m (C, D), 50 μ m (E, F).



Fig. 4.6.2. dCryAB is involved in stabilisation of structural integrity of third instar larval somatic muscles by interacting with IF proteins, part 2. TEM images show in RNAi *dcryAB* line swollen mitochondria (arrowheads) with barely visible mitochondrial crests, comparing to the WT **(A, B)**. MitoTrackerRed reaction, visualised in confocal microscope, detects a lower number of active mitochondria around the nucleus (arrowheads) and in the Z-line area (asterisks), comparing to the wild type **(C, D)**. TEM images show increased deposits of the glycogen (asterisks) and shifted Z-lines (arrowheads) in muscles of RNAi *dcryAB* line, comparing to the control **(E, F)**. Scale bars : 1 μm (A, B), 5 μm (C, D), 2.5 μm (E, F).



Fig. 4.7.1. The vimentin-like meshwork recuperation in third instar larval muscles, after 2 hours of recovery from heat shock. Immunocytochemical reaction, visualised in confocal microscope, show that dCryAB is present in larval muscles in sarcomeres (arrowhead) and in the perinuclear area (asterisk) **(A)**. The vimentin-like protein restores its normal sharp pattern in Z-line (arrowhead) and in the perinuclear area (asterisk) **(B)**. dCryAB and the vimentin-like protein accumulate together in muscle cells (asterisk) **(C)**. Western blot shows dCryAB level in muscle cells in normal conditions and after 2 hours of recovery from heat shock **(D)**. Scale bars: 20 μm (A-C).



Fig. 4.8.1. Comparison of amino acid sequences of αB-crystallin (CryAB) with dCryAB and comparison of the nucleotide sequence of *dcryAB* **with and without mutation R120G.** Comparison of amino acid sequences of human αBcrystallin with drosophila dCryAB, in red pointed conserved arginine in codon 120th **(A)**. DNA sequence of *dcryAB* and *dcryAB^{R120G}*, mutation R120G marked in red **(B)**.

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A	CryAB	9	WIRRPFFPFHSPSRLFDQFFGEHLLESDLFPTSTSLSPFYLRPPSFLRAPSWFDTGL	65
	dCryAB	11	W FP + SRL DQ FG+ L DL + + P LR +LR W L WWDELDFPMRT-SRLLDQHFGQGLKRDDLMSSVWNSRPTVLRS-GYLRPWHTNSLQKQ	66
	CryAB	66	SEMRLEKDRFSVNLDVKHFSPEELKVKVLGDVIEVHGKHEERQDEHGFISREFHRKY	122
	dCryAB	67	ESGSTLNIDSEKFEVILDVQQFSPSEITVKVADKFVIVEGKHEEKQDEHGYVSRQFSRRY	126
	CryAB	123	RIPADVDPLTITSSLSSDGVLTVNGPRKQVSGPERTIPITR 163	
	dCryAB	127	QLPSDVNPDTVTSSLSSDGLLTIKAPMKALPPPQTERLVQITQ 169	

B

WT: AGG \longrightarrow Mutant: GGG R120 \longrightarrow G120 R=arginin G=glycine

Fig. 4.8.2. Effects of the R120G mutation in dCryAB on the sarcomere organisation in *Drosophila* **third instar larval somatic muscles.** Confocal images show the lack of dCryAB^{R120G}-GFP in sarcomeres of some muscle parts, indicated by arrowheads **(A)**. Muscle parts with the lack of dCryAB^{R120G}-GFP contain accumulations of actin (asterisks) without perceptible sarcomeric organisation **(B, C)**. dCryAB^{R120G}-GFP localises ectopically in muscle fibres: in some sarcomeres dCryAB^{R120G}-GFP does not occur in Z-lines but appears in the middle of M-lines, whereas in other sarcomeres it is present in Z-lines but also accumulates on edges of the I-band; Z-line shift (arrowhead) is also observed **(D, E)**. Ultrathin section of larval muscle observed in TEM shows misaligned and a shifted Z-line (dashed line marks Z-lines), elongated mitochondria with a reduced cristae (arrowheads) and a glycogen deposits (asterisks). N-nucleus. Scale bars, 20 μm (A-E), 2 μm (F).



Fig. 4.8.3. Effect of the R120G mutation in dCryAB on the accumulation of dCryAB^{R120G} aggregates, formation of smaller nuclei and a vimentin-like meshwork collapse in *Drosophila* third instar larval somatic muscles development. Confocal images show accumulations of dCryAB^{R120G}-GFP (arrowheads) in sarcomeres (A) and presence of small nuclei (arrowheads) in muscle fibres (B). In larval muscles, expressing *dcryAB* with provided R120G mutation the vimentin-like protein losses regular sarcomeric localisation and accumulates around nucleus (D, E), comparing to the control (C). Three-dimensional modelling of created muscles labeled by adequate antibodies, show complexes compound of dCryAB^{R120G}-GFP and the vimentin-like protein positioned around and inside of nuclei (arrows), and in the sarcomeric part of the muscle fibre (F). The diagram shows a number of individuals with misarranged nuclei position and visible changes of dCryAB and the vimentin-like protein localisation, observed in Mef>*dcryAB*^{R120G} larvae, comparing to the WT (G). N-nucleus. Scale bars, 20 µm (A, B, E, F), 50 µm (C, D).



Fig. 4.9.1. Effects of the *dcryAB*^{*R120G*} **overexpression on the third instar larval muscle morphology.** Diagrams A-E present results of adequate muscle measurements. Muscle measurements show that muscles with overexpressed *dcryAB*^{*R120*} have a smaller length **(A)**, width **(B)**, number of sarcomeres **(C)**, insignificantly changed sarcomere size **(D)** and contain a lower number of nuclei **(E)**, comparing to the WT. Asterisks indicate statistical level of significance of observed differences: *p<0.1, **p<0.5, ***p<0.001.







□ WT

■ Mef>UAS-dcryAB-GFP

■ Mef>UAS-dcryAB R120G-GFP

Fig. 4.10.1. Effects of the *dcryAB*^{*R120G*} **overexpression on the third instar larva motility and life span.** Behavioural assays indicate that the movement ability of Mef>UAS*dcryAB*^{*R120R-GFP*} larvae are significantly affected. Diagrams show that they need significantly more time to revert their body in the righting assay **(A)**, to crawl 5 cm the distance in the journey test **(B)** and execute less peristaltic movements during the time of 30 seconds **(C)**. Muscles overexpressing *dcryAB*^{*R120G-GFP*} larvae are characterised by a lower contractility index **(D)**. *dcryAB*^{*R120R-GFP*} flies show **a** higher mortality rate **(E)**. Asterisks indicate a statistical level of significance of observed differences: *p<0.1, **p<0.5, ***p<0.001.



Fig. 4.11.1. Localisation in larval muscle cells of human α B-crystallin inserted to the *Drosophila* genome. Confocal images show larval muscles overexpressing human α B-crystallin and labeled with adequate antibodies. α B-crystallin occurs together with dCryAB in the Z-line and in the perinuclear area, is present in the Mline and inside of the nucleus but also localises unspecifically in all muscle cytoplasm area (A, A', C, C'). α B-crystallin attaches to the vimentin-like meshwork in the Z-line but also is present together with the vimentin-like protein inside of

the nucleus (B, B', C, C'). N-nucleus. Scale bars: 20 µm (A,B,C), 10 µm (A', B', C').

