Evolutionary history of wild goat (Capra aegagrus) and the goat (C. hircus) based on the analysis of mitochondrial and nuclear DNA polymorphism: Implications for conservation and for the origin of the domestication

Saeid Naderi

THESE

Pour obtenir le grade de DOCTEUR DE L'UNIVERSITE JOSEPH FOURIER

Spécialité Biodiversité-Ecologie-Environnement

Préparée au Laboratoire d'Ecologie Alpine (LECA)

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Présentée et soutenue publiquement le 11 Décembre 2007 par

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A l'Iran, mon cher Pays

A ma chère famille

Et tous ceux qui me sont chers

Remerciements

Je voudrais remercier les membres du jury, Monsieur le Professeur Paolo Ajmone-Marsan et Monsieur le Docteur Olivier Hanotte pour avoir accepté d'être les rapporteurs de ma thèse, et Messieurs les Docteurs Jean-Denis Vigne, Pierre Taberlet et François Pompanon pour avoir accepté d'être présents pour juger mon travail.
Ce travail fait partie d'un programme de coopération Scientifique et Technique Franco-Iranien sous l'égide du Ministère de la Science, de la Recherche et de la Technologie Iranien et du SFERE (La Société Française d'Exportation des Ressources Educatives).

Mon travail de recherche a été effectué au sein du laboratoire d'écologie Alpine (LECA) à Grenoble, sous la direction de M. Pierre Taberlet, Directeur de Recherche au CNRS, à qui j'adresse ici mes sincères remerciements pour m'avoir accueilli dans son laboratoire.

Mes remerciements vont également au Ministère de la Science, de la Recherche et de la Technologie d'Iran grâce auquel j'ai pu bénéficier d'une bourse doctorale (Numéro 800125). Un grand merci aux conseillers scientifiques d'Iran à Paris, Messieurs Rahmati et Abdollahi, ainsi que de l'organisme SFERE, pour tout le soutien et la gentillesse qu'ils m'ont témoigné.
Je tiens à remercier ici tous ceux qui m'ont aidé, soutenu et encouragé pendant ma thèse.
Je suis très heureux de pouvoir exprimer ma profonde gratitude envers mes directeurs de thèse M. Pierre Taberlet, et M. François Pompanon.
Je ne sais comment remercier Pierre, de m'avoir encouragé et guidé tout au long de mon travail, tout en m'accordant sa confiance. Il m'a inspiré mon travail et su me diriger avec beaucoup de patience et de sympathie. J'ai pu, au cours des quatre années passées au laboratoire apprécier non seulement sa conscience scientifique mais aussi et surtout ses remarquables qualités humaines, qu'il trouve ici l'expression de ma profonde reconnaissance.
J'adresse mes sincères remerciements à François, vraiment. Il a toujours été présent pour mes questions avec sa bonne humeur et son sourire habituel. Je le remercie infiniment pour son aide, ses conseils, ses encouragements, sa disponibilité et aussi sa patience.

Je tiens également à remercier très chaleureusement M. Ali Sarraf Moghaddam, mon très cher enseignant de biologie qui m'a gentiment familiarisé avec les sciences de la nature, un grand merci toujours pour ses encouragements, ses qualités humaines rares dont la gentillesse.
J'exprime ma sincère gratitude à M. Dr. Kiabi, mon très cher professeur d'Université en Iran, qui m'a appris l'esprit de la recherche scientifique, celui du travail en équipe, l'autonomie et la modestie dans le travail, tout en pensant à notre futur et en nous ouvrant à des opportunités de continuation dans le domaine de la recherche. Je tiens à le remercier pour ses conseils qui m'aident chaque jour.
Un grand remerciement à mes deux très chers amis et collègues, M. Hamid-Reza Rezaei et M. Hamid-Reza Naghash, pour leur amitié, ainsi que pour les bons moments où nous avons travaillé ensemble. J'espère que nous pourrons de nouveau travailler ensemble dans le futur.
J'adresse mes sincères remerciements à tous ceux qui m'ont aidé pour l'échantillonnage en Iran, surtout M. Hamid-Reza Rezaei, M. Hamid-Reza Naghash, M. Javad Ramezani, M. Ebrahim Ghaderi, M. Afshin Karami, M. Rasul Marsouli, M. Abbas Rafat ainsi qu'aux agents de l'Organisation pour l'Environnement et la conservation en Iran, qui par

leur dévouement m'ont apporté une aide inestimable sur le terrain. Un remerciement tout particulier à M. RamazanAli Ghaemi et M. Bijan Farhang Darehshoori pour leurs avis d'experts. Sans le dévouement, l'aide et le soutien de vous tous, un échantillonnage à si grande échelle n'aurait pu être possible.
Je tiens également à remercier sincèrement M. Aykut Kence, M. Deniz Ozut, Mme Ozge Balkiz, M. Paul Weinberg et M. Amjad Tahir Virk, pour leurs échantillons de Turquie, Azerbaidjan, Dagestan, Turkménistan et Pakistan.
Ensuite, beaucoup de manips n'auraient pu être réalisées sans l'aide de mes collègues, Christian, Delphine, Stéphanie, Ludovic, Carole. Mille mercis à eux.
Je tiens à remercier tous mes collègues du LECA. C'est avec joie que j'ai partagé ces quatre années avec eux. Que tous mes collègues, Carole, Christian, Patrik, Cyrille, Alice, Bahar, Olivier, Mihai, Julien, Sébastien, Delphine, Stéphanie, Ludovic, Margot, Bénédicte, Pierre, Matthieu, Morana, Toni, Florence, Jean-Marie, Olivier, Anthony, Wasim et …, ne soient pas oubliés pour leur collaboration et leur contribution à l'ambiance bien sympathique du laboratoire.
Je tiens à remercier tout particulièrement Christian et Carole pour leurs qualités humaines extraordinaires, leur gentillesse. Ce fût pour moi une suite d'encouragements.
Je dois grand remerciement également à Dr. Jean-Denis Vigne et Dr. Marjan Mashkour pour leurs aides en partie d'Archeaozoology et aussi Dr. Michael Blum et Dr. Ricardo Negrini pour leurs aides en analyse de données.
Je remercie très sincèrement Marjan Mashkour, Catherine Hänni, Sandrine Hughes, Héléna Fernández pour l'intérêt qu'elles ont porté à mon travail et leurs précieux conseils lors des comités de thèse.
Je remercie tous les professeurs et chercheurs du LECA, Irène, Philippe, Roberto, Oscar, Laurence, Serge et…, pour leurs discussions scientifiques qui m'ont guidé au cours de mon travail, et toujours dans une ambiance bien sympathique.
De même, je remercie les membres de l'équipe de foot du LECA, pour leur amitié et pour tous les fantastiques moments passés ensemble dans une excellente ambiance, qui m'ont donné la santé et la motivation pour la bonne continuation de ma thèse : Cyrille, Seb, Fred, Julien, Tarafa, Ozgur, Abdé, Amandine, Margot, Michael, Jérôme, Thierry,…

Je remercie tous mes amis iraniens pour leur soutien et pour tous les fantastiques moments passés ensemble qui sont vraiment pour moi parmi les meilleurs souvenirs de ma thèse tout au long de mon séjour en France, particulièrement à Grenoble.

J'adresse mes remerciements très chaleureux à tous mes amis iraniens, Abbas Akbaripasand, Alireza mirzajani, Reza Amini, Javad Ramezani, Mehrdad Khoshchin, Ayoub Dadbaz, Hossein Najari, Ali Masood Evaz, Abbas Pahlavani, Hassan Rajabi, Rasul Fesharakifard, Babak Nosrati, Ahmad Amini, Mohammad Hassani, Mohammad-Reza Nahal Tahmasbi, Seyed Mojtaba Vaezi, Ali Zamanifard, … pour leur amitié et le soutien moral permanent de proche ou de loin.

Je tiens évidement à remercier mes parents, mes sœurs pour m'avoir suivi dans l'inconnu, pour m'avoir soutenu et pour m'aimer autant; leur bienveillance permanente et leur amour inconditionnel sont mes joies et mes espoirs.

J'adresse mes remerciements plus particulièrement à ma chère épouse, Simin, qui a été toujours présente à mes côtés, à tous les instants pour m'apporter son aide, son soutien et son amour pour pouvoir franchir les plus durs moments de ma thèse. Je n'y serais pas arrivé sans toi, cette thèse c'est aussi la tienne.

Abbreviations

ADN-mt	**ADN mit**ochondrial
AFLP	**A**mplified **F**ragment **L**ength **P**olymorphism
AMOVA	**A**nalysis of **Mo**lecular **Va**riance
Bp	**B**ase **p**air
Ca.	**C**irc**a**
Cal. B.P.	**Cal**ibrated **B**efore **P**resent
CI	**C**onfidence **I**nterval
Cytb	**Cyt**ochrome **b**
dNTP	**d**i-desoxy **N**ucleotide **T**ri **P**hosphate
D-loop	**D**isplacement**-loop**
ESUs	**E**volutionary **S**ignificant **U**nit**s**
FCA	**F**actorial **C**orrespondence **A**nalysis
HVI	**H**yper **V**ariable **I**
indel	**in**sertion/**del**etion
K2P	**K**imura 2-**P**arameters
mtDNA	**mit**ochondrial **DNA**
MB	**M**r**B**ayes
ML	**M**aximum **L**ikelihood
Myr, MYA	**M**illion **Y**ea**r**s , **M**illion **Y**ears **A**go
NJ	**N**eighbour **J**oining
Pb	**p**aire de **b**ase
PCR	**P**olymerase **C**hain **R**eaction
PPNB	**P**re**P**ottery **N**eolithic **B**
SNP	**S**ingle **N**ucleotide **P**olymorphism
TBR	**T**ree **B**isection **R**econnection
TMRCA	**T**ime to the **M**ost **R**ecent **C**ommon **A**ncestor
Ts	**T**ran**s**itions
Tv	**T**rans**v**ersion
YBP	**Y**ears **B**efore **P**resent

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Chapter 1. Version abrégée en français: Histoire évolutive de l'Aegagre (*Capra aegagrus*) et de la chèvre (*C.hircus*) basée sur l'analyse du polymorphisme de l'ADN mitochondrial et nucléaire : Implications pour la conservation et pour l'origine de la domestication

1. Les outils pour comprendre l'origine des animaux domestiques et pour mesurer leur diversité

1.1. Caractérisation moléculaire

La diversité génétique des espèces est la conséquence des évènements génétiques et démographiques qui ont eu lieu durant son évolution. La structure actuelle de cette diversité garde la signature de ces évènements, ce qui nous permet de reconstituer l'histoire évolutive. Parmi les facteurs environnementaux qui affectent l'évolution des espèces, l'homme tient une place particulière. Il exerce des contraintes sélectives directes ou indirectes sur un bon nombre d'espèces. Un type de relation particulier s'est établi entre l'Homme et certains organismes dans le cadre du processus de domestication. Si l'on ne prend en compte que les espèces animales, plus de 40 d'entre elles sont aujourd'hui domestiquées (FAO 2006).

La diversité génétique de ces espèces résulte des processus génétiques et démographiques liés à l'histoire de leur domestication. Elle dépend par exemple de leur dispersion géographique qui s'est faite à travers le monde en suivant les migrations humaines, des flux géniques qui ont découlés des échanges commerciaux. Dans ce contexte de flux géniques constants mais assez faibles, plusieurs milliers d'années de sélection ont conduit à l'adaptation de races locales à leur environnement. Ces races locales, ainsi que les espèces sauvages proches des domestiques représentent cependant une ressource génétique inestimable. Depuis quatre à cinq décennies, cette vaste diversité intra-spécifique se réduit fortement par le remplacement progressif de ces races locales par un petit nombre de races industrielles, sélectionnées. Ainsi l'analyse de la diversité génétique des espèces domestiques et de leurs proches ancêtres sauvages permet de reconstituer l'histoire de la domestication et a également des applications dans la gestion des ressources génétiques.

Le polymorphisme de l'ADN (marqueurs nucléaire et mitochondriaux) est utilisé pour mesurer la diversité génétique des animaux domestiques. La plupart des études ne concernent pas les gènes responsables de caractères dont la variation est liée au processus de domestication. Elles se focalisent plutôt sur l'analyse du polymorphisme neutre afin de permettre la reconstitution de l'histoire évolutive des espèces domestiques et de leurs ancêtres sauvages (Zeder *et al.* 2006a).

Le marqueur moléculaire idéal pour étudier l'origine de la domestication doit être suffisamment conservé pour permettre l'identification des taxons sauvages à l'origine des espèces domestiques. Mais il doit également être suffisamment variable et structuré géographiquement pour permettre de localiser les lieux de domestication. Son évolution doit aussi se faire à un taux constant. Il est difficile de trouver un marqueur parfait, cependant plusieurs zones de l'ADN mitochondrial approchent la plupart de ces conditions. C'est pour cela que les marqueurs mitochondriaux sont de loin les plus utilisés pour les études moléculaires sur les animaux domestiques (Bruford *et al.* 2003).

1.2. Approches archéobiologiques

La combinaison des approches archéologiques et génétiques a conduit depuis une vingtaine d'années à une véritable explosion des connaissances sur l'origine de la domestication. Les études d'ADN ancien permettent de génotyper les ossements retrouvés sur les sites archéologiques. De telles données nous informent sur l'origine et les routes migratoires des espèces domestiques (Fernández *et al.* 2005). L'étude des variations de la diversité génétique au cours du temps chez les domestiques et les sauvages sont utiles pour tenter de distinguer les phénomènes de domestication locale des introgressions à partir des animaux domestiques (Luikart *et al.* 2006).

Les études archéologiques apportent des données complémentaires qui concernent directement les animaux (morphologie) mais aussi leur environnement (contexte écologique) et l'Homme qui les a domestiqués (outils en relation avec le processus de domestication). Les caractères morphologiques mesurés peuvent être modifiés en raison d'une réponse adaptative aux forces sélectives résultant de la domestication (marqueurs Animal-orientés). Ils reflètent donc l'impact évolutif de la domestication sur les populations. D'autres caractères peuvent être modifiés dans le cadre d'une réponse plastique du phénotype. Les variations morphologiques varient alors en nature et en intensité en fonction de facteurs locaux et peuvent changer rapidement au cours du temps.

D'autres marqueurs ne sont pas liés aux animaux et démontrent l'existence d'un contrôle et d'une gestion des troupeaux par l'Homme (marqueurs Humain-orientés). Ces types d'indices sont particulièrement intéressants quand ils précèdent les réponses morphologiques adaptatives des animaux à la domestication. Ils peuvent consister en des outils, des restes de corrals (Zeder *et al.* 2006a).

La caractérisation démographique apporte aussi des informations importantes. Elle est basée sur l'hypothèse que l'âge et le sexe des animaux tués par des chasseurs diffère de celui des animaux capturés par des gardiens de troupeaux, car les deux modes de capture ne répondent pas aux mêmes contraintes. Des données ostéométriques à partir desquelles on caractérise l'âge et le sexe des restes d'animaux sur les sites archéologiques permettent de distinguer la gestion de troupeaux de différentes pratiques de chasse (sélective et non sélective).

Enfin, des données d'abondance et de biogéographie sont également informatives. L'apparition d'espèces potentiellement domestiques en dehors de leur aire de répartition naturelle est généralement interprétée comme résultant de mouvements contrôlés par l'Homme. Ces mouvements auraient concerné des troupeaux domestiques, mais aussi des animaux sauvages en cours de domestication (Zeder 2006).

2. Biodiversité des animaux domestiques

Depuis plus de 10 000 ans, les mutations, l'adaptation locale, la dérive génétique et la sélection des races ont modelé la diversité génétique des populations domestiques. Ces mécanismes ont concerné une quarantaine d'espèces sur les 50 000 que nous connaissons chez les oiseaux et mammifères. Au total, 7 616 races ont été identifiées, la majorité d'entre elles étant originaires d'Europe et d'Asie (FAO 2007).

Chez la vache, la chèvre et le mouton, on trouve un haut niveau de polymorphisme de l'ADN mitochondrial. Pour chaque espèce, l'existence de plusieurs haplogroupes est le résultat de multiples origines maternelles (Figure 1.1). Ces origines multiples peuvent découler de plusieurs évènements de domestication en différents lieux et/ou à différentes périodes, ou bien de la capture de plusieurs haplotypes au cours d'un unique événement de domestication. Le polymorphisme nucléaire est également élevé (e.g. Maudet *et al.* 2002), comparable à celui trouvé chez les espèces sauvages (Taberlet *et al.* 2007). Il apparaît également que la diversité des espèces animales domestiques est en premier lieu répartie selon un axe Est-Ouest (MacHugh & Bradley 2001).

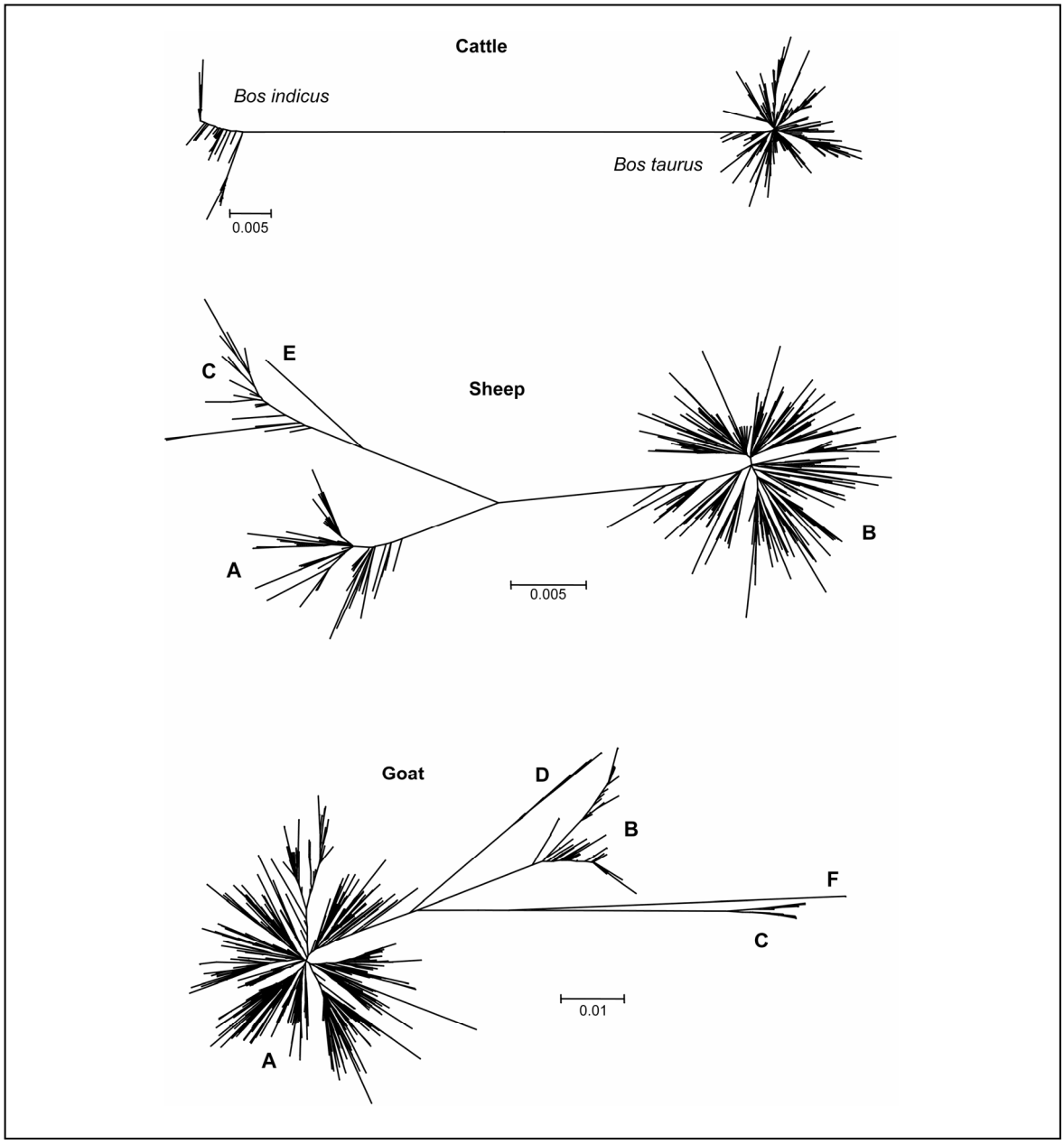

Figure 1.1. Arbres phylogénétiques non racinés réalisés avec la méthode Neighbor-joining et démontrant le polymorphisme de l'ADNmt pour 744 vaches, 640 moutons et 1813 chèvres (Taberlet *et al.* 2007).

3. Etudes portant sur la chèvre

Le genre Capra est composé de la chèvre et des espèces sauvages apparentées : l'Aegagre, le Markhor, les Bouquetins et les Turs. Si l'on excepte l'espèce domestique, le genre est uniquement présent dans l'ancien monde. Les données fossiles suggère une origine en Asie Centrale suivie d'une radiation au Plio-pleistocene. Peu de données archéologiques sont disponibles pour ces espèces, leurs habitats montagnards étant peu propices à la conservation des fossiles. Il en résulte une histoire évolutive mal connue, sans doute également à cause de la rapidité de la radiation du genre, qui rend difficile l'inférence des relations phylogénétiques entre espèces. Le nombre et le statut des taxons composant le genre Capra fait encore débat, et l'on définit de 6 à 9 espèces (Figure 1.2, Pidancier *et al.* 2006).

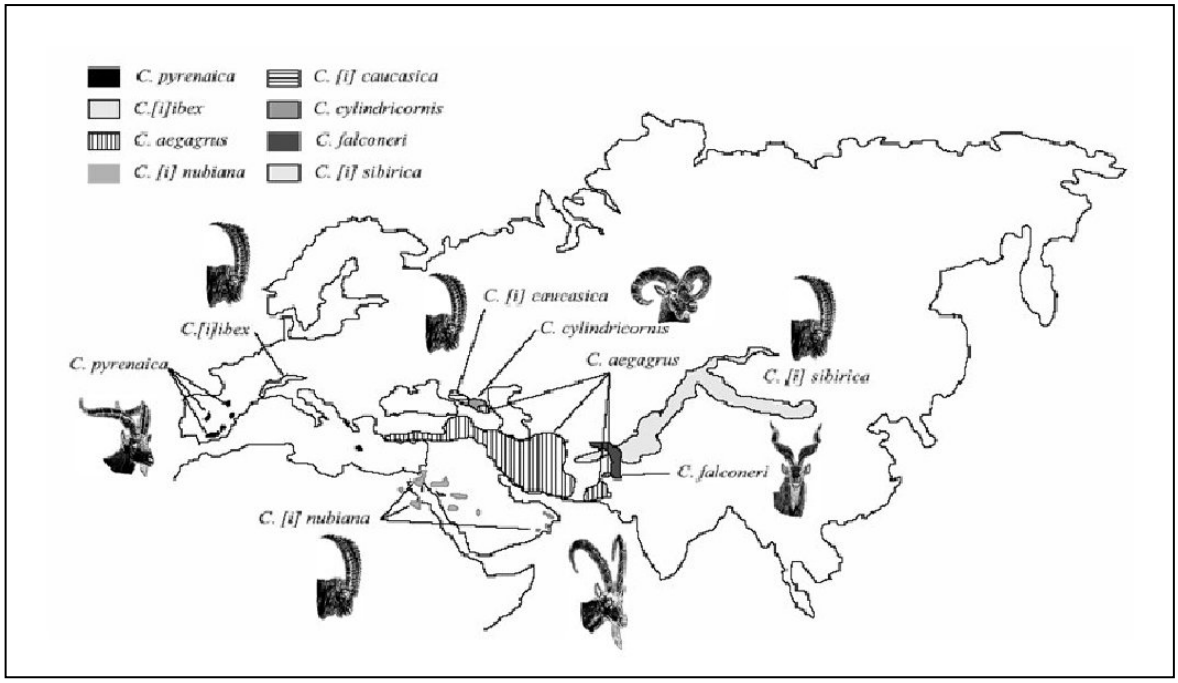

Figure 1.2. Distribution géographique des taxons sauvages du genre Capra. (d'après Pidancier *et al.* 2006, modifié).

Les études sur la diversité génétique de la chèvre domestique (*Capra hircus*) ont permis de définir jusqu'à présent 6 haplogroupes mitochondriaux. (Luikart *et al.* 2001; Sultana *et al.* 2003; Joshi *et al.* 2004). La plupart de cette diversité apparaît au sein des groupes, et seulement 10% est due aux différences entre continents. Luikart *et al.* (2001) ont estimé le temps de divergence entre haplogroupes à plus de 200 000 ans, bien avant le moment de la domestication. Cela suggère que la diversité observée aujourd'hui ne provient pas uniquement d'une population unique qui aurait existé il y a 10 000 ans. La structuration géographique de la diversité génétique de la chèvre est plus nette avec des marqueurs microsatellites qui montrent qu'une grande proportion de la diversité génétique qui existe entre races s'explique par l'origine géographique (Cañon *et al.* 2006).

La diversité génétique passée a également pu être mesurée à partir d'étude d'ADN ancien, qui montrent l'origine et les routes de migration des différents haplogroupes du Moyen-Orient vers l'Europe. Jusqu'alors deux des haplogroupes définis actuellement (A et C) ont été retrouvés dans des sites archéologiques (Fernández *et al.* 2006).

4. La Domestication

La domestication est un phénomène complexe et graduel qui trouve son origine dans la propension des chasseurs-cueilleurs à l'apprivoisement et à la gestion des animaux sauvages. A la fin du Pléistocène, le climat est devenu plus chaud avec des saisons plus marquées. Cela a accru la nécessité de nourriture stockable et la mise en place de cultures et d'élevages. Ces phénomènes ont commencé au début du Néolithique il y a 12 000 à 14 000 ans et ont conduit à la révolution agricole (Diamond 2002). En ce qui concerne les animaux d'élevage, au moins une douzaine de centres de domestication ont été mis en évidence à travers le monde (FAO 2007).

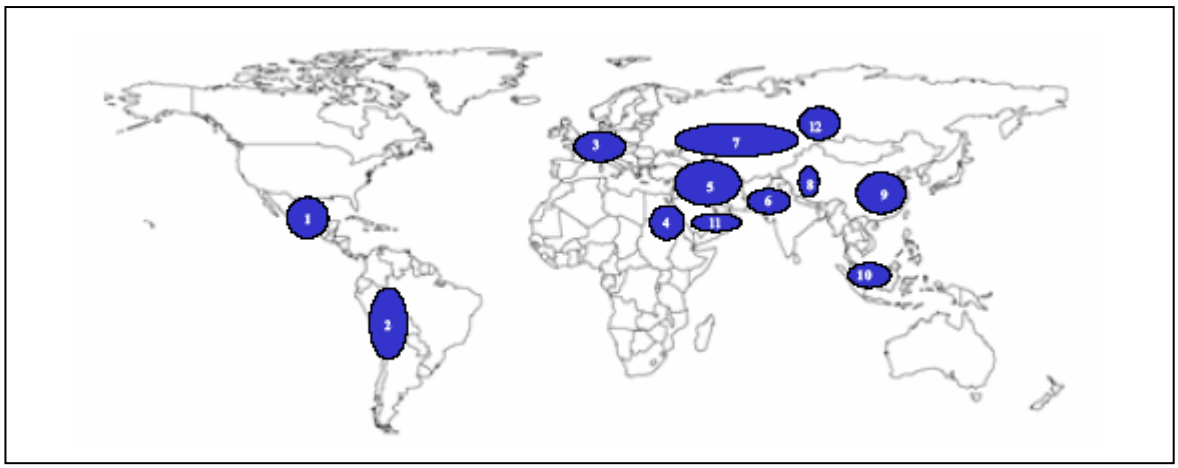

Figure 1.3. Principaux centres de domestication en fonction de données génétiques et archéologiques d'après la FAO (2007) (1) dinde - (2) cobaye, lama, alpaga - (3) cochon, lapin - (4) vache, âne - (5) vache, cochon, chèvre, mouton, chameau - (6) vache, chèvre, poulet, buffle - (7) cheval - (8) yack - (9) cochon, buffle, poulet – (10) poulet, cochon, vache - (11) dromadaire, (12) renne.

Les analyses génétiques ont montré une grande diversité des processus de domestication, en terme nature et nombre de progéniteurs ayant contribué au pool génétique de l'espèce domestiquée (Bruford *et al.* 2003).

La chèvre a été parmi les premiers animaux d'élevage domestiqués, il y a plus de 10 000 ans, contribuant à la révolution Néolithique (Zeder & Hesse 2000). Les connaissances acquises sur la domestication de la chèvre nous permettent de mieux comprendre l'origine et la propagation de l'agriculture. Les données archéologiques et morphologiques suggèrent que la chèvre a été domestiquée à partir de l'aegagre (*Capra aegagrus*) dans le Croissant Fertile (e.g. Peters *et al.* 1999; Peters *et al.* 2005; Zeder 2005) Cette origine a été confirmée par des études génétiques basées sur l'analyse d'ADN mitochondrial et nucléaire (Luikart *et al.* 2006; Takada *et al.* 1997). Les données archéologiques situent la domestication il y a environ 10 500 ans dans les vallées de l'Euphrate et du Tigre, dans le Sud-Est de l'Anatolie (Peters *et al.* 1999; Peters *et al.* 2005) et entre 9 900 et 9 500 ans dans les Monts Zagros à l'Ouest de l'Iran (Zeder & Hesse 2000; Zeder *et al.* 2005; Zeder *et al.* 2006b). La transition de la chasse à la gestion de troupeau est marquée par la capture très majoritaire de jeunes mâles sub-adultes. Les chèvres de cette période ressemblaient sans doute beaucoup aux aegagres sauvages, du point de vue morphologique et génétique. Quelques 500 ans plus tard, les hommes et leur cheptel quittèrent ces montagnes vers les plaines voisines qui constituaient des environnements défavorables à la vie des aegagres. La migration vers ces plaines mit un

terme à la possibilité d'hybridation entre les animaux domestiques et sauvages. Il est possible que, couplé à cette interruption du flux génique, les conditions plus arides et les pâtures plus pauvres rencontrées dans ces nouveaux milieux aient contribué à la réduction de taille de l'espèce domestique (Zeder 2006). De nombreux changements sont également intervenus par la suite sous l'effet de la sélection par l'homme. Il est certain qu'une taille plus petite rend aussi les animaux plus facilement contrôlables, et qu'elle peut être liée à une acquisition plus précoce de la maturité sexuelle (Hall 2004).

Après ces événements initiaux, les données archéologiques nous montrent que la culture Néolithique diffusa vers l'Europe le long de deux routes principales, la route méditerranéenne et la route Danubienne, assurant ainsi la dispersion des chèvres (Fernández *et al*. 2006).

Figure 1.4. *Capra aegagrus* (Photo par Saeid Naderi).

5. Génétique de la conservation

La génétique moléculaire peut être utilisée pour la gestion scientifique et la conservation des animaux sauvages et domestiques. Il est important de mesurer la diversité génétique des sauvages et des domestiques, de connaître les relations de parenté entre ces espèces, leur phylogéographie, pour mettre en place des plans de conservation. La préservation des espèces sauvages ainsi que des races locales rustiques est essentielle pour le maintien des ressources génétiques. Une grande diversité d'allèles issue de ces stocks pourrait être nécessaire pour renforcer la diversité génétique des races industrielles modernes dans le cadre d'une gestion durable des élevages.

Article 1. Analyse à grande échelle de la diversité génétique chez la chèvre domestique

Ce chapitre est basé sur l'article "Large-scale mitochondrial DNA analysis of the domestic goat reveals six haplogroups with high diversity" de S. Naderi, H.-R. Rezaei, P. Taberlet, S. Zundel, S.-A. Rafat, H.-R. Naghash, M.A.A. El-Barody, O. Ertugrul[6], F. Pompanon et le consortium Econogene, publié dans PLoS ONE (PLoS ONE 2(10): e1012. doi:10.1371/journal.pone.0001012).

Depuis les débuts de la domestication, le transport par l'homme des animaux domestiques, pour des raisons économiques et commerciales, a gouverné les processus démographiques et génétiques qui expliquent la répartition actuelle de ces animaux et la structure génétique de leurs populations. C'est pourquoi une bonne connaissance de la diversité génétique des animaux domestiques est un pré-requis essentiel pour la compréhension de l'histoire de la domestication. C'est en particulier le cas pour la chèvre qui a été l'un des premiers ongulés domestiqués en marge du Croissant Fertile il y a environ 10 000 ans (e.g. Peters *et al.* 1999; Zeder & Hesse 2000; Peters *et al.* 2005; Zeder 2005; Luikart *et al.* 2006).

Dans ce cadre, cette étude a pour objectif de fournir une méthode standardisée pour décrire la diversité actuelle des espèces domestiques, et de décrire précisément la diversité génétique de la chèvre domestique à l'échelle mondiale. La diversité des chèvres a été caractérisée à partir de 2430 individus provenant du monde entier. Elle inclut notamment 946 nouveaux individus provenant de régions très peu étudiées jusqu'à présent, notamment la zone du Croissant Fertile. L'étude a porté sur le segment hyper variable HVI de la région de contrôle de l'ADN mitochondrial. On dénote une extrême diversité de cette région puisque les 2430 individus correspondent à 1540 haplotypes. Cette analyse ayant été faite à l'échelle mondiale, elle permet d'établir clairement la nomenclature des haplogroupes maternels. Selon nos résultats, seulement 5 des 6 groupes décrits jusqu'alors sont suffisamment divergents pour pouvoir être décrits comme des haplogroupes différents. De plus, un nouvel haplogroupe mitochondrial a été décrit, et correspond à des individus localisés autour du Croissant Fertile (Figure 1.5 A).

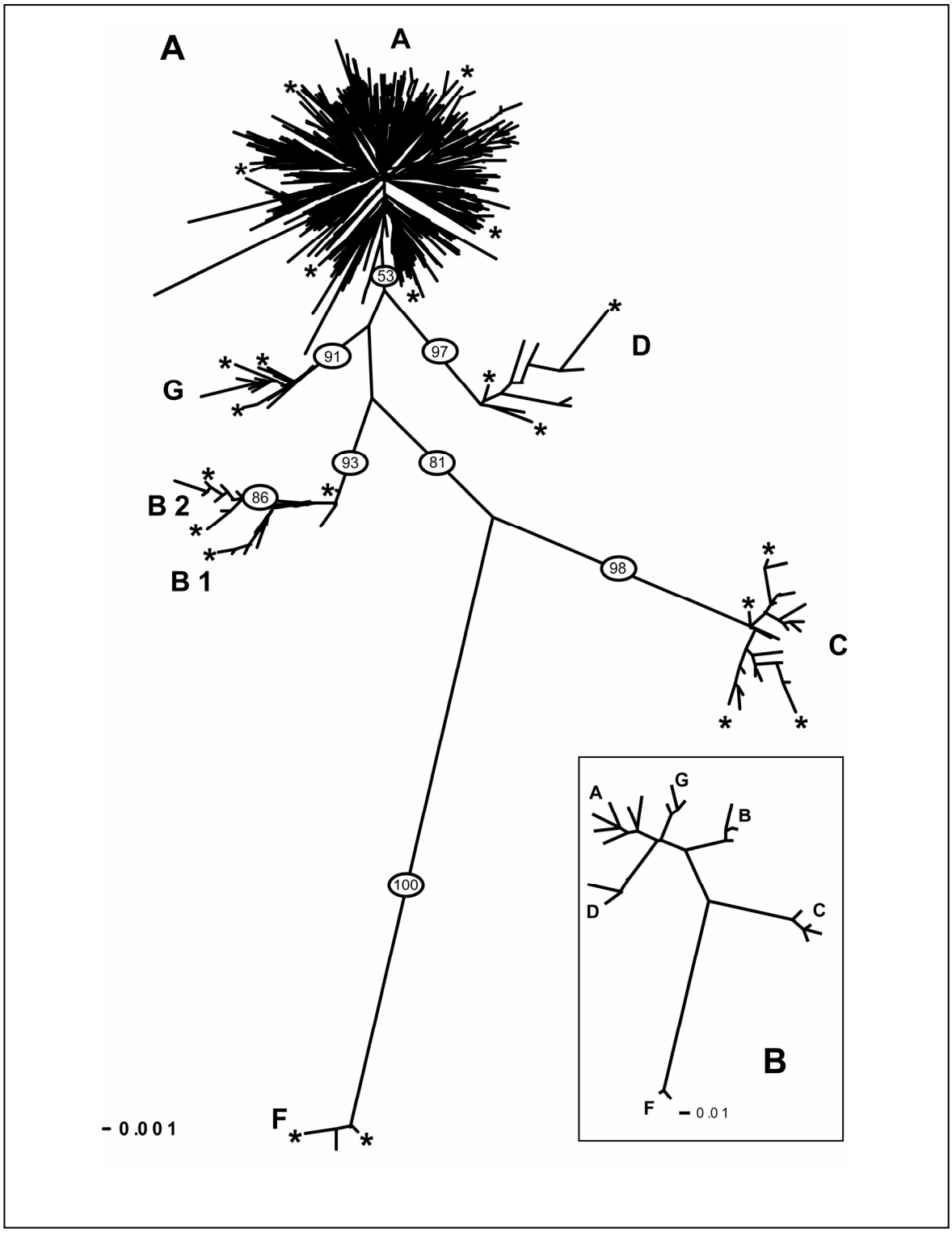

Figure 1.5. A. Les six haplogroupes mitochondriaux de chèvres domestiques détectés à partir de l'analyse de 1540 haplotypes (A, B, C, D, F, G). L'arbre représenté a été réalisé par la méthode de Neighbor-Joining. Les chiffres donnent les valeurs de bootstraps. Les étoiles représentent la position de 22 individus choisis comme références représentant la diversité totale et dont l'arbre neighbor-joining est donné dans l'encadré B.

Une forte diversité génétique est retrouvée au sein de chacun de ces groupes. La plupart de la diversité est répartie entre haplogroupes à l'intérieur des régions géographiques. Cette faible structure phylogéographique résulte probablement de l'ubiquité de l'haplogroupe A qui est fortement dominant, et représente plus de 90% des individus (Figure 1.6). La large répartition des autres haplogroupes (à une exception près), serait liée aux migrations humaines. L'ADN mitochondrial caractérisé ne permet pas de distinguer la fragmentation récente des populations locales de chèvres en races isolées.

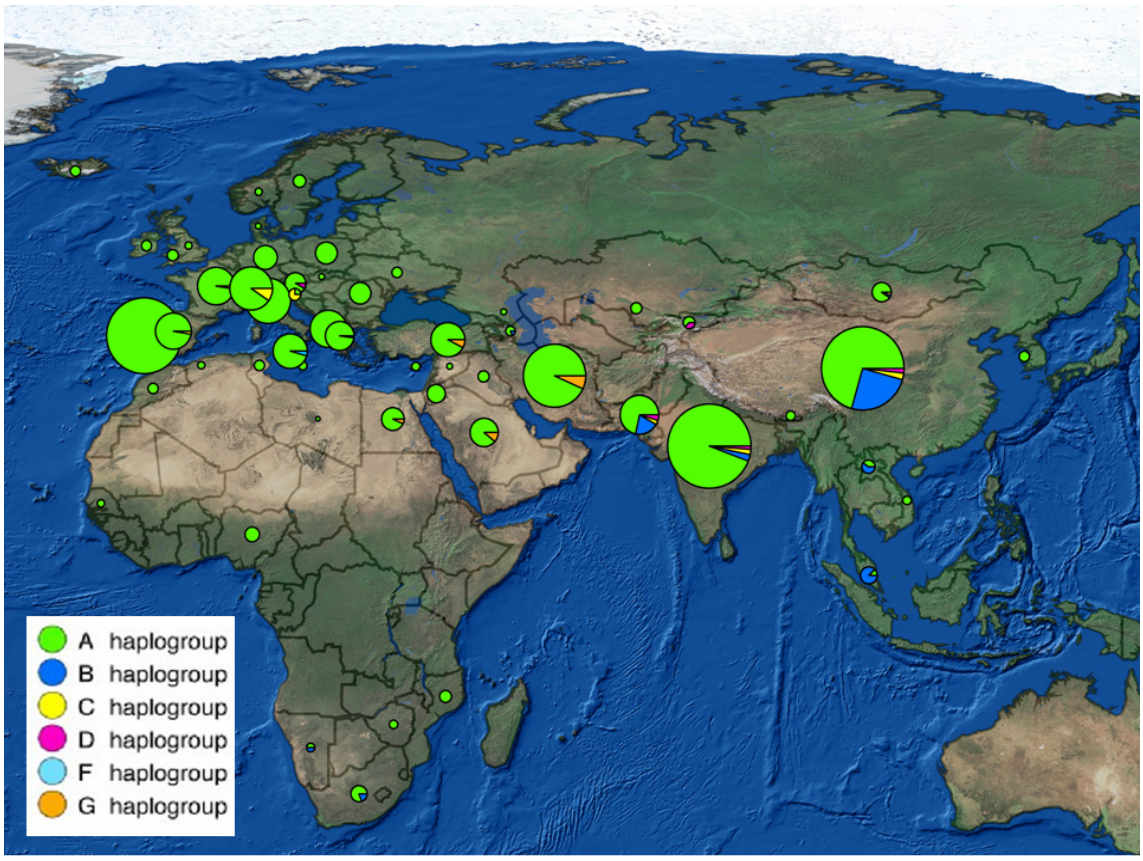

Figure 1.6. Distribution géographique des haplogroupes d'ADNmt chez la chèvre domestique.

L'estimation des paramètres démographiques, réalisée à partir d'analyses de mésappariements ("mismatch analysis"), montre que tous les haplogroupes ont subit une expansion démographique récente dont la date correspond approximativement à la période de domestication. Cependant, même avec un jeu de données aussi grand que celui utilisé

ici, il est très difficile de donner des dates relatives exactes selon les groupes, les intervalles de confiance étant très importants.

Au cours de cette étude, nous proposons également des critères standards pour la définition des haplogroupes mitochondriaux. Ils sont basés en partie sur l'utilisation des analyses de mésappariements qui permettent de définir un nombre de mutations seuil au delà duquel les individus appartiennent à des groupes différents (Figure 1.7).

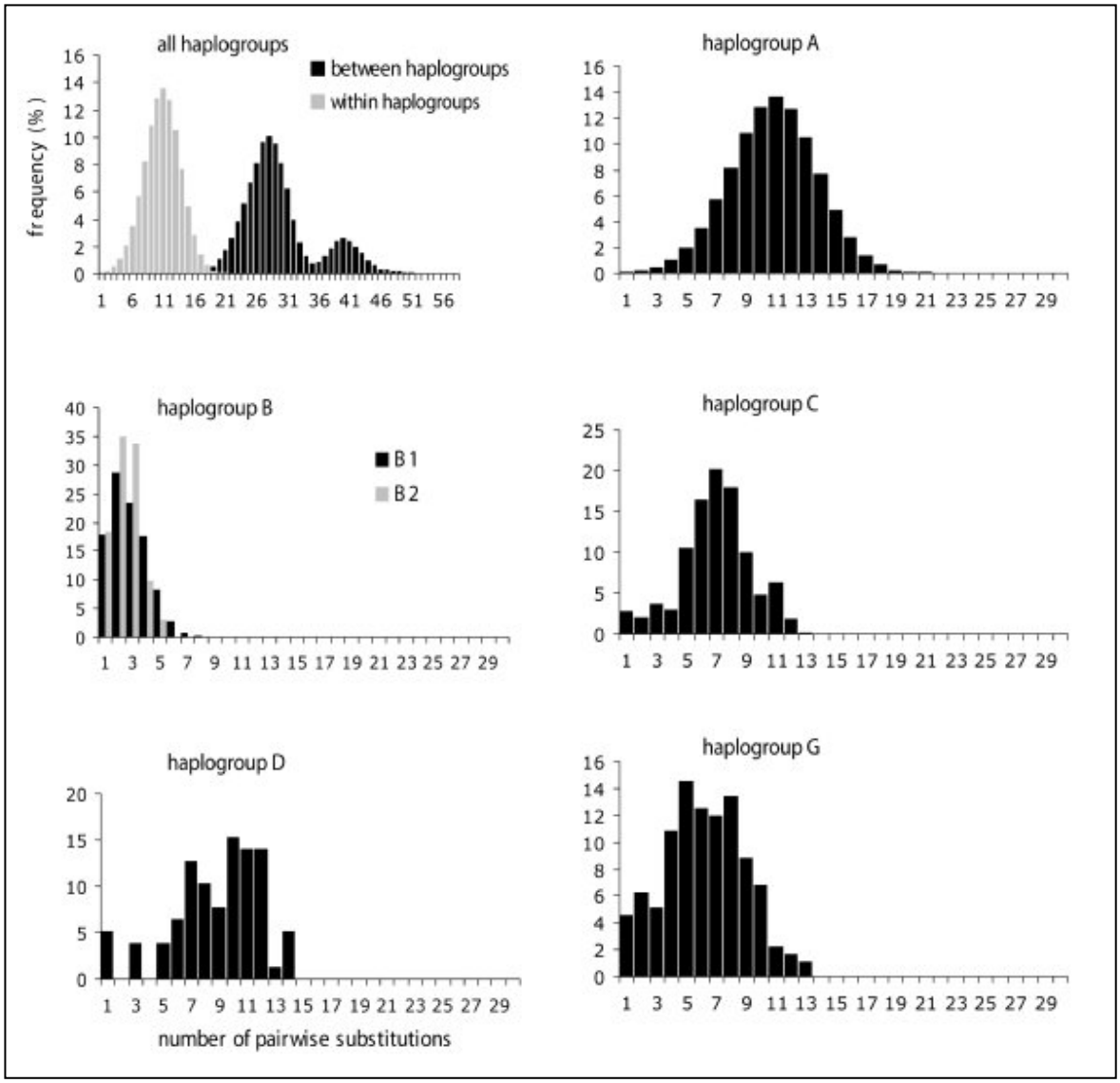

Figure 1.7. Distribution des substitutions entre paires d'haplotypes pour les haplogroupes d'ADNmt.

La réalisation d'un arbre phylogénétique est également nécessaire pour placer de nouveaux individus relativement aux haplotypes déjà définis. Pour faciliter cette tâche, nous fournissons 22 séquences de référence qui permettent une première analyse rapide de nouveaux jeux de données (Figure 1.5 B). Cette méthodologie peut également s'appliquer pour standardiser et clarifier la nomenclature des haplogroupes mitochondriaux chez d'autres espèces domestiques.

Article 2. Arguments génétiques en faveur d'un événement de domestication à grande échelle chez la chèvre

Ce chapitre est basé sur l'article "Goat domestication: a single large-scale event without bottleneck" de S. Naderi, H.-R. Rezaei, F. Pompanon, M. G. B. Blum, R. Negrini, H.-R. Naghash, Ö. Balkız, M. Mashkour, O. Gaggiotti, P. Ajmone-Marsan, A. Kence, J.-D. Vigne, P. Taberlet, soumis.

Les premières traces archéologiques de la domestication de la chèvre permettent de dater celle-ci il y a environ 10 500 ans dans les Vallées du Tigre et de l'Euphrate, dans le Sud-Est de l'Anatolie (Peters *et al.* 1999; Peters *et al.* 2005), et il y a moins de 10 000 ans dans le Zagros (Zeder & Hesse 2000; Zeder *et al.* 2005). Bien que moins probable, l'hypothèse d'une domestication plus récente (Horwitz *et al.* 2000) encore dans la basse vallée de l'Indus n'a pas été contestée (Meadow 1996). La chèvre a été domestiquée à partir de l'aegagre (*Capra aegagrus*), et la mise en évidence de trois haplogroupes mitochondriaux chez la chèvre domestique par Luikart *et al.* 2001, a été interprétée comme l'existence de plusieurs évènements de domestication indépendants. En faisant l'hypothèse d'un seul haplogroupe domestiqué par haplogroupe et en supposant un temps de coalescence de 10 000 ans pour l'haplogroupe majoritaire (groupe A), ces auteurs ont daté les autres évènements de domestication il y a environ 6 000 ans et 2 000 ans pour les haplogroupes C et B respectivement. Ce scénario est complètement remis en question depuis la découverte de la présence de chèvres de l'haplogroupe C dans le Sud de la France il y a 7 500 ans, très loin des centres de domestication plausibles (Fernández *et al.* 2006).

Dans ce contexte, notre objectif est de mieux comprendre le processus de domestication par une analyse extensive de la diversité génétique des chèvres domestiques et des représentants actuels de son ancêtre sauvage. Nous avons donc analysé la région de contrôle de l'ADN mitochondrial chez 487 aegagres échantillonnés dans 43 localités recouvrant la majeure partie de l'aire de répartition de l'espèce. Les 251 haplotypes obtenus ont été analysés conjointement aux 1540 haplotypes domestiques connus à ce jour (voir chapitre 4; Figure 1.8).

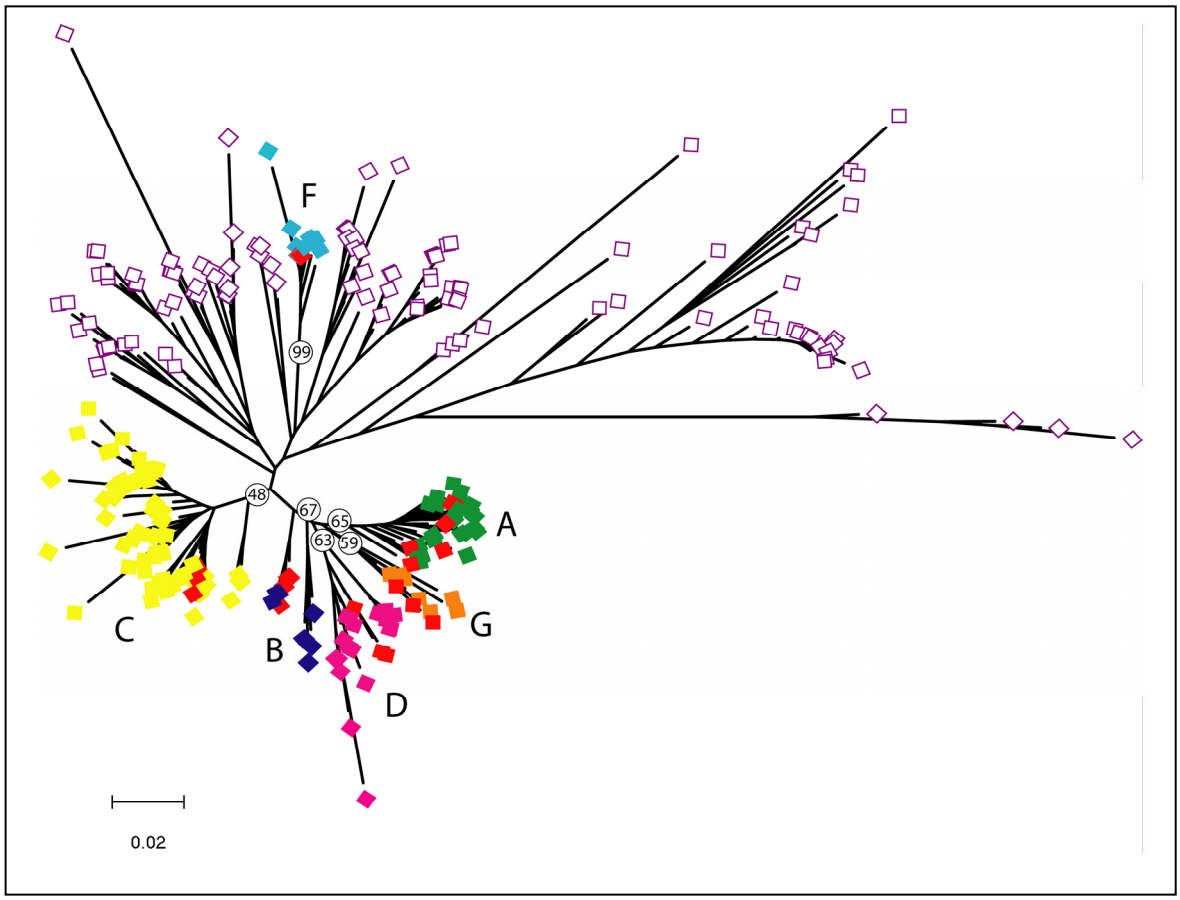

Figure 1.8. Relations phylogénétiques des 251 aegagres et des 22 haplotypes de référence représentatifs de la diversité des chèvres. Les haplotypes des six haplogroupes définis chez les domestiques sont représentés par: vert = A, bleu foncé = B, jaune = C, rose = D, bleu clair = F et orange = G. Les haplotypes rouges correspondent aux sauvages proches des domestiques, ceux représentés en blanc correspondent aux sauvages n'appartenant pas à un haplogroupe domestiqué.

Une analyse de la diversité nucléaire a également été menée en comparant à l'aide de marqueurs AFLP le polymorphisme des aegagres à ceux de races domestiques iraniennes et européennes (italiennes).

L'estimation de paramètres caractérisant l'histoire démographique des populations à partir des données génétiques montre une signature d'expansion plus forte chez les aegagres dont le génotype est proche des chèvres domestiques. Cela signifie qu'une partie des sauvages a subit une expansion démographique avant la domestication effective, qui pourrait être liée à une phase de gestion durable de troupeaux sauvages par l'homme. Cette phase de pré-domestication corrobore des données archéologiques qui suggèrent le contrôle et la protection des populations de chèvres sauvages. Elle aurait duré plusieurs siècles. Dans le Zagros, elle aurait notamment été caractérisée par le prélèvement de jeunes mâles et de vieilles femelles dans les troupeaux, ce qui n'était pas le cas pour les aegagres chassés. Plus tard, les animaux issus de ces populations sauvages gérées, éventuellement transférés loin de leur aire de distribution naturelle, auraient été à l'origine des chèvres domestiques. La localisation actuelle des aegagres génétiquement proches des chèvres domestiques comprend une zone qui inclut l'Est de l'Anatolie, le Zagros, le Plateau Central Iranien et le Nord-Est de l'Iran. La phase de pré-domestication n'a donc pas été un phénomène local, mais une pratique bien plus vaste que ne le laissait penser les seuls arguments archéologiques. On peut faire l'hypothèse que la phase de pré-domestication dans le Sud du Zagros et dans le Plateau Central Iranien. En effet, des haplotypes identiques à ceux de cette région se retrouvent à plusieurs milliers de kilomètres, ce qui est inhabituel chez les animaux (excepté chez les oiseaux ; e.g. Ball *et al.* 1988 ; Questiau *et al.* 1999). Il est donc probable que les hommes aient transporté des animaux dès la phase de pré-domestication, à partir de cette région (Sud Zagros, Plateau Central Iranien) où la pré-domestication aurait été initiée (Figure 1.9).

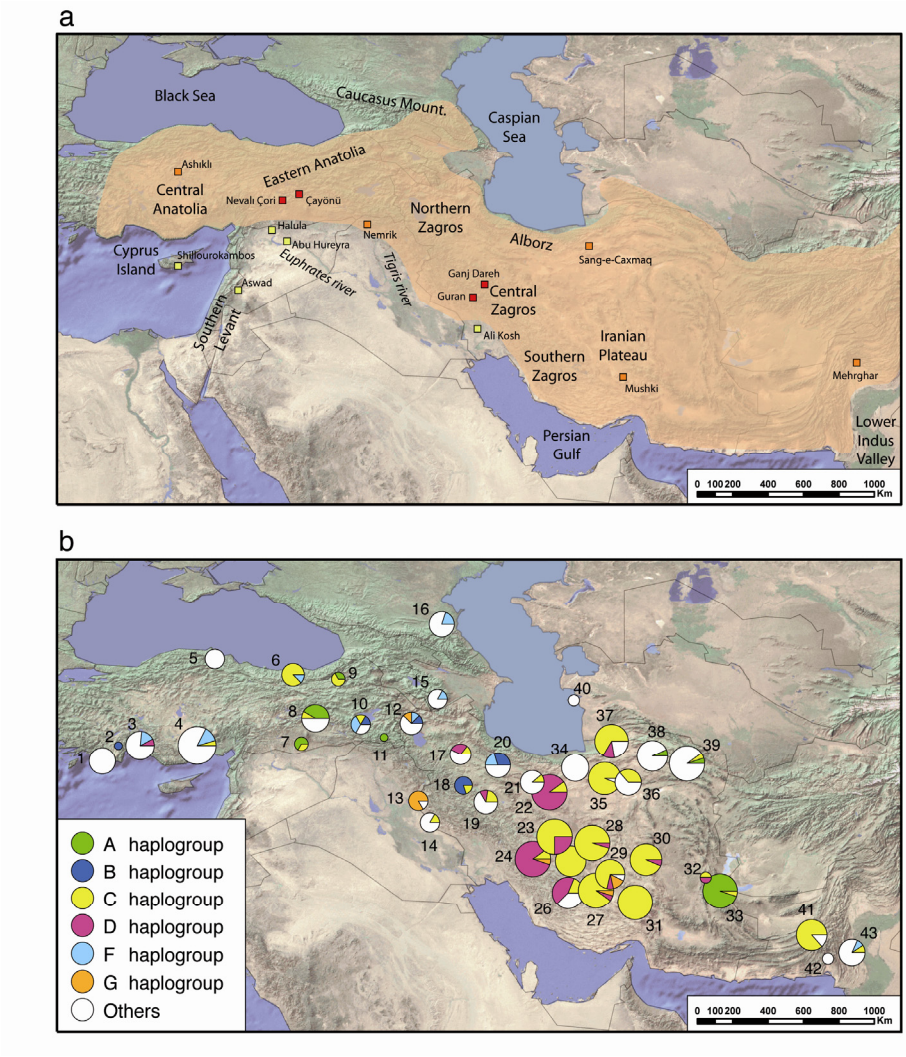

Figure 1.9. Région étudiée et distribution géographique des haplogroupes d'ADNmt pour l'aegagres. a) Distribution naturelle du aegagre d'après Uerpmann (Uerpmann 1987). Les sites archéologiques qui démontrent la domestication pré-Néolithique locale de chèvre sont représentés en rouge. Les sites qui suggèrent la domestication locale de la chèvre, ou le transfert de chèvres domestiquées au début de la période néolithique dite de « pré-poterie », sont représentés en orange. Les sites qui fournissent l'évidence d'un transfert de chèvres hors de la région géographique originelle de l'aegagre vers le milieu du 10 ème millénaire Cal. B. P, sont représentés en jaune. b) Distribution géographique des haplogroupes de mtDNA pour l'aegagre. La taille des cercles est proportionnelle au nombre d'individus analysés. Les différents haplogroupes d'aegagre sont en codes couleurs identiques à ceux utilisés pour la Figure 1.4. Les différentes localités identifiées par des nombres, correspondent à celles décrites dans le tableau n°1 annexé à l'article n°2.

La comparaison de la diversité génétique des aegagres sauvages avec celle des chèvres domestiques et l'estimation du nombre d'haplotypes ancestraux capturés lors de la domestication convergent pour montrer que la phase de domestication effective a aussi concerné un grand nombre d'individus. Plusieurs dizaines voire centaines d'haplotypes mitochondriaux ont très probablement été capturés. Cela n'a pu se faire qu'à une vaste échelle géographique à partir des troupeaux sauvages prédomestiqués. Il est clair que contrairement à ce qui a été démontré chez plusieurs plantes, la chèvre n'a pas subi de fort goulot d'étranglement pendant sa phase de domestication.

La localisation des zones impliquées dans la phase de domestication effective est possible en recherchant les populations sauvages actuelles présentant les génotypes les plus proches des chèvres domestiques. En ce qui concerne l'haplogroupe domestique le plus représenté (groupe A), l'origine le plus probable est l'Est de l'Anatolie qui serait donc un centre de domestication. La présence d'haplotypes du groupe A au sud-est de l'Iran serait plus vraisemblablement due à des introgressions à partir des domestiques. La répartition géographique des haplotypes sauvages proches des autres haplogroupes domestiques montrent qu'en plus de l'Est de l'Anatolie, le Zagros (Sud et Centre) serait aussi impliqué dans la phase de domestication. Toutes ces conclusions concordent avec les données archéologiques. Il est possible que ces différents évènements se soient produits à différents moments entre 10 000 et 7 000 ans. Quoi qu'il en soit, nos résultats ne soutiennent pas l'hypothèse d'un centre de domestication de la chèvre dans la basse vallée de l'Indus.

Le scénario de la domestication de la chèvre que nous proposons remet donc en question plusieurs hypothèses admises jusqu'à présent. La domestication se serait faite à une vaste échelle géographique, sans doute sur une longue période de temps et en deux étapes. La première étape, la pré-domestication, aurait consisté en une gestion durable des troupeaux sauvages et avec des premiers déplacements d'animaux par l'homme. La seconde étape, la domestication effective, aurait aussi concerné un grand nombre d'individus d'où une absence de fort goulot d'étranglement permettant de capturer une grande partie de la diversité génétique sauvage. Ces résultats soulèvent maintenant la question de la généralisation de ce type de scénario, et notamment de l'existence d'une phase de pré-domestication et l'absence de goulot d'étranglement, chez les autres animaux domestiques.

Article 3. Les vaches, les moutons et les chèvres sont-elles des espèces menacées?

Ce chapitre est basé sur l'article "Are cattle, sheep, and goats endangered species?" de P. Taberlet, A. Valentini, H.R. Rezaei, S. Naderi, F. Pompanon, R. Negrini, P. Ajmone-Marsan publié dans Molecular Ecology (2007, doi: 10.1111/j.1365-294X.2007.03475.x)

Depuis une dizaine de milliers d'années, les fermiers ont géré les vaches, les moutons et les chèvres de façon durable, ce qui a abouti à des cheptels bien adaptés aux conditions locales dans lesquelles ils sont élevés. Il y a environ 200 ans, la situation a commencé à changer dramatiquement avec la montée en puissance du concept de race. Tous les animaux d'une même race ont commencé à être sélectionnés pour exprimer des traits phénotypiques communs. Ainsi, la reproduction entre individus de races différentes a fortement décliné, conduisant à une forte fragmentation des populations initiales.

Depuis quelques décennies les pressions de sélection ont encore augmenté avec l'objectif d'augmenter la productivité, sans que la préservation de la diversité génétique globale ne soit suffisamment prise en compte. Si l'efficacité des méthodes modernes de sélection a permis une augmentation des rendements de production animale, elle a également eu pour effet une diminution alarmante de la variabilité génétique. De nombreuses races industrielles sont maintenant fortement consanguines avec des tailles efficaces de populations inférieures à 50. Avec le développement de ces races, les éleveurs subissent de plus en plus des pressions économiques les conduisant à abandonner leurs races traditionnelles. Cela a déjà eu pour conséquence la disparition récente d'un grand nombre d'entre elles. Ainsi, les ressources génétiques d'animaux d'élevage tels que la vache, le mouton et la chèvre sont fortement menacées, essentiellement dans les pays développés.

Il nous apparaît donc essentiel de promouvoir des mesures conduisant à une gestion durable des ressources génétiques. Il faut avant tout préserver *in situ* les races menacées. Il est aussi nécessaire de mettre en place des programmes de sélection afin de restaurer la diversité génétique des races industrielles. Enfin, il est indispensable de protéger les espèces sauvages proches des espèces domestiques qui peuvent devenir une ressource génétique très utile.

Conclusion

Depuis le début de la domestication, les processus démographiques, les mutations, la dérive génétique, l'adaptation locale, et la sélection des races ont façonné la diversité génétique des populations domestiques. Une bonne connaissance de la structure génétique des populations domestiques et sauvages est donc essentielle pour comprendre l'histoire de la domestication, mais aussi pour mettre en place des programmes de conservation. Cela a été le cadre du travail que nous avons mené sur la chèvre domestique (*Capra hircus*), l'un des premiers ongulés domestiqués il y a plus de 10 000 ans dans le Croissant Fertile. L'histoire de la domestication a été abordée par l'analyse comparée de la diversité génétique des chèvres domestiques et de celle de son ancêtre sauvage (*Capra aegagrus*).

Nous avons tout d'abord mis au point une méthode standard permettant d'établir une nomenclature claire des haplogroupes mitochondriaux, et aussi de définir de nouveaux haplogroupes lorsque cela s'avère pertinent. Cette méthode a été utilisée pour analyser 2430 séquences d'ADN mitochondrial (fragment HV1 de la région de contrôle), incluant 946 nouveaux échantillons issus de régions très peu étudiées jusqu'ici (notamment le Croissant Fertile). Cinq des six haplogroupes mitochondriaux présentent une forte diversité génétique, mais la diversité est essentiellement distribuée entre haplogroupes au sein des régions géographiques. Cette faible structure phylogéographique résulterait surtout de l'ubiquité de l'haplogroupe A (plus de 90% des chèvres), mais aussi de la vaste répartition des autres groupes, conséquence très probable des migrations humaines.

Même avec un jeu de données aussi important que celui analysé ici, il est très difficile de comprendre l'histoire de la domestication en se basant uniquement sur l'analyse des animaux domestiques. Par exemple, il est difficile d'estimer précisément si les expansions démographiques dont on voit la signature génétique sont antérieures ou postérieures à la domestication. De plus, il n'est pas possible d'identifier le(s) centre(s) de domestication de la chèvre à cause de la faible structure phylogéographique observée. On n'identifie aucun gradient de diversité, alors que l'on attend une diversité décroissante à partir du centre de domestication. Enfin, les données génétiques sur les domestiques seuls ne permettent pas de tester précisément l'hypothèse d'un goulot d'étranglement au moment de la domestication. C'est l'étude conjoint des ancêtres sauvages (les aegagres) et des chèvres qui a apporté les nouvelles informations permettant de reconstituer l'histoire de la domestication. Ces nouvelles informations concernent la localisation spatiale des aegagres génétiquement proche des chèvres domestiques, la comparaison de la diversité

nucléaire et mitochondriale des domestiques et des sauvages, et la reconstitution des processus démographiques passés chez les aegagres. Ces données ont été acquises à partir d'un échantillonnage extensif composé de 487 aegagres issus de 43 localités recouvrant l'ensemble de l'aire de répartition de l'espèce. Elles ont permi d'établir un nouveau scénario de domestication de la chèvre en deux étapes. La première étape correspond à une phase de gestion des troupeaux sauvages par l'homme qui précède la domestication *sensu stricto*. Pendant cette phase de pré-domestication, les troupeaux d'aegagres concernés ont subi une expansion démographique dont la signature génétique est toujours visible actuellement. L'estimation des paramètres démographiques montre en effet un taux de croissance démographique plus fort chez les aegagres génétiquement proches des chèvres que chez les aegagres d'haplotypes très divergents des domestiques. L'étape suivant la pré-domestication est la domestication *sensu stricto* réalisée à partir d'individus issus des troupeaux gérés par l'homme.

Les aegagres génétiquement proches des chèvres sont actuellement répartis sur une vaste zone qui inclut l'Est de l'Anatolie, l'ensemble du Zagros, le Plateau Iranien Central et le Nord Est de l'Iran. Cette distribution démontre que les phénomènes de pré-domestication et de domestication ont été réalisés à grande échelle du point de vue géographique. Ils ont également été de grande ampleur du point de vue génétique. L'analyse comparée de la diversité nucléaire et mitochondriale chez les chèvres et les aegagres démontre qu'une grande partie de la diversité génétique sauvage a été capturée par les domestiques. Il n'y a donc pas eu de goulot d'étranglement au moment de la domestication de la chèvre. Ce scénario est très différent des modèles précédents qui mettaient en avant des phénomènes se produisant à une échelle réduite, avec des centres de domestication très localisés et de fortes réductions de la diversité génétique.

Perspectives

L'utilisation plus poussée de marqueurs nucléaires devrait permettre de mieux comprendre l'histoire de la domestication. Le séquençage de nombreux gènes nucléaires apporterait une masse d'information permettant d'estimer de façon fiable les dates d'expansion des aegagres génétiquement proches des chèvres. Une expansion démographique des aegagres antérieure à celle des chèvres domestiques confirmerait l'existence de la phase de pré-domestication.

L'étude d'échantillons de chèvres issus de sites archéologiques apporterait également des éléments nouveaux. La comparaison d'échantillons anciens et actuels devrait permettre d'identifier des mutations expliquant les variations phénotypiques apparues et sélectionnées pendant le processus de domestication, conduisant ainsi à l'identification des gènes de la domestication.

Il paraît enfin nécessaire de tester si des scénarii de domestication à grande échelle comme celui que nous avons pu mettre en évidence chez la chèvre sont plausibles chez d'autres animaux domestiques. En d'autres termes, il s'agit de tester si l'absence de goulot d'étranglement au moment de la domestication est nécessaire pour garantir le succès d'une domestication animale durable.

Figure 1.10. *Capra aegagrus* à Malayer, zone protégée en Iran (Photo par HR. Rezaei).

Chapter 2. Introduction

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We are becoming more and more aware of the importance of the world's biodiversity – the variety of its plants, animals and micro-organisms, and of the ecosystems in which they live. For a sustainable management of these genetic resources, we need at first to know the evolutionary history of the organisms. The present structure of the genetic diversity retains the signatures of past demographic events and helps to reconstitute the evolutionary history (Luikart *et al.* 2003). Nature and human impacts are the most important forces that always affected the evolutionary history of organisms. One of the most important human impacts on organisms is the domestication process (Pääbo 1999). A few wild species became domesticated. The precise analysis of the genetic structure of both wild and domestic species can provide invaluable data to track and understand the domestication process itself.

Beside the wild ancestor when it still exists, the different domestic breeds can be considered as genetic resources. Breeds with the highest genetic diversity represent the most valuable resources, and are expected to be found close to the domestication centres (Bruford *et al.* 2003). As a consequence, the precise knowledge of wild ancestors, of domestication centres, and of colonization routes is of prime importance for tracking genetic resources (Zeder *et al.* 2006a).

The 40-plus livestock species contributing to today's agriculture and food production are shaped by a long history of domestication and development. Selection pressures resulting from environmental stress factors, and the controlled breeding and husbandry imposed by humans, have been combined to produce a large variety of genetically distinct breeds. This diversity, developed over thousands of years, is a valuable resource for today's livestock keepers. Genetically diverse livestock populations provide a greater range of options for meeting future challenges, whether associated with environmental change, emerging disease threats, new knowledge of human nutritional requirements, fluctuating market conditions or changing societal needs (FAO 2007).

If the domestication process was the major initiating event in the development of today's livestock diversity, the subsequent dispersion and migration of domesticated species across all five continents was equally important. This process played a major role

in the emergence of the current geographic distribution of livestock diversity. The main factors at the root of the early dispersion of livestock species were the expansion of agriculture, trade, and military conquests. This resulted in genetic (e.g. selection, gene flow) and demographic processes that explain the present worldwide distribution (Diamond 2002). After the initial plant and animal domestications in the Near East, ca. 11,500 and 10,500, respectively, years ago (ya) (Harris 1996), Neolithic culture diffused into Europe along two main routes: ‘‘Mediterranean” route and ‘‘Danubian’’ route (Diamond & Bellwood 2003).

From the beginning of animal husbandry in prehistory to the mid-twentieth century, gene flow generally enhanced diversity. However, during the past five decades the development of intensive selection to increase the production led to a reduction in diversity. Furthermore, the large-scale replacement of local breeds with a small number of globally successful breeds also contributed to a strong overall diversity in domestic breeds. This process was particularly intense in North America and Europe, where 50 percent of documented breeds are classified as extinct, critical or endangered. It is now being replicated in developing countries, and represents a major threat to the conservation and utilization of indigenous animal genetic resources (FAO 2007).

Clarification of the geographic pattern and history of the dispersal of livestock is essential to the identification of original geographic areas with high levels of diversity, which are potential priority areas for conservation efforts. This requires extensive mapping of genetic diversity. Thus, if distant livestock populations are relatively similar genetically, we can infer that humans transported animals. Up to now, very few studies have been undertaken in this field.

In summary, the combined effects of portability/mobility on the one hand (goats and horses) and introgression on the other (cattle, sheep and pigs) has shaped the distribution of genetic diversity that we see in livestock on a global scale today (Bruford *et al.* 2003). How gene flow will impact diversity in the future will depend primarily on the policy and legislative frameworks that are now in the process of being developed. It seems likely that the transfer of livestock selection programs will continue and even increase rapidly in developing countries. The crowding out of locally adapted breeds will probably accelerate in many developing countries, unless appropriate support is given to local livestock keepers for promoting in situ conservation.

It is critical that the analysis of the domestication history be conducted with not only an appreciation of the biology of domesticated plants and animals, but also with an

understanding of the cultural context of the human partners in the process. And this is where genetics and archaeology come together to provide a richly detailed understanding of domestication (Zeder *et al.* 2006a). As the origin and diffusion of livestock is intimately linked to human evolution and migrations, data from domestic goats, sheep, cattle and other species can be used as a way to study the history of human populations (Fernández *et al.* 2006).

1. Tools to understand livestock origin and diversity

1.1. Genetic tools

Genetic tools have a central role in many biological investigations. For instance, genetic analysis can provide insights into diverse investigations such as evolutionary histories of species (Avise *et al.* 1987), interactions and relationships among populations (Luikart *et al.* 2001; Meadows *et al.* 2007), or individuals (Queller *et al.* 1993), evaluation of the success of specific management actions and conservation (Manceau *et al.* 1999b ; Vernesi *et al.* 2002), population and behavioral ecology (Scribner & Chesser 2001) and food habits (Symondson 2002). DNA-based markers have been developed since the 1970s (Karp *et al.* 1997; Sunnucks 2000) but have only been actively applied to studies of animal domestication and diversity since the early 1990s (Loftus *et al.* 1994).

A series of recent genetic studies has revealed the remarkably complex picture of livestock domestication. By comparing mitochondrial (mtDNA) and nuclear DNA sequences of modern breeds with their potential wild ancestors, we have gained new insights into the timing and location of domestication event(s) that produced the farm animals. Recognizing of real number of domestication events and the locations in which they took place are very important for determination of our approach to conserving livestock biodiversity resources in the future (Bruford *et al.* 2003).

1.1.1. Choosing molecular markers

To help understand the origins of domestication of a livestock species, the ideal molecular marker should have several characteristics. First, it should be sufficiently conserved to allow the identification of the wild taxon or population from which the species descends. Second, the marker should be variable and structured enough across the geographical range of the wild ancestor so that the approximate locality of domestication can be identified. Third, the marker should evolve at a rapid but constant rate — this feature allows the origin of a particular polymorphism to be dated. This combination of characteristics is difficult to find, but fortunately, in animal evolutionary studies, there is such a marker: mtDNA. At present, mtDNA is by far the most widely used molecular tool in domestication studies (Bruford *et al.* 2003).

Protein polymorphisms were the first molecular markers used in population studies. A large number of studies, particularly during the 1970s, documented the characterization of blood group and allozyme systems. However, the level of polymorphism observed in proteins is often low, which reduces the general applicability of protein typing in diversity studies (Randi *et al.* 1990).

DNA-based polymorphisms are now the markers of choice for molecular-based surveys of genetic diversity. Many genetic studies of plant and animal domesticates do not focus on the particular genes responsible for the changes in morphology, behavior, and physiology that distinguish domesticates from their wild progenitors. Instead, these studies generally concentrate on variation in neutral genes or in non-coding genetic regions that can be used to trace the evolutionary history of domesticates and their wild progenitors (Zeder *et al.* 2006a).

1.1.2. Mitochondrial DNA

Mitochondrial DNA is a small DNA molecule (less than 20 kb in most mammals) that is located only in mitochondria. It is the most widely used DNA marker for studies of closely related populations such as domestic breeds. Especially the highly variable section of this molecule, the control region, has a rapid rate of evolution, which leads to a high level variability within species. It represents an ideal marker for studying the divergence between wild and domestic populations under a relatively short time scale over which domestication operated (Zeder *et al.* 2006a). For instance, in a study of the control region

diversity in domestic goats (*Capra hircus*), 331 haplotypes were identified from 406 individuals (Luikart *et al.* 2001). The lack of recombination associated with exclusive maternal inheritance allows the identification of maternal lineages that have diverged through time only via accumulation of new mutations. Moreover, the presence of mtDNA at a high copy number in most cells facilitates its extraction from ancient material, thus making it very suitable for archaeological genetic studies (Fernández *et al.* 2005).

Also this marker is less sensitive to introgression from wild species than nuclear DNA. Nuclear gene histories may have been complicated through more ephemeral encounters between wild males and tame females (Bruford *et al.* 2003). Since the effective population size of mtDNA is one-quarter that of nuclear DNA, it has proven particularly useful in the study of population dynamics because it is capable of detecting population bottlenecks that are likely to occur in domesticates, but which have less impact on nuclear DNA (Zeder *et al.* 2006a). For interspecific studies the mtDNA cytochrome *b* gene (cyt *b)* is more appropriate than the control region because it evolves less rapidly, being under functional constraint as a coding gene. Thus, it is easier to align between species (without sequence gaps) and, in conjunction with the fossil record to calibrate a molecular clock, easier to use for estimating divergence dates between taxa (e.g., sheep and goat diverged - 6 MYA) (Luikart *et al.* 2006).

In summary, mtDNA sequences are the markers of choice for domestication studies. More specifically, mtDNA sequences are used to identify putative wild progenitors, the number of maternal haplogroups and their geographic origins. It can also be used to track geographic patterns of diversity and evolution (phylogeography). Mitochondrial DNA can also tell us about the recent demographic processes affecting a population, for example whether a population has undergone a recent demographic expansion, or has a more complex history (Bruford *et al.* 2003).

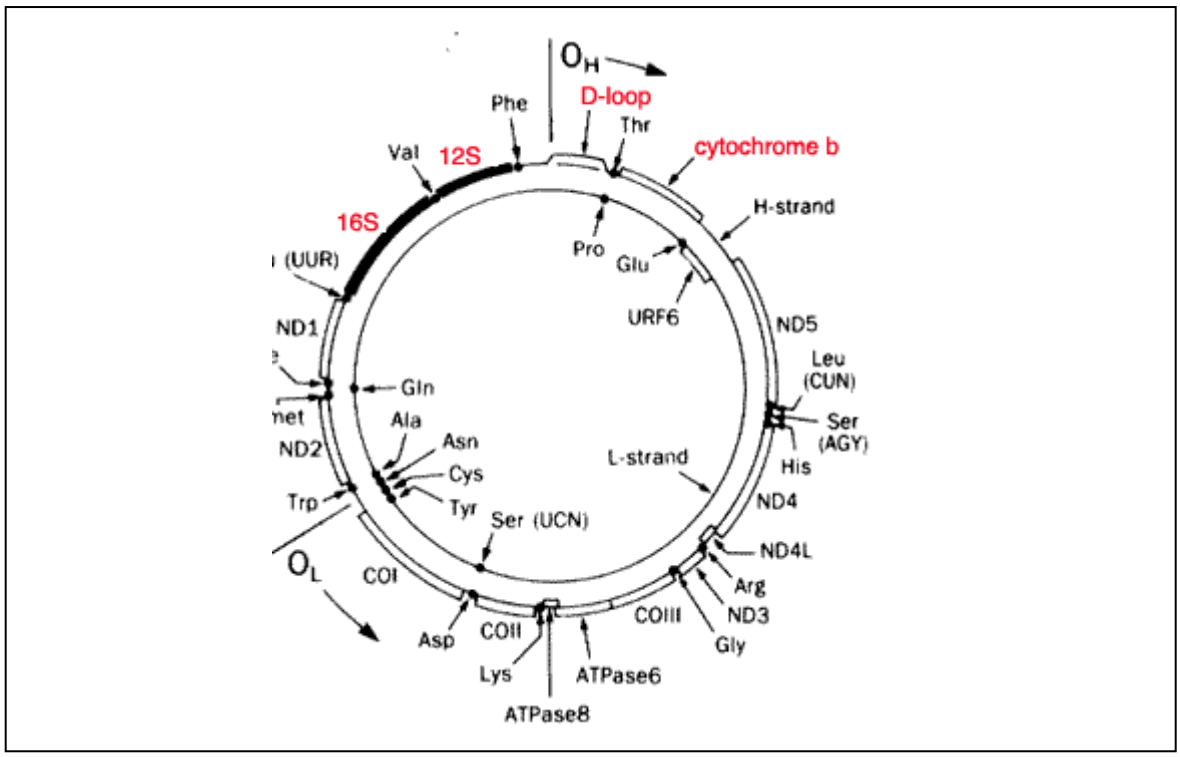


Figure 2.1. Schema of the Mammalian mitochondrial genome

However, there are some limitations. Mitochondrial DNA can be a poor predictor of overall genomic diversity, because it behaves like a single locus and is an extra-nuclear genetic marker with specific evolutionary dynamics. Crucially, as it is maternally inherited, mtDNA does not detect male mediated gene flow, which has had a powerful influence on the evolution of livestock species in modern times. Thus, although nuclear DNA is less variable than mtDNA in animals and therefore generally less useful in phylogenetic studies of relatively shallow time depth, studies on nuclear genes are needed because they give information on gene flow and selection processes that had a great influence on the evolution of livestock species (MacHugh *et al.* 1997).

1.1.3. Amplified fragment length polymorphism (AFLP)

This multilocus marker screens many loci distributed randomly throughout the genome, simultaneously. This is a relatively cheap, easy, fast and reliable technique based on DNA fingerprinting that detects hundreds of informative genomic restriction fragments by PCR amplification (Mueller & Wolfenbarger 1999). Fingerprints are produced without prior sequence knowledge using a limited set of generic primers. The number of fragments detected in a single reaction can be 'tuned' by selection of specific primer sets. The

technique will display presence or absence of restriction fragments rather than length differences. In general, there is an almost linear correlation between numbers of amplified fragments and genome size (Vos *et al.* 1995).

AFLP markers have proved useful for assessing genetic differences among individuals, populations and independently evolving lineages, such as species. Because of the rapidity and ease with which reliable, high-resolution markers can be generated, AFLPs are emerging as a powerful addition to the molecular toolkit of ecologists and evolutionary biologists (Ajmone-Marsan *et al.* 2001), and increasingly used in plant and animal domestication studies (Bruford *et al.* 2003).

The main disadvantage of AFLP markers is that they show a dominant mode of inheritance, i.e. heterozygotes cannot be characterized. This reduces the power of population genetic analyses, which generally require more informative codominant markers allowing heterozygosity analyses (Bruford *et al.* 2003).

1.1.4. Y-chromosome DNA

This DNA marker is transmitted by males only, without recombination. It is especially useful for reconstructing paternal lineages, and thus represents the "male view" of evolutionary history. Information from Y-chromosome is complementary to mtDNA data, although its DNA sequences are generally far less polymorphic, and therefore less informative (Luikart *et al.* 2006; Hanotte *et al.* 2000). The nucleotide diversity present on the mammalian Y-chromosome appears generally lower than that found on autosomes (Hellborg & Ellegren 2004). Information from the Y-chromosome is likely to be particularly important in domestic animals where the contribution of a small number of males has been disproportionately large during breed development, leading to a reduction of the polymorphism. In addition, examination of the Y-chromosome has the capacity to reveal the identity of those wild ancestors at the origin of the domestic breeds (Meadows *et al.* 2004). However, the possibility of paternal gene flow from wild males that mate with domestic females might have a confounding effect (Luikart *et al.* 2006). In case of hybridization between different breeds, the analysis of Y-chromosome polymorphism might allow to detect and to quantify male-mediated admixture (Hanotte & Jianlin 2005).

1.1.5. Microsatellites

Simple sequence repeats (SSR), also known as microsatellite repeats, consist of short nucleotide sequences (e.g. CAT) that are repeated many times in tandem (…CATCATCAT…). SSR are codominantly inherited. The number of SSR tandem repeats can vary in a sequence, and many such variants (alleles) can exist in a population. The repeated sequences is often simple, consisting of two, three or four nucleotides (di-, tri- and tetranucleotide repeats, respectively), and can be repeated 10 to 100 times. As there are often many alleles present at a microsatellite locus, the origin of a particular allele can be identified, provided that the pedigrees are known (Goldstein *et al.* 1995).

Microsatellites are the most useful DNA markers for measuring and comparing levels of diversity (e.g., number of alleles) within populations because these markers are highly variable, often having 5-10 alleles per locus. The analytical strengths of microsatellite markers are co-dominance and hypervariability (Queller *et al.* 1993). These markers can thus be used to compare levels of diversity within populations from different continental regions (e.g. inside and outside the centres of domestication). Microsatellites can also be useful for assessing genetic relationships among closely related populations (isolated for only several dozen generations) (Luikart *et al.* 2006).

Microsatellites have three primary uses in domestication studies. First, they can be used to quantify genetic variation within and among livestock populations or breeds. Second, they allow the documentation of admixture (genetic mixing) among livestock populations. Third, microsatellite data can be used to assign individuals to genetically similar groups at the population, breed or species levels. Microsatellites markers are also highly sensitive to genetic bottlenecks and selection, both of which are likely to have occurred during domestication events (Bruford *et al.* 2003).

Microsatellites also have some limitations. This type of marker developed for a particular species can often be applied to closely related species, but the percentage of loci that successfully amplify may decrease with increasing genetic distance. In other words, microsatellite primers developed for one species can rarely be used beyond the very closest relatives. Furthermore, the risk of null alleles (non-amplifying alleles) increases when the primer sequences were not designed specifically for the species under study. Therefore, it is better to develop microsatellite markers for each species. Finally, the

implementation of a microsatellite study is technically demanding, and the development is time-consuming and expensive (Jarne & Ladoga 1996).

The molecular markers used to characterize diversity in livestock have up to now little to do with the genes under selection for economically important traits. The identification of causative mutations for phenotypic variation will add a new dimension to the characterization of animal domestication, as it will allow researchers to trace selection and the spread of economically important alleles. Such analysis is potentially very powerful, especially when combined with single nucleotide polymorphism (SNP) screening methods, and indicates that there are exciting new avenues of research in this area. With the publication of genome sequences for key domestic species (for example for cattle genome see in: http://www.ncbi.nlm.nih.gov/genome/guide/cow/ and for chicken genome see in: http://www.ncbi.nlm.nih.gov/genome/guide/chicken/) and the increasing availability of expressed sequence tag (EST) databases, we can expect an exponential increase in the availability of both neutral and selected markers. It is exciting that in the future we should be able to simultaneously detect male and female demographic history and the signatures of selection, past and present, within the genomes of our domestic livestock (Bruford *et al.* 2003).

1.2. Archaeobiological approaches

Advances in molecular genetic and archaeobiological techniques in the interdisciplinary investigations over the past two decades have resulted in a virtual explosion of studies exploring the origins of plant and animal domestication.

1.2.1. Ancient DNA

It appears necessary to complete the analysis of the modern DNA diversity with ancient DNA (aDNA) studies that can potentially facilitate our understanding of the origin and the routes of diffusion of domestic species. This is feasible through both research of the DNA diversity of the wild progenitors just before the earliest domestication, and by the analysis of the evolution of the DNA diversity of domestics through times. In fact, ancient DNA provides a tremendous opportunity for the integration of archaeology and biology in the study of plant and animal domestication (Fernández *et al.* 2005).

Ancient DNA studies could be particularly helpful in pinpointing the site of domestication. For example, evidence for a local domestication would be provided by finding a DNA haplogroup in ancient domestic animals from one location (e.g., the Fertile Crescent) but not from other locations (e.g. East Asia). Even more compelling would be the discovery of a unique DNA haplogroup in both wild and domestic animals from one location, but a different DNA haplogroup in the wild and domestics from another location. Moreover, distinguishing between local domestication versus introgression might be facilitated by using ancient DNA samples from wild and domestic animals sampled through time (e.g. 12,000 to 5,000 years ago) in regions where domestication likely occurred (Luikart *et al.* 2006).

However, there are limitations in the utilization of aDNA in domestication studies. DNA is poorly preserved in warm climates corresponding to the putative centres of domestication. Up to now, no aDNA was recovered from bones of animal dating to the earliest phases of the domestication process, but a few studies analyzed more recent samples from European sites (Fernández *et al.* 2006; Larson *et al.* 2007). However, we can expect that future studies of aDNA combined with archaeozoology, will likely yield new discoveries greatly advancing our understanding of the origin and spread of farm animals and their role in ancient human societies. It will also be possible, for domesticated

animals, to track the timing of genetic change along with that of the other non-morphological and morphological indicators domestication (Zeder *et al.* 2006a).

1.2.2. Archaeological markers

The archaeological markers may take the form of morphological change in the target species, changes in its genetic structure, a restructuring of its population biology, or the transformation of its ecological context. Markers of domestication may also be found in the tools, settlement patterns, or even the ideology of the human partners in the domestication process (Zeder *et al*. 2006).

The archaeological markers for animal species domestication studies can be divided into two categories: 1- Morphological markers 2- Nonmorphological markers

1.2.2.1. Morphological Markers

1.2.2.1.1. Genetically driven markers

Those are that reflect genetically driven, selective responses to domestication passed from one generation to the next. These markers reflect the evolutionary impact of domestication on the animal on a population level (Animal-oriented markers). The domestic animals display a set of changes in behavioral, physiological, and morphological characteristics that can be directly tied to selection for less aggressive behavioral traits, such as earlier onset of sexual maturity and more frequent receptivity, smaller brain size and other changes in neurological organization, shortening of the snout, tooth-size reduction and changes in tooth number, the changes in the size and shape of horns, smaller bodies, and lessening of sexual dimorphism (Zeder 2006b).

Clearly, beside of domestication there are a number of other factors that may cause morphological changes in organisms. The impact of these factors will also vary depending on the biology of different species and the nature of their interaction with humans. For example change in body size is the most widely used marker of animal domestication today. But, there are other factors that affect body size in both wild and domestic species that have nothing to do with domestication (e.g., sexual dimorphism, age, geography and climate changes and habitat destruction)(Zeder 2006b). Most importantly, the cause and effect mechanisms that link domestication to body-size reduction are still less than

adequately known (Zeder 2006c). Such morphological changes, if related to the process of domestication at all, are only delayed, and possibly indirect, artifacts of human management (Zeder *et al.* 2006).

1.2.2.1.2. Plastic Responses to domestication

These markers operate on individual animals and will vary in degree and nature depending on highly localized factors that may change over time. A beveling on the lower second premolars of horses in the Eurasian steppe has been interpreted as definitive evidence of bit wear and therefore domestication (Brown & Anthony 1998). Recently, a number of researchers have begun to explore the potential of dietary shifts as detected by isotopic analysis as a marker of initial domestication in animals (e.g., Balasse *et al.* 2000, for sheep and goats). Again, it is important to remember that dietary conditions of early domestic animals will vary depending on the environment in which they are raised and the management practices used by their human masters. Therefore, it would be a mistake to attempt to apply any single isotopic or other chemically detected shift in diet as a definitive marker of domestication in any species in any single region, and certainly not as a widely applicable marker across species and regions (Zeder 2006b).

1.2.2.2. Non-morphological Markers

These markers seek to detect evidence of human management or control of animals (Human-oriented markers), especially those that may precede any detectable, genetically driven morphological change (Zeder 2006b).

1.2.2.2.1. Demographic profiling

Demographic profiling was one of the first of non-morphological markers that has been applied to animal domestication studies. The technique is based on the assumption that the age and sex of animals taken by hunters interested in maximizing the return from their hunt will differ from the age and sex of those harvested by herders interested in promoting the long-term growth of their herds. The demographic profiling, particularly sex-specific harvest profiles, constructed by combining osteometric data and precise radiocarbon dating (using accelerator mass spectrometer; AMS), are capable of

distinguishing between herd management and a range of selective and non-selective hunting practices (Zeder 2006c). However, this method has limitations in the techniques used to reconstruct these profiles. Most importantly, until recently, it has not been possible to construct separate harvest profiles for male and female animals, which is essential in order to distinguish certain hunting practices from herding (Zeder 2006b).

1.2.2.2.2. Zoogeography and abundance

The appearance of a potential domestic species outside its presumed natural range is often taken as a signal of human involvement in the movement of animals, either as already domesticated herds or as captive wild animals undergoing domestication. The zoogeographic data can sometimes be problematic in making the case for animal domestication. Without direct dating, it is difficult to know if a specimen is contemporary with the strata in which it was found or with a later intrusion into earlier strata (Zeder 2006b).

Moreover, present-day distributions of wild progenitor species have been strongly affected by over-hunting and by the loss of habitat due to agriculture and urban settlement. Past distributions are therefore likely to be quite different today from what they were during the Early Holocene. The use of relative abundance data to mark initial stages of the domestication process faces similar problems, especially in assemblages from sites within or close to the likely natural habitat of wild progenitors. Without additional evidence of domestic status (i.e. morphological change or domestic demographic patterns), it is difficult to tell if an increase in the use of a potential domestic species signals the adoption of herd management or the intensification of hunting strategies (Zeder 2006c).

1.2.2.2.3. Different types of more circumstantial evidence of human control

Remnants of pens or corrals, sometimes with associated dung pellets, have been used as evidence for domestication. The architectural features (i.e. corals and other animal shelters), artefacts associated with the use of animal resources (i.e. chums or milk strainers), and artistic renderings that feature domesticates or herding activities (Zeder 2006b).

There is no single prescription for animal domestication studies that can be universally applied to all species in all regions. Instead, researchers need to choose the best methods according to both the species and the cultural context that they face. Combining genetic and archaeological information provides the most fruitful approach for unlocking the secrets of the origins of domestic animals. Determining the time and location of origin of ancient genetic lineages can be best done using reliably dated fossils from archaeozoologists. Similarly, tracking the diffusion of these different genetics lineages requires well-dated fossil material from each of several archaeological sites (Luikart *et al.* 2006).

Also, with intraspecific study of genetic variation, linkages with other types of data are needed. These other attributes include geography, morphology, and ecology. The partnering of these varied sources of information with genetic variation falls into the emerging field of phylogeography, where aspects of the past of an organism are read from modern distributions of phylogenetically related sequence variants. Phylogeography has been described as a subject with two orthogonal dimensions: the horizontal one of the geography of genetic diversity and the vertical one representing the time through which this geography emerges (Avise 2000). Therefore, the study of domestication must follow an interdisciplinary approach (Bradley 2006).

2. Livestock biodiversity

2.1. Current knowledge

2.1.1. Species diversity

Mutation, selective breeding, and adaptation have shaped the diversity of livestock populations. Only about 40 of the 50,000 known avian and mammalian species have been domesticated. On a global scale, five species – cattle, sheep, chickens, goats, and pigs – show widespread distribution and particularly large numbers. The first three are the most widely distributed domestic species globally, while the latter two are less evenly spread (Figure 2.2). Goats are much less numerous in the Americas, Europe and Caucasus than in other regions (FAO 2007).

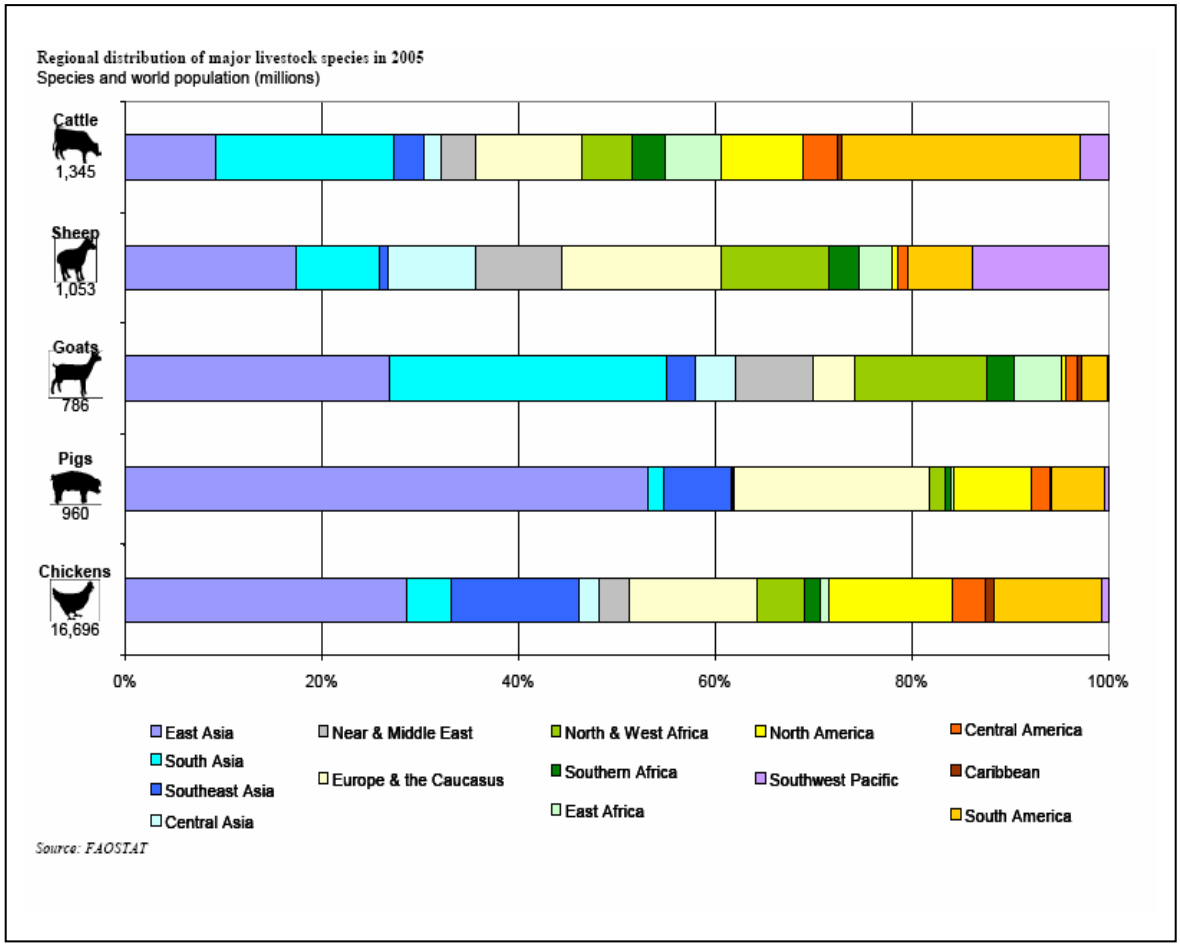


Figure 2.2. Global distribution of five major domestic species: cattle, sheep, chickens, goats, and pigs.

2.1.2. Breed diversity

Definition of breed adopted by FAO

Either a subspecific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species or a group for which geographical and/or cultural separation from phenotypically similar groups has led to acceptance of its separate identity (FAO 1999).

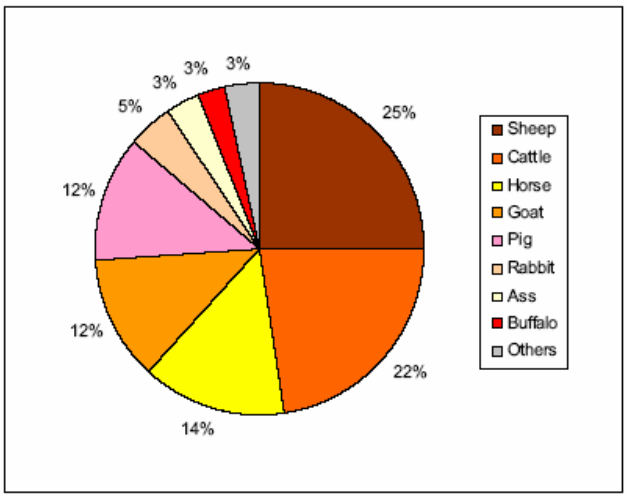
The total number of breed records in the Global Databank has increased greatly since the publication of the World Watch List for Domestic Animal Diversity (WWL–DAD: 3, Scherf 2000).

Table 2.1. Status of information in the Global Databank for Animal Genetic Resources (FAO 2007).

Year of analysis	Mammalian species			Avian species		Countries covered
	Number of national breed populations	% with population data		Number of national breed populations	% with population data	
1993	2 719	53		-	-	131
1995	3 019	73		863	85	172
1999	5 330	63		1 049	77	172
2006	10 512	43		3 505	39	182*

**No data recorded for Andorra, Brunei Darussalam, Gaza Strip, Holy See, Liechtenstein, Marshall Islands, Federated States of Micronesia, Monaco, Nauru, Qatar, San Marino, Singapore, Timor-Leste, United Arab Emirates, West Bank, Western Sahara*

A global total of 7 616 breeds have been reported. Europe and the Caucasus, and Asia are home to the largest share of breeds of most of the world's major livestock species. Camels are the exception, with the largest number of breeds being found in Africa. In terms of population size, Asia is the dominant region for most species. Exceptions include camels (Africa), turkeys (Europe and the Caucasus) and horses (44 percent of which are found in Latin America and the Caribbean) (FAO 2007).



Mammalian species with more than 100 recorded breeds are displayed separately; the remaining mammalian species are aggregated as others.

Figure 2.3. Distribution of the world's mammalian breeds by species

2.2. Livestock's genetic diversity

Overall, the level of mtDNA polymorphism in cattle, sheep, and goats is high, and contains evidence of multiple maternal origins. Such multiple origins correspond either to several domestication events in different locations and/or at different periods, or to the capture of several mtDNA haplotypes during a single domestication event. Furthermore, nuclear DNA polymorphism seems high (see e.g. Maudet *et al*. 2002), comparable to what is found in wild species (Taberlet *et al.* 2007).

2.3. Goat and its general situation

The genus *Capra*, which contains domestic goats and their wild relatives (Bezoar, Markhor, Spanish ibex, Alpine ibex, Nubian ibex, Walia ibex, East Caucasian tur, West Caucasian tur and Siberian ibex) displays an old-world distribution. Fossil data suggest that the *Capra* first appeared in Central Asia (Pilgrim 1947) and that a species radiation occurred in the Plio-pleistocene (Pilgrim 1947; Hartl *et al.* 1990). Very few paleontological data are available for species of this genus because their preferred mountainous habitats are not favourable for fossil preservation. Consequently, the evolutionary history of *Capra* species is poorly understood. This is compounded by the fact that the radiation of *Capra* taxa apparently occurred rapidly (Hartl *et al.* 1990; Manceau *et al*. 1999a), making it difficult to assess the number of species and their phylogenetic relationships. The number and status of *Capra* species and subspecies is still under debate, with estimates ranging from 6 to 9 species (Schaller 1977; Shackleton 1997; Pidancier *et al*. 2006).

This species is most hardy of all livestock species and will thrive and breed on the minimum of food and under extremes of temperatures and humidity. They can provide with clothing, meat and milk as well as bone, sinew, dung and manure (Pringle 1998; Clutton-Brock 1999). Goats were also easy to transport in boats over long distances, as well as by land, following humans better than sheep or cattle. For these reasons, goats were among the first farm animals domesticated and were important in the economies of societies as long as 10,000 years ago (Clutton-Brock 1999; Zeder & Hesse 2000). Subsequently, goats were taken along during human migrations and colonizations, and in more recent times, on ships exploring new continents (Porter 1996).

Goats are the least numerous of the five major livestock species. There are about 800 million worldwide – one for every eight people. Some 70 percent of the world's goats are in Asia and the Near and Middle East. Goat breeds contribute 12 percent to the total number of recorded mammalian breeds in the world (FAO 2007).

Goats are of major economic significance for smallholders in the South, particularly in ecologically marginal areas such as drylands and mountains, where other domestic animals cannot easily be kept. They are of limited importance in Northern agriculture, though some highly productive dairy breeds have been developed in central Europe through upgrading local stock with dairy breeds of Swiss origin. Rising living standards in the Near and Middle East and the migration of people who prefer goat meat, have increased the demand for goat meat, furthering the spread of the Boer goat during the past few decades (Alandia Robles *et al*. 2006).

2.4. Goat genetics diversity results, up to now

Up to now, 5 mtDNA haplogroups have been recognized based on different regional and worldwide scale genetic studies. According these studies, most of the genetic diversity occurred within breeds, and only about 10% of the total mtDNA variation was due to differences among continents. This is far lower than the published estimates of 54-80% in cattle for the same mtDNA region. This suggests that in the past goats were transported far more extensively than cattle. The very weak geographic structure has been interpreted as the result of the extensive transportation of goats among continents (Luikart *et al*. 2001; Sultana *et al*. 2003; Joshi *et al*. 2004).

Interestingly, the percentage of mtDNA variation (HVI) between continents for humans is surprisingly similar (10%) to that in goats. This similarity might be coincidental, but it is intriguing to speculate that goats have had similar amounts of high intercontinental movement because they have been more important during human movements (migrations, colonizations) or more used in historical commerce and trade than cattle (Luikart *et al*. 2006).

The molecular clock approach allows the time of divergence between haplogroups to be estimated based on the fact that the mutation rate is approximately constant through time. Since mitochondrial genes are not affected by environmental selection pressures, the number of mutations is roughly proportional to time. In this way, using published sheep

cytochrome *b* sequences and established dates based on fossil data for the split between *Capra* and *Ovis*, Luikart *et al*. (2001) estimated the divergence time between these haplogroups more than 200,000 years ago, well before the time of domestication. This timeframe is much earlier than domestication, suggesting that the mtDNA in today's domestic goats does not originate from within one local population only 10,000 years ago. These highly divergent haplogroups could not have evolved (i.e., accumulated so many mutations) in only 10,000 years. It is more likely that three genetic origins occurred from three different wild populations that already carried quite distinct mtDNA 10,000 years ago. This suggests that the wild progenitors of the three lineages probably belonged to different populations of wild goats (Luikart *et al*. 2001).

Additionally, on the base of a restricted study, at least three distinct groups of domestic goats were found based on Y-chromosome polymorphism (Pidancier *et al*. 2006). Interestingly, all individuals from a given divergent mtDNA lineage did not always come from the same distinctive Y-chromosome lineage. This is not surprising, because of the extensive gene flow among goat populations and regions, which is likely to mix maternal and paternal lineages within and among breeds. In contrast to mtDNA, Y-chromosome data seems to suggest a higher diversity in the Fertile Crescent region than in other regions. For example, two Y-chromosome lineages were found in contemporary goats from Jordan and Turkey, but not in other regions (Luikart *et al*. 2006).

The origin and spread routes of the different goat haplogroups across the Old World was analyzed by Fernández *et al.* (2005), using 130 bp of the mtDNA control region of the ancient DNA extracted from samples of archaeological sites in Europe and the Middle-East. They found that several ancient samples from the prehistoric sites of the Qazvin Plain in the northern part of the Iranian Central Plateau belong to A haplogroup, the main haplogroup that was found worldwide in modern goats. In another study, Fernández *et al*. (2006) were able to analyze several ancient samples from Europe (Southern France) belong to the A and C haplogroups. But, none of other haplogroups have been found in ancient sequences up to now.

An extensive survey to examine patterns of thirty microsatellites variation in 1426 domestic goats from 45 traditional or rare breeds in 15 European and Middle Eastern countries, clearly indicates a geographical partitioning of goat diversity, with a large proportion of the genetic diversity found among breeds. About 41% of the genetic variability among the breeds could be explained by their geographical origin. A decrease in genetic diversity from the south-east to the north-west was accompanied by an increase

in the level of differentiation at the breed level. These observations support the hypothesis that domestic livestock migrated from the Middle East towards western and northern Europe and indicate that breed formation was more systematic in north-central Europe than in the Middle East (Cañón *et al.* 2006).

3. Domestication

3.1. The domestication process in general

Domesticated animals are considered to be those species that are bred in captivity, and modified from their wild ancestors to make them more useful to humans, who control their reproduction (breeding), care (shelter, protection against predators) and food supply (Diamond 2002; Mignon-Grasteau 2005). Domestication includes the following steps: initial association with free breeding; confinement; confinement with breeding in captivity; and selective breeding and breed improvement (Zeuner 1963).

At domestication time, at the end of the Pleistocene the climate had started to become warmer and more seasonal, favouring plants with large roots and tubers and large seeded annual plants. Such species are easy to harvest, cultivate and store and so are well suited to farming. These species probably became increasingly important food resources during seasons in which other food was unavailable. With the climatic reversal of the Younger Dryas cold period (12,200–11,100 YBP), the demand for cultivated and storable food increased and led to the domestication of species such as rice, wheat and legumes. As the climate warmed, some human populations started expanding rapidly and population centres became established in regionally important sites. Settlements tended to be located in naturally fertile areas that were suitable for agriculture, or in locations that linked different landmasses, and so were natural stopping-off points for migrating peoples (Salamini *et al*. 2002). The indigenous population, together with migratory populations, needed to be supplied with food, and this would have provided another stimulus for farming and the domestication of agricultural species. From this time very few animal species have been successfully domesticated. Domestication was a complex and gradual process, which altered the behaviour and morphological characteristics of the ancestral animals. The circumstances and pressures that affected the domestication of animals remain uncertain, and may have varied from one geographic area to another and from one species to another. But, it seems that the root of animal domestication is probably related

to the ubiquitous tendency of hunter-gatherers to try to tame or manage wild animals. In this situation, the main object of animal domestication may have been the desire to secure the availability of "favourite" foods. The potential of some domesticated species to provide support to crop farming (e.g. ploughing with oxen or buffalo), or as pack and riding animals (e.g. llamas, dromedaries, Bactrian camels, horses, donkeys and even cattle) being realized later (Diamond 2002).

Clearly there are some universal principles that come into play in domestication process story, both cultural and biological. Climate, community, optimization, adaptation, co-evolution, and selection all serve to shape the process of domestication wherever it occurred. But there are other highly localized factors that play important roles in each instance. Understanding what these factors are and how they shaped the unfolding process of domestication are equally, perhaps even more, important in explaining domestication (Zeder 2006).

Among the 148 non-carnivorous mammalian species weighing more than 45 kg, only 15 have been domesticated. Thirteen of these species are from Europe and Asia, and two originate from South America. Moreover, only six species have become widespread on all continents (cattle, sheep, goats, pigs, horses, and donkeys), while the remaining nine (dromedaries, Bactrian camels, llamas, alpacas, reindeer, water buffalo, yaks, Bali cattle, and mithan) are important in more limited areas of the globe (FAO 2007).

3.2. Domestication history

The history of animal domestication started around 12 000 to 14 000 years ago during the agricultural revolution of the early Neolithic, with the domestication of major crop and livestock species. The control of food production by early farmers led to major demographic, technological, political, and military changes. The domestication of animals and plants is considered to be one of the most important developments in history, and one of the prerequisites for the rise of human civilizations (Diamond 2002). After the initial domestication events, the spread of farming into nearly all terrestrial habitats followed rapidly (Diamond & Bellwood 2003, Figure 2.4). During thousands of years, natural and human selection, genetic drift, inbreeding and cross-breeding have contributed to today's animal genetic resources diversity and have allowed the development of sustainable

livestock production in a variety of environments (agro-ecological zones) and production systems (Bruford *et al*. 2003).

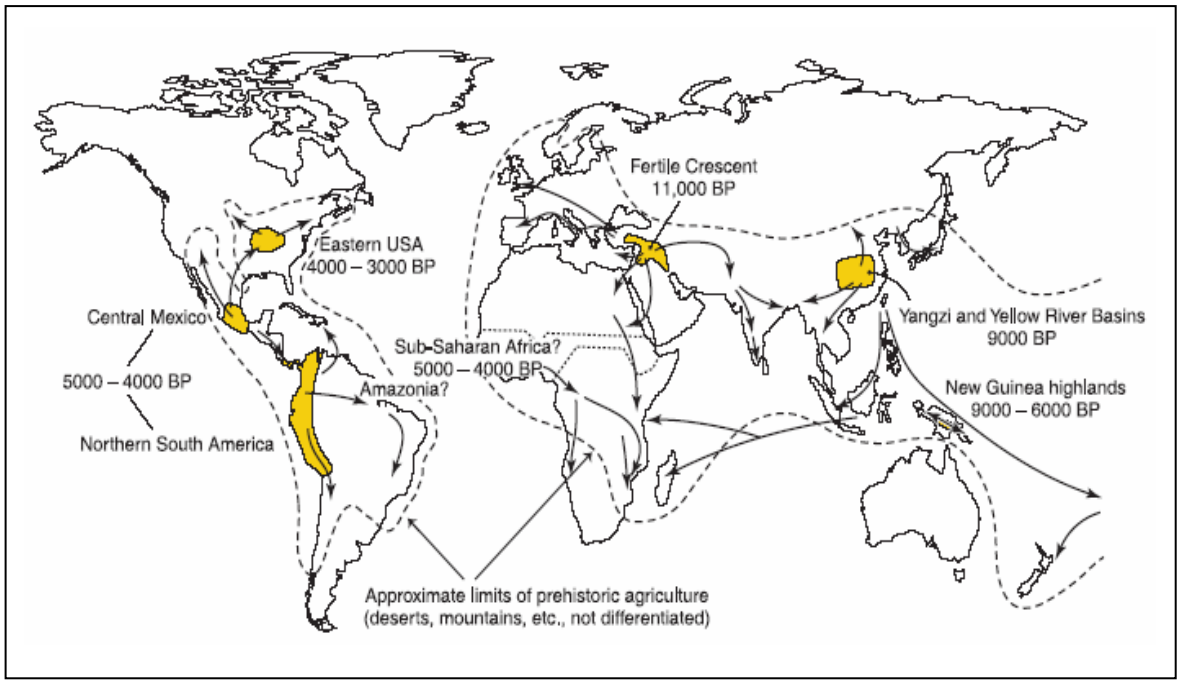


Figure 2.4. Archaeological map of agricultural homelands and spread of Neolithic/Formative, with approximate radiocarbon dates (Diamond & Bellwood 2003).

However, based on molecular genetics and archaeological data, exact dating of domestication events has proved to be particularly challenging. Animals undergoing the initial process of domestication would not have been significantly different in morphology from their wild ancestors, and dates relying on morphological characters will undoubtedly underestimate the age of domestication events, because the expression of morphological changes is often delayed in domestic animals (Zeder 2006; Dobney & Larson 2006). The process of molecular dating, while independent of morphological changes, is typically characterized by large confidence intervals, and often relies on uncertain calibration points. In fact, the molecular-clock hypothesis is controversial in general, for any timescale, taxon, or genome type. Even if one ignores the evidence for unequal mutation rates among different groups and different genomes, the timescale of domestication is much too short to be appropriate for molecular clocks, which are better calibrated for species that diverged millions or tens of millions of years ago, not populations (such as domesticates) diverging thousands of years ago (see Ho *et a1*. 2005; Ho & Larson 2006; Ho *et al*. 2007).

Approaches including demographic profiling techniques for identifying initial attempts at livestock management by humans, and calibration of molecular clocks using ancient DNA information, are providing new approaches for pinpointing the dates of domestication. However, the precise dating of domestication events might come from the genetic analysis of fossil bones properly dated by archaeozoologists (Zeder 2006).

3.3. Domestication centers

Livestock domestication is now thought to have occurred in at least twelve areas of the world. Interestingly, not all centres of domestication are closely associated with the homelands of our crop species. While in some cases (e.g. the Fertile Crescent), domestication centres of both crops and livestock are intermingled, in others (e.g. the African continent) crop and livestock domestication seem largely to have occurred independently (FAO 2007).

Clearly, inferences about the location of origin from a single type of pattern of molecular data (e.g. diversity levels) should only be made with caution because they can be unsatisfactory or even potentially misleading. For example, levels of molecular diversity in domestic breeds are expected to be highest near the centre of origin, assuming that dispersal away from the centre would lead to loss of genetic variation due to repeated founder effects (Loftus *et a1*. 1999). This pattern is indeed seen in cattle (Troy *et al*. 2001) and sheep (Townsend 2000), but in goats, mtDNA variation is apparently not higher in the Fertile Crescent region compared to most other continental regions. For example, the mtDNA diversity (mean number of base changes between two sequences) within the Near East, Europe, and Asia is approximately equal (10 bp differences). Rather, it is advisable to incorporate information from several analyses, such as the geographic distribution of haplogroups and also historical or temporal distributions, e.g. using ancient DNA, and archaeological data (Luikart *et al*. 2001; Luikart *et al*. 2006).

However there are still uncertainties about the existence of some domestication centres for some species, the following geographic areas are important primary centres of origin and, therefore, diversity of livestock species: the Andean chain of South America (llamas, alpacas, guinea pigs); central America (turkeys, Muscovy ducks); northeast Africa (cattle, donkeys); southwest Asia including the Fertile Crescent (cattle, sheep, goats, pigs); the Indus valley region (cattle, goats, chickens, riverine buffaloes); Southeast Asia

(chickens, Bali cattle); east China (pigs, chicken, swamp buffaloes); the Himalayan plateau (yaks); and north Asia (reindeer) (FAO 2007).

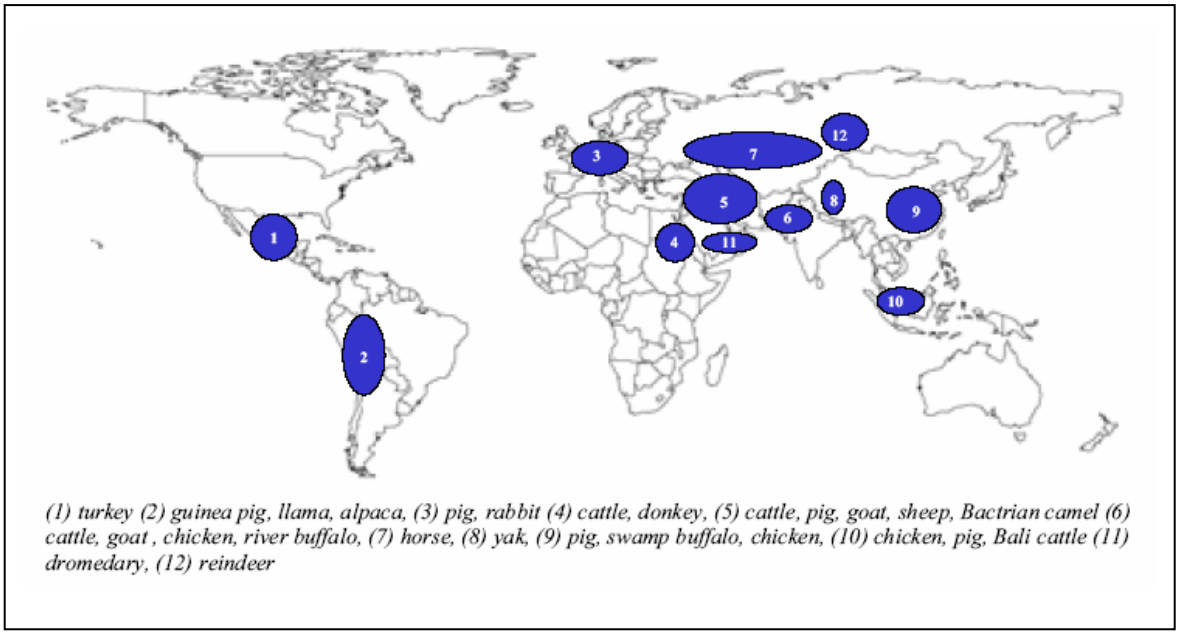


Figure 2.5. Major centres of livestock domestication, based on archaeological and molecular genetic information.

It is important to remember, however, that genetically independent domestication events are not necessarily culturally, or even entirely biologically, independent. Knowledge of domestication can move between peoples and be applied to local wild plant and animal resources. It is also possible that many of the apparently independent domestication events in animals arose when either domestic males or females (or perhaps both) were moved into an area and served as a kind of seed stock, breeding with local wild populations. Depending on the sex of the domestic seed stock and the lineage traced by genetic markers (maternal or paternal), this level of contact could well go undetected. Ancient livestock DNA studies and osteometric information from archaeological sites are important tools to address these issues (Zeder 2006).

3.4. Complex patterns of genetic structure of domesticates

The use of genetic markers has revealed an extraordinary amount of variation and complexity in the domestication of livestock, in terms of the numbers and types of progenitors that contributed genetic material during domestication, and the number of occasions that similar stocks were domesticated. So, what do these complex patterns of past domestication imply for modern patterns of genetic diversity across individuals, breeds, domestic 'species' and geographical zones? (Bruford et al. 2003)

Table 2.2. Summary of genetic and archaeological information for different domestic species (FAO 2007).

Domestic species	Wild Ancestor	MtDNA clades	Domest. events*	Time B.P.	Location
Cattle	Aurochs (3 subspecies) (extinct)				
Bos taurus taurus	*B. primigenius primigenius*	4	1	~ 8000	Near and Middle East (west Asia)
	B. p. opisthonomous	2	1	~ 9500	northeast Africa
Bos taurus indicus	*B. p. nomadicus*	2	1	~ 7000	northern Indian subcontinent
Yak	Wild yak				
Poephagus grunniens	*P. mutus*	3	1	~ 4500	Qinghai-Tibetan Plateau
Goat	Bezoar				
Capra hircus	*Capra aegragus* (3 subspecies)	5	2	~ 10000	Near and Middle East, northern Indian subcontinent
Sheep	Asian mouflon				
Ovis aries	*Ovis orientalis*	4	2	~ 8500	Near and Middle East/Turkey (Central Anatolia)
Water buffalo	Asian wild buffalo				
Riverine *B. bubalus bubalus*		ND	1	~ 5000	Islamic Republic of Iran/Iraq, Indian subcontinent
Swamp *B. bubalus carabensis*		ND	1	~ 4000	Southeast Asia, China
Pigs	Wild boar				
Sus scrofa domesticus	*Sus scrofa* (16 subspecies)	6	6	~ 9000	Europe, Near and Middle East, China Indian subcontinent, Southeast Asia

Horse	Extinct				
Equus caballus		17	multiple	~ 6500	Eurasian steppe
Donkey	African wild donkey				
Equus asinus	*Equus africanus*			~ 6000	northeast Africa
	Nubian wild ass *E. a. africanus*	1	1		
	Somali wild ass *E. a. somali*	1	1		
Llama					
Lama glama	2 subspecies	ND	1	~ 6500	Andes
	L. guanicoe guanicoe				
	L. guanicoe cacsiliensis				
Alpaca					
Vicugna pacos	2 subspecies	ND	1	~ 6500	Andes
	V. vicugna vicugna				
	V. vicugna mensalis				
Bactrian Camel	Extinct**				
Camelus bactrianus	*C. b. ferus*	ND	1	~ 4500	Central Asia (eastern Republic of Iran)
Dromedary	Extinct				
Camelus dromedarius		ND	1	~ 5000	southern Arabian Peninsula
Domestic chicken	Red Junglefowl				
Gallus domesticus	*Gallus gallus* (4 subspecies	5	2	~ 5000	Indian subcontinent
	G. g. spadiceus, G. g. jabouillei			~ 7500	China – Southeast Asia
	G. g. murghi, G. g. gallus)				

Source: adapted and updated from Bruford et al. (2003); Hanotte and Jianlin (2005)
**Minimun number of domestication events; **Recent genetic evidence suggests that the endangered wild population are not the ancestral maternal populations of today's domestic Bactrian (Jianlin et al., 1999), ND = not determined*

3.5. Goat Domestication

Goats were among the first farm animals domesticated, 10,500 years ago, contributing to the rise of the ‘‘Neolithic revolution’’. Goat domestication was an integral part of the rise of agriculture and the adoption of agricultural practices throughout much of the world. Insights into the evolution and spread of goats are likely to deepen our understanding of the origin and spread of agriculture and the rise of early human civilizations. Archaeological and morphological studies suggested that the domestic goat

(*Capra hircus*) was domesticated from the bezoar (*Capra aegagrus*) in the Fertile Crescent (Meadow 1996; Porter 1996; Pringle 1998; Zeder & Hesse 2000; Zeder 2005; Zeder 2006c). This origin was confirmed by genetic studies based on mitochondrial (Manceau *et al.* 1999a; Mannen *et al.* 2001; Takada *et al.* 1997) and nuclear DNA (Pidancier *et al*.2006; Luikart *et al*. 2006). The first archaeological evidence traces back as far as ca. 10,500 cal. B.P. in the high Euphrates and Tigris valleys, in Southeastern Anatolia (Peters *et al.*1999; Peters *et al*. 2005) and 9,900-9,500 cal. B.P. in the Zagros mountains (Zeder & Hesse 2000; Zeder 2005).

People began to domesticate wild goats in highland area of Ganj Dareh in the Zagros Mountains of western Iran. Metrical analyses of patterns of sexual dimorphism in modern bezoars (*Capra aegagrus*) skeletons using direct accelerator mass spectrometry radiocarbon dates allow sex-specific age curves to be computed for archaeofaunal assemblages. A distinct shift to selective harvesting of sub-adult males marks initial human management and the transition from hunting to herding of the species. In fact, early herders mainly killed young males for meat and kept most females and a few older males as breeding stock. In contrast, hunters interested in a quicker return on their effort often targeted the largest males in a herd or killed many animals at once. Goats in these early-managed herds probably looked much like wild goats, both physically and genetically. As much as 500 years later, managed herds and their herders expanded out of this highland homeland of initial domestication and into adjacent, less-optimal areas like Dehluran Plain, where Ali Kosh is situated. Moving into these lowland areas undoubtedly represented a substantial departure from the environmental conditions that prevailed in their native highland habitats. It also ended any potential for interbreeding between managed and wild goats. The more conservative harvest profile at Ali Kosh, later slaughter of both young males and older females may be a response to the loss of easy access to wild animals for restocking. The genetic isolation from wild populations, plus the impact of tighter human control of breeding, undoubtedly resulted in the changes in horn morphology documented at Ali Kosh. These factors, coupled with more arid environmental conditions and poorer pasture opportunities, also may have contributed to a reduction in the size of these animals (Zeder 2006c). Over time, isolation of managed herds and the introduction of selective breeding produced changes in domesticated goats.

After the initial plant and animal domestications in the Near East, *ca.* 11,500 and 10,500, respectively, years ago (Harris 1996; Cauvin 2000), Neolithic culture diffused into

Europe along two main routes (Diamond & Bellwood 2003). From their initial domestication areas, goats also were introduced into Europe by following these routes. Archaeological data and radiocarbon dates on seeds or bones provide support for an earlier arrival in Western Europe (namely France) via the ‘‘Mediterranean’’ route rather than the ‘‘Danubian’’ route (Figure 2.6).

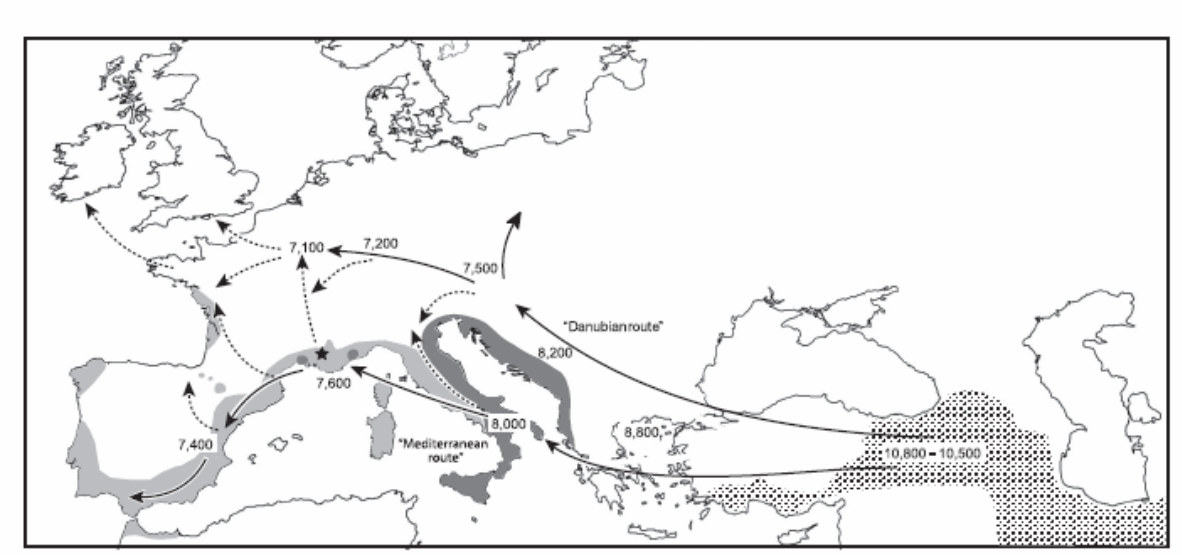


Figure 2.6. Map of goats introduction routes from their initial domestication areas into Europe along ‘‘Mediterranean’’ and ‘‘Danubian’’ route (From Guilaine 2003; Fernández *et al*. 2006).

Map of Figure 2.6 shows occidental part of the current geographic distribution of the wild goat, *Capra aegagrus* (dotted area), as well as the two main waves for the initial advancement of the Neolithic culture into Europe: the Mediterranean route and the Danubian route. The location of Baume d’Oullen (an archaeological site in France) is indicated by a star. The dates on the map are calibrated radiocarbon date-derived B.P. (cal. B.P.). Solid-line arrows indicate main flow; broken-line arrows indicate possible secondary flows. Dark gray zones indicate the area of the Impressa culture (8,000–7,500 cal. B.P.); light gray zones indicate the area of the Cardial and cultures (between 7,500 and 6,800 cal. B.P.) (Fernández *et al*. 2006).

This diffusion has been verified by archaeozoological analyses at Baume d’Oullen and at a range of Early Neolithic sites from Southern Europe. In these sites, the number of goats was low compare with sheep and even to cattle. These data indicate that Early

Neolithic farmers were breeding and transporting relatively small flocks of goats. These small local flocks were, however, probably more or less interbred at the regional scale with other Early Neolithic flocks, because the contacts between the small human communities were strong enough to generate large and rather homogeneous culture. Therefore, the presence of high genetic diversity of such small goat populations in southern France can be explained by extensive gene flow during the Neolithic expansion between the Eastern and the Western Mediterranean Basin. Therefore, such an early diversity seems likely to be explained by a diverse founding pool and a large effective population size (i.e. global *N*e) (Fernández *et al*. 2006).

4. Livestock transformations following domestication and consequences on genetic diversity

The domestication process resulted in many changes in animals. Human favoured several morphological changes. Domestic animals are generally smaller than their wild ancestors. Smaller animals are easier to manage and to handle. They may also reach puberty sooner, and large flocks or herds can be kept more easily (Hall 2004). In some cases, human selection has deliberately resulted in extreme size differences, illustrated by the small size of the Shetland pony and the large size of the Shire horse (Clutton-Brock 1999). These body size and form transformations from the wild ancestors were realized to satisfy the demand for meat products (e.g. European beef breeds), or to cope with new environmental pressures (e.g. Sahelian goats). Selection for muscular mass has often resulted in greater muscular development of the hind quarters relative to the shoulders (Hall 2004). An extreme example of selection for muscular mass is the double muscling trait observed in some European beef breeds, and in some sheep and pigs breeds. In cattle, the trait results from mutation at a single gene – the myostatin gene (Grobet *et al.* 1998). In sheep it involves the callipyge gene (Cockett *et al.* 2005).

Fat pattern deposition may also show changes following domestication. For example, reduced predation has encouraged fat deposition in domestic poultry. In domesticated mammals, the hump of the Zebu and the tails of fat-tailed and fat-rumped sheep are striking examples of selection for fat deposition. This exaggerated fat deposition may be quite ancient, with fat-tailed sheep already common in western Asia by 3000 BC, and

humped cattle depicted on cylinder seals from the ancient civilizations of Mohenjo-Daro and Harappa in the Indus Valley about 2500 to 1500 BC (Clutton-Brock 1999).

Great variation is found in the wool and hair coats of most domestic species. For example, sheep breeds of alpine regions have particularly thick woolly coats, while breeds from the African Sahel lack wool. These changes were probably the result of mutations followed by artificial selection, perhaps as early as 6000 BC, as illustrated by a statuette of a woolly sheep found in Iran (Clutton-Brock 1999).

Coat and plumage colorations were also selected by the environment, with light coloured animals being more adapted to hotter environments and dark coloured animals to cooler environments (Hall 2004). Coat colours have also been influenced by cultural selection. Livestock breeders in the developed world often favour uniformity in coat colour, but in the tropics diversity in coat colour may be preferred for ceremonial reasons, or simply to facilitate the identification of individual animals (Poland *et al.* 2003).

Understanding the origin and the subsequent history and evolution of domestic animals is essential to the design of sustainable conservation and utilization strategies of the genetic resources. Livestock diversity originates from the wild ancestors, and was subsequently shaped through the processes of mutation, genetic drift, and natural and human selection. Only a subset of the diversity present in the ancestral species survived, in the domestic counterparts. However, domestic livestock diversity has been continuously evolving. Reshuffling of genes at each generation, mutation, and cross-breeding or admixture of different gene pools has offered new opportunities for natural and human selection. This has been the basis of the enormous gains in productivity achieved in commercial breeds, and of the adaptation of indigenous livestock to highly diverse and challenging environments. However, the world's livestock diversity is currently shrinking, with rapid and uncontrolled loss of unique and often uncharacterized animal genetic resources. If a breed or population becomes extinct, this means the loss of its unique adaptive attributes, which are often under the control of many interacting genes, and are the results of complex interactions between the genotype and the environment.

5. Conservation Genetics and implications for conservation

Molecular genetic studies results can be utilized for scientific management and conservation of wild animals and their domestic descendents. In the past, the domestication of plants and animals was a key step in human evolution, allowing the development of our current societies. We can anticipate that domestic plants and animals will continue to play a key role in the future, but many plant varieties and animal breeds are endangered (Esquinas-Alcazar 2005; Taberlet *et al*. 2007). Genetic data should help to promote a sustainable use of the genetic resources. Sound conservation strategies must rely on the knowledge of the levels of genetic diversity within and between breeds, the knowledge of the adaptive geographic variation, the inventories of potential genetic resources including the wild ancestor, and the assessment of colonisation routes out of the domestication centres. Particular attention should be paid to wild ancestors, and to traditional breeds located close to the domestication centres. Finally, as for wild animals, it might be useful to consider the concept of evolutionary significant units (ESUs) (Ryder 1986; Moritz 1994) and to also apply it to domestic species. According to the current loss of genetic diversity in domestic breed at the worldwide level (FAO 2007), it is extremely important to design in the short term sound strategies for preserving the evolutionary potential of domestic animals and achieving sustainable animal farming.

Figure 2.7. The habitat of *Capra aegagrus* in Dena Protected Area in Iran (Photo by S. Naderi)

Chapter 3. mtDNA diversity of goats

Chapter 3. Large-scale mitochondrial DNA analysis of the domestic goat reveals six haplogroups with high diversity

Research Article

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PLoS ONE 2(10): e1012. doi:10.1371/journal.pone.0001012

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Key words: Domestic goat, Mitochondrial DNA (HVI), haplogroup, Genetic structure, phylogeny, *Capra hircus*

Abstract

Background. From the beginning of domestication, the transportation of domestic animals resulted in genetic and demographic processes that explain their present distribution and genetic structure. Thus studying the present genetic diversity helps to better understand the history of domestic species. *Methodology/Principal Findings*. The genetic diversity of domestic goats has been characterized with 2430 individuals from all over the old world, including 946 new individuals from regions poorly studied until now (mainly the Fertile Crescent). These individuals represented 1540 haplotypes for the HVI segment of the mitochondrial DNA (mtDNA) control region. This large-scale study allowed the establishment of a clear nomenclature of the goat maternal haplogroups. Only five of the six previously defined groups of haplotypes were divergent enough to be considered as different haplogroups. Moreover a new mitochondrial group has been localized around the Fertile Crescent. All groups showed very high haplotype diversity. Most of this diversity was distributed among groups and within geographic regions. The weak geographic structure may result from the worldwide distribution of the dominant A haplogroup (more than 90% of the individuals). The large-scale distribution of other haplogroups (except one), may be related to human migration. The recent fragmentation of local goat populations into discrete breeds is not detectable with mitochondrial markers. The estimation of demographic parameters from mismatch analyses showed that all groups had a recent demographic expansion corresponding roughly to the period when domestication took place. But even with a large data set it remains difficult to give relative dates of expansion for different haplogroups because of large confidence intervals. *Conclusions/Significance*. We propose standard criteria for the definition of the different haplogroups based on the result of mismatch analysis and on the use of sequences of reference. Such a method could be also applied for clarifying the nomenclature of mitochondrial haplogroups in other domestic species.

Introduction

More than 10,000 years ago, the transition of humans from hunting to the manipulation of the behavior of certain animals lead to the process of domestication [1]. This process contributed to the rise of human civilization by enabling people to settle into a sedentary lifestyle. The goat was one of the first domesticated animals [2-4]. It was a source of milk, meat, dung for fuel and materials for clothing and building such as hair, bone and skin [1,5]. Archaeological studies suggested that the domestic goat *Capra hircus* was domesticated from the bezoar *Capra aegagrus* in the Fertile Crescent [e.g. 6-8]. This origin was confirmed by genetic studies based on mitochondrial [e.g. 9,10] and nuclear DNA [11].

From the beginning of the domestication process, the exchange and transportation of domestic animals has been related to human migration and trade. This resulted in genetic (e.g., selection, gene flow) and demographic processes that explain the present worldwide distribution of more than 300 different breeds of *Capra hircus* and their genetic structure [2]. Thus, the present genetic diversity bears the molecular signature of past events, such as rapid demographic expansions. Therefore, the study of this diversity helps to reconstitute the evolutionary history of the goat [12] and could bring new facts that help to understand the history of domestication.

Mitochondrial DNA is commonly used for the study of domesticated species. The control region has been especially used for describing the genetic polymorphism of goats [13], because it is variable and structured enough across the geographical range of the species, and evolves at a constant rate [12]. Moreover, it allows maternal lineages to be followed and is less sensitive to introgression from wild species than nuclear DNA [13]. However, studies on nuclear genes are needed because they give information on gene flow and selection processes that had a great influence on the evolution of livestock species [12].

Luikart et al. [13] conducted the first study of the overall genetic structure of domestic goats at the worldwide scale. They analyzed 406 individuals representing 88 breeds from the old world. They found three mitochondrial haplogroups (A, B and C) that diverged more than 200,000 years ago and have undergone demographic expansion at different times. This would suggest multiple maternal origins of domestic goats or introgression of other haplotypes after the first domestication event. Moreover, they

showed that most of genetic diversity occurred within breeds, and interpreted the very weak geographic structure as the result of the extensive transportation of goats among continents.

The initial global survey by Luikart et al. [13] has been followed by regional studies describing more precisely the genetic diversity of goat breeds. However, these studies were always realized in restricted geographic regions corresponding to different countries such as Pakistan [14], India [15], China [16], South Korea [17], Sicily [18], Spain [19,20] and Portugal [21]. The existence of three new haplogroups has been suggested [14,15,18]. However, this has sometimes been based only on a few individuals, and without comparing the new divergent haplotypes to a sample representative of the worldwide haplotype diversity. In general, the identification of a new haplogroup might be controversial in the absence of standardized criteria. All previous studies describing the mitochondrial polymorphism of domestic animals use the term of "maternal lineage" for characterizing a group of closely related haplotypes. However, this term is ambiguous as it usually corresponds to many haplotypes, and thus to many maternal lineages *sensu stricto*. As a consequence, we propose to use "mitochondrial haplogroup" instead of "maternal lineage", a term that is already in common use in genetic studies.

In this context, the goals of the present study are (i) to characterize the domestic goat mtDNA diversity based on a worldwide sampling and make a global synthesis including previous studies, (ii) to establish the relationships between mitochondrial haplogroups and to propose a clear nomenclature, and (iii) to give standard criteria for the definition of mitochondrial haplogroups. For this purpose we used data from previous studies (1484 sequences retrieved from GeneBank), and we analyzed 946 new samples from all over the old world. New samples were especially taken from localities that have not been adequately sampled before, and that may have played an important role in the history of goat domestication (i.e., Middle East and especially the Fertile Crescent).

Results

Sequence polymorphism

The HVI fragment of the control region shows a high polymorphism with 336 variable sites over the 558 bp of the alignment. We observed 285 substitutions (226 transitions and 59 transversions) and 110 insertions/deletions (from 1 to 76 bp). The 2430 individuals correspond to 1540 different haplotypes.

Phylogenetic analysis and genetic structure of domestic goats

The Neighbor-joining tree of the 2430 domestic goats (Figure 3.1) shows 6 highly divergent groups corresponding to different mitochondrial haplogroups called A, B, C, D, F (according to previous studies) and G. Each group has high haplotype diversity (Table 3.1), and has been defined by high bootstrap values (except a bootstrap of 53 % for A; Figure 3.1A), and by high mean pairwise distance with all other groups (see below). The A haplogroup is the most represented when considering either the number of individuals or the number of haplotypes and is highly dominant all over the old world (Table 3.1 and Figure 3.2). Except for two individuals situated at the base of the B group, this clade is composed of two sub-groups, B1 (35 haplotypes) and B2 (9 haplotypes), as previously defined by Chen et al. [16]. The B group is mostly found in whole Asia, with a few individuals from the Sub-Saharan Africa and one European goat from Greece. The B2 individuals are restricted to China and Mongolia. Goats from the C group are from whole Asia and Europe and the D group is present in the whole Asia and Northern Europe. The three goats from the F group are from Sicily. The G group has not been reported until now, and is present in Middle East and Northern Africa, near the Fertile Crescent.

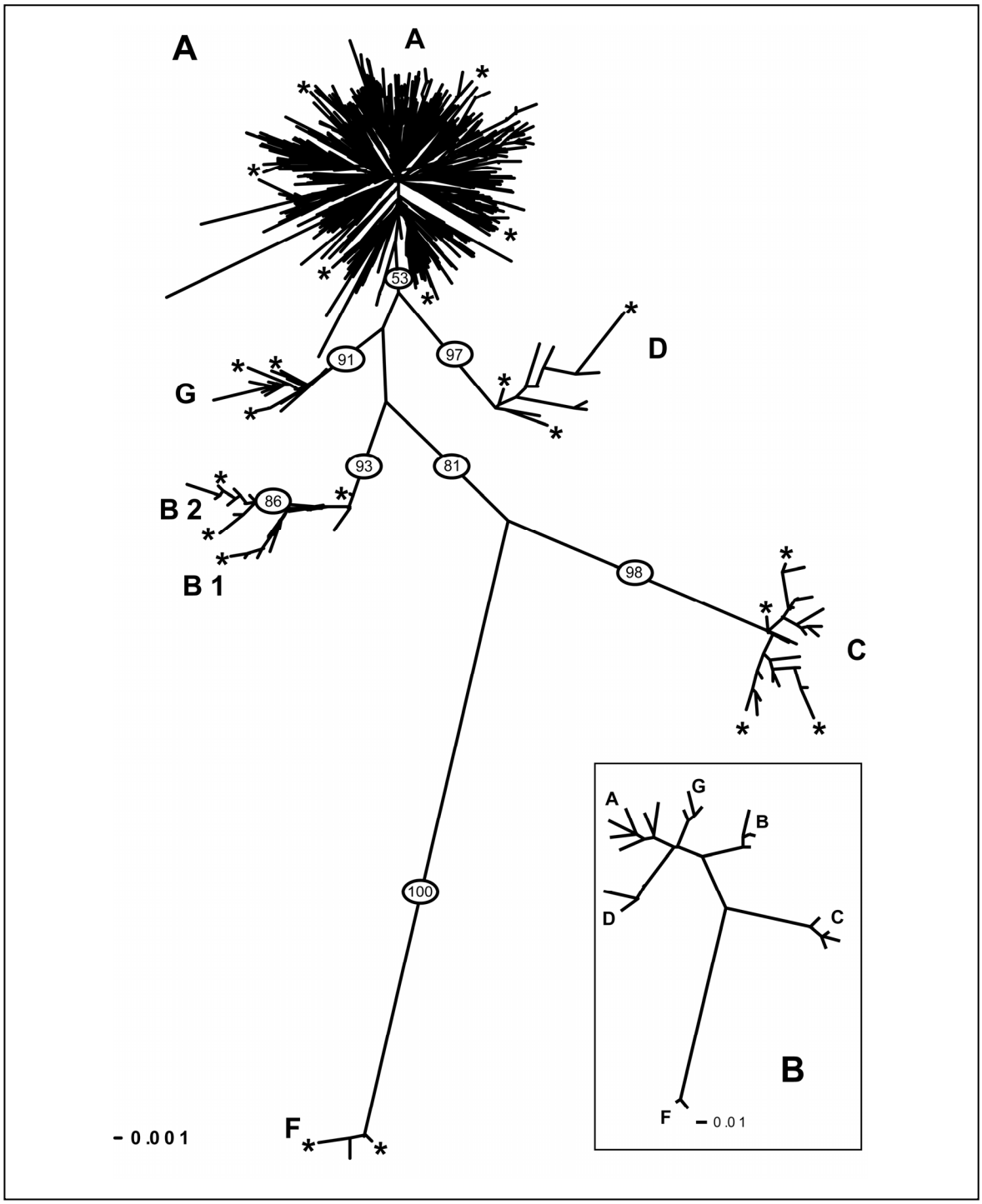

Figure 3.1. Neighbor-joining trees of domestic goat based on 1540 mtDNA haplotypes (A) and on the 22 reference mtDNA haplotypes (B). Distances were calculated using the Kimura 2-Parameter model with gamma correction (alpha = 0.28). On the (A) tree, the numbers on the branches represent bootstrap values out of 1000 replications, and the stars point out the position of reference individuals for each haplogroup used to construct the (B) tree (see Table 3.5).

Table 3.1. Genetic diversity of goat mtDNA haplogroups

haplogroup	# individuals (%)	# haplotypes (%)	haplotype diversity
A	2208 (90.86)	1440 (93.51)	0.9992 ± 0.0001
B	144 (5.92)	46 (2.99)	0.9000 ± 0.0197
B1	107 (4.40)	35 (2.27)	0.8402 ± 0.0333
B2	35 (1.44)	9 (0.58)	0.8151 ± 0.0481
C	35 (1.44)	23 (1.49)	0.9714 ± 0.0136
D	13 (0.54)	10 (0.65)	0.9487 ± 0.0506
F	3 (0.12)	3 (0.19)	1.0000
G	27 (1.11)	18 (1.17)	0.9544 ± 0.0254

The haplotype diversity is very high all over the Eurasia and Africa with a value above 0.97 in 39 of the 54 studied countries (Table 3.2). More than 77% of the mtDNA variation is distributed within breeds while about 11% is found among breeds within geographic regions and 12 % among geographic regions (Table 3.3). Nevertheless this low but significant geographic structure is coherent with the fact that all breeds are composed of individuals from the A group, with eventually a lower percentage of individuals from other haplogroups (for about 25% of the breeds). This low geographic structure is also confirmed by the distribution of all haplogroups that are present in several regions (except for F). Most of the mtDNA diversity is distributed among groups and within geographic regions, while less than 4% of this variability is found among regions within groups (Table 3.3).

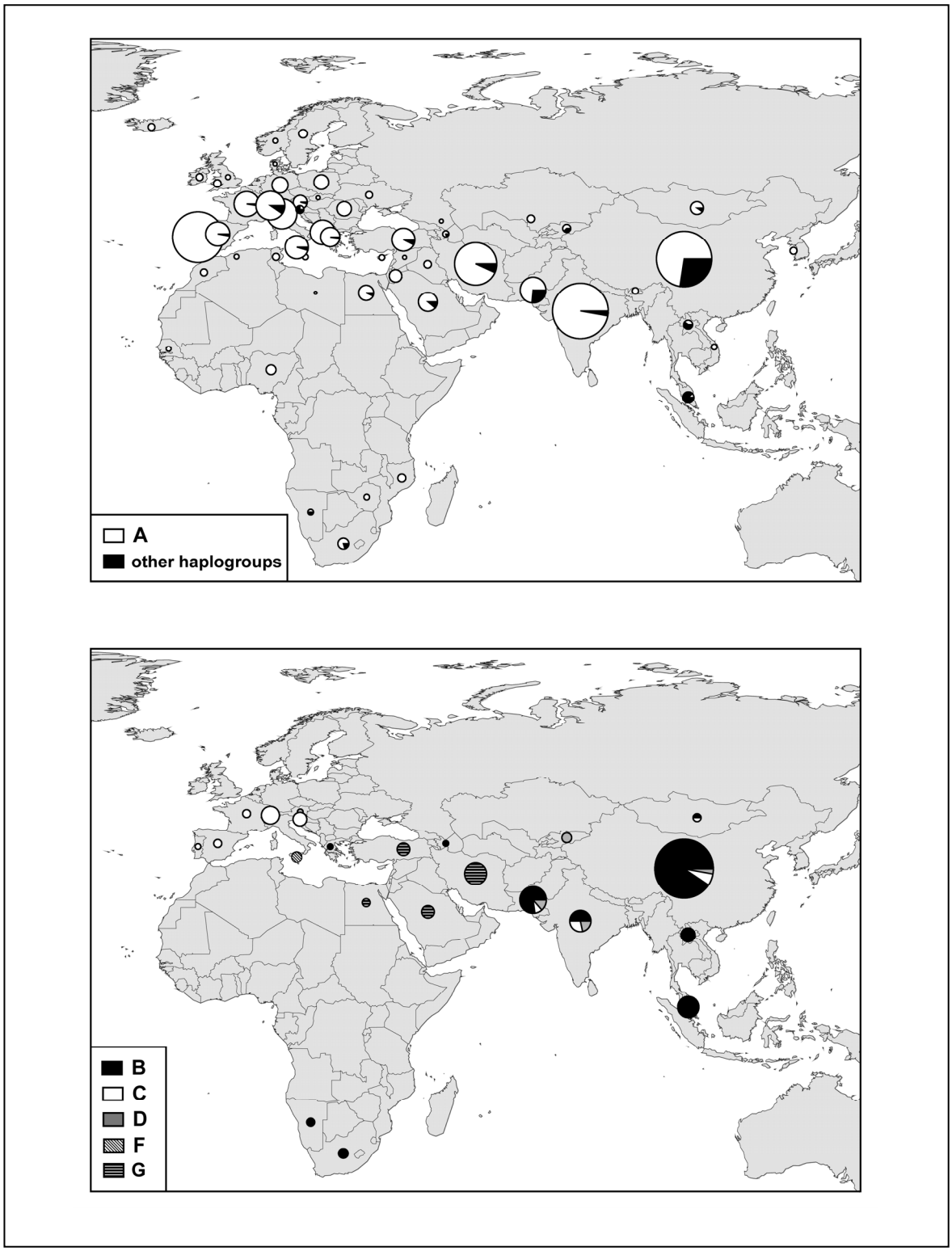

Figure 3.2. Geographic distribution of domestic goat mtDNA haplogroups. The size of each circle is proportional to the sample size and each specific haplotype is represented by a different colour.

Table 3.2. Geographic origin and characteristics of the studied domestic goat

region	country	# of breeds	# of individuals	# of haplotypes	# ind / haplogroup	Haplotype diversity	Accession numbers
Eastern Asia (EA)	Bhutan	1	5	5	A:5	1.0000+/-0.1265	AJ317851-55 (Luikart et al. 2001)
	China	13+U	382	154	A:275; B1: 63; B2: 34; C:7; D: 3	0.9827+/-0.0027	AJ317569-70 (Luikart et al. 2001); DQ089106-13; DQ089116; DQ089135; DQ089147; DQ089155-9; DQ089186-8; DQ089191-209; DQ089212-16; DQ089218-19; DQ089221-2; DQ089237-47; DQ089249-54; DQ089256-57; DQ089269-70; DQ089272-80; DQ089282-304 ; DQ089350 (Chen et al. 2005); AY853278-301 (Zhang et al. 2004); DQ121491-588; DQ121590-618 (Liu et al. 2006); DQ188849-903 (Liu et al. 2005); AY860871-942 (Zhang et al. 2004)
	Laos	1	10	7	A:4; B1: 6	0.9778+/-0.0540	AB044295- 304 (Mannen et al. 2001)
	Malaysia	1	16	6	A:2; B1:14	0.8583+/-0.0626	AJ317553; AJ317831-32; AJ317828-29 (Luikart et al. 2001); EF618221- 31
	Mongolia	2+U	21	21	A:19; B2:1; C:1	1.0000+/-0.0147	AJ317534 -38; AJ317545-52; AJ317833-34 (Luikart et al. 2001); EF618234- 39
	South Korea	U	6	4	A:6	1.0000+/-0.0962	DQ217780- 85 (Lee et al. 2005)
	Vietnam	1	4	3	A:4	0.8333+/-0.2224	AJ317566-68 (Luikart et al. 2001); EF618541
Middle East (ME)	Iran	3+U	222	161	A:207 ; G:15	0.9970+/-0.0008	EF617863- EF618084
	Iraq	1	7	6	A:7	1.0000+/-0.0764	AJ317762-68 (Luikart et al. 2001)
	Jordan	2	19	16	A:19	0.9825+/-0.0223	AJ317769-73 (Luikart et al. 2001); EF618191- 204
	Pakistan	18	73	55	A:56; B1:12; C: 2 ; D: 3	0.9855+/-0.0076	AJ317533; AJ317539;AJ317554-55; AJ317557-59; AJ317563-65; AJ317826; AJ317845-50; AJ317861-63 (Luikart et al. 2001); AB110552-589(Sultana et al. 2003); EF618253- 63
	Saudi Arabia	3	45	39	A:40; G: 5	0.9949+/-0.0058	AJ317752-59 (Luikart et al. 2001); EF618309- 45
	Syria	1	2	2	A:2	1.0000+/-0.5000	AJ317760-61 (Luikart et al. 2001)
	Turkey	5	66	56	A:61; G: 5	0.9953+/-0.0038	AJ317736-751; AJ317842-43 (Luikart et al. 2001); EF618492-539
Western Asia (WA)	Azerbaijan	1	5	5	A:4 ; B1:1	1.0000+/-0.1265	EF617702- 6
	Dagestan	1	2	2	A:2	1.0000+/-0.5000	EF617708- 9
	India	5+U	387	207	A:373 ; B1:7; C:4; D:3	0.9937+/-0.0008	AJ317827; AJ317856-57; AJ317540-41; AJ317830; AJ317542-44; AJ317560-62; AJ317571-72 (Luikart et al. 2001); AY155674-AY156039 (Joshi et al. 2004); EF617856 - 62
	Kazakhstan	1	7	7	A:7	1.0000+/-0.0764	EF618205- 11
	Kyrgyzstan	1	8	7	A:5 ; D: 3	0.9643+/-0.0772	EF618212- 19
Northern Africa (NAF)	Algeria	1	3	3	A:3	1.0000+/-0.2722	AJ317777-79 (Luikart et al. 2001)
	Egypt	3	29	24	A:27 ; G: 2	0.9901+/-0.0116	AJ317780-83; AJ317795-801 (Luikart et al. 2001); EF617711-28

	Libya	U	1	1	A:1	1.0000+/-0.0000	EF618220
	Morocco	1	6	5	A:6	0.9333+/-0.1217	AJ317784 -88 (Luikart et al. 2001); EF618233
	Nigeria	3	12	12	A:12	1.0000+/-0.0340	AJ317810-811; AJ317823-25 (Luikart et al. 2001); EF618246-52
	Senegal	1	3	3	A:3	1.0000+/-0.2722	AJ317816-18 (Luikart et al. 2001)
	Tunisia	1+U	6	5	A:6	1.0000+/-0.0962	AJ317789-794 (Luikart et al. 2001)
Sub-Saharan Africa (SAF)	Mozambique	1	8	5	A:8	0.9286+/-0.0844	AJ317804-809 (Luikart et al. 2001); EF618240- 1
	Namibia	2	4	1	A:2; B1: 2	0.8333+/-0.2224	EF618242- 5
	South Africa	3+U	15	11	A:12; B1: 3	0.9429+/-0.0542	AJ317812-15; AJ317819-20; AJ317844; AJ317821-22 (Luikart et al. 2001); EF618351- 56
	Zimbabwe	1	4	2	A:4	0.8333+/-0.2224	AJ317802-803 (Luikart et al. 2001); EF618545- 6
Northern Europe (NE)	Austria	2	24	18	A:23; D:1	0.9783+/-0.0187	EF617678- 701
	Denmark	1	2	1	A:2	1.0000+/-0.5000	AJ317650 (Luikart et al. 2001) ; EF617710
	England	1	3	2	A:3	0.6667+/-0.3143	AJ317592; AJ317841 (Luikart et al. 2001); EF617729
	France	7	79	61	A:77 ; C: 2	0.9932+/-0.0039	AJ317575-83; AJ317713-19; AJ317723-25; AJ317629-30 (Luikart et al. 2001); EF617730-87
	Germany	5	32	25	A:32	0.9919+/-0.0099	AJ317586; AJ317627-28 ; AJ317649 (Luikart et al. 2001); EF617788- 815
	Iceland	6	6	1	A:6	0.0000+/-0.0000	AJ317587 (Luikart et al. 2001); EF617851- 55
	Ireland	1	6	4	A:6	0.8667+/-0.1291	AJ317588-91 (Luikart et al. 2001); EF618085- 6
	Norway	1	3	3	A:3	1.0000+/-0.2722	AJ317593-95 (Luikart et al. 2001)
	Poland	4	27	22	A:27	0.9943+/-0.0119	AJ317584-85; AJ317651-52 (Luikart et al. 2001); EF618264-86
	Slovakia	1	2	2	A:2	1.0000+/-0.5000	AJ317653-54 (Luikart et al. 2001)
	Slovenia	1	8	3	A:2; C: 6	0.7143+/-0.1227	AJ317731; AJ317835; AJ317837 (Luikart et al. 2001); EF618346-50
	Sweden	1	9	7	A:9	0.9722+/-0.0640	AJ317637 (Luikart et al. 2001); EF618415- 22
	Switzerland	11	104	74	A:94; C:10	0.9925+/-0.0026	AJ317573-74; AJ317596-99; AJ317605; AJ317619-24; AJ317626; AJ317631-36; AJ317836; AJ317838- 40; AJ317638-48 (Luikart et al. 2001); EF618423- 91
	Ukraine	1	6	4	A:6	0.9333+/-0.1217	AJ317600-604 (Luikart et al. 2001); EF618540
	Wales	7	7	4	A:7	0.8095+/-0.1298	AJ317655-58 (Luikart et al. 2001); EF618542 - 44
Southern Europe (SE)	Albania	6	77	65	A:77	0.9969+/-0.0028	EF617601- 77
	Cyprus	1	4	3	A:4	0.8333+/-0.2224	AJ317774-76 (Luikart et al. 2001); EF617707
	Greece	2+U	47	39	A:46 ; B1:1	0.9935+/-0.0061	AJ317686-97 (Luikart et al. 2001); EF617816- 50
	Italy	11	115	95	A:115	0.9969+/-0.0018	AJ317674-78; AJ317680-85 (Luikart et al. 2001); EF618087-190
	Malta	2	4	4	A:4	1.0000+/-0.1768	AJ317659-AJ317702-AJ317708 (Luikart et al. 2001); EF618232

Portugal	8	321	164	A:320 ; C:1	0.9941+/-0.0009	AJ317660-69; AJ317698-701; AJ317720-22; AJ317726-30; AJ317732-35 (Luikart et al. 2001); AY961629-697; AY961700- 916 (Pereira et al_2005); EF618287- 95
Romania	6	26	23	A:26	0.9908+/-0.0133	AJ317606-618 (Luikart et al. 2001); EF618296- 308
Sicily	1	67	22	A:64; F: 3	0.9701+/-0.0073	DQ241305-71 (Sardina et al. 2006)
Spain	9+U	73	59	A:71;C:2	0.9962+/-0.0032	AJ317625; AJ317670-73; AJ317679; AJ317703-4;AJ317705-7; AJ317709-12 (Luikart et al. 2001);EF618357-414

Note: U: Individuals from undefined breed(s)

Table 3.3. Partition of the genetic variance among haplogroups, breeds and continental regions revealed by hierarchical AMOVAs

	AMOVA haplogroups / regions			AMOVA regions / breeds		
Source of variation	Among haplogroups	Among regions within haplogroups	Within regions	Among regions	Among breeds within regions	Within breeds
d.f.	5	20	2404	6	166	1429
% of variation	74.62	3.56	21.82	12.06	10.79	77.14
P value	<0.0001	<0.0001		<0.0001	<0.0001	

Demography of mitochondrial haplogroups

Because of the low number of goats in the F group, demographic parameters were not estimated for this group. The overall mismatch distribution shows a multi-modal distribution (Figure 3.3). The first peak with a maximum of 10 pairwise differences corresponds to the differences between haplotypes from the same group. Two other peaks with maxima at 27 and 39 pairwise differences correspond to differences between haplotypes from different groups. The distributions of within-groups and between-groups pairwise differences have a very thin overlap around 20 mismatches. The mismatch distribution analysis reveals a unimodal bell-shaped distribution of pairwise sequence differences for all haplogroups (Figure 3.3), except for B that is bimodal (data not shown). B1 and B2 are unimodal, and individuals from these sub- groups generally differ by 8 or 9 mismatches (always less than 14 mismatches). This unimodal pattern that is less clear for

the D group, perhaps because of the low sample size (n=13), would be coherent with recent demographic expansions. The time of expansion would differ according to the group, as suggested by the different means of pairwise distribution (Figure 3.3) and the estimations made under a model of pure demographic expansion [22] (Table 3.4). However, the validity of the expansion model used for estimating the expansion time is only accepted for the A, C groups (SSD *P*-Values <0.00001 and ≤ 0.05 respectively see Table 3.4). All groups have high growth rates indicating high demographic expansion (Table 3.4). The estimates differ according to the groups, but the overlapping of confidence intervals, as well as the different sample sizes, preclude further interpretation.

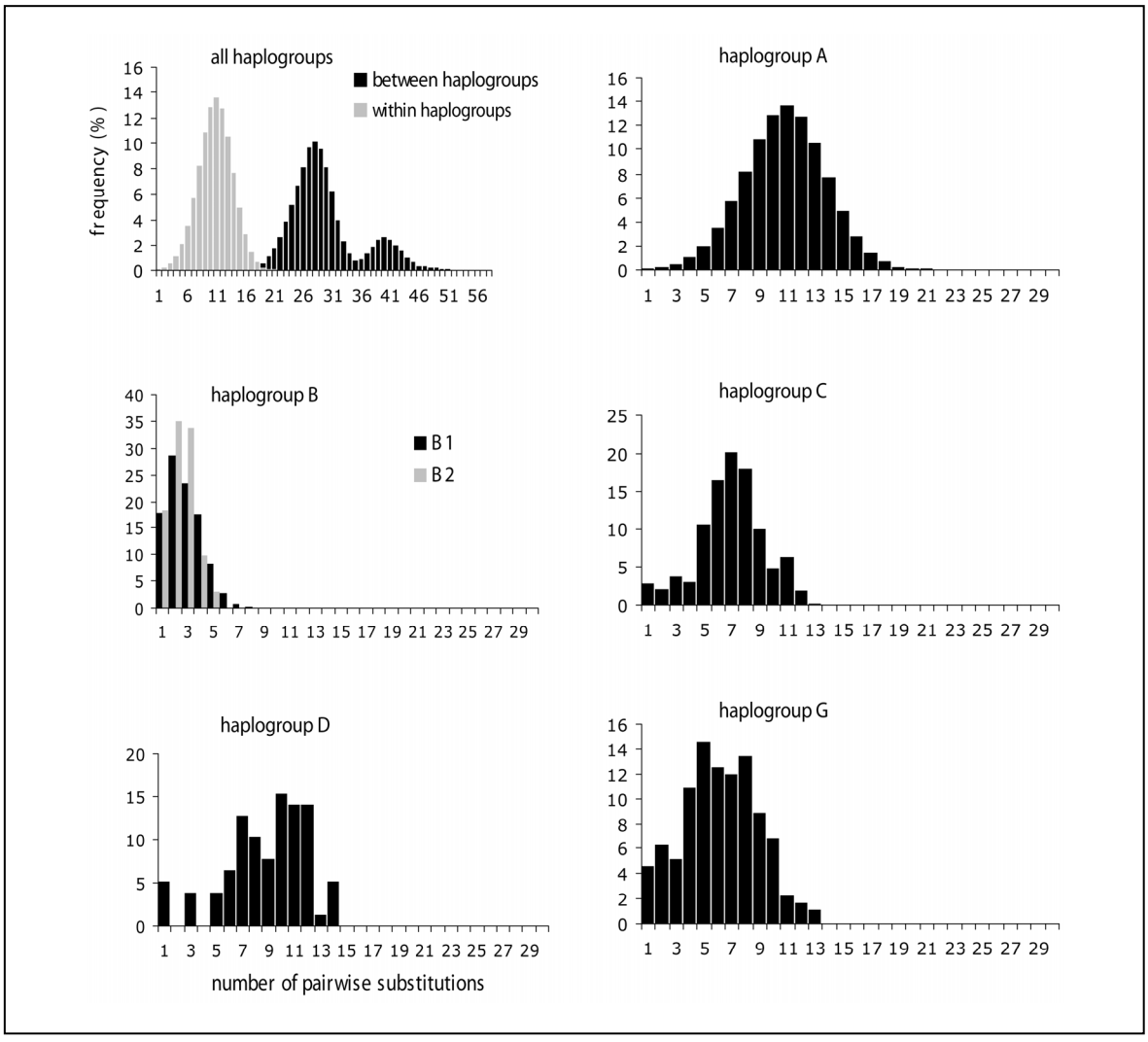

Figure 3.3. Mismatch distributions for mtDNA haplogroups of domestic goats. For the overall dataset, the distribution of pairwise differences were realized separately for comparisons between and within haplogroups.

Table 3.4. Estimation of demographic parameters from genetic data

haplogroups	τ (0.95 CI)	Validity of the expansion model SSD (*P*-value)	Rough estimation of Expansion time	Growth rate (0.95 CI)
A	10.07 (9.74-10.42)	0.00071 (***P* <0.0001**)	~ 9000 - 9700	308 (199-344)
B1	1.855 (0.73-3.19)	0.0008 (*P* =0.70)	-	333 (201-412)
B2	1.584 (1.10-2.65)	0.0095 (*P* =0.20)	-	108 (14-324)
C	6.37 (4.99-7.84)	0.00795 (***P* =0.05**)	~ 4600 - 7300	185 (158-291)
D	9.10 (5.50-13.01)	0.0141 (*P* =0.20)	-	334 (173-509)
G	5.79 (2.85-11.22)	0.0021 (*P* =1.00)	-	209 (144-293)

Note. - See material and methods for the methods used for estimating the demographic parameters. CI: Confidence Interval. SSD: sum of square deviations between the observed and the expected mismatch distributions.

Discussion

High mtDNA diversity in domestic goat

The very high mt DNA diversity may partly result from a high mutation rate of the control region. Higher pedigree divergence rates than phylogenetic divergence rates have been shown for the control region in human [23] and other animals (e.g.,[24, 25]). This could explain that we observe a higher diversity than the one expected with the phylogenetic mutation rate estimated for Bovidae (i.e., 30.1 % of divergence per Myr on the total control region sequence based on the *Bos*/*Bison* divergence [26]). Such high variability could also result from the selection of polymorphism but, to our knowledge, this has never been shown for the control region. Another explanation would be the capture of a large part of the diversity of the wild ancestor (i.e., the bezoar) during the domestication, with a large maternal effective population size. Testing this last hypothesis requires comparing the diversity of goats to that of the bezoar [27].

Characteristics and nomenclature of mitochondrial haplogroups

Five reliable mitochondrial haplogroups have previously been described in domestic goats [13-15,18]. However, most of the previous studies were based on local samples and

thus only considered a part of the whole haplotype variability. Therefore, it may be difficult to assess the pertinence of defining a new group on the base of few haplotypes. It would also be difficult to make the correspondence between several studies analyzing samples from different geographic origins. Our study can lead to a clear nomenclature of goat mitochondrial haplogroups, because we analyzed 2430 goats representing 1540 different haplotypes from all over Africa, Asia and Europe (946 new sequences mainly from the region of domestication and 1484 sequences from previous studies). We revealed the existence of 6 highly divergent groups. Five of them (A, B, C, D and F) have already been described, and one (G) is a new group. The two sequences that have been previously used to define the E group [15] now fall within the A haplogroup. This is partly due to the finding of new haplotypes, which are intermediate between those from A and E used by Joshi et al. [15]. Therefore, the E group cannot be considered as a mitochondrial haplogroup anymore. The B clade is composed of two groups (B1 and B2) that have previously been described as "sub-lineages" by Chen et al. [16]. We agree that the B1 and B2 are part of the same haplogroup because the genetic divergence between them (pairwise differences always lower than 14 mismatches) is lower than the divergence between all pairs of haplogroups (more than 20 mismatches). They must be considered as two subgroups because even with a low divergence they are supported by robust bootstrap values.

Standard criteria for defining goat mitochondrial haplogroups

More generally, previous considerations point out the problem of defining groups and sub-groups. A new haplogroup is defined when it highly diverges from all other haplotypes. However, the haplogroups may change over time, as more and more haplotypes will be available. We faced this situation for the E haplogroup that is no valid any more. There is therefore a need for standard and easy-to-use criteria in order to assign new goat haplotypes to existing haplogroups or to define new haplogroups. A haplotype can be related to an existing group if it presents a moderate genetic divergence from this group. The difficulty may be to define what is a “moderate” divergence. It can be deduced from the distributions of pairwise sequence differences within and between haplogroups. For goats, almost all haplotypes from the same group differ by less than 20 mismatches (whatever the group) while haplotypes from different groups usually present more than 20

mismatches (Figure 3.3). This threshold value would give a quick and easy indication for almost all studied haplotypes. However, it may be inadequate for some haplotypes (about 1% in our study) because the two mismatch distributions overlap.

Given the increasing number of sequences available, analyzing new haplotypes together with all previously published sequences will be time consuming and will require huge computational resources. Moreover several programs cannot be used because the algorithm complexity does not allow managing such datasets. Especially when a few haplotypes from restricted localities are studied, their assignation to haplogroups should be quick and easy. For a first approach, an accurate solution would be to place the new different haplotypes in a phylogenetic tree containing sequences of reference representative of the diversity of *C. hircus* mitochondrial DNA. For this purpose we have selected 22 haplotypes representing the variability of the 6 present goat mitochondrial haplogroups (Table 3.5 and Figure 3.1B).

Table 3.5. The 22 reference individuals of the 6 domestic goat haplogroups

haplogroup	Geographic origin (Country)	Accession Number	Reference
A	India	AY155721	Joshi et al. 2004
A	Italy	EF618134	This Study
A	France	EF617779	This Study
A	Jordan	EF618200	This Study
A	Iran	EF617945	This Study
A	Iran	EF617965	This Study
B1	Laos	AB044303	Mannen et al. 2001
B1	Azerbaijan	EF617706	This Study
B2	Mongolia	AJ317833	Luikart et al. 2001
B2	China	DQ121578	Liu et al. 2006
C	India	AY155708	Joshi et al. 2004
C	Switzerland	AJ317838	Luikart et al. 2001
C	Spain	EF618413	This Study
C	China	DQ188892	Liu et al. 2005
D	India	AY155952	Joshi et al. 2004
D	Austria	EF617701	This Study
D	China	DQ188893	Liu et al. 2005
F	Sicily	DQ241349	Sardina et al. 2006
F	Sicily	DQ241351	Sardina et al. 2006
G	Iran	EF618084	This Study
G	Turkey	EF618535	This Study
G	Egypt	EF617727	This Study

Four of the 1540 haplotypes present a tandemly repeated sequence of 76 bp. Three individuals are from the A group (from Iran, Morocco and India) and one from the B1 sub-group (Malaysia). Such tandem repeats are common in vertebrate species [28] and have already been found in the Bovidae family [29]. They are attributed to slippage-mispairing events that are more likely to appear in regions where the polymerase activity is interrupted [28]. This phenomenon corresponding to a single duplication event is found in a few individuals from different haplogroups, and has occurred more than once in the history of goats.

Genetic structure of domestic goats

Our results show that most of the genetic variation is found among goat haplogroups, with a weak phylogeographic structure. The strongly dominant A group (91 % of the goats) is distributed worldwide, and even if the other groups have more restricted distributions they still occupy large geographic areas (Figure 3.2). The F group is the exception, with three haplotypes restricted to a single locality (Sicily) that could have been brought along from recently captured wild goats. However, the sampling effort may still be insufficient to see the whole distribution of haplogroups other than A, because of their low frequency. The differences among geographic regions at the worldwide scale are low (about 12%) but significant. This is concordant with previous results showing a very weak phylogeographic structure of goats [13] and sheep [30,31] compared to cattle [32,33]. The genetic differences among continental regions could partly result from the differential geographic distribution of mitochondrial haplogroups. However, there is still a low but significant genetic variation (3.5%) among region within groups, indicating regional differentiations of haplotypes. At the regional scale, the lack of geographic structure has also been reported in several places [16,19,21] while a structure has been found in India [15]. The weak phylogeographic structure found today in goats has been explained by a high mobility of this species in relation to human migration and commercial trade [12,13,34]. This mobility would have been higher than those of cattle due to their versatility in feeding habits and ability to live under extreme conditions [1]. However, the mixing of goat haplogroups could have existed before the worldwide translocation of goats. The presence of goats in Cyprus 10,000 years ago [35] suggests that goats could have been translocated within the domestication area since the first domestication events.

Moreover, we cannot exclude that the mt-haplogroups were already mixed in the wild ancestor before domestication. When considering the local scale, the genetic pattern of domestic goats also seems related to human history. For instance, the geographic structure found in Indian goats would have a common historical basis in the sequential migrations of human populations with different cultural and linguistic characteristics [15].

However, the information given by mitochondrial markers is limited because it does not detect male-mediated gene flow and does not predict the nuclear genomic diversity [12]. In particular, the breeds cannot be distinguished on the base of mtDNA [16,19, 20] while nuclear markers show a genetic structure [36-38]. Our study confirmed that more than 77 % of the mtDNA variation is found within breeds and that nearly 25% of the breeds are composed of at least 2 haplogroups. This is in accordance with the recent fragmentation of local goat populations into discrete breeds about 200 years ago, under strong selection pressures on a few phenotypic traits [39]. This structure can be seen on nuclear markers linked to selected parts of the genome, but not on mitochondrial markers. Then, looking at the evolutionary history of breeds using mtDNA markers could lead to misinterpretation. For example, a breed composed of two mitochondrial haplogroups would have a bimodal mismatch distribution due to within- and between-breeds pairwise differences, and should not be interpreted in term of demographic history of the breed. Thus, fully understanding the evolutionary history of domestic goats would also require the use of nuclear markers.

Demography of mitochondrial haplogroups

The present structure of the genetic diversity retains the signature of past demographic events and helps reconstitute the evolutionary history [40]. The estimation of demographic parameters remains difficult because of the difficulties of verifying the hypothesis of the models used, of estimating accurate initial parameters (e.g., absolute date of domestication) and sometimes because of low sample sizes. However, rough estimations from the present work and previous studies [13,15,16] are concordant and agree on the same scenario. All haplogroups had a recent demographic expansion corresponding roughly to the period when domestication took place about 10,000 years ago. It is difficult to give relative dates of expansion because of large confidence intervals, especially for D and G groups, but our results confirm that the expansions of B and C

groups were more recent than that of A [13]. Also, our results show that all groups had high growth rates, with a tendency for slower growth in B2 sub-group and C and G. A faster growth of A relative to C is in accordance with archaeozoological data: the genotyping of fossil goats showed that about 7000 years ago A and C were equally represented in Southern France [34] while A is strongly dominant in Southern Europe now.

Limits of genetic data from domestic goats for reconstituting the history of domestication

Divergence time between haplogroups has been estimated on adequate molecular markers (mainly cytochrome *b*) between 103,000 and 597,800 years [13-16]. All these values are far greater than the domestication time, showing that most of goat genetic diversity existed before domestication, and that several haplogroups were domesticated in one or several events. However, the genetic data available for domestic goats does not permit furthering our understanding of the domestication process and identifying potential domestication centre(s). A higher genetic diversity would have been expected near the Fertile Crescent where the goat domestication took place according to archaeological data, and where extensive sampling has been done. But the haplotype diversity is similar all over the world (more than 80% of the countries with a haplotype diversity greater than 0.9), because of the high migration rates in domestic goats due to human migration and commercial trade.

Moreover, the presence of a possible ancestral haplotype in a particular area does not prove that this is a domestication centre, since many events could have occurred to mask the real history (e.g., coalescence or founder effects). For instance the domestication of a B sub-group in China supported by genetic data [16] is doubtful since the wild ancestor of the domestic goat (i.e. the bezoar *Capra aegagrus*) has credibly never been present in this area [11, 41]. Overall, in order to fully understand the domestication of goats it is necessary to characterize the genetic diversity of wild goat species, and to establish the evolutionary relationships between wild and domesticated haplotypes.

Materials and methods

Sampling and DNA extraction

Samples were collected from 946 individuals from 42 countries of the old world (See Table 3.2) from which 569 individuals were studied within the Econogene project (www.econogene.eu). Samples consisted of ear tissue preserved in ethanol 95% until extraction, or of blood collection. DNA was extracted from tissue using the Qiagen DNeasy tissue kit following the manufacturer's instructions, and from blood samples using QIAamp DNA blood kit.

To have a good coverage of the goat breeds, the dataset was completed with 1484 sequences containing the *Capra hircus* HVI control region (450 to 1200 bp long) retrieved from GenBank (Table 3.2).

DNA amplification and sequencing

The HVI segment of the control region was sequenced for all blood and tissue DNA extracts. Using the primers CAP-F (5'-CGTGTATGCAAGTACATTAC-3') and CAP-R (5'-CTGATTAGTCATTAGTCCATC-3'), we amplified a fragment of 598 bp (without primers) that corresponds to the positions 15,653 to 16,250 on the complete goat mitochondrial sequence of reference ([42]; accession number AF533441). PCR amplifications were conducted in a 25 µl volume with 2 mM $MgCl_2$, 200 µM of each dNTP, 1 µM of each primer and 1 unit of AmpliTaq Gold Polymerase (Applied Biosystems). After a 10 min period at 95°C for polymerase activation, 35 cycles were run with the following steps: 95°C: 30s, 55°C: 30s, 72°C: 1 min. PCR products were purified using the Qiaquick PCR purification kit (Qiagen). 35 ng of purified DNA from this PCR product was used for sequencing with the CAP-F or CAP-R primer. Sequence reactions were performed for both DNA strands by using the ABI PRISM Dye Terminator Cycle Sequencing Reaction Kit (Applied Biosystems) in a 20 µl volume with 2 µM of each primer. 25 cycles were run with the following steps 96°C: 30s, 55°C: 30s, 60°C: 4 min. Excess dye terminators were removed by spin-column purification and the products were electrophorezed on an ABI 3700 PRISM DNA sequencer (Applied Biosystems) using the POP 7 polymer.

Sequences were edited for correction with the SeqScape v2.5 software (Applied Biosystems). All sequences were deposited in GenBank (Accession Numbers EF617601-EF618546, Table 3.2).

Sequences from GenBank and from our dataset were aligned with Mega v3.1 [43], and then adjusted by eye. For further analyses, we only kept the region used by Luikart et al. [13] because this is the part of the sequence available for most of the GenBank records, and also the most informative one. This region is 481 bp long and corresponds to the positions 15,707 to 16,187 on the *Capra hircus* reference sequence (mtDNA complete sequence of *C. hircus*, Accession number AF533441 [42]). According to the insertion/deletion events, the analyzed sequences ranged from 481 to 558 bp. For Indian goats a shorter fragment of 453 bp has been sequenced [15] and the 28 missing nucleotides were treated as missing data. The alignment of the 2430 sequences used in this study is provided as supplementary information.

Data analysis

The substitution model used for the HVI region was the Kimura 2-parameters model, as previously used on several subsets of the present dataset (e.g., [13,15]). The heterogeneity in substitution rates among nucleotide sites was modelled by a gamma distribution. The alpha parameter was estimated as the mean of 10 estimations by a maximum-likelihood method under the Kimura 2-parameters model using PAML v 2.0.2 [44]. Each estimation was based on the analysis of 1000 individuals randomly chosen in the dataset of 2430 individuals. The estimated value (alpha = 0.28) was similar to that estimated for the same region on a smaller sample of domestic and wild goats by Luikart et al. [13]. These settings were used for further phylogenetic reconstruction and analysis of genetic diversity. We used 1484 published sequences for checking the validity of the halpogroups previously defined (see Table 3.2 for references and GenBank accession numbers).

Given the very high number of sequences analyzed, the phylogenetic tree was constructed using the Neighbor-joining method using PAUP* v 4.0 [45], with 1000 bootstraps for measuring branch robustness. The ARLEQUIN v 3.0 software [46] was used for estimating haplotype and nucleotide diversity, for analyzing mismatch distribution within mitochondrial haplogroups, and for estimating the parameters of

demographic expansion. Four individuals that showed a 76 bp insertion were discarded for mismatch analyses and the analyses were thus performed on 481 bp long sequences. The expansion time was estimated under a model of pure demographic expansion [22] with parameters set to default values in ARLEQUIN 3.0. The parameter of demographic expansion τ was estimated according to the method of Schneider and Excoffier [47]. The validity of the expansion model was tested using the sum of square deviations (SSD) between the observed and expected mismatches [47].

Growth rates of mitochondrial haplogroups were estimated with Lamarc v2.2 [48] using a bayesian framework allowing migrations across haplogroups (with a maximum of 10000 migration events, default priors used for migration rates estimation). The estimation of growth rates was done with linear prior (upper bound of 1000 and lower bound of -500), 10 initial chains (500 samples, sampling interval of 20 and burn-in period of 1000) and 2 final chains (10000 samples, sampling interval of 20 and burn-in period of 1000).

In order to test the geographic structure of the mtDNA haplotype diversity, the goat distribution has been partitioned in 7 geographic regions (Northern Europe, Southern Europe, Northern Africa, Sub-Saharan Africa, Middle East, Western Asia and Eastern Asia, see Table 3.2). Two hierarchical AMOVA were performed using ARLEQUIN v3.0 to test the partition of the genetic variance among haplogroups and among continents within haplogroups, as well as among continents and among breeds within continents. This second AMOVA was performed on the 1602 goats for which the breeds were known.

Acknowledgements

We would like to thank Prof. Oscar Gaggiotti for fruitful discussions and constructive comments, Cécile Albert for help with figures, and Jessica Scriven and Alison Cleary for help with the English. We are grateful to Ebrahim Ghaderi and Prof. Mahamoud Abo-Shehada for their help for collecting samples in Iran and Jordan. We also thank two anonymous reviewers for constructive and stimulating comments.

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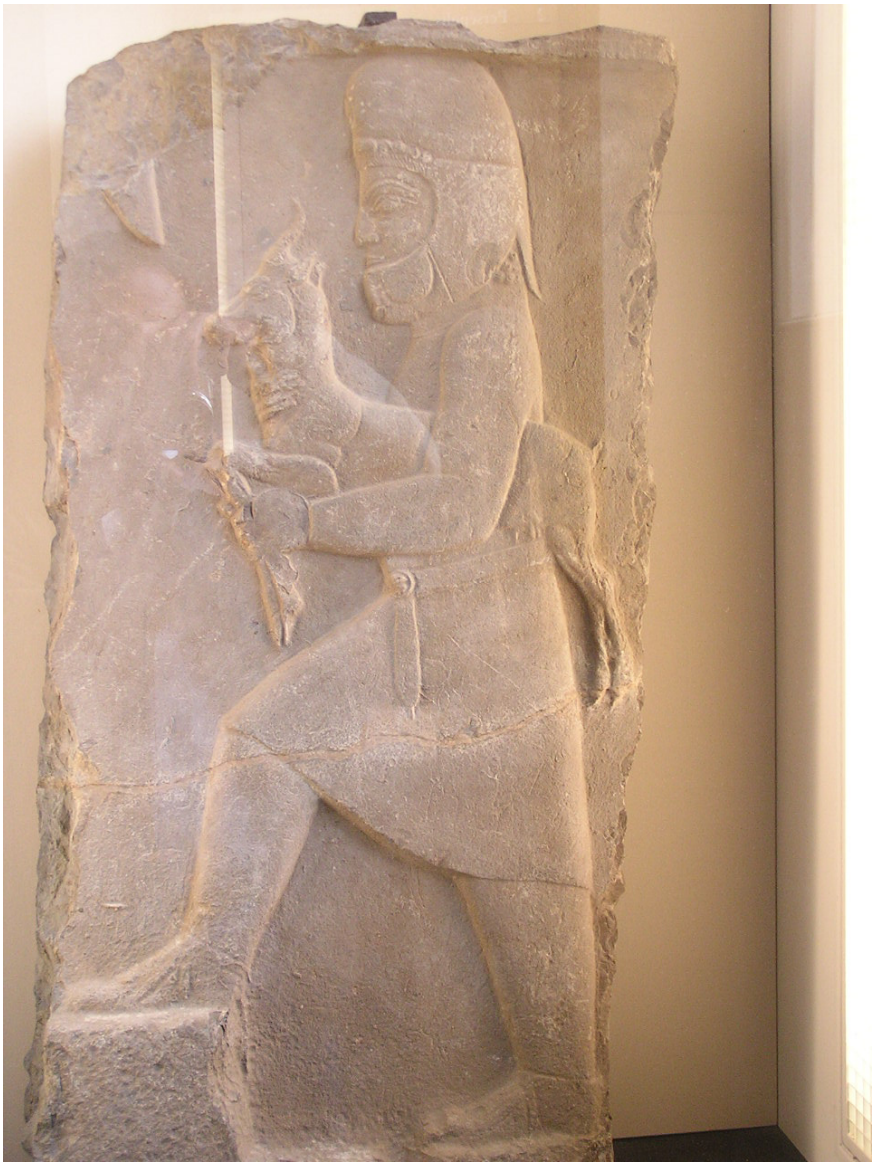
Chapter 4. Goat domestication



Chapter 4. Goat domestication: a single large-scale event without bottleneck

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The emergence of farming during the Neolithic transition, including the domestication of livestock, was a critical point in the evolution of humankind. Together with sheep, cattle and pigs[1-3], the goat (*Capra hircus*) was one of the first domesticated ungulates. While the precise domestication process remains unknown in livestock animals, it has been postulated that a strong reduction of population size - a bottleneck - occurs at the very early phase of domestication[4]. However, we show that goat domestication was in fact a large-scale process, without bottleneck. A comparison based on extensive sampling of goat genetic diversity to that of its wild ancestor, the bezoar, reveals a two-step scenario for goat domestication. A signature of population expansion in bezoars bearing mitochondrial DNA (mtDNA) haplotypes similar to those of goats, suggests an initial phase of management of wild flocks that fits well with some archaeological proposals. A second phase – the effective domestication – occurred mainly in Eastern Anatolia, and possibly in Northern and Central Zagros, and involved the capture of a large number of mtDNA haplotypes. This scenario strongly differs from previous bottleneck models that saw domestication occurring within restricted areas with population reductions. Our results, with their attendant implications for the development of early farming, should direct future research on animal domestication towards testing if the absence of bottleneck is the rule or the exception.

The first archaeological evidence of goat domestication traces back as far as ca. 10,500 calibrated Before Present (cal. B.P.) in the high Euphrates and Tigris valleys, in Southeastern Anatolia[5-6] and 9,900-9,500 cal. B.P. in the Zagros mountains[3,4,7]. While the hypothesis concerning goat domestication in the Southern Levant[8] seems to be more and more debatable, the domestication of local ungulates, especially goats, in the Lower Indus valley during the late 8th /early 7th millennia cal. B.P.[9] has not yet been contested. It is now widely recognized that the goat's wild ancestor is the bezoar, Capra aegagrus[10].

The three goat (*C. hircus)* mtDNA haplogroups (A, B, and C) found by Luikart *et al.*[11] have been interpreted to signify three distinct domestication events. Assuming a single haplotype domesticated per haplogroup and a coalescence time of 10,000 years for the most common A haplogroup, the domestication of B and C haplogroups have been hypothesised to have occurred about 2130 and 6110 years ago, respectively[11]. However, the finding of the C haplogroup dating to 7500 years ago in Southern France[12], far from

putative domestication centres, threw the initial scenario calling for sequential domestications[11] into question. The recent analysis of 2430 goat individuals revealed a total of six different monophyletic mtDNA haplogroups A, B, C, D, F, and G, with the A haplogroup representing more than 90% of individuals[13].

In this context, our main objective was to better understand the domestication process by an extensive analysis of the mtDNA polymorphism both in the domestic goat and in its wild ancestor. More specifically, we aimed to localize the putative domestication centres by finding the present day wild populations that bear the closest genotypes when compared to the domestic populations, using extensive and well-controlled sampling in the field. We also aimed to quantify the amount of mitochondrial and nuclear DNA diversity captured during the domestication process. Thus we analyzed the mtDNA control region of 487 modern bezoars from 43 localities covering most of the distribution range (see Methods and Supplementary Information), and compared it with the polymorphism of the homologous region in goats (Figure 4.1). Using five breeds from Iran and three from Italy we also compared the nuclear DNA polymorphism (via AFLP[14]) between the bezoar and domestic breeds.

Our first main finding is that bezoars bearing haplotypes close to domestic goats have had a significantly higher population growth rate, compared to other bezoars (Table 4.1). This evidence of a population size increase of the domestics' antecedents, suggests a phase of sustainable management of some wild flocks of bezoars, probably before true domestication. Such a population increase fits well with some archaeozoological findings, which suggest both the "controlling and protecting herds of [wild] caprines"[15] and the subsequent management of animals morphologically indistinguishable from wild populations[7,16], before incipient domestication / population isolation, as defined by Horwitz[17]. This phase of "pre-domestication"[16] might have lasted several centuries or millennia, as suggested by some archaeologists specializing in the Near East[18]. In the Central Zagros, the "pre-domestic" phase would have been characterized by culling more young males and older females, which is not the case for hunted bezoars[7]. Later on, individuals from these managed bezoar flocks transferred from their natural distribution area (Figure. 4.2a) would have been the source of fully domestic goats, and may even have become partly feralized, as they did ca. 10.000 cal. B.P. in Cyprus[16,19]. Consequently, a large proportion of the modern bezoar populations might come from herds that were managed by humans during these early pre-Neolithic and Neolithic periods. Indeed, the current geographic distribution of bezoars genetically close-to-domestics, with a

population expansion signature, encompasses a large area that includes Eastern Anatolia, the whole Zagros, the Central Iranian Plateau, and Northeastern Iran. Thus, the phase of pre-domestic management was not a local phenomenon, but a widespread practice in numerous localities spread over an area much larger than suggested by archaeozoology.

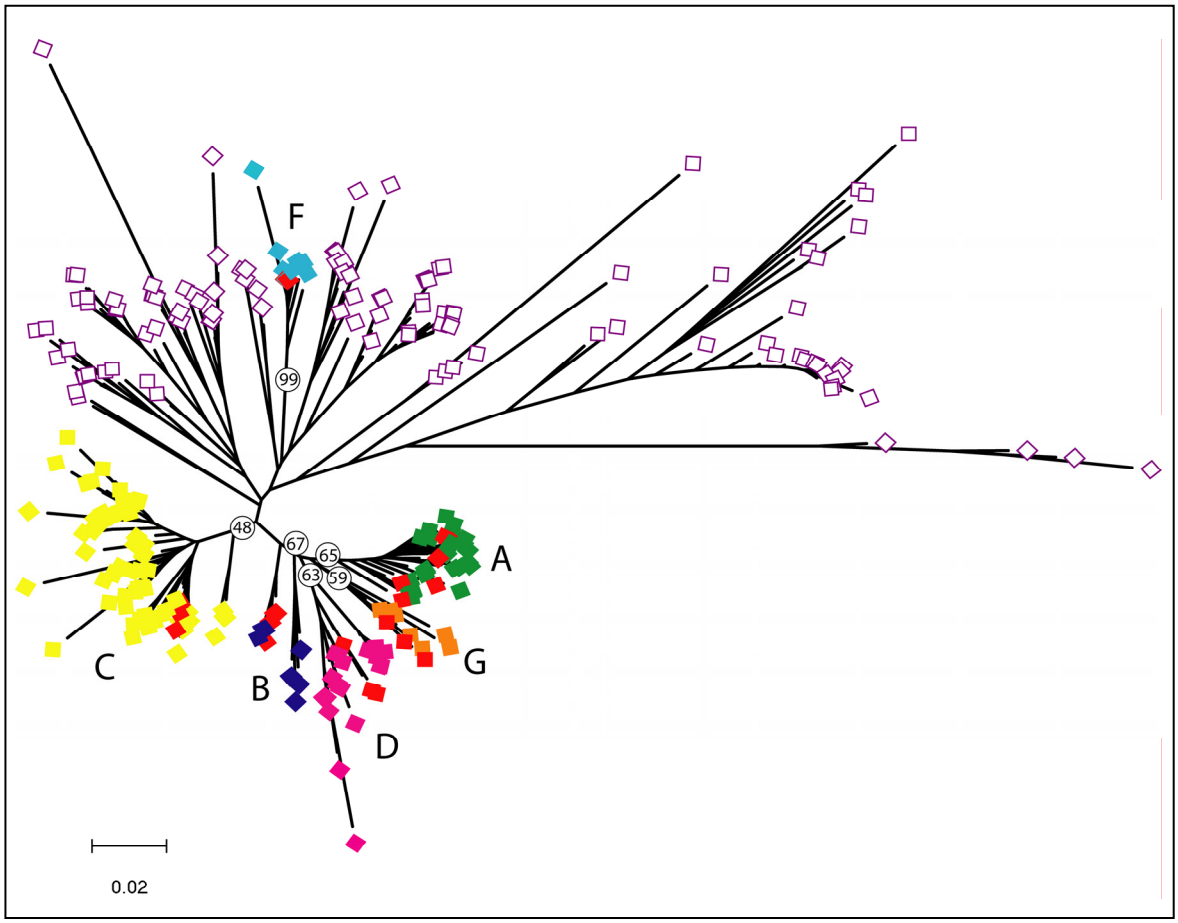

Figure 4.1. **Phylogenetic relationship of the 251 haplotypes from the 487 bezoars studied.** This tree was obtained with the neighbour joining method (see Methods). In order to identify shared mtDNA haplogroups, 22 haplotypes chosen to represent the overall diversity of modern goats[13] have also been included in the analysis (in red). The scale represents the genetic distance. The different colors correspond to the haplotypes from the different mtDNA haplogroups found in goat (A: green, B: dark blue, C: yellow, D: purple, F: light blue, G: orange). The other bezoar haplotypes are represented in white.

Table 4.1. Estimation of population growth rates (most probable estimates) for domestic goat and for two categories of bezoar (wilds close-to-domestics; wilds non close-to-domestics) using Lamarc v2.2[25].

	Growth rate	95% percentile
No gene flow with domestics		
Domestics	260.73	252.77-268.47
Wilds close-to-domestics	71.11	52.75-81.97
Wilds non close-to-domestics	19.47	13.25-23.62
Gene flow with domestics		
Domestics	108.57	95.53-112.59
Wilds close-to-domestics	67.44	59.52-77.59
Wilds non close-to-domestics	29.91	24.27-40.29

The demographic model always considers migration between wild populations. Results presented in the upper half of the table assume no migration between wilds and domestics. Results presented in the bottom half assume migration between wilds and domestics. Four independent runs gave similar results (one run presented). The growth rate given is equal to g/μ, where g is the parameter governing the exponential growth model used by Lamarc and μ is the mutation rate.

The phylogeographic structure of the bezoar is weak compared to other wild ungulates (see e.g. ref. 20), and the same mtDNA haplotypes can be found in very distant localities (e.g. 1635 km for haplotype 54 found in localities 8 and 28; 3022 km for haplotype 136 found in localities 6 and 43; etc.). Such a mixing of haplotypes is very unusual in natural populations (except for animals with high dispersal abilities such as birds; e.g. ref. 21, 22). The most likely explanation for such a mixing in bezoars is that humans translocated many animals in the past, probably during the pre-domestication phase, before morphological modifications. Such a transfer is archaeologically attested in Cyprus[16,19]. This mixing is particularly obvious for the C haplogroup that now occupies almost all of the bezoar distribution area (Figure 4.2b). According to the strong

predominance of the C haplogroup in Southern Zagros and in the Central Iranian Plateau, one can hypothesize that these two regions were at the origin of the C haplogroup, and that the pre-domestication phase began there.

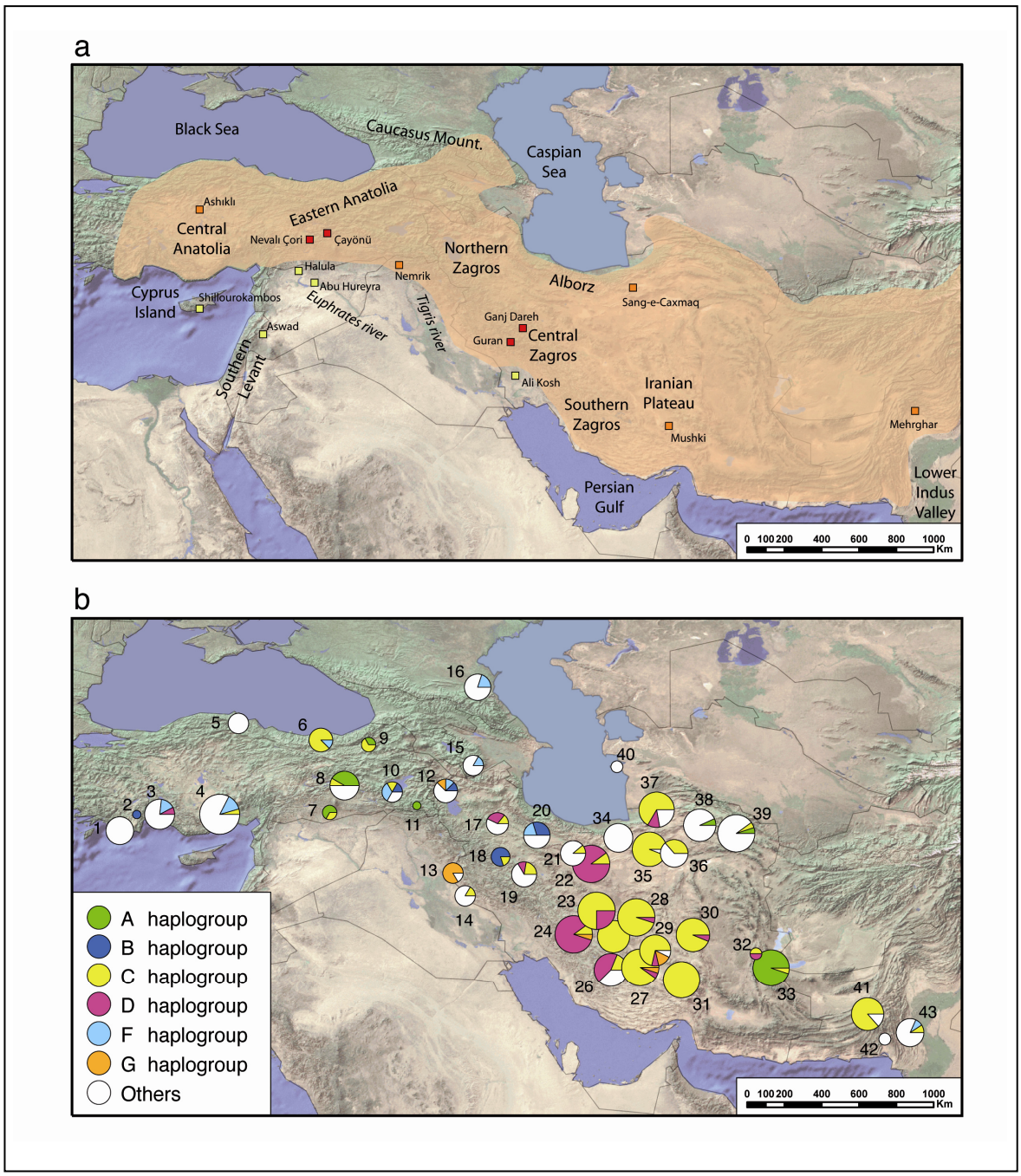

Figure 4.2. **Study area and geographic distribution of the mtDNA haplogroups in the bezoar. a**, Natural distribution of the bezoar according to Uerpmann[28]. This distribution may not have changed since the beginning of goat management/domestication, and stops at the Eastern limit of the map. The archaeological sites that give evidence of local pre-Neolithic goat domestication are represented in red.

(Figure 4.2, continued) The sites that suggest either local goat domestication or early pre-pottery Neolithic transfer of domesticated goat are represented in orange. Finally, the sites that provide evidence of transfer of goats out of the original geographic range of the bezoar before the middle of the 10th millennium cal. B.P. are represented in yellow (Supplementary Table 4.3). **b**, Geographic distribution of the mtDNA haplogroups in the bezoar. The size of the circles is proportional to the number of individuals analyzed. The different bezoar haplogroups are color-coded as in Figure 4.1. Different localities are identified by numbers, as in Supplementary Table 4.1.

Our second main finding deals with the subsequent effective domestication process that led to morphologically different animals. The large number - dozens or hundreds - of mtDNA haplotypes captured at this initial step of the effective domestication argues for a large-scale process (Supporting Information). Such a large number of ancestral goat haplotypes cannot have come from a geographically restricted area. Again, this suggests a process that occurred over a wide range and over several centuries, implying that at least several hundred individuals were taken from the managed populations to initiate domestic flocks. Finally, the fact that several traditional breeds in Iran have a genetic diversity at nuclear loci close to or even higher than the current bezoar populations also argues for very large-scale domestication. Thus, the first domesticated goats were able to capture most of the genetic diversity of their wild ancestors. Clearly, goats do not fit with the bottleneck domestication paradigm that has been extensively documented in plants[4].

The last significant finding concerns the putative location of the true domestication centres. Today, 90% of the goat mtDNA haplotypes belong to the A haplogroup, a proportion which cannot have changed dramatically in the expanding goat population since domestication. (Supplementary Information). The A haplogroup is missing in bezoars from the Zagros and from the Iranian Plateau and its presence in the easternmost locality analyzed in Iran (locality 33, in Figure 4.2b) can be explained by introgression from goats (Supplementary Information). The most likely origin of the A haplogroup in goats therefore lies in Eastern Anatolia, where it is common in wild populations. This is fully consistent with recent archaeological evidence of ca. 10,500 cal. B.P. goat domestication there (e.g. Nevalı Çori, Figure 4.2a). The C haplogroup has a widespread geographic distribution in bezoars, but the closest relatives to the domestics are found in

Eastern Anatolia (Figure 4.3), suggesting that the C haplogroup domestics also originate from this region.

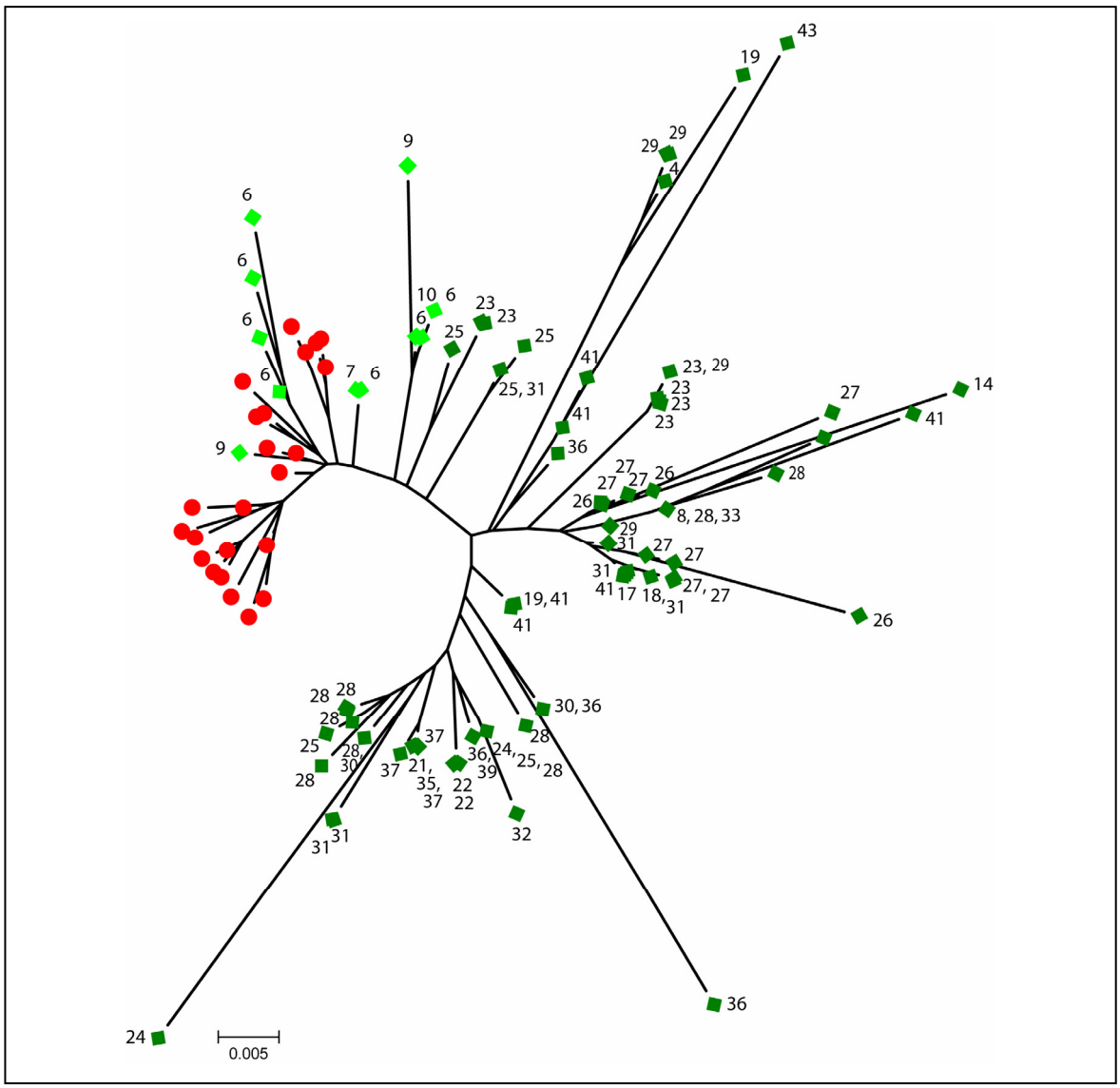

Figure 4.3. **Phylogenetic tree (neighbour joining) of the C haplogroup in both goats (in red) and bezoar (light green from Eastern Turkey, dark green from other locations).** This tree was obtained with the neighbour joining method (see Methods). The close relationships between bezoars from Eastern Turkey and goats demonstrates that the domestication for the C haplogroup occurred in this area. The domestic goat C haplotypes are grouped into at least three clusters, suggesting at least three ancestral haplotypes. The numbers represent the populations as in Figure 4.2b and Supplementary Table 4.1.

The bezoars of the C haplogroup in Eastern Anatolia were probably translocated from the Southern Zagros or the Central Iranian Plateau during the pre-domestic phase, as suggested by the presence of the same C haplotype in localities 8 and 28 (Figure 4.2b).The D haplogroup occupies a wide area in the Zagros, consistent with the second earliest archaeologically known domestication area, ca. 9,900-9,500 cal. B.P. in Central Zagros[7]. Conversely, the rather restricted distribution of the B and G haplogroups in the Northern Zagros, suggest that goats were also domesticated in this area, which was not indicated by archaeology. However, it is possible that these different events occurred at different times, over a long period between the earliest known ungulate domestications, ca. 10,500 cal. B.P. and the latest neolithisation steps in the Near and Middle East, during the 8th-7th millennia cal. B.P. Our results do not support the possible domestication centre for goats in the Lower Indus Valley[9].

To summarize, the domestication process in goats was preceded over a large area and before the 11th millennium B.P., by a period of pre-domestic management of wild flocks that did not induce any detectable morphological change. This first step led to significant increases in population sizes that are still detectable today in the bezoar populations. It seems that Southern Zagros and the Central Iranian Plateau played a key role in this first phase, and were the source of several trans-located populations with C and D haplogroups. The second step consisted of the true domestication and occurred in Eastern Anatolia starting from 11,500 B.P., and possibly in Northern and Central Zagros starting from 10,000 B.P. According to the overrepresentation of the A haplotype in modern goats, Eastern Anatolia was undoubtedly the main contributor. Dozens of mtDNA haplotypes were captured, probably corresponding to the early domestication of hundreds of individuals.

This scenario is very different from previous models, which call for restricted domestication centres and population bottlenecks. The next challenge will be to test if such a large-scale scenario without bottlenecks is also applicable to other domestic animals. Is the absence of bottlenecks during the domestication process a prerequisite for a successful and sustainable domestication?

METHODS SUMMARY

Mitochondrial DNA analyses

483 wild goats were sampled from 42 geographic localities representing the whole distribution area, mostly using a non-invasive approach[23] (Supplementary Table 4.1). A 481 bp fragment of the control region (HVI, hypervariable region I) was sequenced as in ref. 11. These sequences were analyzed using neighbour joining (NJ) methods, Bayesian (MB) and maximum likelihood (ML). The ARLEQUIN v 3.0 software[24] was used to estimate the percentage of variance among regions and localities by an analysis of molecular variance (AMOVA) (See Methods).

Estimation of population growth rate

Growth rates of mitochondrial haplogroups were estimated with Lamarc v2.2[25] using a bayesian framework (See Methods).

Estimation of the number of goat mtDNA haplotypes captured during the domestication process

The number of ancestral haplotypes has been estimated using a phylogenetic approach, assuming a domestication time between 13,000 and 9,000 years B.P., and a divergence time of 200 to 300 thousand years between goat haplogroups A and C[11]. To infer how many goat haplotypes would be found in a sample containing any possible number of sequences, we performed a rarefaction analysis. We also computed the pairwise coalescence times for all pairs of domestic and wild sequences. Finally, assuming a neutral model of evolution, we computed the minimum frequency of the goat A haplogroup at the domestication time (See Methods).

Nuclear DNA analysis

A total of 232 goats (five breeds from Iran and three breeds from Italy) were analyzed, and compared with 19 bezoar samples, using AFLP markers according to the protocol described in Ajmone-Marsan *et al.*[26] (Supplementary Table 4.2). The amount of genetic variation within each goat breed and within the bezoar population was estimated by averaging Jaccard similarity between individuals belonging to the same breed or population[27] (See Methods).

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Figure 4.4. *Capra aegagrus* in Golestan National Park in Iran (Photo by HR. Rezaei).

Acknowledgements

We would like to thank Dr. Bahram Kiabi, Ramezanali Ghaemi and Bijan Farhang Darehshoori for fruitful discussions and constructive comments. We also thank the Iranian Departement of Environment for sampling authorizations (Nb 13/1-36694-1383), and Javad Ramezani and Afshin Karami for their administrative support. We are gratefull to all the guards of National Parks and other protected areas, and to Ebrahim Ghaderi, Rasul Marsooli, Seyed Abbas Rafat, Paul Weinberg, Amjad Tahir Virk, and Gordon Luikart for their help during the field sampling in Iran, Azerbaijan, Dagestan and Pakistan. Thanks are due to the Turkish General Directorate of Nature Protection and National Parks for their cooperation during the field sampling as well. J.-D. Vigne benefited from grants from the ESF OMLL project "Early Bovids" for archaeological field sessions. We greatly appreciated the help of Delphine Rioux, Stéphanie Zundel, Ludovic Gielly, Christian Miquel, and Carole Poillot in the Grenoble laboratory. We thank G.W. Hewitt, R. Geremia, P. Choler and L. Després for their critical reading of the manuscript. S. Naderi and HR. Rezaei were supported by PhD scholarships from the Iranian Ministry of Science, Research, and Technology (number 800125 and, 791135 respectively). F. Pompanon was supported by the Institut National de la Recherche Agronomique.

Author information DNA sequences have been deposited at GenBank/EMBL under accession numbers EF989163-EF989645 (see also Supplementary Information). Reprints and permissions information are available at www.nature.com/reprints. The authors declare no competing financial interests. Correspondence and requests for materials should be addressed to P.T. (e-mail: pierre.taberlet@ujf-grenoble.fr).

METHODS

Mitochondrial DNA analyses

Sampling

Fresh faeces were collected in the field, after observation of the goats from a distance to ensure the species origin of the sample. For each individual two samples were collected and preserved with two methods (silica gel and ethanol 96%). Moreover, some samples consisted of skin and muscle obtained from hunter kills and carcasses. Because of possible hybridization in captivity, no samples from zoos were considered in this study. In addition to the samples collected in the field, we retrieved four sequences of *C. aegagrus* from GenBank. For comparison with domestic goat, the data set was completed with 22 reference sequences of the mtDNA control region of different haplogroups of *C. hircus*[13]. All *C. aegagrus* samples used for the mtDNA analysis are listed in Supplementary Table 4.1.

DNA extraction

The whole genomic DNA was extracted from fecal samples after 20 minutes in washing buffer (Tris-HCl 0.1 M, EDTA 0.1 M, NaCl 0.1 M, N-lauroyl sarcosine 1%, pH 7.5-8.0), using DNAeasy extraction blood kit (Qiagen) following the manufacture's protocol for animal blood except for the incubation with protease (2 hours at 56° C with 55 µl of protease). For tissue samples, total DNA was extracted using the tissue extraction kit QIAamp Animal Tissue kit (Qiagen) following the manufacture's instructions.

DNA amplification

A 598 bp fragment was amplified using the primers CAP-F (5'-CGTGTATGCAAGTACATTAC-3')and CAP-R (5'-CTGATTAGTCATTAGTCCATC-3'). PCR amplifications were conducted in a 25 µl volume with 2 mM $MgCl_2$, 200 µM of each dNTP, 1 µM of each primer and 1 unit of AmpliTaq Gold Polymerase (Applied Biosystems). After a 10 min period at 95°C for polymerase activation, 35 cycles for tissue samples and 40 cycles for faeces samples were run with the following steps: 95°C: 30 sec, 55°C: 30 sec, 72°C: 1 min.

DNA sequencing

PCR products were purified using the Qiaquick PCR purification kit (Qiagen). 35 ng of purified DNA from this PCR product was used for sequencing with the CAP-F/CAP-R primer pair. Sequence reactions were performed for both DNA strands by using the ABI PRISM Dye Terminator Cycle Sequencing Reaction Kit (Applied Biosystems) in a 20 µl volume with 2 µM of each primer. 25 cycles were run with the following steps 96°C: 30 sec, 55°C: 30 sec, 60°C: 4 min. Excess dye terminators were removed by spin-column purification and the products were electrophorezed on an ABI 3700 PRISM DNA sequencer (Applied Biosystems) using the POP 7 polymer.

Sequences were edited for correction with the SeqScape v2.5 software (Applied Biosystems), were aligned with Mega v3.1[29], and adjusted by eye when relevant. For further analyses, we only kept the region used by Luikart *et al.*[11] because this informative region is available for most of the GenBank records. This region is 481 bp long on the *C. hircus* reference sequence (mtDNA complete sequence of *C. hircus*[30], Accession number AF533441). According to the insertion/deletion events, the analyzed sequences ranged from 481 to 558 bp. All sequences were deposited in GenBank (Acc. Numbers EF989163-EF989645, Supplementary Table 4.1).

Data analysis

The substitution model used was the Kimura 2-parameters (K2P) model. The heterogeneity in substitution rates among nucleotide sites was modelled by a gamma distribution. The alpha parameter was estimated by a maximum-likelihood method under the K2P model using PAML v 2.0.2[31]. The estimated value ($\alpha = 0.29$) was similar to that estimated for the same region on a smaller sample of domestic and wild goats[11]. These settings were used for further phylogenetic reconstruction and analysis of genetic diversity.

Data were analyzed using neighbour joining (NJ) methods, Bayesian (MB) and maximum likelihood (ML). Bayesian analyses were performed using MrBayes V3.1.2[32]. The Markov Chain Monte Carlo search was run with $3x10^6$ generations (repeated three times), sampling the Markov chain every 100 generations, with a burn-in of 10,000 trees (as detected by plotting the log likelihood scores against generation number). The most appropriate likelihood model was determined using the Akaike Information Criterion implement in ModelTest 3.07[33]. ML analyses were first performed with PHYML 2.4.4[34], using a K2P model of sequence evolution. Using the best tree found by PHYML as a

starting tree, heuristic ML searches were executed with PAUP* 4.0b10[35], with a tree bisection reconnection (TBR) branch swapping, and all parameter values estimated. Clade stability was estimated by non-parametric bootstrapping in 100 replicates with PHYML. NJ[36] trees constructed by using MEGA v.3.1[29]. We chose the K2P distance matrix[37]; the robustness of each branch was determined by a nonparametric bootstrap test with 1000 replicates and a TBR branch swapping algorithm. The tree topologies obtained with the different phylogenetic methods are very similar, and only the neighbour-joining result is presented in Figure 4.1.

The AMOVA[24] has been performed on 487 wild individuals from the 43 populations divided into 8 geographic regions (Eastern Anatolia, Northern Zagros and Caucasus : 6, 7, 8, 9, 10,11, 12, 15, 16; Central Anatolia: 1, 2, 3, 4, 5 ; Albroz and Turkmenistan: 17, 20, 21, 34, 35, 36, 37, 38, 39, 40; Central Zagros : 13, 14, 18, 19; Southern Zagros : 23, 24, 25, 26; Central Iranian Plateau : 22, 27, 28, 29, 30, 31; Eastern Iranian Plateau : 32, 33; Lower Indus Valley : 41, 42, 43; population numbers refer to Figure 4.2b and Supplementary Table 4.1).

Estimation of population growth rate

LAMARC v2.2[25] was implemented either allowing migrations across haplogroups (with a maximum of 10000 migration events; default priors used for migration rate estimations), or without migrations. The estimation of growth rates was done with a flat prior (upper bound of 1000 and lower bound of -500), 10 initial chains (500 samples, sampling interval of 20 and burn-in period of 1000) and 2 final chains (10000 samples, sampling interval of 20 and burn-in period of 1000).

Estimation of the number of goat mtDNA haplotypes that were captured during the domestication process

Phylogenetic approach

A phylogenetic method was used for estimating the number of ancestral haplotypes leading to the 2427 mtDNA sequences carried by the goats today. The phylogeny of the 2427 goat sequences was reconstructed using the software PHYML 2.4.4[34] assuming the HKY85 model of substitution. Heterogeneity of mutation rate across sites was captured by a gamma distribution with shape parameter 0.29[11]. We used the software PATHD8[38] to create an ultrametric tree from the phylogeny.

Rarefaction analysis of the number of goat mtDNA haplotypes found according to the number of samples analyzed

In order to infer how many haplotypes would be found in a sample containing any possible number of sequences, we performed a rarefaction approach. For different values b of the number of sequences, we sampled at random b sequences among the 2427 sequences and we computed the ancestral number of haplotypes from the ultrametric tree obtained from PATHD8[38]. Extrapolation was then performed using polynomial regression as implemented in the R routine loess (http://www.r-project.org/).

Estimation of the Time to the Most Recent Common Ancestor (TMRCA) for the different goat haplogroups

The estimates of the TMRCA for the different haplogroups were obtained from the ultrametric tree inferred with PATHD8[38] (see above).

Computation of the pairwise coalescence times

For all pairs of domestic and wild sequences we computed the genetic distances defined as the number of site differences. Genetic distances were then rescaled into coalescence times by calibrating the median distance between the A haplogroup and the C haplogroup at 250,000 years[11].

Frequency of the A haplogroup at the time of the domestication

Assuming a neutral model of evolution, we computed the minimum frequency of the A haplogroup at the domestication time compatible with its present frequency. More precisely, we computed the probability of observing more individuals from the A haplogroup than the number of individuals that have actually been sampled (2208). This probability was computed for different values of the frequency x of A haplotypes at the time of the domestication. The smallest frequency value x such that the probability was larger than 0.01 was considered to be the smallest number of haplotypes captured that is compatible with the observed number of A haplotypes that have been sampled.

For a given value k of the number of individuals from the A haplogroup at the time of the domestication and a given value m of the number of ancestral haplotypes, the proportion of the number of individuals from the A haplogroup at the present time can be approximated by a Beta distribution with parameters k and m-k. Therefore, the number of individuals from the A haplogroup today follows a Beta Binomial distribution[39] with parameters k, m-k and n (=2427; the number of individuals analyzed today). The ancestral

number of individuals from the A haplogroup k is unknown and its distribution is a binomial with parameters m and x. As a consequence the probability of getting more than 2208 individuals from the A haplogroup today was given by the survival function of the Beta Binomial distribution integrated over the possible values for the number of ancestral A haplotypes.

Nuclear DNA analysis

Sampling

The list of samples is given in Supplementary Table 4.2.

DNA extraction

DNA was extracted with the GenElute Mammalian Genomic DNA miniprep kit [Sigma G1N-70], following the instruction supplied by the manufacturer. DNA quality and concentration were visually checked by electrophoresis on 1% agarose gel stained with ethidium bromide.

AFLP procedure

EcoRI/TaqI AFLP molecular markers were produced according to the protocol described in Ajmone Marsan *et al.*[26]. Three highly polymorphic primer pairs carrying ACA/ACT, ATA/AAG and ATG/AAC as selective nucleotides were assayed on all animals sampled. AFLP polymorphisms were visually scored as dominant markers, coding 1 the presence and 0 the absence of the band.

Data analysis.

Allele frequencies of each marker were estimated in each population using a Bayesian approach with uniform distribution of allele frequencies (AFLP-surv 1.0[40]; http://www.ulb.ac.be/sciences/lagev/aflp-surv.html). Following this method, the frequency of the null allele at each locus is computed on the basis of two parameters: sample size and number of individuals that lack the AFLP fragment. Allele frequencies were used to calculate summary statistics, as the percentage of polymorphic loci laying within the frequency range 0.05 to 0.95 and the unbiased average expected heterozygosity[41], assuming Hardy-Weinberg equilibrium. Statistical significance of differences between population expected heterozygosity values was tested by Kruskal Wallis non-parametric test.

The genetic relationship between individuals was investigated by Factorial Correspondence Analysis (FCA) using the software Genetix v4.05[42]. FCA[43] is a multivariate method for the analysis of categorical variables analogous to the Principal Components Analysis. It allows the simultaneous representation of OTUs and loci as a cloud of points in a metric space. Axes are independent and are ranked according to fractions of information explained. Inertia, or dispersion, measures this information. The direction of maximum inertia is the direction in which the cloud of points is most scattered.

The amount of genetic variation within populations was estimated by averaging Jaccard similarity[27] between individuals belonging to the same population. Variation in Mantel test generated by Monte Carlo resampling procedures was used to test the significance of the difference between population Jaccard values (MANTEL-STRUCT software[44], http://www.marksgeneticsoftware.net/).

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SUPPLEMENTARY INFORMATION

Supplementary results

Partitioning of the mtDNA genetic variance within and among localities

The total genetic variation was distributed within populations (52.90 %) and among populations within a geographic region (37.70 %). Only 9.40 % of the diversity was distributed among regions, which reflects the low phylogeographic structure in bezoars (Supplementary Table 4.4).

Estimation of the number of goat mtDNA haplotypes that have been captured during the domestication process

Phylogenetic approach

Using 200 to 300 thousand years as the divergence time between A and C haplogroups[1], we found that the number of ancestral haplotypes of the 2427 sequences, at the domestication time, ranges from 1308 to 1900. The domestication was assumed to occur between 9,000 and 13,000 years B.P.

Another calibration based on the fact that the C haplogroup has been found in Southern France 7500 years ago[2] can be carried out, assuming that the C haplogroup comes from the domestication of a single haplotype, and assuming that its domestication occurred either 7500 or 9500 years ago. When the TMRCA of the C haplogroup was fixed at 7500 years B.P., we found 12 ancestral haplotypes 9500 years ago for the whole goat dataset, and 10 ancestral haplotypes 10500 years ago. Obviously, these estimates correspond to an important underestimation of the number of ancestral haplotypes, because first the C haplogroup had been domesticated before 7500 years B.P., and second because several C haplotypes have probably been domesticated, as suggested by the clustering of domestic goat C haplotypes into at least three clusters within the bezoar phylogeny (Figure 4.3).

When the TMRCA of the C haplogroup was fixed at 9500 years B.P. (a more realistic date allowing the spread of the C haplogroup from the domestication area to Southern France), we found 103 ancestral haplotypes 9500 years ago and 16 ancestral haplotypes 10500 years ago. Again, if several C haplotypes had been domesticated, this corresponds to an underestimate.

Rarefaction analysis of the number of goat mtDNA haplotypes found according to the number of samples analyzed.

The results are displayed in Supplementary Figure 4.1 and demonstrate that analyzing more samples would lead to an increase of the estimated number of ancestral haplotypes.

Estimation of the TMRCA for the different goat haplogroups

Results are presented in Supplementary Table 4.5.

Computation of the pairwise coalescence times.

The proportion of pairs of sequences that coalesced more recently than 13,000 years ago (an upper bound for the domestication time) is smaller than 1% (Supplementary Figure 4.2). When using a divergence time of 200,000 years or 300,000 years, the proportion of pairs of sequences that coalesced before the domestication remained smaller than 1%. When the calibration was done using a mtDNA control region mutation rate of $2.5*10^{6}$ site/generation as it has been found in humans[3], we found that only 2.5% of the pairs coalesced before 13,000 years. When using other genetic distances, the proportion of pairs that coalesced more recently than the domestication remains similar (Results not shown).

Frequency of the A haplogroup at the time of the domestication.

It is highly unlikely that the frequency of individuals from the A haplogroup at the time of domestication was below 0.87 (Supplementary Figure 4.3).

Nuclear DNA analysis

The results of the AFLP analysis of eight breeds of domestic goats, compared with the bezoar are presented on Supplementary Figure 4.4.

Supplementary Discussion

Introgression from the domestics to the wilds in southeastern Iran

Mitochondrial DNA introgression from the domestics to the wilds might make the current results difficult to interpret. It is therefore important to identify such events in our dataset. Currently, individuals from the A haplogroups represent 90.86 % of domestic goats. This proportion cannot have dramatically changed since their domestication, and thus the A haplogroups were always the most numerous during goat history (see above

section "Frequency of the A haplogroup at the time of the domestication"). As a consequence, if an introgression occurred from the domestic to the wild, it should have mainly concerned the A haplogroup. Furthermore, the introgressed haplotypes should be expected to appear in many clades of the phylogenetic tree of the A haplogroup, as would do the A haplotypes of a goat population today. On the contrary, a wild population without introgression should only show a very limited number of clustered haplotypes.

As the A haplogroup is absent in bezoars from the Iranian Plateau and from the Zagros, we can deduce that no mtDNA introgression from the domestics to the wilds occurred in these areas. However, the situation is very different in Lar Mountains (Sistan Province, Southeast Iran, locality 33 in Figure 4.2b). The bezoar haplotypes of the A haplogroups in this locality are distributed among many clades of the phylogeny of the A haplogroup (Supplementary Figure 4.5). This is a strong indication that the bezoars from this region have been heavily introgressed by goats. As a consequence, we cannot take into account Lar Mountains as the possible origin of the A haplogroup in goats. This introgression is also supported by a phylogeographic argument. The phylogenetic tree of the bezoar (Fig. 4.1) is composed of three main groups: (i) haplogroups non close-to-domestics and F, (ii) haplogroup C, (iii) haplogroups A, B, D, G. Individuals from haplogroups A, B, D, and G are clustered together in the phylogenetic tree, and thus are supposed to be geographically close. Clearly, the only individuals of the A haplogroup that are not consistent with their position in the phylogeny are in localities 33, 38, and 39. These introgressions occurred after the effective domestication and thus concerned the most frequent A haplogroup in goats.

Number of mtDNA haplotypes captured during the domestication process

Luikart *et al.*[1] estimated that the domestication of the C haplogroup occurred around 6, 000 years ago, assuming both a similar and limited amount of mtDNA diversity within each founder haplogroup, and a domestication of the A haplogroup 10,000 years ago. The origin of the C haplogroup 6,000 years ago is impossible because domestic goats from this haplogroup were already present in Europe about 1,500 years earlier. The mtDNA analysis of bones from an Early Neolithic site from Southwestern Europe showed that at least two distinct haplotypes from each of the A and C haplogroups were present in this site 7,500 years ago[2]. This finding demonstrates that the effective domestication of the C haplogroup is much more ancient. It occurred in the same area (Eastern Anatolia) than the A

haplogroup, and most probably at the same time. Therefore, this contradicts the assumption that each haplogroup in goats originated from a single bezoar haplotype.

All our results are concordant with the domestication of large number of goat individuals. A first set of arguments suggests that most of the present mtDNA diversity observed in goats already existed at the beginning of the domestication process. The estimation of the TMRCA for the main different goat haplogroups is more ancient than the time of domestication (Supplementary Table 4.5), and very few pairs of sequences (less than 1%) coalesced more recently than 13,000 years ago (an upper bound for the domestication time). Moreover, the fact that the same haplotype is found in bezoars in very distant locations even today supports a very low number of mutations since the domestication. Such translocations probably occurred during the pre-domestication phase, as it does not make sense to translocate wild animals after the goats have been effectively domesticated. A second set of arguments posits that the domestication process may have caught a large amount of genetic diversity by capturing a large number of individuals. Several methods have been used for estimating the number of ancestral haplotypes that were captured. The less realistic hypothesis for calibrating the method (i.e., assuming the domestication of a single C haplotype 7,500 years ago) gave 10 ancestral haplotypes for the present goat dataset. This estimate is clearly an important underestimation (see additional results). More realistic assumptions lead to an estimation of more than 1,000 domesticated haplotypes. A rarefaction analysis showed that finding new domestic haplotypes would increase the estimated number of ancestral haplotypes.

To summarize, both our mtDNA and nuclear DNA results, are consistent with the capture of a large genetic diversity during the goat domestication process, with no bottleneck. While bottleneck during domestication has been extensively documented in plants[4], it does not fit with the genetic data available in goats. This might not be an exception as the capture of a high genetic variability has already been shown in yak[5] and horse[6].

Supplementary Tables and Figures

Supplementary Table 4.1. Geographic origin and characteristics of the wild goat samples for mt-DNA sequence study.

Sample number	Code	Haplotypes	Haplogroup	Species	Country	Population	Longitude (E)	Latitude (N)	Sample Type	Collector	Accession Number
1	Ca001	1	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989163
2	Ca002	2	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989164
3	Ca003	17	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989165
4	Ca004	3	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989166
5	Ca005	4	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989167
6	Ca006	5	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989168
7	Ca007	6	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989169
8	Ca008	7	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989170
9	Ca009	8	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989171
10	Ca010	9	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989172
11	Ca011	10	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989173
12	Ca012	11	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989174
13	Ca013	12	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989175
14	Ca014	11	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989176
15	Ca015	13	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989177
16	Ca016	14	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Tissue	S. Naderi	EF989178
17	Ca017	15	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Tissue	S. Naderi	EF989179
18	Ca018	16	A	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Feces	S. Naderi	EF989180
19	Ca019	17	A	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989181

20	Ca020	18	A	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Tissue	S. Naderi	EF989182
21	Ca021	19	A	*C. aegagrus*	Turkey	Artvin (9)	41.49	41.11	Tissue	A. Kence	EF989183
22	Ca022	15	A	*C. aegagrus*	Turkey	Tunceli (8)	39.34	39.07	Tissue	A. Kence	EF989184
23	Ca023	15	A	*C. aegagrus*	Turkey	Tunceli (8)	39.34	39.07	Tissue	A. Kence	EF989185
24	Ca024	15	A	*C. aegagrus*	Turkey	Tunceli (8)	39.34	39.07	Tissue	A. Kence	EF989186
25	Ca025	20	A	*C. aegagrus*	Turkey	Tunceli (8)	39.34	39.07	Bone	A. Kence	EF989187
26	Ca026	21	A	*C. aegagrus*	Turkey	Tunceli (8)	39.34	39.07	Bone	A. Kence	EF989188
27	Ca027	22	A	*C. aegagrus*	Turkey	Gaziantep (7)	37.72	38.45	Liver	A. Kence	EF989189
28	Ca028	23	A	*C. aegagrus*	Turkey	Sumbul (11)	43.78	37.53	Tissue	A. Kence	EF989190
29	Ca029	24	A	*C. aegagrus*	Turkey	Gaziantep (7)	37.72	38.45	Tissue	A. Kence	EF989191
30	Ca030	25	B	*C. aegagrus*	Iran	Marakan (12)	45.24	38.85	Feces	HR. Rezaei	EF989192
31	Ca031	26	B	*C. aegagrus*	Iran	Ghorveh (18)	47.82	35.06	Feces	HR. Rezaei	EF989193
32	Ca032	27	B	*C. aegagrus*	Iran	Ghorveh (18)	47.82	35.06	Feces	HR. Rezaei	EF989194
33	Ca033	26	B	*C. aegagrus*	Iran	Ghorveh (18)	47.82	35.06	Feces	HR. Rezaei	EF989195
34	Ca034	28	B	*C. aegagrus*	Iran	Ghorveh (18)	47.82	35.06	Feces	HR. Rezaei	EF989196
35	Ca035	29	B	*C. aegagrus*	Iran	Ghazvin (20)	49.57	36.09	Tissue	HR. Rezaei	EF989197
36	Ca036	30	B	*C. aegagrus*	Iran	Ghazvin (20)	49.57	36.09	Tissue	HR. Rezaei	EF989198
37	Ca037	31	B	*C. aegagrus*	Iran	Ghazvin (20)	49.57	36.09	Tissue	HR. Rezaei	EF989199
38	Ca038	32	B	*C. aegagrus*	Turkey	Van (10)	43.22	38.29	Tissue	A. Kence	EF989200
39	Ca039	33	B	*C. aegagrus*	Turkey	Antalya (2)	30.95	36.9	Feces	A. Kence	EF989201
40	Ca040	34	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989202
41	Ca041	34	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989203
42	Ca042	34	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989204
43	Ca043	34	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989205
44	Ca044	34	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989206
45	Ca045	34	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989207
46	Ca046	35	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989208
47	Ca047	36	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989209
48	Ca048	36	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989210
49	Ca049	36	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989211
50	Ca050	36	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989212
51	Ca051	55	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989213

52	Ca052	37	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Tissue	S. Naderi	EF989214
53	Ca053	37	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989215
54	Ca054	37	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989216
55	Ca055	37	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989217
56	Ca056	37	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989218
57	Ca057	37	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989219
58	Ca058	37	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989220
59	Ca059	37	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989221
60	Ca060	37	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989222
61	Ca061	37	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989223
62	Ca062	37	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989224
63	Ca063	37	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989225
64	Ca064	37	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989226
65	Ca065	38	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989227
66	Ca066	39	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989228
67	Ca067	40	C	*C. aegagrus*	Iran	Bavanat (25)	53.91	30.31	Feces	S. Naderi	EF989229
68	Ca068	41	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989230
69	Ca069	41	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989231
70	Ca070	41	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989232
71	Ca071	41	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989233
72	Ca072	41	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989234
73	Ca073	41	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989235
74	Ca074	41	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989236
75	Ca075	41	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989237
76	Ca076	41	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989238
77	Ca077	42	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989239
78	Ca078	41	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989240
79	Ca079	41	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989241
80	Ca080	41	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Tissue	S. Naderi	EF989242
81	Ca081	43	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989243
82	Ca082	44	C	*C. aegagrus*	Iran	Malayer (19)	48.95	34.21	Feces	HR. Rezaei	EF989244
83	Ca083	45	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989245

84	Ca084	45	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989246
85	Ca085	45	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989247
86	Ca086	45	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989248
87	Ca087	45	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989249
88	Ca088	46	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989250
89	Ca089	46	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989251
90	Ca090	46	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989252
91	Ca091	46	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989253
92	Ca092	47	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989254
93	Ca093	48	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989255
94	Ca094	48	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989256
95	Ca095	48	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989257
96	Ca096	49	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989258
97	Ca097	50	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989259
98	Ca098	51	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989260
99	Ca099	52	C	*C. aegagrus*	Iran	Khartooran (36)	55.86	35.77	Feces	S. Naderi	EF989261
100	Ca100	66	C	*C. aegagrus*	Iran	Khartooran (36)	55.86	35.77	Feces	S. Naderi	EF989262
101	Ca101	67	C	*C. aegagrus*	Iran	Khartooran (36)	55.86	35.77	Tissue	S. Naderi	EF989263
102	Ca102	53	C	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989264
103	Ca103	53	C	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989265
104	Ca104	53	C	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989266
105	Ca105	53	C	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989267
106	Ca106	53	C	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989268
107	Ca107	53	C	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989269
108	Ca108	54	C	*C. aegagrus*	Iran	Lar, Sistan (33)	60.88	29.68	Tissue	S. Naderi	EF989270
109	Ca109	55	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989271
110	Ca110	54	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989272
111	Ca111	54	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Tissue	S. Naderi	EF989273
112	Ca112	56	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989274
113	Ca113	57	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989275
114	Ca114	57	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989276
115	Ca115	54	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989277

116	Ca116	57	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989278
117	Ca117	57	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989279
118	Ca118	57	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989280
119	Ca119	57	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989281
120	Ca120	58	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989282
121	Ca121	59	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989283
122	Ca122	59	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989284
123	Ca123	59	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989285
124	Ca124	60	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989286
125	Ca125	41	C	*C. aegagrus*	Iran	Ghorveh (18)	47.82	35.06	Feces	HR. Rezaei	EF989287
126	Ca126	61	C	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989288
127	Ca127	62	C	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989289
128	Ca128	63	C	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989290
129	Ca129	63	C	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989291
130	Ca130	63	C	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989292
131	Ca131	64	C	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989293
132	Ca132	64	C	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989294
133	Ca133	64	C	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989295
134	Ca134	65	C	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989296
135	Ca135	64	C	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989297
136	Ca136	64	C	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989298
137	Ca137	64	C	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989299
138	Ca138	64	C	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989300
139	Ca139	64	C	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989301
140	Ca140	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989302
141	Ca141	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989303
142	Ca142	57	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989304
143	Ca143	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989305
144	Ca144	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989306
145	Ca145	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989307
146	Ca146	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989308
147	Ca147	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989309

148	Ca148	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989310
149	Ca149	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989311
150	Ca150	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989312
151	Ca151	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989313
152	Ca152	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989314
153	Ca153	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989315
154	Ca154	66	C	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989316
155	Ca155	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989317
156	Ca156	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989318
157	Ca157	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989319
158	Ca158	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989320
159	Ca159	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989321
160	Ca160	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989322
161	Ca161	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989323
162	Ca162	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989324
163	Ca163	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989325
164	Ca164	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989326
165	Ca165	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989327
166	Ca166	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989328
167	Ca167	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989329
168	Ca168	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989330
169	Ca169	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989331
170	Ca170	64	C	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989332
171	Ca171	64	C	*C. aegagrus*	Iran	Khojir (21)	51.72	35.63	Feces	S. Naderi	EF989333
172	Ca172	67	C	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Tissue	S. Naderi	EF989334
173	Ca173	55	C	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989335
174	Ca174	68	C	*C. aegagrus*	Iran	Mahneshan (17)	47.67	36.66	Feces	HR. Rezaei	EF989336
175	Ca175	69	C	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989337
176	Ca176	70	C	*C. aegagrus*	Turkey	Erzincan (6)	39.31	39.42	Tissue	A. Kence	EF989338
177	Ca177	71	C	*C. aegagrus*	Turkey	Gaziantep (7)	37.72	38.45	Tissue	A. Kence	EF989339
178	Ca178	72	C	*C. aegagrus*	Turkey	Van (10)	43.22	38.29	Tissue	A. Kence	EF989340
179	Ca179	54	C	*C. aegagrus*	Turkey	Tunceli (8)	39.34	39.07	Tissue	A. Kence	EF989341

180	Ca180	73	C	*C. aegagrus*	Turkey	Artvin (9)	41.49	41.11	Tissue	A. Kence	EF989342
181	Ca181	74	C	*C. aegagrus*	Turkey	Erzincan (6)	39.31	39.42	Tissue	A. Kence	EF989343
182	Ca182	75	C	*C. aegagrus*	Turkey	Erzincan (6)	39.31	39.42	Tissue	A. Kence	EF989344
183	Ca183	76	C	*C. aegagrus*	Turkey	Erzincan (6)	39.31	39.42	Tissue	A. Kence	EF989345
184	Ca184	77	C	*C. aegagrus*	Turkey	Erzincan (6)	39.31	39.42	Tissue	A. Kence	EF989346
185	Ca185	78	C	*C. aegagrus*	Turkey	Erzincan (6)	39.31	39.42	Tissue	A. Kence	EF989347
186	Ca186	79	C	*C. aegagrus*	Turkey	Erzincan (6)	39.31	39.42	Tissue	A. Kence	EF989348
187	Ca187	80	C	*C. aegagrus chiltanensis*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989349
188	Ca188	81	C	*C. aegagrus chiltanensis*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989350
189	Ca189	44	C	*C. aegagrus chiltanensis*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989351
190	Ca190	44	C	*C. aegagrus chiltanensis*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989352
191	Ca191	82	C	*C. aegagrus chiltanensis*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989353
192	Ca192	44	C	*C. aegagrus chiltanensis*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989354
193	Ca193	44	C	*C. aegagrus chiltanensis*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989355
194	Ca194	81	C	*C. aegagrus chiltanensis*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989356
195	Ca195	82	C	*C. aegagrus chiltanensis*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989357
196	Ca196	44	C	*C. aegagrus chiltanensis*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989358
197	Ca197	81	C	*C. aegagrus*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989359
198	Ca198	83	D	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989360
199	Ca199	84	D	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989361
200	Ca200	84	D	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989362
201	Ca201	84	D	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989363
202	Ca202	84	D	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989364
203	Ca203	84	D	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989365
204	Ca204	84	D	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989366
205	Ca205	85	D	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989367
206	Ca206	86	D	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989368
207	Ca207	87	D	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989369
208	Ca208	87	D	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989370
209	Ca209	87	D	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989371
210	Ca210	87	D	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989372
211	Ca211	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989373

212	Ca212	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989374
213	Ca213	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989375
214	Ca214	89	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989376
215	Ca215	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989377
216	Ca216	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989378
217	Ca217	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989379
218	Ca218	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989380
219	Ca219	90	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989381
220	Ca220	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989382
221	Ca221	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989383
222	Ca222	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989384
223	Ca223	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989385
224	Ca224	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989386
225	Ca225	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989387
226	Ca226	91	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989388
227	Ca227	88	D	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989389
228	Ca228	88	D	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989390
229	Ca229	97	G	*C. aegagrus*	Iran	Marakan (12)	45.24	38.85	Feces	HR. Rezaei	EF989391
230	Ca230	92	G	*C. aegagrus*	Iran	Zalzard (13)	45.63	34.06	Feces	HR. Rezaei	EF989392
231	Ca231	93	G	*C. aegagrus*	Iran	Zalzard (13)	45.63	34.06	Feces	HR. Rezaei	EF989393
232	Ca232	94	G	*C. aegagrus*	Iran	Zalzard (13)	45.63	34.06	Feces	HR. Rezaei	EF989394
233	Ca233	92	G	*C. aegagrus*	Iran	Zalzard (13)	45.63	34.06	Feces	HR. Rezaei	EF989395
234	Ca234	95	G	*C. aegagrus*	Iran	Zalzard (13)	45.63	34.06	Feces	HR. Rezaei	EF989396
235	Ca235	96	G	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989397
236	Ca236	97	G	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989398
237	Ca237	97	G	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989399
238	Ca238	98	G	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989400
239	Ca239	99	C	*C. aegagrus*	Iran	Dena (24)	51.32	31.06	Feces	S. Naderi	EF989401
240	Ca240	100	C	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989402
241	Ca241	101	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989403
242	Ca242	102	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Feces	S. Naderi	EF989404
243	Ca243	103	C	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989405

244	Ca244	104	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989406
245	Ca245	105	C	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989407
246	Ca246	106	C	*C. aegagrus*	Iran	Shoorab (32)	61.46	30.13	Feces	S. Naderi	EF989408
247	Ca247	107	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989409
248	Ca248	108	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989410
249	Ca249	108	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989411
250	Ca250	108	C	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989412
251	Ca251	109	C	*C. aegagrus*	Iran	Kalmand (28)	54.79	31.28	Tissue	S. Naderi	EF989413
252	Ca252	110	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989414
253	Ca253	111	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989415
254	Ca254	111	C	*C. aegagrus*	Iran	Khabr (31)	56.48	28.84	Feces	S. Naderi	EF989416
255	Ca255	112	C	*C. aegagrus*	Iran	Godghool (27)	55.14	29.45	Feces	S. Naderi	EF989417
256	Ca256	113	C	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989418
257	Ca257	113	C	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989419
258	Ca258	114	C	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989420
259	Ca259	115	C	*C. aegagrus*	Iran	Mehran (14)	46.12	33.31	Feces	HR. Rezaei	EF989421
260	Ca260	116	C	*C. aegagrus*	Iran	Malayer (19)	48.95	34.21	Feces	HR. Rezaei	EF989422
261	Ca261	117	C	*C. aegagrus*	Iran	Khartooran (36)	55.86	35.77	Feces	S. Naderi	EF989423
262	Ca262	118	Wild	*C. aegagrus*	Iran	Mehran (14)	46.12	33.31	Tissue	HR. Rezaei	EF989424
263	Ca263	119	D	*C. aegagrus*	Iran	Kolahghazi (23)	51.81	32.42	Feces	S. Naderi	EF989425
264	Ca264	120	D	*C. aegagrus*	Iran	Shoorab (32)	61.46	30.13	Feces	S. Naderi	EF989426
265	Ca265	121	D	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989427
266	Ca266	122	D	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	HR. Rezaei	EF989428
267	Ca267	123	D	*C. aegagrus*	Iran	Malayer (19)	48.95	34.21	Feces	HR. Rezaei	EF989429
268	Ca268	124	D	*C. aegagrus*	Iran	Mahneshan (17)	47.67	36.66	Feces	HR. Rezaei	EF989430
269	Ca269	125	D	*C. aegagrus*	Iran	Mahneshan (17)	47.67	36.66	Feces	HR. Rezaei	EF989431
270	Ca270	126	D	*C. aegagrus*	Iran	Bafgh (30)	56.76	31.56	Feces	S. Naderi	EF989432
271	Ca271	127	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989433
272	Ca272	127	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989434
273	Ca273	127	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989435
274	Ca274	127	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989436
275	Ca275	127	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989437

276	Ca276	127	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989438
277	Ca277	127	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989439
278	Ca278	127	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989440
279	Ca279	127	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989441
280	Ca280	127	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989442
281	Ca281	127	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989443
282	Ca282	127	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989444
283	Ca283	128	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989445
284	Ca284	128	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989446
285	Ca285	128	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989447
286	Ca286	129	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989448
287	Ca287	130	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989449
288	Ca288	130	D	*C. aegagrus*	Iran	Kavir (22)	52.19	34.71	Feces	S. Naderi	EF989450
289	Ca289	131	C	*C. aegagrus*	Turkey	Artvin (9)	41.49	41.11	Tissue	A. Kence	EF989451
290	Ca290	132	Wild	*C. aegagrus*	Turkey	Tunceli (8)	39.34	39.07	Bone	A. Kence	EF989452
291	Ca291	133	C	*C. aegagrus*	Pakistan	Kirthar (43)	67.43	25.81	Feces	A. T. Virk	EF989453
292	Ca292	134	Wild	*C. aegagrus*	Pakistan	Kirthar (43)	67.43	25.81	Feces	A. T. Virk	EF989454
293	Ca293	134	Wild	*C. aegagrus*	Pakistan	Kirthar (43)	67.43	25.81	Feces	A. T. Virk	EF989455
294	Ca294	135	Wild	*C. aegagrus*	Pakistan	Kirthar (43)	67.43	25.81	Feces	A. T. Virk	EF989456
295	Ca295	136	F	*C. aegagrus*	Iran	Ghazvin (20)	49.57	36.09	Tissue	HR. Rezaei	EF989457
296	Ca296	136	F	*C. aegagrus*	Iran	Marakan (12)	45.24	38.85	Feces	HR. Rezaei	EF989458
297	Ca297	136	F	*C. aegagrus*	Pakistan	Kirthar (43)	67.43	25.81	Feces	A. T. Virk	EF989459
298	Ca298	136	F	*C. aegagrus*	Turkey	Erzincan (6)	39.31	39.42	Tissue	A. Kence	EF989460
299	Ca299	136	F	*C. aegagrus*	Dagestan	AudiKoisu (16)	46.71	43.25	Tissue	P. Weinberg	EF989461
300	Ca300	137	F	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Feces	A. Kence	EF989462
301	Ca301	137	F	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989463
302	Ca302	137	F	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989464
303	Ca303	137	F	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Feces	A. Kence	EF989465
304	Ca304	138	F	*C. aegagrus*	Azerbaijan	Nakhitchevan (15)	45.26	39.25	Feces	P. Weinberg	EF989466
305	Ca305	139	F	*C. aegagrus*	Turkey	Van (10)	43.22	38.29	Tissue	A. Kence	EF989467
306	Ca306	140	F	*C. aegagrus*	Iran	Ghazvin (20)	49.57	36.09	Tissue	HR. Rezaei	EF989468
307	Ca307	141	F	*C. aegagrus*	Dagestan	AudiKoisu (16)	46.71	43.25	Tissue	P. Weinberg	EF989469

308	Ca308	142	F	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989470
309	Ca309	143	Wild	*C. aegagrus*	Turkey	Finike (1)	30.8	36.17	Feces	A. Kence	EF989471
310	Ca310	144	Wild	*C. aegagrus*	Turkey	Finike (1)	30.8	36.17	Feces	A. Kence	EF989472
311	Ca311	145	Wild	*C. aegagrus*	Turkey	Finike (1)	30.8	36.17	Feces	A. Kence	EF989473
312	Ca312	145	Wild	*C. aegagrus*	Turkey	Finike (1)	30.8	36.17	Feces	A. Kence	EF989474
313	Ca313	145	Wild	*C. aegagrus*	Turkey	Finike (1)	30.8	36.17	Feces	A. Kence	EF989475
314	Ca314	145	Wild	*C. aegagrus*	Turkey	Finike (1)	30.8	36.17	Feces	A. Kence	EF989476
315	Ca315	145	Wild	*C. aegagrus*	Turkey	Finike (1)	30.8	36.17	Feces	A. Kence	EF989477
316	Ca316	145	Wild	*C. aegagrus*	Turkey	Finike (1)	30.8	36.17	Feces	A. Kence	EF989478
317	Ca317	145	Wild	*C. aegagrus*	Turkey	Finike (1)	30.8	36.17	Feces	A. Kence	EF989479
318	Ca318	145	Wild	*C. aegagrus*	Turkey	Finike (1)	30.8	36.17	Feces	A. Kence	EF989480
319	Ca319	145	Wild	*C. aegagrus*	Turkey	Finike (1)	30.8	36.17	Feces	A. Kence	EF989481
320	Ca320	146	Wild	*C. aegagrus*	Iran	Khartooran (36)	55.86	35.77	Feces	S. Naderi	EF989482
321	Ca321	147	Wild	*C. aegagrus*	Iran	Khartooran (36)	55.86	35.77	Feces	S. Naderi	EF989483
322	Ca322	147	Wild	*C. aegagrus*	Iran	Khartooran (36)	55.86	35.77	Feces	S. Naderi	EF989484
323	Ca323	148	Wild	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Feces	A. Kence	EF989485
324	Ca324	149	Wild	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Feces	A. Kence	EF989486
325	Ca325	149	Wild	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Tissue	A. Kence	EF989487
326	Ca326	149	Wild	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Tissue	A. Kence	EF989488
327	Ca327	150	Wild	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Tissue	A. Kence	EF989489
328	Ca328	151	Wild	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Tissue	A. Kence	EF989490
329	Ca329	152	Wild	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Feces	A. Kence	EF989491
330	Ca330	153	Wild	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Tissue	A. Kence	EF989492
331	Ca331	154	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989493
332	Ca332	154	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Tissue	A. Kence	EF989494
333	Ca333	155	Wild	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Tissue	A. Kence	EF989495
334	Ca334	156	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Tissue	A. Kence	EF989496
335	Ca335	157	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989497
336	Ca336	158	Wild	*C. aegagrus*	Dagestan	AudiKoisu (16)	46.71	43.25	Tissue	P. Weinberg	EF989498
337	Ca337	159	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989499
338	Ca338	159	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989500
339	Ca339	160	Wild	*C. aegagrus*	Iran	Khoshyeylagh (35)	55.43	36.71	Feces	S. Naderi	EF989501

340	Ca340	161	Wild	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Tissue	S. Naderi	EF989502
341	Ca341	162	Wild	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	S. Naderi	EF989503
342	Ca342	163	Wild	*C. aegagrus*	Iran	Khojir (21)	51.72	35.63	Feces	S. Naderi	EF989504
343	Ca343	163	Wild	*C. aegagrus*	Iran	Khojir (21)	51.72	35.63	Feces	S. Naderi	EF989505
344	Ca344	164	Wild	*C. aegagrus*	Iran	Parvar (34)	53.51	35.97	Feces	S. Naderi	EF989506
345	Ca345	164	Wild	*C. aegagrus*	Iran	Parvar (34)	53.51	35.97	Feces	S. Naderi	EF989507
346	Ca346	165	Wild	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Feces	S. Naderi	EF989508
347	Ca347	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989509
348	Ca348	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989510
349	Ca349	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989511
350	Ca350	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989512
351	Ca351	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989513
352	Ca352	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989514
353	Ca353	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989515
354	Ca354	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989516
355	Ca355	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989517
356	Ca356	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989518
357	Ca357	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989519
358	Ca358	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989520
359	Ca359	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989521
360	Ca360	166	Wild	*C. aegagrus*	Iran	Salook (38)	57.26	37.22	Feces	S. Naderi	EF989522
361	Ca361	167	Wild	*C. aegagrus*	Iran	Parvar (34)	53.51	35.97	Feces	S. Naderi	EF989523
362	Ca362	167	Wild	*C. aegagrus*	Iran	Parvar (34)	53.51	35.97	Feces	S. Naderi	EF989524
363	Ca363	168	Wild	*C. aegagrus*	Iran	Parvar (34)	53.51	35.97	Feces	S. Naderi	EF989525
364	Ca364	168	Wild	*C. aegagrus*	Iran	Parvar (34)	53.51	35.97	Feces	S. Naderi	EF989526
365	Ca365	169	Wild	*C. aegagrus*	Iran	Parvar (34)	53.51	35.97	Feces	S. Naderi	EF989527
366	Ca366	169	Wild	*C. aegagrus*	Iran	Parvar (34)	53.51	35.97	Feces	S. Naderi	EF989528
367	Ca367	169	Wild	*C. aegagrus*	Iran	Parvar (34)	53.51	35.97	Feces	S. Naderi	EF989529
368	Ca368	169	Wild	*C. aegagrus*	Iran	Parvar (34)	53.51	35.97	Feces	S. Naderi	EF989530
369	Ca369	169	Wild	*C. aegagrus*	Iran	Parvar (34)	53.51	35.97	Feces	S. Naderi	EF989531
370	Ca370	170	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989532
371	Ca371	171	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989533

372	Ca372	171	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989534
373	Ca373	171	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989535
374	Ca374	171	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989536
375	Ca375	171	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989537
376	Ca376	171	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989538
377	Ca377	171	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989539
378	Ca378	171	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989540
379	Ca379	171	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Tissue	S. Naderi	EF989541
380	Ca380	172	Wild	*C. aegagrus*	Iran	Parvar (34)	53.51	35.97	Feces	S. Naderi	EF989542
381	Ca381	173	Wild	*C. aegagrus*	Iran	Khartooran (36)	55.86	35.77	Tissue	S. Naderi	EF989543
382	Ca382	174	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989544
383	Ca383	174	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989545
384	Ca384	174	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Feces	S. Naderi	EF989546
385	Ca385	174	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Tissue	S. Naderi	EF989547
386	Ca386	174	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Tissue	S. Naderi	EF989548
387	Ca387	174	Wild	*C. aegagrus*	Iran	Tandooreh (39)	58.87	37.41	Tissue	S. Naderi	EF989549
388	Ca388	175	Wild	*C. aegagrus*	Iran	Khartooran (36)	55.86	35.77	Feces	S. Naderi	EF989550
389	Ca389	175	Wild	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Feces	A. Kence	EF989551
390	Ca390	176	Wild	*C. aegagrus*	Iran	Marakan (12)	45.24	38.85	Feces	HR. Rezaei	EF989552
391	Ca391	177	Wild	*C. aegagrus*	Azerbaijan	Nakhitchevan (15)	45.26	39.25	Tissue	P. Weinberg	EF989553
392	Ca392	177	Wild	*C. aegagrus*	Turkey	Soyuk (5)	35.17	41.51	Tissue	A. Kence	EF989554
393	Ca393	178	Wild	*C. aegagrus*	Turkey	Soyuk (5)	35.17	41.51	Tissue	A. Kence	EF989555
394	Ca394	179	Wild	*C. aegagrus*	Iran	Marakan (12)	45.24	38.85	Feces	HR. Rezaei	EF989556
395	Ca395	180	Wild	*C. aegagrus*	Iran	Marakan (12)	45.24	38.85	Feces	HR. Rezaei	EF989557
396	Ca396	180	Wild	*C. aegagrus*	Iran	Marakan (12)	45.24	38.85	Feces	HR. Rezaei	EF989558
397	Ca397	181	Wild	*C. aegagrus*	Dagestan	AudiKoisu (16)	46.71	43.25	Tissue	A. Kence	EF989559
398	Ca398	182	Wild	*C. aegagrus*	Dagestan	AudiKoisu (16)	46.71	43.25	Tissue	P. Weinberg	EF989560
399	Ca399	183	Wild	*C. aegagrus*	Dagestan	AudiKoisu (16)	46.71	43.25	Tissue	P. Weinberg	EF989561
400	Ca400	184	Wild	*C. aegagrus*	Turkey	Van (10)	43.22	38.29	Tissue	A. Kence	EF989562
401	Ca401	185	Wild	*C. aegagrus*	Iran	Dahaj (29)	54.87	30.57	Feces	S. Naderi	EF989563
402	Ca402	186	Wild	*C. aegagrus*	Iran	Malayer (19)	48.95	34.21	Tissue	HR. Rezaei	EF989564
403	Ca403	186	Wild	*C. aegagrus*	Iran	Malayer (19)	48.95	34.21	Tissue	HR. Rezaei	EF989565

404	Ca404	187	Wild	*C. aegagrus*	Iran	Malayer (19)	48.95	34.21	Feces	HR. Rezaei	EF989566
405	Ca405	188	Wild	*C. aegagrus*	Iran	Malayer (19)	48.95	34.21	Feces	HR. Rezaei	EF989567
406	Ca406	189	Wild	*C. aegagrus*	Iran	Malayer (19)	48.95	34.21	Feces	HR. Rezaei	EF989568
407	Ca407	190	Wild	*C. aegagrus*	Pakistan	Hazarganji (41)	66.11	27.28	Horn	A. T. Virk	EF989569
408	Ca408	191	Wild	*C. aegagrus*	Iran	Mehran (14)	46.12	33.31	Feces	HR. Rezaei	EF989570
409	Ca409	192	Wild	*C. aegagrus*	Iran	Mehran (14)	46.12	33.31	Tissue	HR. Rezaei	EF989571
410	Ca410	193	Wild	*C. aegagrus*	Iran	Mehran (14)	46.12	33.31	Feces	HR. Rezaei	EF989572
411	Ca411	194	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989573
412	Ca412	195	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989574
413	Ca413	196	Wild	*C. aegagrus*	Turkey	Tunceli (8)	39.34	39.07	Tissue	A. Kence	EF989575
414	Ca414	197	Wild	*C. aegagrus*	Turkey	Tunceli (8)	39.34	39.07	Tissue	A. Kence	EF989576
415	Ca415	198	Wild	*C. aegagrus*	Iran	Mehran (14)	46.12	33.31	Tissue	HR. Rezaei	EF989577
416	Ca416	199	Wild	*C. aegagrus*	Iran	Malayer (19)	48.95	34.21	Tissue	HR. Rezaei	EF989578
417	Ca417	200	Wild	*C. aegagrus*	Turkey	Soyuk (5)	35.17	41.51	Horn	A. Kence	EF989579
418	Ca418	201	Wild	*C. aegagrus*	Turkey	Soyuk (5)	35.17	41.51	Horn	A. Kence	EF989580
419	Ca419	201	Wild	*C. aegagrus*	Turkey	Soyuk (5)	35.17	41.51	Horn	A. Kence	EF989581
420	Ca420	201	Wild	*C. aegagrus*	Turkey	Soyuk (5)	35.17	41.51	Tissue	A. Kence	EF989582
421	Ca421	201	Wild	*C. aegagrus*	Azerbaijan	Nakhitchevan (15)	45.26	39.25	Tissue	P. Weinberg	EF989583
422	Ca422	201	Wild	*C. aegagrus*	Azerbaijan	Nakhitchevan (15)	45.26	39.25	Feces	P. Weinberg	EF989584
423	Ca423	201	Wild	*C. aegagrus*	Azerbaijan	Nakhitchevan (15)	45.26	39.25	Feces	P. Weinberg	EF989585
424	Ca424	202	Wild	*C. aegagrus*	Iran	Golestan (37)	56.14	37.43	Tissue	HR. Rezaei	EF989586
425	Ca425	203	Wild	*C. aegagrus*	Iran	Ghazvin (20)	49.57	36.09	Tissue	HR. Rezaei	EF989587
426	Ca426	204	Wild	*C. aegagrus*	Iran	Ghazvin (20)	49.57	36.09	Tissue	HR. Rezaei	EF989588
427	Ca427	205	Wild	*C. aegagrus*	Iran	Ghazvin (20)	49.57	36.09	Tissue	HR. Rezaei	EF989589
428	Ca428	206	Wild	*C. aegagrus*	Iran	Ghazvin (20)	49.57	36.09	Tissue	HR. Rezaei	EF989590
429	Ca429	207	Wild	*C. aegagrus*	Iran	Mahneshan (17)	47.67	36.66	Feces	HR. Rezaei	EF989591
430	Ca430	208	Wild	*C. aegagrus*	Iran	Mahneshan (17)	47.67	36.66	Feces	HR. Rezaei	EF989592
431	Ca431	209	Wild	*C. aegagrus*	Turkey	Tunceli (8)	39.34	39.07	Tissue	A. Kence	EF989593
432	Ca432	210	Wild	*C. aegagrus*	Turkey	Tunceli (8)	39.34	39.07	Tissue	A. Kence	EF989594
433	Ca433	211	Wild	*C. aegagrus*	Turkey	Tunceli (8)	39.34	39.07	Tissue	A. Kence	EF989595
434	Ca434	212	Wild	*C. aegagrus*	Iran	Mahneshan (17)	47.67	36.66	Feces	HR. Rezaei	EF989596
435	Ca435	213	Wild	*C. aegagrus*	Iran	Khojir (21)	51.72	35.63	Feces	S. Naderi	EF989597

436	Ca436	214	Wild	*C. aegagrus*	Iran	Khojir (21)	51.72	35.63	Feces	S. Naderi	EF989598
437	Ca437	215	Wild	*C. aegagrus*	Iran	Khojir (21)	51.72	35.63	Feces	S. Naderi	EF989599
438	Ca438	216	Wild	*C. aegagrus*	Iran	Khojir (21)	51.72	35.63	Feces	S. Naderi	EF989600
439	Ca439	217	Wild	*C. aegagrus*	Iran	Khojir (21)	51.72	35.63	Feces	S. Naderi	EF989601
440	Ca440	218	Wild	*C. aegagrus*	Iran	Khojir (21)	51.72	35.63	Feces	S. Naderi	EF989602
441	Ca441	219	Wild	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989603
442	Ca442	220	Wild	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989604
443	Ca443	221	Wild	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989605
444	Ca444	222	Wild	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989606
445	Ca445	223	Wild	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989607
446	Ca446	224	Wild	*C. aegagrus*	Iran	Bamoo (26)	52.68	29.69	Feces	S. Naderi	EF989608
447	Ca447	225	Wild	*C. aegagrus*	Iran	Khartooran (36)	55.86	35.77	Feces	S. Naderi	EF989609
448	Ca448	226	Wild	*C. aegagrus*	Iran	Khartooran (36)	55.86	35.77	Feces	S. Naderi	EF989610
449	Ca449	227	Wild	*C. aegagrus*	Iran	Mahneshan (17)	47.67	36.66	Feces	HR. Rezaei	EF989611
450	Ca450	228	Wild	*C. aegagrus*	Iran	Marakan (12)	45.24	38.85	Feces	HR. Rezaei	EF989612
451	Ca451	229	Wild	*C. aegagrus*	Iran	Ghazvin (20)	49.57	36.09	Tissue	HR. Rezaei	EF989613
452	Ca452	230	Wild	*C. aegagrus*	Iran	Zalzard (13)	45.63	34.06	Feces	HR. Rezaei	EF989614
453	Ca453	231	C	*C. aegagrus*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989615
454	Ca454	232	C	*C. aegagrus*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989616
455	Ca455	233	D	*C. aegagrus*	Turkey	Akseki (3)	31.47	37.21	Tissue	A. Kence	EF989617
456	Ca456	234	C	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Tissue	A. Kence	EF989618
457	Ca457	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989619
458	Ca458	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989620
459	Ca459	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989621
460	Ca460	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989622
461	Ca461	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989623
462	Ca462	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989624
463	Ca463	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989625
464	Ca464	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989626
465	Ca465	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989627
466	Ca466	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989628
467	Ca467	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989629

468	Ca468	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989630
469	Ca469	235	Wild	*C. aegagrus*	Turkey	Mersin (4)	34.36	36.21	Feces	A. Kence	EF989631
470	Ca470	236	Wild	*C. aegagrus*	Turkey	Van (10)	43.22	38.29	Tissue	A. Kence	EF989632
471	Ca471	236	Wild	*C. aegagrus*	Azerbaijan	Nakhitchevan (15)	45.26	39.25	Tissue	P. Weinberg	EF989633
472	Ca472	237	Wild	*C. aegagrus*	Pakistan	Hazarganji (41)	66.11	27.28	Feces	A. T. Virk	EF989634
473	Ca473	238	Wild	*C. aegagrus*	Dagestan	AudiKoisu (16)	46.71	43.25	Tissue	P. Weinberg	EF989635
474	Ca474	239	Wild	*C. aegagrus*	Dagestan	AudiKoisu (16)	46.71	43.25	Tissue	P. Weinberg	EF989636
475	Ca475	240	Wild	*C. aegagrus*	Dagestan	AudiKoisu (16)	46.71	43.25	Tissue	P. Weinberg	EF989637
476	Ca476	241	Wild	*C. aegagrus*	Dagestan	AudiKoisu (16)	46.71	43.25	Tissue	P. Weinberg	EF989638
477	Ca477	242	Wild	*C. aegagrus*	Pakistan	Kirthar (43)	67.43	25.81	Feces	A. T. Virk	EF989639
478	Ca478	243	Wild	*C. aegagrus*	Pakistan	Kirthar (43)	67.43	25.81	Feces	A. T. Virk	EF989640
479	Ca479	244	Wild	*C. aegagrus*	Pakistan	Kirthar (43)	67.43	25.81	Feces	A. T. Virk	EF989641
480	Ca480	245	Wild	*C. aegagrus*	Pakistan	Kirthar (43)	67.43	25.81	Feces	A. T. Virk	EF989642
481	Ca481	246	Wild	*C. aegagrus*	Pakistan	Dureji (42)	67.43	25.81	Tissue	A. T. Virk	EF989643
482	Ca482	247	Wild	*C. aegagrus*	Pakistan	Dureji (42)	67.43	25.81	Tissue	A. T. Virk	EF989644
483	Ca483	248	F	*C. aegagrus*	Turkey	Van (10)	43.22	38.29	Tissue	A. Kence	EF989645
484	Ca484	249	Wild	*C. aegagrus*	Turkmenistan	Turkmenistan (40)	65.49	38.37	Tissue	G. Luikart	AJ317866
485	Ca485	250	Wild	*C. aegagrus*	Turkmenistan	Turkmenistan (40)	65.49	38.37	Tissue	G. Luikart	AJ317867
486	Ca486	251	Wild	*C. aegagrus blythi*	Pakistan	Kirthar (43)	67.43	25.81	Tissue	Sultana	AB110590
487	Ca487	251	Wild	*C. aegagrus blythi*	Pakistan	Kirthar (43)	67.43	25.81	Tissue	Sultana	AB110591

Supplementary Table 4.2. Geographic origin and characteristics of the domestic and wild goat samples used for AFLP study.

(Abbreviations used for the different breeds: CAE, *C. aegagrus*; VAL, Valdostana; BIO, Bionda dell'Adamello; CAM, Camosclata; RAI, Raini; LOC, Iranian local breeds; KUR, Kurdi; KSH, Kermanshah; SAN, Sanandaj).

NO.	Code	Species	Country	Population (Breed)	Longitude(E)	Latitude(N)	Sample Type	Collector
1	ChIr01	*C. hircus*	IRAN	Bashgol Ghazvin (LOC)	49.56	36.12	Tissue	HR. Rezaei
2	ChIr02	*C. hircus*	IRAN	Bashgol Ghazvin (LOC)	49.56	36.12	Tissue	HR. Rezaei
3	ChIr03	*C. hircus*	IRAN	Bashgol Ghazvin (LOC)	49.56	36.12	Tissue	HR. Rezaei
4	ChIr04	*C. hircus*	IRAN	Bashgol Ghazvin (LOC)	49.56	36.12	Tissue	HR. Rezaei
5	ChIr05	*C. hircus*	IRAN	Bashgol Ghazvin (LOC)	49.56	36.12	Tissue	HR. Rezaei
6	ChIr06	*C. hircus*	IRAN	Bashgol Ghazvin (LOC)	49.56	36.12	Tissue	HR. Rezaei
7	ChIr07	*C. hircus*	IRAN	Bashgol Ghazvin (LOC)	49.56	36.12	Tissue	HR. Rezaei
8	ChIr08	*C. hircus*	IRAN	Alamout Gazvin (LOC)	49.57	36.11	Tissue	HR. Rezaei
9	ChIr09	*C. hircus*	IRAN	Alamout Gazvin (LOC)	49.57	36.11	Tissue	HR. Rezaei
10	ChIr10	*C. hircus*	IRAN	Alamout Gazvin (LOC)	49.57	36.11	Tissue	HR. Rezaei
11	ChIr11	*C. hircus*	IRAN	Alamout Gazvin (LOC)	49.57	36.11	Tissue	HR. Rezaei
12	ChIr12	*C. hircus*	IRAN	Angouran Zanjan – Mahneshan (LOC)	47.67	36.67	Tissue	HR. Rezaei
13	ChIr13	*C. hircus*	IRAN	Marakan, Western Azarbaijan (LOC)	45.24	38.84	Tissue	HR. Rezaei
14	ChIr14	*C. hircus*	IRAN	Marakan, Western Azarbaijan (LOC)	45.24	38.84	Tissue	HR. Rezaei
15	ChIr15	*C. hircus*	IRAN	Marakan, Western Azarbaijan (LOC)	45.24	38.84	Tissue	HR. Rezaei
16	ChIr16	*C. hircus*	IRAN	Marakan, Western Azarbaijan (LOC)	45.24	38.84	Tissue	HR. Rezaei
17	ChIr17	*C. hircus*	IRAN	Ghorveh Sanandadj (LOC)	47.82	35.06	Tissue	HR. Rezaei
18	ChIr18	*C. hircus*	IRAN	Ghorveh Sanandadj (LOC)	47.82	35.06	Tissue	HR. Rezaei
19	ChIr19	*C. hircus*	IRAN	Mehran (LOC)	46.11	33.31	Tissue	HR. Rezaei
20	ChIr20	*C. hircus*	IRAN	Mehran (LOC)	46.11	33.31	Tissue	HR. Rezaei

21	ChIr21	*C. hircus*	IRAN	Dareh Shahr Ilam (LOC)	47.38	33.19	Tissue	HR. Rezaei
22	ChIr22	*C. hircus*	IRAN	Dareh Shahr Ilam (LOC)	47.38	33.19	Tissue	HR. Rezaei
23	ChIr23	*C. hircus*	IRAN	Khoram- Abad (LOC)	48.16	33.58	Tissue	HR. Rezaei
24	ChIr24	*C. hircus*	IRAN	Azna (LOC)	49.35	33.44	Tissue	HR. Rezaei
25	ChIr25	*C. hircus*	IRAN	Azna (LOC)	49.35	33.44	Tissue	HR. Rezaei
26	ChIr26	*C. hircus*	IRAN	Azna (LOC)	49.35	33.44	Tissue	HR. Rezaei
27	ChIr27	*C. hircus*	IRAN	Parvar (LOC)	55.51	36.01	Tissue	S. Naderi
28	ChIr28	*C. hircus*	IRAN	Parvar (LOC)	55.51	36.01	Tissue	S. Naderi
29	ChIr29	*C. hircus*	IRAN	Khosh Yeylagh, Dasht_e_Zardabeh (LOC)	55.47	34.75	Tissue	S. Naderi
30	ChIr30	*C. hircus*	IRAN	Khosh Yeylagh, Dasht_e_Zardabeh (LOC)	55.47	34.75	Tissue	S. Naderi
31	ChIr31	*C. hircus*	IRAN	Khosh Yeylagh, Dasht_e_Zardabeh (LOC)	55.47	34.75	Tissue	S. Naderi
32	ChIr32	*C. hircus*	IRAN	Khartooran (LOC)	55.86	35.79	Tissue	S. Naderi
33	ChIr33	*C. hircus*	IRAN	Khartooran (LOC)	55.86	35.79	Tissue	S. Naderi
34	ChIr34	*C. hircus*	IRAN	Nosratabad Systan & Baloochestan (LOC)	59.87	29.97	Tissue	S. Naderi
35	ChIr35	*C. hircus*	IRAN	Ghamishloo (LOC)	51.22	32.85	Tissue	S. Naderi
36	ChIr36	*C. hircus*	IRAN	Ghamishloo (LOC)	51.22	32.85	Tissue	S. Naderi
37	ChIr37	*C. hircus*	IRAN	Ghamishloo (LOC)	51.22	32.85	Tissue	S. Naderi
38	ChIr38	*C. hircus*	IRAN	Ghamishloo (LOC)	51.22	32.85	Tissue	S. Naderi
39	ChIr39	*C. hircus*	IRAN	Kooh-e-Bafgh (LOC)	55.67	31.85	Tissue	S. Naderi
40	ChIr40	*C. hircus*	IRAN	Kooh-e-Bafgh (LOC)	55.67	31.85	Tissue	S. Naderi
41	ChIr41	*C. hircus*	IRAN	Kooh-e-Bafgh (LOC)	55.67	31.85	Tissue	S. Naderi
42	ChIr42	*C. hircus*	IRAN	Kooh-e-Bafgh (LOC)	55.67	31.85	Tissue	S. Naderi
43	ChIr43	*C. hircus*	IRAN	Kooh-e-Bafgh (LOC)	55.67	31.85	Tissue	S. Naderi
44	ChIr44	*C. hircus*	IRAN	Khabr National Park (LOC)	56.48	28.84	Tissue	S. Naderi
45	ChIr45	*C. hircus*	IRAN	Khabr National Park (LOC)	56.48	28.84	Tissue	S. Naderi
46	ChIr46	*C. hircus*	IRAN	Khabr National Park (LOC)	56.48	28.84	Tissue	S. Naderi
47	ChIr47	*C. hircus*	IRAN	Khabr National Park (LOC)	56.48	28.84	Tissue	S. Naderi
48	ChIr48	*C. hircus*	IRAN	Khabr National Park (LOC)	56.48	28.84	Tissue	S. Naderi

49	ChIr49	*C. hircus*	IRAN	Khabr National Park (LOC)	56.48	28.84	Tissue	S. Naderi
50	ChIr50	*C. hircus*	IRAN	Khabr National Park (LOC)	56.48	28.84	Tissue	S. Naderi
51	ChIr51	*C. hircus*	IRAN	God-e-Ghool Restricted Area (LOC)	55.14	29.45	Tissue	S. Naderi
52	ChIr52	*C. hircus*	IRAN	God-e-Ghool Restricted Area (LOC)	55.14	29.45	Tissue	S. Naderi
53	ChIr53	*C. hircus*	IRAN	God-e-Ghool Restricted Area (LOC)	55.14	29.45	Tissue	S. Naderi
54	ChIr54	*C. hircus*	IRAN	God-e-Ghool Restricted Area (LOC)	55.14	29.45	Tissue	S. Naderi
55	ChIr55	*C. hircus*	IRAN	God-e-Ghool Restricted Area (LOC)	55.14	29.45	Tissue	S. Naderi
56	ChIr56	*C. hircus*	IRAN	God-e-Ghool Restricted Area (LOC)	55.14	29.45	Tissue	S. Naderi
57	ChIr57	*C. hircus*	IRAN	God-e-Ghool Restricted Area (LOC)	55.14	29.45	Tissue	S. Naderi
58	ChIr58	*C. hircus*	IRAN	Dahaj Shahr Babak (LOC)	54.87	30.57	Tissue	S. Naderi
59	ChIr59	*C. hircus*	IRAN	Dahaj Shahr Babak (LOC)	54.87	30.57	Tissue	S. Naderi
60	ChIr60	*C. hircus*	IRAN	Dahaj Shahr Babak (LOC)	54.87	30.57	Tissue	S. Naderi
61	ChIr61	*C. hircus*	IRAN	Dahaj Shahr Babak (LOC)	54.87	30.57	Tissue	S. Naderi
62	ChIr62	*C. hircus*	IRAN	Basiran (LOC)	52.85	30.88	Tissue	S. Naderi
63	ChIr63	*C. hircus*	IRAN	Basiran (LOC)	52.85	30.88	Tissue	S. Naderi
64	ChIr64	*C. hircus*	IRAN	Basiran (LOC)	52.85	30.88	Tissue	S. Naderi
65	ChIr65	*C. hircus*	IRAN	Basiran (LOC)	52.85	30.88	Tissue	S. Naderi
66	ChIr66	*C. hircus*	IRAN	Basiran (LOC)	52.85	30.88	Tissue	S. Naderi
67	ChIr67	*C. hircus*	IRAN	Basiran (LOC)	52.85	30.88	Tissue	S. Naderi
68	ChIr68	*C. hircus*	IRAN	Basiran (LOC)	52.85	30.88	Tissue	S. Naderi
69	ChIr69	*C. hircus*	IRAN	Zaraab, Around Baft City in Kerman Province (RAI)	56.61	29.23	Tissue	A. Rafat
70	ChIr70	*C. hircus*	IRAN	Zaraab, Around Baft City in Kerman Province (RAI)	56.61	29.23	Tissue	A. Rafat
71	ChIr71	*C. hircus*	IRAN	Absaalaan-sad, Around Baft City in Kerman Province (RAI)	56.61	29.24	Tissue	A. Rafat
72	ChIr72	*C. hircus*	IRAN	Absaalaan-sad, Around Baft City in Kerman Province (RAI)	56.61	29.24	Tissue	A. Rafat
73	ChIr73	*C. hircus*	IRAN	Zaraab, Around Baft City in Kerman Province (RAI)	56.61	29.23	Tissue	A. Rafat
74	ChIr74	*C. hircus*	IRAN	Zaraab, Around Baft City in Kerman Province (RAI)	56.61	29.23	Tissue	A. Rafat
75	ChIr75	*C. hircus*	IRAN	Khabr, Around Baft City in Kerman Province (RAI)	56.82	29.41	Tissue	A. Rafat
76	ChIr76	*C. hircus*	IRAN	Jangal-cha, Around Baft City in Kerman Province (RAI)	56.37	29.93	Tissue	A. Rafat

77	ChIr77	*C. hircus*	IRAN	Jangal-cha, Around Baft City in Kerman Province (RAI)	56.37	29.93	Tissue	A. Rafat
78	ChIr78	*C. hircus*	IRAN	Ghaasemi, Around Baft City in Kerman Province (RAI)	56.81	29.65	Tissue	A. Rafat
79	ChIr79	*C. hircus*	IRAN	Ghaasemi, Around Baft City in Kerman Province (RAI)	56.81	29.65	Tissue	A. Rafat
80	ChIr80	*C. hircus*	IRAN	Gorguye, Around Baft City in Kerman Province (RAI)	56.21	29.23	Tissue	A. Rafat
81	ChIr81	*C. hircus*	IRAN	Gorguye, Around Baft City in Kerman Province(RAI)	56.21	29.23	Tissue	A. Rafat
82	ChIr82	*C. hircus*	IRAN	Zaraab, Around Baft City in Kerman Province (RAI)	56.6	29.23	Tissue	A. Rafat
83	ChIr83	*C. hircus*	IRAN	Zaraab, Around Baft City in Kerman Province (RAI)	56.6	29.23	Tissue	A. Rafat
84	ChIr84	*C. hircus*	IRAN	Baft (RAI)	56.6	29.44	Tissue	A. Rafat
85	ChIr85	*C. hircus*	IRAN	Baft (RAI)	56.6	29.44	Tissue	A. Rafat
86	ChIr86	*C. hircus*	IRAN	Baft (RAI)	56.6	29.44	Tissue	A. Rafat
87	ChIr87	*C. hircus*	IRAN	Baft (RAI)	56.6	29.44	Tissue	A. Rafat
88	ChIr88	*C. hircus*	IRAN	Baft-Hoseinabad, Around Baft City in Kerman Province (RAI)	56.26	29.23	Tissue	A. Rafat
89	ChIr89	*C. hircus*	IRAN	Baft-Hoseinabad, Around Baft City in Kerman Province (RAI)	56.26	29.23	Tissue	A. Rafat
90	ChIr90	*C. hircus*	IRAN	Baft, Jamalabad, Around Baft City in Kerman Province (RAI)	56.32	29.73	Tissue	A. Rafat
91	ChIr91	*C. hircus*	IRAN	Baft, Jamalabad, Around Baft City in Kerman Province (RAI)	56.32	29.73	Tissue	A. Rafat
92	ChIr92	*C. hircus*	IRAN	Chalekuye, Around Baft City in Kerman Province (RAI)	56.91	29.87	Tissue	A. Rafat
93	ChIr93	*C. hircus*	IRAN	Chalekuye, Around Baft City in Kerman Province (RAI)	56.91	29.87	Tissue	A. Rafat
94	ChIr94	*C. hircus*	IRAN	Baft-mahdabad, Around Baft City in Kerman Province (RAI)	56.05	29.32	Tissue	A. Rafat
95	ChIr95	*C. hircus*	IRAN	Baft-mahdabad, Around Baft City in Kerman Province (RAI)	56.05	29.32	Tissue	A. Rafat
96	ChIr96	*C. hircus*	IRAN	Baft-dughan, Around Baft City in Kerman Province (RAI)	56.58	29.32	Tissue	A. Rafat
97	ChIr97	*C. hircus*	IRAN	Baft-dughan, Around Baft City in Kerman Province (RAI)	56.58	29.32	Tissue	A. Rafat
98	ChIr98	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat
99	ChIr99	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat
100	ChIr100	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat
101	ChIr101	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat
102	ChIr102	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat
103	ChIr103	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat
104	ChIr104	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat

105	ChIr105	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat
106	ChIr106	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat
107	ChIr107	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat
108	ChIr108	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat
109	ChIr109	*C. hircus*	IRAN	Armarde-DashtBozorg, Around Baneh city (KUR)	46.28	36.55	Tissue	A. Rafat
110	ChIr110	*C. hircus*	IRAN	Armarde-DashtBozorg, Around Baneh city (KUR)	46.28	36.55	Tissue	A. Rafat
111	ChIr111	*C. hircus*	IRAN	Armarde-DashtBozorg, Around Baneh city (KUR)	46.28	36.55	Tissue	A. Rafat
112	ChIr112	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat
113	ChIr113	*C. hircus*	IRAN	Torjan (KUR)	46.17	36.55	Tissue	A. Rafat
114	ChIr114	*C. hircus*	IRAN	Armarde-DashtBozorg, Around Baneh city (KUR)	46.28	36.55	Tissue	A. Rafat
115	ChIr115	*C. hircus*	IRAN	Armarde-DashtBozorg, Around Baneh city (KUR)	46.28	36.55	Tissue	A. Rafat
116	ChIr116	*C. hircus*	IRAN	Armarde-DashtBozorg, Around Baneh city (KUR)	46.28	36.55	Tissue	A. Rafat
117	ChIr117	*C. hircus*	IRAN	Armarde-DashtBozorg, Around Baneh city (KUR)	46.28	36.55	Tissue	A. Rafat
118	ChIr118	*C. hircus*	IRAN	Saqqez (KUR)	46.29	36.13	Tissue	A. Rafat
119	ChIr119	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
120	ChIr120	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
121	ChIr121	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
122	ChIr122	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
123	ChIr123	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
124	ChIr124	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
125	ChIr125	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
126	ChIr126	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
127	ChIr127	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
128	ChIr128	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
129	ChIr129	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
130	ChIr130	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
131	ChIr131	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
132	ChIr132	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash

133	ChIr133	*C. hircus*	IRAN	Kurdistan-Kermanshah (KSH)	46.73	34.25	Tissue	HR. Naghash
134	ChIr134	*C. hircus*	IRAN	Kurdistan-Sanandaj (SAN)	46.85	35.45	Tissue	HR. Naghash
135	ChIr135	*C. hircus*	IRAN	Kurdistan-Sanandaj (SAN)	46.85	35.45	Tissue	HR. Naghash
136	ChIr136	*C. hircus*	IRAN	Kurdistan-Sanandaj (SAN)	46.85	35.45	Tissue	HR. Naghash
137	ChIr137	*C. hircus*	IRAN	Kurdistan-Sanandaj (SAN)	46.85	35.45	Tissue	HR. Naghash
138	ChIr138	*C. hircus*	IRAN	Kurdistan-Sanandaj (SAN)	46.85	35.45	Tissue	HR. Naghash
139	ChIr139	*C. hircus*	IRAN	Kurdistan-Sanandaj (SAN)	46.85	35.45	Tissue	HR. Naghash
140	ChIr140	*C. hircus*	IRAN	Kurdistan-Sanandaj (SAN)	46.85	35.45	Tissue	HR. Naghash
141	ChIr141	*C. hircus*	IRAN	Kurdistan-Sanandaj (SAN)	46.85	35.45	Tissue	HR. Naghash
142	ChIr142	*C. hircus*	IRAN	Kurdistan-Sanandaj (SAN)	46.85	35.45	Tissue	HR. Naghash
143	CaIRI01	*C. aegagrus*	IRAN	Khartooran Protected Area (CAE)	55.86	35.77	Tissue	S. Naderi
144	CaIRI04	*C. aegagrus*	IRAN	Gazvin (CAE)	49.57	36.09	Tissue	HR. Rezaei
145	CaIRI05	*C. aegagrus*	IRAN	Gazvin (CAE)	49.57	36.09	Tissue	HR. Rezaei
146	CaIRI06	*C. aegagrus*	IRAN	Lashkar-Dar Malayer (CAE)	48.95	34.21	Tissue	HR. Rezaei
147	CaIRI08	*C. aegagrus*	IRAN	Mehran (CAE)	46.12	33.31	Tissue	HR. Rezaei
148	CaIRI11	*C. aegagrus*	IRAN	Tandooreh National Park (CAE)	58.87	37.41	Tissue	S. Naderi
149	CaIRI12	*C. aegagrus*	IRAN	Tandooreh National Park (CAE)	58.87	37.41	Tissue	S. Naderi
150	CaIRI14	*C. aegagrus*	IRAN	Gazvin (CAE)	49.57	36.09	Tissue	HR. Rezaei
151	CaIRI15	*C. aegagrus*	IRAN	Gazvin (CAE)	49.57	36.09	Tissue	HR. Rezaei
152	CaIRI17	*C. aegagrus*	IRAN	Golestan National Park (CAE)	56.14	37.43	Tissue	HR. Rezaei
153	CaIRI19	*C. aegagrus*	IRAN	Gazvin (CAE)	49.57	36.09	Tissue	HR. Rezaei
154	CaIRI20	*C. aegagrus*	IRAN	Gazvin (CAE)	49.57	36.09	Tissue	HR. Rezaei
155	CaIRI26	*C. aegagrus*	IRAN	Kalmand-Bahadoran Protected Area (CAE)	54.79	31.28	Tissue	S. Naderi
156	CaIRI28	*C. aegagrus*	IRAN	Gazvin (CAE)	49.57	36.09	Tissue	HR. Rezaei
157	CaIRI33	*C. aegagrus*	IRAN	Gazvin (CAE)	49.57	36.09	Tissue	HR. Rezaei
158	CaIRI35	*C. aegagrus*	IRAN	Mehran (CAE)	46.12	33.31	Tissue	HR. Rezaei
159	CaIRI36	*C. aegagrus*	IRAN	Lashkar-Dar Malayer (CAE)	48.95	34.21	Tissue	HR. Rezaei
160	CaIRI39	*C. aegagrus*	IRAN	Bavanat Restricted Area (CAE)	53.91	30.31	Tissue	S. Naderi
161	CaIRI40	*C. aegagrus*	IRAN	Bavanat Restricted Area (CAE)	53.91	30.31	Tissue	S. Naderi
162	ChItCAM01	*C. hircus*	ITALY	Boario_Brescia_Lombardy (CAM)	10.1465	45.8846	Whole blood	S. Giovenzana
163	ChItCAM02	*C. hircus*	ITALY	Boario_Brescia_Lombardy (CAM)	10.1465	45.8846	Whole blood	S. Giovenzana

164	ChItCAM03	*C. hircus*	ITALY	Boario_Brescia_Lombardy (CAM)	10.1465	45.8846	Whole blood	S. Giovenzana
165	ChItCAM04	*C. hircus*	ITALY	Boario_Brescia_Lombardy (CAM)	10.1439	45.8961	Whole blood	S. Giovenzana
166	ChItCAM05	*C. hircus*	ITALY	Boario_Brescia_Lombardy (CAM)	10.1439	45.8961	Whole blood	S. Giovenzana
167	ChItCAM06	*C. hircus*	ITALY	Boario_Brescia_Lombardy (CAM)	10.1439	45.8961	Whole blood	S. Giovenzana
168	ChItCAM07	*C. hircus*	ITALY	Boario_Brescia_Lombardy (CAM)	10.2311	45.9297	Whole blood	S. Giovenzana
169	ChItCAM08	*C. hircus*	ITALY	Boario_Brescia_Lombardy (CAM)	10.2311	45.9297	Whole blood	S. Giovenzana
170	ChItCAM10	*C. hircus*	ITALY	Boario_Brescia_Lombardy (CAM)	10.2311	45.9297	Whole blood	S. Giovenzana
171	ChItCAM11	*C. hircus*	ITALY	Prestine_Brescia_Lombardy (CAM)	10.321	45.9229	Whole blood	S. Giovenzana
172	ChItCAM12	*C. hircus*	ITALY	Prestine_Brescia_Lombardy (CAM)	10.321	45.9229	Whole blood	S. Giovenzana
173	ChItCAM14	*C. hircus*	ITALY	Prestine_Brescia_Lombardy (CAM)	10.321	45.9229	Whole blood	S. Giovenzana
174	ChItCAM16	*C. hircus*	ITALY	Pincamuno_Brescia_Lombardy (CAM)	10.3212	45.9343	Whole blood	S. Giovenzana
175	ChItCAM17	*C. hircus*	ITALY	Pincamuno_Brescia_Lombardy (CAM)	10.3212	45.9343	Whole blood	S. Giovenzana
176	ChItCAM18	*C. hircus*	ITALY	Pincamuno_Brescia_Lombardy (CAM)	10.3212	45.9343	Whole blood	S. Giovenzana
177	ChItCAM19	*C. hircus*	ITALY	Piantedo_Sondrio_Lombardy (CAM)	9.4389	46.1408	Whole blood	S. Giovenzana
178	ChItCAM20	*C. hircus*	ITALY	Piantedo_Sondrio_Lombardy (CAM)	9.4389	46.1408	Whole blood	S. Giovenzana
179	ChItCAM21	*C. hircus*	ITALY	Piantedo_Sondrio_Lombardy (CAM)	9.4389	46.1408	Whole blood	S. Giovenzana
180	ChItCAM22	*C. hircus*	ITALY	San pellegrino terme_Bergamo_Lombardy (CAM)	9.6384	45.869	Whole blood	S. Giovenzana
181	ChItCAM23	*C. hircus*	ITALY	San pellegrino terme_Bergamo_Lombardy (CAM)	9.6384	45.869	Whole blood	S. Giovenzana
182	ChItCAM24	*C. hircus*	ITALY	San pellegrino terme_Bergamo_Lombardy (CAM)	9.6384	45.869	Whole blood	S. Giovenzana
183	ChItCAM25	*C. hircus*	ITALY	Valmadrera_Lecco_Lombardy (CAM)	9.3352	45.8287	Whole blood	S. Giovenzana
184	ChItCAM26	*C. hircus*	ITALY	Valmadrera_Lecco_Lombardy (CAM)	9.3352	45.8287	Whole blood	S. Giovenzana
185	ChItCAM27	*C. hircus*	ITALY	Valmadrera_Lecco_Lombardy (CAM)	9.3352	45.8287	Whole blood	S. Giovenzana
186	ChItCAM28	*C. hircus*	ITALY	Malgrate_Lecco_Lombardy (CAM)	9.3563	45.8481	Whole blood	S. Giovenzana
187	ChItCAM29	*C. hircus*	ITALY	Malgrate_Lecco_Lombardy (CAM)	9.3563	45.8481	Whole blood	S. Giovenzana
188	ChItCAM31	*C. hircus*	ITALY	Malgrate_Lecco_Lombardy (CAM)	9.3563	45.8481	Whole blood	S. Giovenzana
189	ChItCAM32	*C. hircus*	ITALY	Vedeseta_Bergamo_Lombardy (CAM)	9.5661	45.899	Whole blood	S. Giovenzana
190	ChItCAM33	*C. hircus*	ITALY	Vedeseta_Bergamo_Lombardy (CAM)	9.5661	45.899	Whole blood	S. Giovenzana
191	ChItVAL02	*C. hircus*	ITALY	Avise_Aosta_Valle d'Aosta (VAL)	7.1556	45.7008	Whole blood	S. Giovenzana
192	ChItVAL03	*C. hircus*	ITALY	Avise_Aosta_Valle d'Aosta (VAL)	7.1556	45.7008	Whole blood	S. Giovenzana
193	ChItVAL04	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.0686	45.7643	Whole blood	S. Giovenzana
194	ChItVAL05	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.0686	45.7643	Whole blood	S. Giovenzana
195	ChItVAL06	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.0686	45.7643	Whole blood	S. Giovenzana

196	ChItVAL07	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.0646	45.7471	Whole blood	S. Giovenzana
197	ChItVAL08	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.0646	45.7471	Whole blood	S. Giovenzana
198	ChItVAL09	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.0646	45.7471	Whole blood	S. Giovenzana
199	ChItVAL10	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.301	45.762	Whole blood	S. Giovenzana
200	ChItVAL11	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.301	45.762	Whole blood	S. Giovenzana
201	ChItVAL12	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.301	45.762	Whole blood	S. Giovenzana
202	ChItVAL13	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.3234	45.7622	Whole blood	S. Giovenzana
203	ChItVAL14	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.3234	45.7622	Whole blood	S. Giovenzana
204	ChItVAL15	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.3234	45.7622	Whole blood	S. Giovenzana
205	ChItVAL16	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.6821	45.6524	Whole blood	S. Giovenzana
206	ChItVAL17	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.6821	45.6524	Whole blood	S. Giovenzana
207	ChItVAL18	*C. hircus*	ITALY	Morgex_Aosta_Valle d'Aosta (VAL)	7.6821	45.6524	Whole blood	S. Giovenzana
208	ChItVAL19	*C. hircus*	ITALY	Pont st martin_Aosta_Valle d'Aosta (VAL)	7.7817	45.5904	Whole blood	S. Giovenzana
209	ChItVAL20	*C. hircus*	ITALY	Pont st martin_Aosta_Valle d'Aosta (VAL)	7.7817	45.5904	Whole blood	S. Giovenzana
210	ChItVAL21	*C. hircus*	ITALY	Pont st martin_Aosta_Valle d'Aosta (VAL)	7.7817	45.5904	Whole blood	S. Giovenzana
211	ChItVAL22	*C. hircus*	ITALY	Jovencan_Aosta_Valle d'Aosta (VAL)	7.2953	45.7203	Whole blood	S. Giovenzana
212	ChItVAL23	*C. hircus*	ITALY	Jovencan_Aosta_Valle d'Aosta (VAL)	7.2953	45.7203	Whole blood	S. Giovenzana
213	ChItVAL25	*C. hircus*	ITALY	Gressan_Aosta_Valle d'Aosta (VAL)	7.3269	45.7193	Whole blood	S. Giovenzana
214	ChItVAL26	*C. hircus*	ITALY	Gressan_Aosta_Valle d'Aosta (VAL)	7.3269	45.7193	Whole blood	S. Giovenzana
215	ChItVAL27	*C. hircus*	ITALY	Gressan_Aosta_Valle d'Aosta (VAL)	7.3269	45.7193	Whole blood	S. Giovenzana
216	ChItVAL28	*C. hircus*	ITALY	Aosta_Aosta_Valle d'Aosta (VAL)	7.3121	45.7845	Whole blood	S. Giovenzana
217	ChItVAL29	*C. hircus*	ITALY	Aosta_Aosta_Valle d'Aosta (VAL)	7.3121	45.7845	Whole blood	S. Giovenzana
218	ChItVAL30	*C. hircus*	ITALY	Aosta_Aosta_Valle d'Aosta (VAL)	7.3121	45.7845	Whole blood	S. Giovenzana
219	ChItVAL31	*C. hircus*	ITALY	Arnad_Aosta_Valle d'Aosta (VAL)	7.6797	45.6577	Whole blood	S. Giovenzana
220	ChItVAL32	*C. hircus*	ITALY	Arnad_Aosta_Valle d'Aosta (VAL)	7.6797	45.6577	Whole blood	S. Giovenzana
221	ChItVAL33	*C. hircus*	ITALY	Arnad_Aosta_Valle d'Aosta (VAL)	7.6797	45.6577	Whole blood	S. Giovenzana
222	ChItBIO02	*C. hircus*	ITALY	Angolo terme_Brescia_Lombardy (BIO)	10.1526	45.8856	Whole blood	S. Giovenzana
223	ChItBIO03	*C. hircus*	ITALY	Angolo terme_Brescia_Lombardy (BIO)	10.1526	45.8856	Whole blood	S. Giovenzana
224	ChItBIO04	*C. hircus*	ITALY	Prestine_Brescia_Lombardy (BIO)	10.3211	45.9343	Whole blood	S. Giovenzana
225	ChItBIO06	*C. hircus*	ITALY	Prestine_Brescia_Lombardy (BIO)	10.3211	45.9343	Whole blood	S. Giovenzana
226	ChItBIO08	*C. hircus*	ITALY	Ceto_Brescia_Lombardy (BIO)	10.3512	46.0033	Whole blood	S. Giovenzana
227	ChItBIO09	*C. hircus*	ITALY	Ceto_Brescia_Lombardy (BIO)	10.3512	46.0033	Whole blood	S. Giovenzana

228	ChItBIO10	*C. hircus*	ITALY	Ceto_Brescia_Lombardy (BIO)	10.3526	46.005	Whole blood	S. Giovenzana
229	ChItBIO12	*C. hircus*	ITALY	Ceto_Brescia_Lombardy (BIO)	10.3526	46.005	Whole blood	S. Giovenzana
230	ChItBIO13	*C. hircus*	ITALY	Ceto_Brescia_Lombardy (BIO)	10.3675	46.0751	Whole blood	S. Giovenzana
231	ChItBIO15	*C. hircus*	ITALY	Ceto_Brescia_Lombardy (BIO)	10.3675	46.0751	Whole blood	S. Giovenzana
232	ChItBIO16	*C. hircus*	ITALY	Ceto_Brescia_Lombardy (BIO)	10.3792	46.0792	Whole blood	S. Giovenzana
233	ChItBIO17	*C. hircus*	ITALY	Ceto_Brescia_Lombardy (BIO)	10.3792	46.0792	Whole blood	S. Giovenzana
234	ChItBIO18	*C. hircus*	ITALY	Ceto_Brescia_Lombardy (BIO)	10.3792	46.0792	Whole blood	S. Giovenzana
235	ChItBIO19	*C. hircus*	ITALY	Saviore dell'adamello_Brescia_Lombardy (BIO)	10.4371	46.0702	Whole blood	S. Giovenzana
236	ChItBIO20	*C. hircus*	ITALY	Saviore dell'adamello_Brescia_Lombardy (BIO)	10.4371	46.0702	Whole blood	S. Giovenzana
237	ChItBIO21	*C. hircus*	ITALY	Saviore dell'adamello_Brescia_Lombardy (BIO)	10.4371	46.0702	Whole blood	S. Giovenzana
238	ChItBIO22	*C. hircus*	ITALY	Valle di saviore_Brescia_Lombardy (BIO)	10.4371	46.0702	Whole blood	S. Giovenzana
239	ChItBIO23	*C. hircus*	ITALY	Valle di saviore_Brescia_Lombardy (BIO)	10.4371	46.0702	Whole blood	S. Giovenzana
240	ChItBIO24	*C. hircus*	ITALY	Valle di saviore_Brescia_Lombardy (BIO)	10.4371	46.0702	Whole blood	S. Giovenzana
241	ChItBIO25	*C. hircus*	ITALY	Cevo_Brescia_Lombardy (BIO)	10.4028	46.0721	Whole blood	S. Giovenzana
242	ChItBIO27	*C. hircus*	ITALY	Cevo_Brescia_Lombardy (BIO)	10.4028	46.0721	Whole blood	S. Giovenzana
243	ChItBIO28	*C. hircus*	ITALY	Cedegolo_Brescia_Lombardy (BIO)	10.3561	46.0753	Whole blood	S. Giovenzana
244	ChItBIO29	*C. hircus*	ITALY	Cedegolo_Brescia_Lombardy (BIO)	10.3561	46.0753	Whole blood	S. Giovenzana
245	ChItBIO30	*C. hircus*	ITALY	Cedegolo_Brescia_Lombardy (BIO)	10.3561	46.0753	Whole blood	S. Giovenzana
246	ChItBIO31	*C. hircus*	ITALY	Darfo_Brescia_Lombardy (BIO)	10.1945	45.8733	Whole blood	S. Giovenzana
247	ChItBIO32	*C. hircus*	ITALY	Darfo_Brescia_Lombardy (BIO)	10.1945	45.8733	Whole blood	S. Giovenzana

Supplementary Table 4.3. Additional information about the archeological sites indicated in Fig. 2a.

Site	Region	Country	Culture	Date cal. B.P.	Origin of early domestic goats	References
Nevalı Çori	Eastern Anatolia	Turkey	Early PPNB	ca. 10,500	local	7
Shillourokambos	Cyprus	Cyprus	Early/Middle PPNB	10,300-10,200	transferred	8,9
Aswad	Damascus plain	Syria	Early/Middle PPNB	10,300-10,000	transferred	10
Çayönü	Eastern Anatolia	Turkey	Middle PPNB	ca. 10,000	?	11
Aşıklı	Central Anatolia	Turkey	Middle PPNB	10,000-9500	?	12
Nemrik	Eastern Anatolia	Iraq	Middle PPNB	10,000-9500	?	13
Ganj Dareh	Central Zagros	Iran	Aceramic Neolithic	9900-9700	local	14-16
Halula	Euphrates Valley	Syria	Middle PPNB	9800-9500	transferred	17
Abu Hureyra	Euphrates Valley	Syria	Middle PPNB	9800-9500	transferred	18,19
Tapeh Guran	Central Zagros	Iran	Aceramic Neolithic	9500-9200	?	14-16
Ali Kosh	Zagros lowlands	Iran	Aceramic Neolithic	9500-9400	transferred	14-16
Tal-i-Mushki	Fars	Iran	Aceramic Neolithic	8000-8500	?	20
Mehrgahr	Indus Valley	Pakistan	Early Neolithic	?8000-7500	?	21-23

PPNB: PrePottery Neolithic B

Supplementary Table 4.4. Partition of the genetic variance among geographic regions and populations by Analysis of molecular variance for bezoars (*Capra aegagrus*).

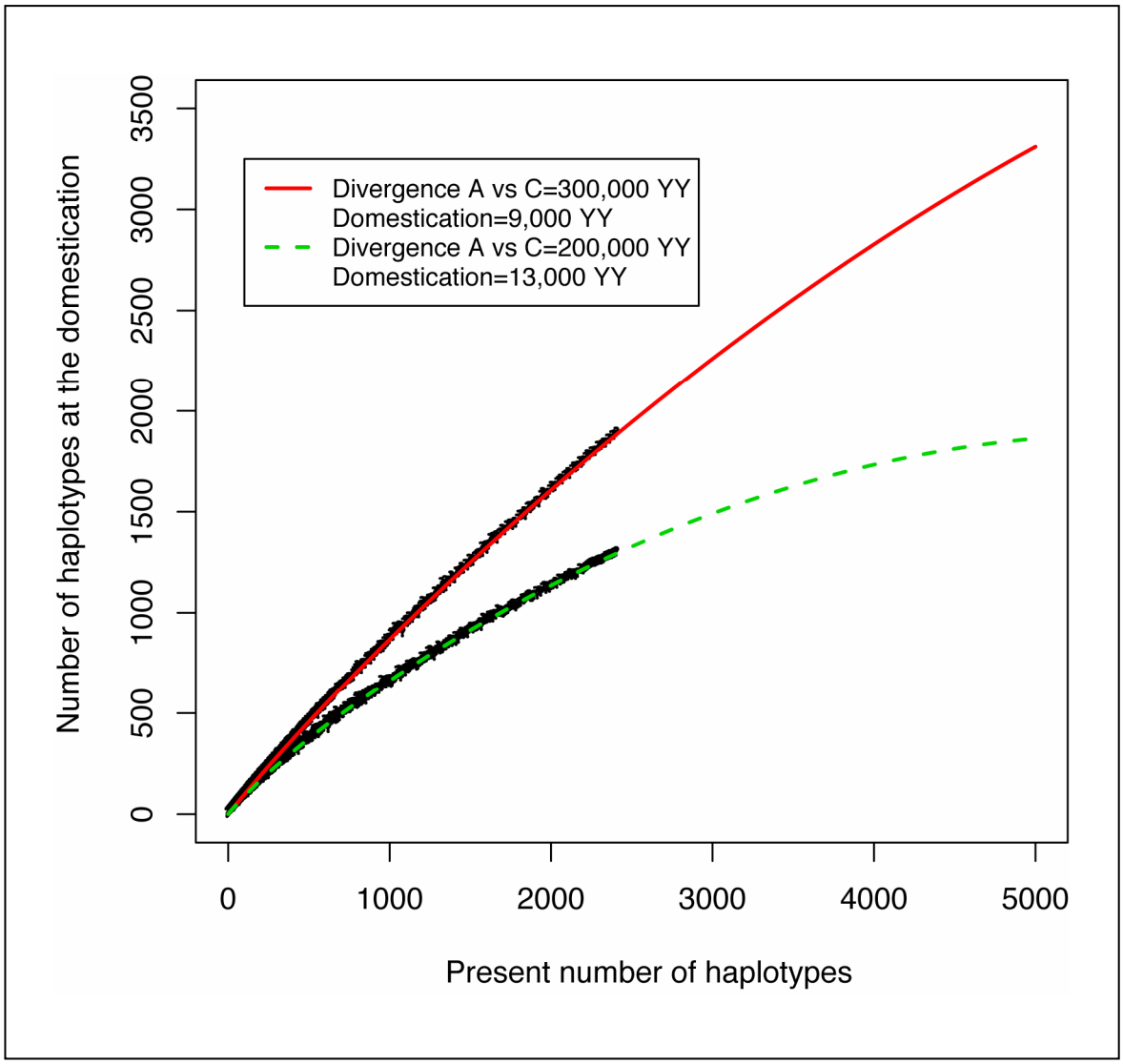
All percentages of variations are significantly different from 0 (*: P< 0.001 ; **: P<0.00001). d.f.: degree of freedom.

Source of variation	d.f.	Sum of squares	Variance components	% of variation
Among Regions	7	4079.332	4.89819	9.40**
Among populations within regions	35	8340.091	19.64446	37.70**
Within populations	444	12240.671	27.56908	52.90*
Total	486	24660.094	52.11173	

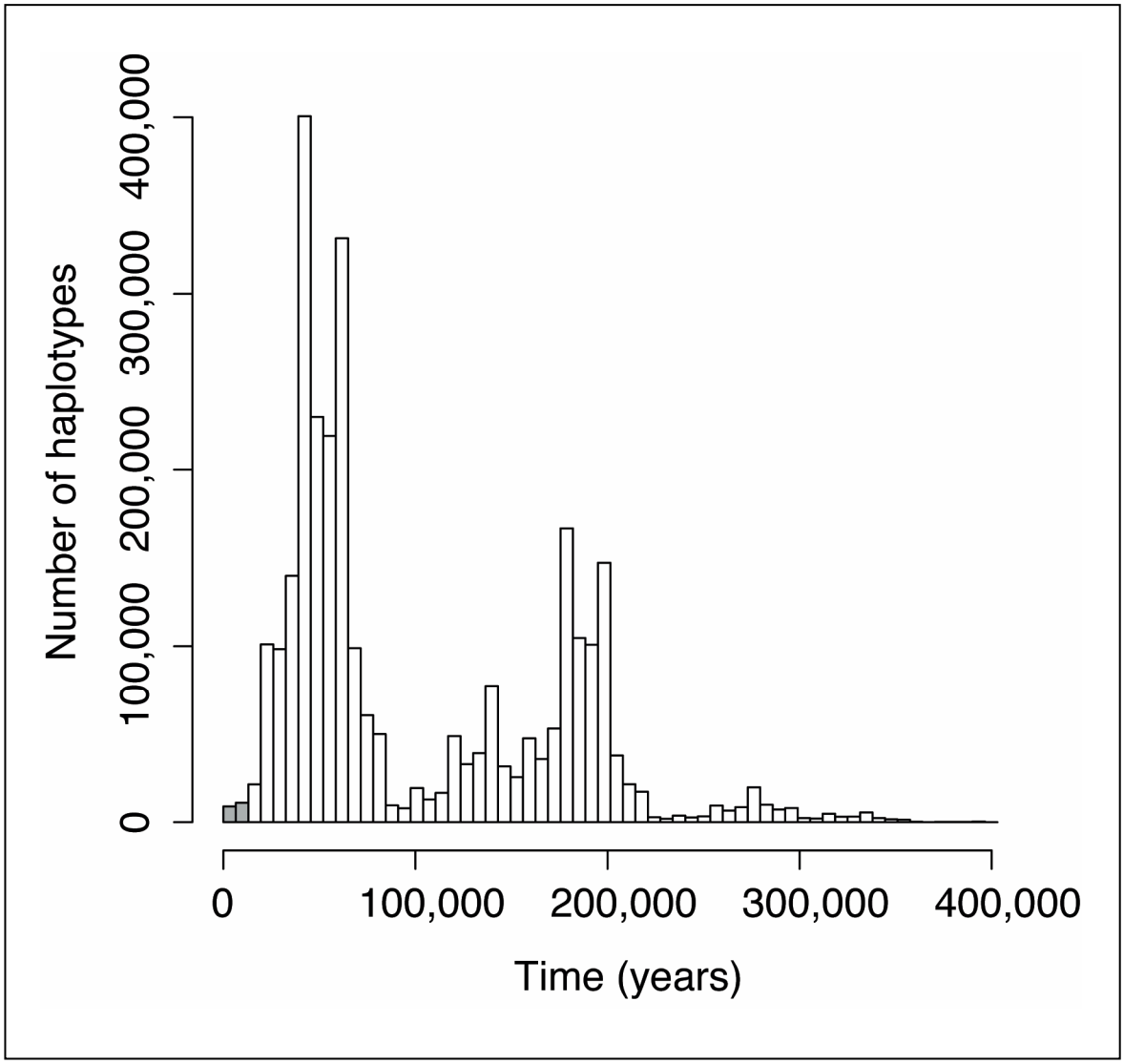
Supplementary Table 4.5. TMRCA for different mtDNA haplogroups of goats (*Capra hircus*).

Divergence A versus C (years)	A haplogroup (years)	B haplogroup (years)	C haplogroup (years)	D haplogroup (years)
200,000	55,000	29,000	29,000	36,000
300,000	83,000	44,000	44,000	53,000

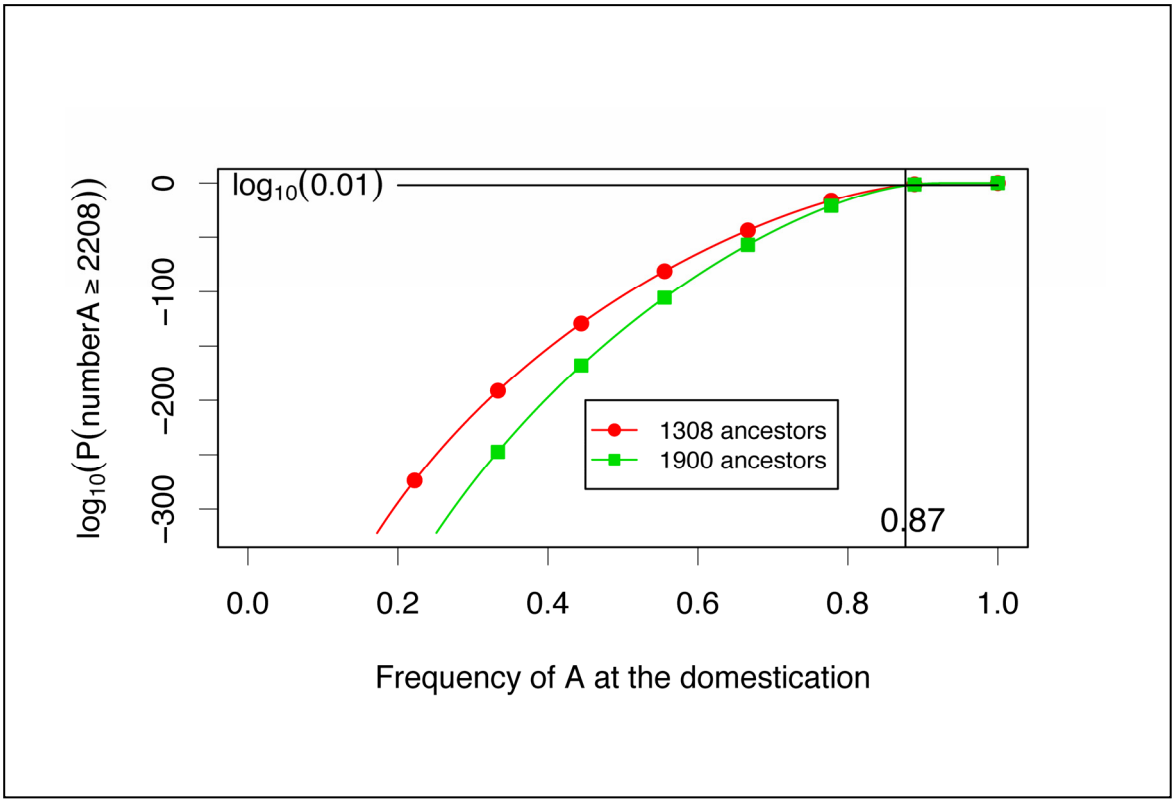
Supplementary Figure 4.1. Number of ancestral haplotypes at the time of domestication as a function of the size of the sample. The dots correspond to the bootstrap replicates and the curves have been obtained using a polynomial regression.



Supplementary Figure 4.2. Pairwise coalescence times of goat (*Capra hircus*) mtDNA haplotypes. Genetic distances are computed as the number of differences between pairs of sequences and are then rescaled in time by using 250,000 years for the divergence time between A and C haplogroups. The shaded part of the histogram corresponds to the pairs of sequences that coalesced more recently than the domestication.

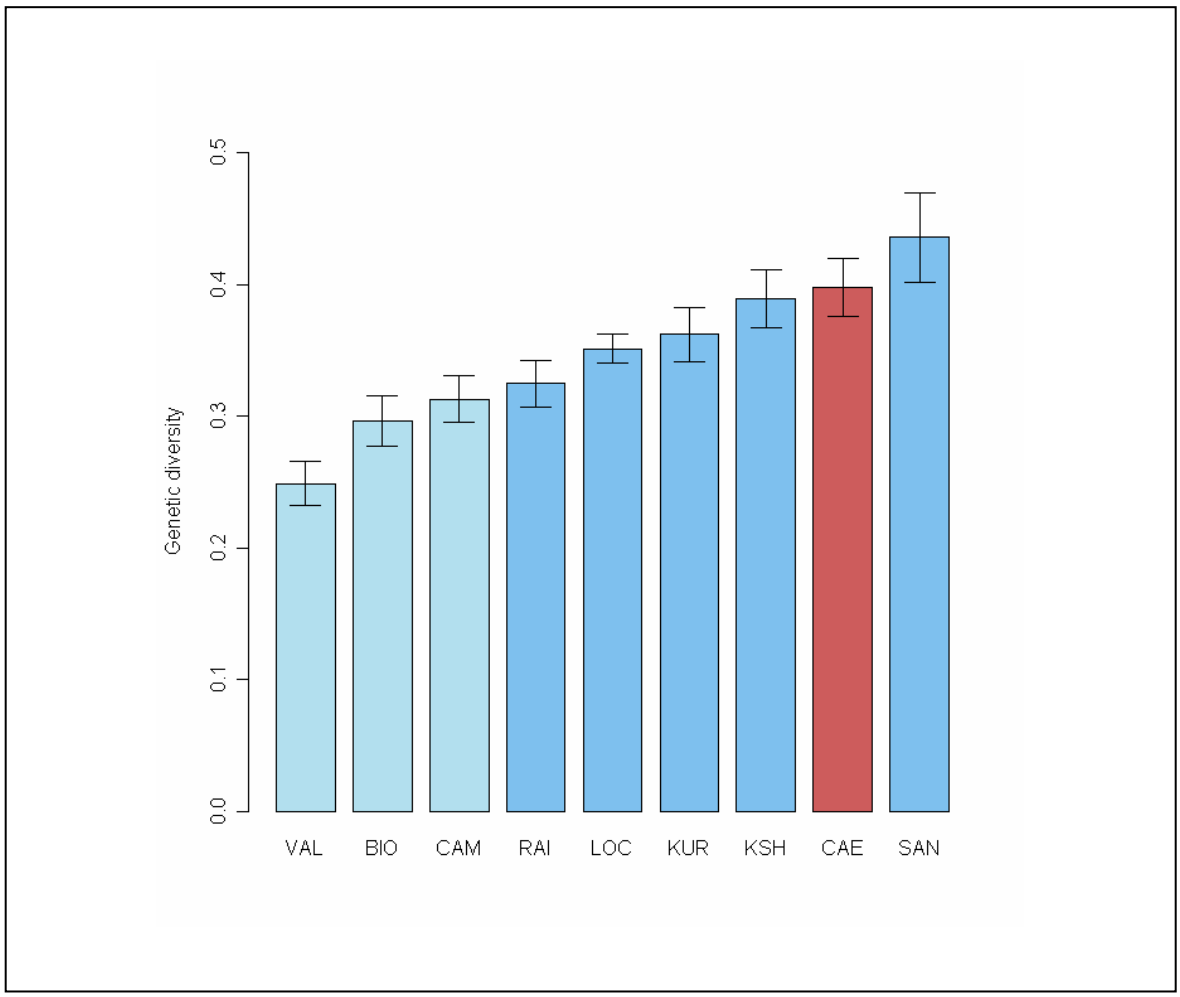


Supplementary Figure 4.3. Probability of observing more than the present number of individuals from the A haplogroup as a function of the frequency of the individuals from the A haplogroup at the time of the domestication.

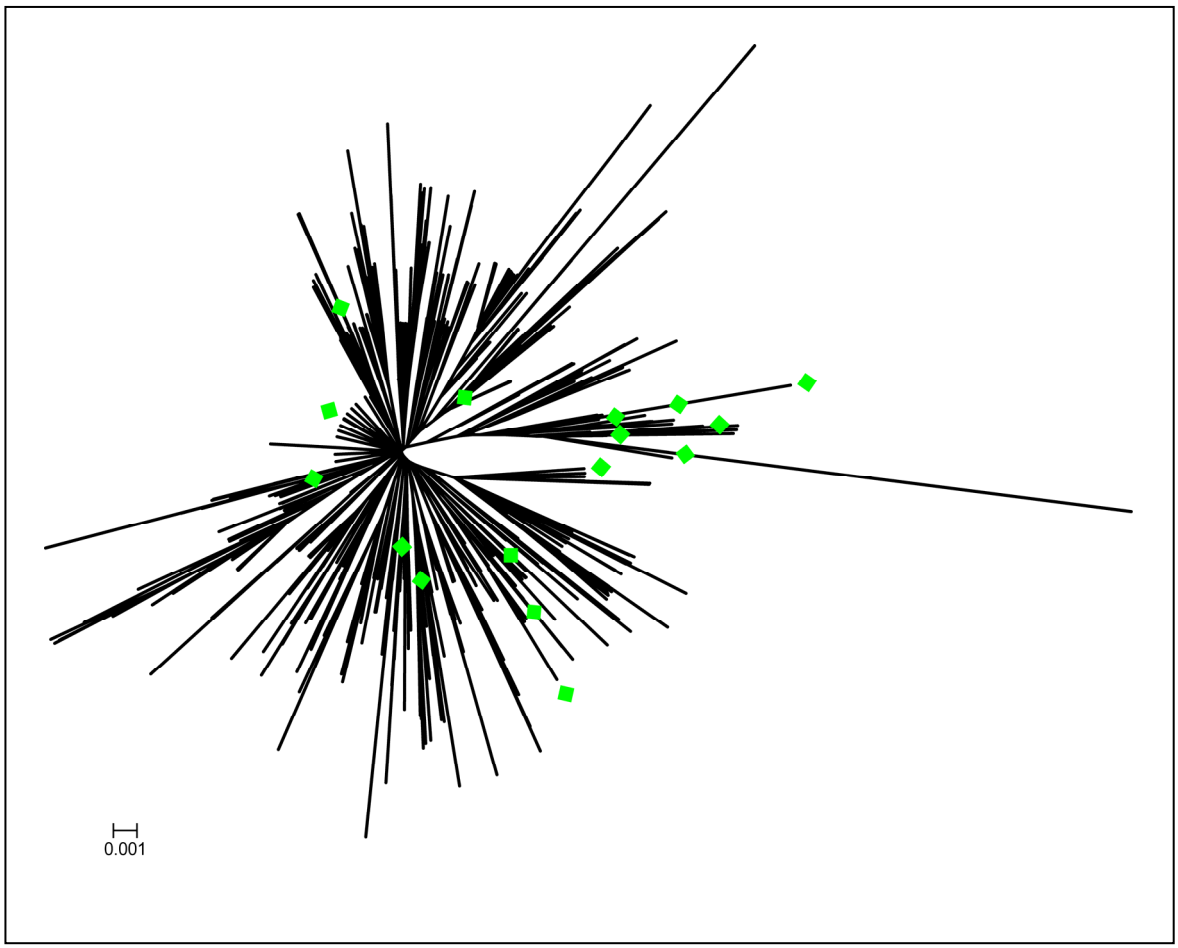


Supplementary Figure 4.4. Levels of genetic polymorphism of nuclear DNA inferred from AFLP analysis for the bezoar (*Capra aegagrus*) and for eight goat (*Capra hircus*) breeds, five from Iran, three from Italy.

CAE, *C. aegagrus*; VAL, Valdostana; BIO, Bionda dell'Adamello; CAM, Camosclata; RAI, Raini; LOC, Iranian local breeds; KUR, Kurdi; KSH, Kermanshah; SAN, Sanandaj.



Supplementary Figure 4.5. Placement of the bezoars of the A haplogroup from the Lar Mountains (Southeast Iran, locality 33 in Figure 2b) within the phylogeny of the A haplogroup of goats. The presence of bezoar haplotypes (in green) in many different clades of the phylogeny indicates a likely introgression from the domestics to the wilds.



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Supplementary Figure 4.6. The habitat of *Capra aegagrus* in Dahaj protected area in Iran (Photo by Saeid Naderi)**.**

Chapter 5. Are cattle, sheep, and goats endangered species?

Chapter 5. Are cattle, sheep, and goats endangered species?

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Molecular Ecology: (2008) 17, 275–284

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Keywords: breeds, conservation genetics, genetic diversity, livestock

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Running title: Are cattle, sheep, and goats endangered species?

Abstract

For about 10000 years, farmers have been managing cattle, sheep, and goats in a sustainable way, leading to animals that are well adapted to the local conditions. About two hundreds years ago, the situation started to change dramatically, with the rise of the concept of breed. All animals from the same breed began to be selected for the same phenotypic characteristics, and reproduction among breeds was seriously reduced. This corresponded to a strong fragmentation of the initial populations. A few decades ago, the selection pressures were increased again in order to further improve productivity, without enough emphasis on the preservation of the overall genetic diversity. The efficiency of modern selection methods successfully increased the production, but with a dramatic loss of genetic variability. Many industrial breeds now suffer from inbreeding, with effective population sizes falling below 50. With the development of these industrial breeds came economic pressure on farmers to abandon their traditional breeds, and many of these have recently become extinct as a result. This means that genetic resources in cattle, sheep, and goats are highly endangered, particularly in developed countries. It is therefore important to take measures that promote a sustainable management of these genetic resources, first by *in situ* preservation of endangered breeds, second by using selection programs to restore the genetic diversity of industrial breeds, and finally by protecting the wild relatives that might provide useful genetic resources.

Introduction

According to the Food and Agriculture Organization of the United Nations (FAO), the population sizes of domestic cows, sheep, and goats, are about 1,400, 1,100, and 700 million, respectively (Scherf 2000; Table 5.1). Over the past 15 years, about 300 of 6000 breeds of farm animals identified by the FAO have become extinct. Furthermore, 1350 breeds of domestic animals currently face extinction in the near future (Scherf 2000). This trend of loss of cattle, sheep, and goat breeds appears particularly strong in Europe (Table 5.1), possibly because it remains poorly documented in developing countries. At the worldwide level, 17% of cattle and 14% of sheep breeds have already been lost (Scherf 2000).

Table 5.1. Population sizes, current number of breeds, number of extinct breeds for cattle, sheep, and goats in different regions (source: FAOSTAT from Scherf (2000); statistics concerning 170 countries).

		Cattle	Sheep	Goat
Africa	Population size ('000)	174 556	127 440	137 104
	Current number of breeds	251	147	89
	Number of extinct breeds	23	8	0
Asia and Pacific	Population size ('000)	461 197	408 098	390 433
	Current number of breeds	236	233	146
	Number of extinct breeds	19	7	1
Europe	Population size ('000)	162 119	185 035	26 092
	Current number of breeds	482	629	187
	Number of extinct breeds	171	142	14
Latin America and Caribbean	Population size ('000)	356 069	89 372	40 752
	Current number of breeds	107	42	34
	Number of extinct breeds	24	0	0
Near East	Population size ('000)	71 913	242 770	114 572
	Current number of breeds	86	201	94
	Number of extinct breeds	12	11	1
North America	Population size ('000)	141 481	7 891	1 428
	Current number of breeds	62	61	20
	Number of extinct breeds	5	13	1
Total population size ('000)		1 367 335	1 060 606	710 381

The International Union for the Conservation of Nature and Natural Resources (IUCN) regards a species as critically endangered, endangered, or vulnerable when its effective population size falls below 50, 250, or 1000, respectively (IUCN 2000). The rule-of-thumb in conservation biology considers that the effective population size should not be lower than 50 to avoid extinction in the short-term, and not lower than 500 to avoid extinction in the long term (Franklin 1980).

Thus, it seems irrelevant to consider these three domestic species as endangered, considering their numbers that in the case of random mating result in effective population sizes way above the critical thresholds. However, such conclusions based purely on the

number of individuals are often overly simplistic. After a brief presentation of the domestication history of these three species, we will separately consider the cases of highly productive breeds and of local breeds with low population sizes. We will examine the potential threats that cattle, sheep, and goats might suffer from, with emphasis on the current management, particularly in developed countries. These three domestic species are divided into many breeds (Table 5.1), and each breed can be considered as an independent genetic unit, as crosses are not usually employed for reproduction in developed countries. Is the current management of breeds of high commercial value sustainable? What is the impact of managing these breeds separately, of the extensive use of artificial insemination, and of increasing the selection pressure for higher production? What are the optimal management guidelines for a sustainable use of genetic resources in cattle, sheep, and goats?

From a conservation biology point of view, our goal is also to show the possible parallel between domestic and wild species. Do domestic and wild species suffer from the same threats? Should the same concepts be used for managing wild and domestic animals?

Wild ancestors and the domestication process

Beside the wild ancestor when it still exists, the breeds to be used as genetic resources (i.e. the breeds with the highest genetic diversity) are expected to be found close to the domestication centres. As a consequence, precise knowledge of wild ancestors, of domestication centres, and of colonization routes is of prime importance for tracking genetic resources.

Information about cattle, sheep, and goat domestication comes from archaeological evidence, mostly from osteometry and morphometry, but also from genetic data (Vigne *et al.* 2005). Up to now, genetic studies on domestication mainly concerned the analysis of mitochondrial DNA (mtDNA) polymorphisms, either in the domestic species itself, or by comparing the domestic species with its wild ancestor.

Cattle

It is now widely recognized that the wild ancestor of all domesticated cattle was the auroch (*Bos primigenius*) (Zeuner 1963). The aurochs are now extinct. For domestic cattle, the common usage accepts two taxa (*Bos taurus* and *B. indicus*) that fully interbreed. *B.*

indicus differs from *B. taurus* by the presence of a prominent hump. The mtDNA polymorphism reflects this dichotomy (Fig. 5.1), but the reality is much more complex due to extensive hybridization among these two cattle haplogroups in Africa (Bradley *et al.* 1996).

The presence of two mtDNA haplogroups is interpreted as an indication of two main domestication events, one in the Fertile Crescent leading to *B. taurus*, and one in the Indian sub-continent leading to *B. indicus* (Loftus *et al.* 1994; Bradley *et al.* 1996; Bradley & Magee 2006). Eighty four percent of the mitochondrial variation is partitioned among Europe, Asia, and Africa (Bradley *et al.* 1996). The earliest archaeological evidence of cattle domestication dates from 8800 to 8300 BC (calibrated) in the Fertile Crescent (Helmer *et al.* 2005).

Sheep

Archaeological evidence indicates that domestic sheep, *Ovis aries*, were also domesticated in the Fertile Crescent, *circa* 8500 BC (calibrated) (Peters *et al.* 2005). However, their wild ancestors have not yet been identified with certainty, as no extensive genetic studies have been carried out on the putative ancestors. The wild candidates are *Ovis gmelini* (the Asiatic mouflon), *O. vignei* (the urial), and *O. ammon* (the argali), with a preference for *O. gmelini*, which shows the same chromosomal numbers as the domestic species (Bruford & Townsend 2006).

To date, four main mitochondrial DNA haplogroups have been found in domestic sheep, indicating multiple maternal origins (Fig. 5.1), and 35% of the mtDNA variation is partitioned among continents (Townsend 2000, cited by Bruford *et al.* 2003).

Goats

Goat domestication is very well documented. The first archaeological evidence traces back as far as 8500-7900 BC (calibrated) in the Zagros mountains (Fertile Crescent) (Zeder 2005), and the wild ancestor is the bezoar, *Capra aegagrus* (Fernández *et al.* 2005; Luikart *et al.* 2006).

The main characteristic of goat mtDNA polymorphism is its large haplotypic variation and its weak intercontinental phylogeographic structure, with only 10% partitioned among continents, suggesting high historical gene flow among continents

(Luikart *et al.* 2001). A recent ancient DNA study suggested that high gene flow already occurred during the Neolithic expansion into Europe (Fernández *et al.* 2006). Up to now, five different mtDNA haplogroups have been found (Fig. 5.1), indicating multiple maternal origins, as in sheep and cattle.

Dispersal from the domestication centres

During the 3000-4000 years following the initial domestication events in the Fertile Crescent, agriculture spread over Europe, Africa, and Asia. Archaeological evidence showed that two main colonization routes took place in Europe (Fig. 5.2): the Mediterranean route and the Danubian route. A decrease of genetic diversity likely occurred during this colonization process in Europe. This has been demonstrated for cattle mtDNA, for which populations in Western Europe exhibit lower polymorphism than those in the Near East (Troy et al. 2001; Bradley & Magee 2006). A number of secondary livestock migrations accompanied human migrations in more recent historical times and contributed to the shaping of local gene pools. For instance an introgression of the African gene pool is observed in Iberian cattle breeds (Cymbron *et al.* 1999; Miretti *et al.* 2004; Anderung *et al.* 2005; Beja-Pereira *et al.* 2006), possibly linked to the Moorish occupation or to even earlier events. Also, a surprisingly high level of mtDNA variation and close genetic relationship was discovered between Tuscan cattle breeds and Near Eastern breeds. This pattern might be linked either to the sailing and docking in Tuscany of Middle Eastern people in the late Bronze Age and to the onset of the Etruscan civilization in Central Italy (Pellecchia *et al.* 2007), or to an introgression from local aurochs (Beja-Pereira *et al.* 2006).

Overall, the level of mtDNA polymorphism in cattle, sheep, and goats (Fig. 5.1) is high, and contains evidence of multiple maternal origins. Such multiple origins correspond either to several domestication events in different locations and/or at different periods, or to the capture of several mtDNA haplotypes during a single domestication event. Furthermore, nuclear DNA polymorphism seems high (see e.g. Maudet *et al.* 2002), comparable to what is found in wild species. During crop domestication, many species went through a strong bottleneck (see references in Zeder 2006), but this is clearly not the case for livestock. All the current evidence suggests that cattle, sheep, and goats have very large gene pools on which human induced-selection was acting to produce the very large diversity of breeds we observe today.

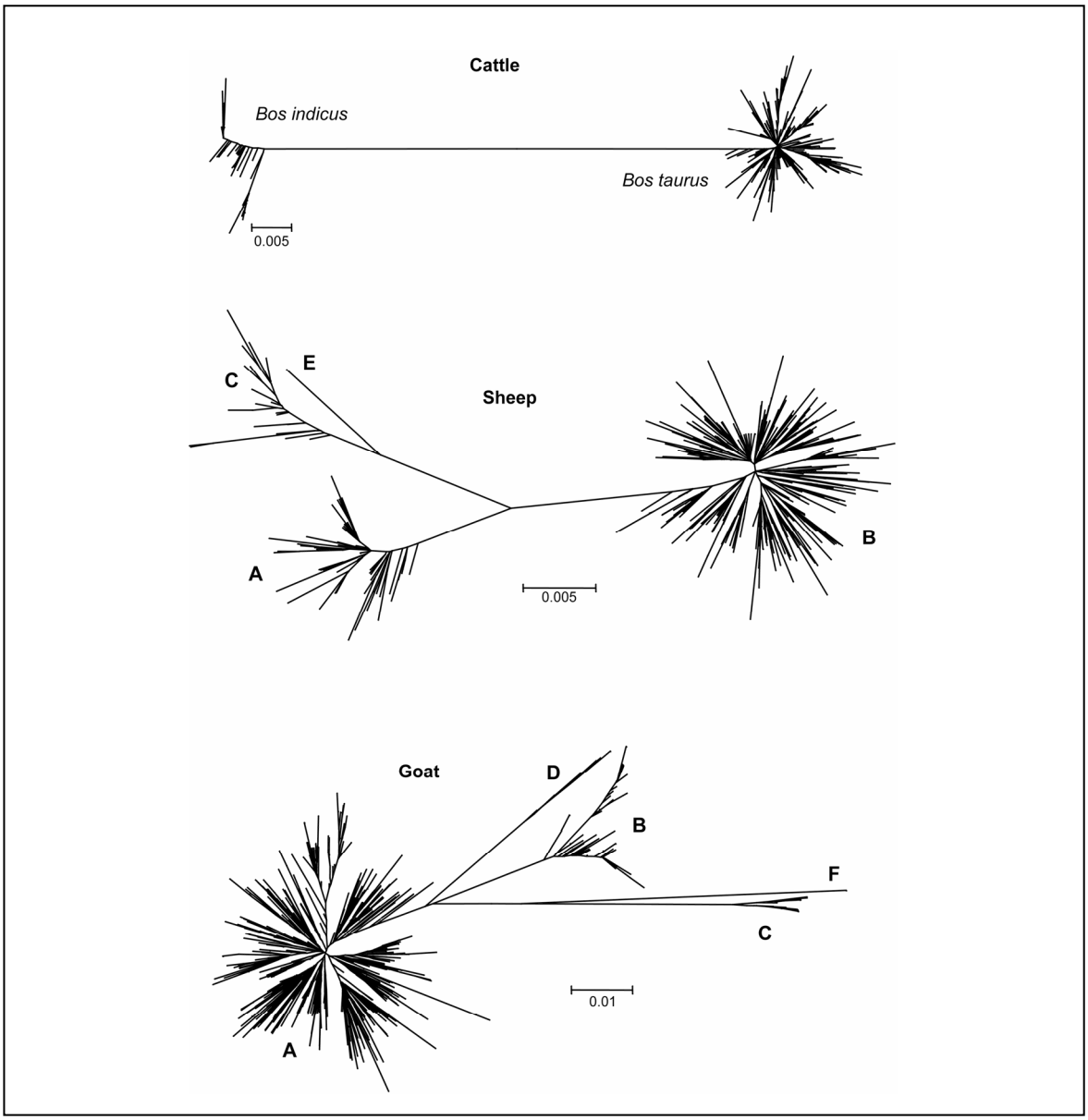

Figure 5.1. Unrooted neighbor-joining trees showing the mtDNA polymorphism of cattle, sheep, and goats. The phylogenetic analyses were conducted using MEGA version 3.1, Kumar *et al.* 2004, with control region sequences. A total of 744 sequences from Loftus *et al.* 1994, Bradley *et al.*1996, and Troy *et al.* 2001 were used for cattle. A total of 640 sequences from Wood & Phua 1996, Hiendleder *et al.* 1998, Guo *et al.* 2005, Pedrosa *et al.* 2005, Meadows *et al.* 2006, and Tapio *et al.* 2006 were used for sheep. A total of 1813 sequences from Luikart *et al.* 2001, Sultana *et al.* 2003, Joshi *et al.* 2004, Azor *et al.* 2005, Chen *et al.* 2005, Odahara *et al.* 2005, Pereira *et al.* 2005, Li *et al.* 2006, Sardina *et al.* 2006, and Liu *et al.* 2007 were used for goats. The letters A, B, C, etc. in the trees for sheep and goats represent the different mtDNA haplogroups described in the literature.

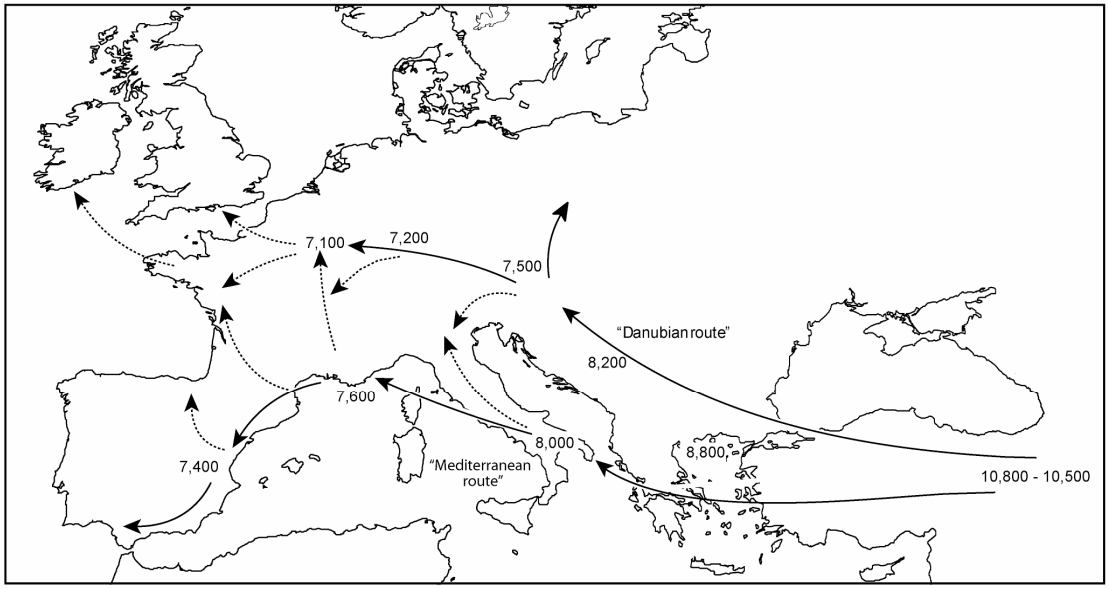

Figure 5.2. The two main initial advancements of the Neolithic culture into Europe (from Fernàndez *et al.* 2006). The dates on the map are calibrated radiocarbon date-derived BP, and correspond to the arrival of agriculture in the corresponding region.

The threats on highly productive breeds

Fragmentation into discrete breeds

About 10000 years ago, farmers started controlling the reproduction of their animals, by favouring the reproduction of animals with preferred phenotypes, and using males either from their own farm, or from another farm located in the same area. As a consequence, farm animals slowly became locally adapted. About two hundred years ago, the situation started to dramatically change. Stronger selection pressures were applied to local populations followed by standardization of the desired conformation and performance. The first cattle herd book was published in Britain in 1822 (Epstein & Mason 1984). This led to the concept of breed. All animals from the same breed began to exhibit the same phenotypic characteristics, and reproduction among different phenotypes (i.e. among different breeds) was seriously reduced. A few decades ago, selection pressures were increased again in order to further improve productivity. To summarize, farm animals underwent relatively low selection pressures during about 98% of their

common history with humans, and later their populations were suddenly fragmented into many well-defined breeds, with high selection constraints.

Effects of artificial insemination and other reproductive technologies

Artificial insemination offers the possibility of easily obtaining thousands of progeny from a single sire, permitting the dissemination of valuable genes (Vishwanath 2003). It is widely used in cattle, particularly in dairy farms, and is the main method of reproduction in many breeds in the developed world, while in sheep and goats it is limited to a few highly productive breeds. This has greatly sped up the rate of genetic change of livestock populations by increasing the selection pressure and the reliability of sire breeding values, estimated from the performance of a large number of relatives. "Improved" germplasm has flooded almost every market, displacing locally adapted populations and inducing the loss of many genetic variants.

The effect of artificial insemination on effective population size is sometimes striking (Table 5.2). For example, *Ne* is as low as 46 in French Holstein, a breed that counts 2.5 million animals across France (Boichard *et al.* 1996). An even more extreme result was found in Japan, where the Japanese Black cattle had a *Ne* of 17.2 in between 1993 and 1997, despite a census size of 0.53 million reproductive cows (Nomura *et al.* 2001). A reduction in effective population size has also been documented in sheep (Maiwashe & Blackburn 2004; Tapio *et al.* 2005), and is probably occurring in goat breeds where artificial insemination has been implemented. Surprisingly, rather high levels of genetic diversity at the nuclear DNA level still appear to exist in the Holstein cattle population, with observed heterozygosity above 0.6 (0.67 in Maudet *et al.* 2002; 0.61 in Vallejo *et al.* 2003). Such a level of heterozygosity is probably highly overestimated due to an ascertainment bias produced by non-random sampling of the genetic markers used (Rogers & Jorde 1996). The microsatellites used were selected among a large set of potential markers, with the goal of maximizing the level of polymorphism and/or heterozygosity. They are probably mainly located in chromosomal regions that have not been under selection. The markers that are either monomorphic or have a low level of polymorphism are simply ignored and are usually not reported in the literature.

Table 5.2. Examples of effective population sizes in some cattle breeds.

Cattle breed	Country	Period	Census population size[a]	Effective population size (Ne)	Reference
Holstein	Denmark	1983-1992	-	68	Sørensen et al. 2005
Holstein	Germany	1999	≈ 2,200,000	52	Koenig & Simianer 2006
Holstein	Denmark	1993-2003	≈ 3,700,000	49	Sørensen et al. 2005
Holstein	France	1988-1991 (?)	≈ 2,500,000	46	Boichard et al. 1996
Holstein	USA	1999	≈ 8,500,000	39	Weigel 2001
Jersey	Denmark	1977-1991	-	87	Sørensen et al. 2005
Jersey	Denmark	1993-2003	≈ 640,000	53	Sørensen et al. 2005
Jersey	USA	1999	≈ 550,000	30	Weigel 2001
Danish red	Denmark	1977-1998	-	157	Sørensen et al. 2005
Danish red	Denmark	2001-2003	≈ 560,000	47	Sørensen et al. 2005
Japanese black	Japan	1986-1990	-	30	Nomura et al. 2001
Japanese black	Japan	1993-1997	≈ 530,000	17	Nomura et al. 2001
Montbéliarde	France	1988-1991 (?)	≈ 700,000	125	Boichard et al. 1996
Abondance	France	1988-1991 (?)	≈ 65,000	106	Boichard et al. 1996
Normande	France	1988-1991 (?)	≈ 800,000	47	Boichard et al. 1996
Tarentaise	France	1988-1991 (?)	≈ 14,000	27	Boichard et al. 1996

[a] The census population sizes were obtained either from the cited references, or from other sources such as breeder associations.

Another problem could be the oversimplification of the models for estimating genetic values, only involving simple linear models that do not consider interactions between factors. As a consequence, they do not take into account dominance and epistasis effects, thus overestimating the genetic value of heterozygotes which are consequently more likely to be selected for reproduction (Cappuccio *et al.* 2003). Nevertheless, attention needs to be paid to the maintenance of sufficient within breed genetic diversity, to preserve

populations from falling into the extinction vortex (Soulé & Mills 1998) and guarantee the long-term sustainable exploitation of livestock.

Inbreeding has always been avoided by breeders. Traditional practices included the exchange of parents among herds, culling of parents when daughters became sexually mature or confinement in breeding groups with mating with alternate males. Artificial insemination made these practices unfeasible. Most semen doses in the market arise from related bulls and this information is not easily available to single breeders, so unwanted inbreeding is likely to occur; semen doses are available for a long time after a bull is dead, making an insemination with its descendants more likely; most pedigrees do not go back more than three generations and therefore grouping females according to the common recent ancestry will not prevent mating with a relative male.

Artificial selection always reduces the number of genetic variants passed on to the following generation and with time it leads to the fixation of the desired alleles. The high level of linkage disequilibrium observed in livestock species (Farnir *et al.* 2000; Khatkar *et al.* 2006) may favour additional fixation of rather large chromosome regions flanking genes under intense selection, by the hitch-hiking process (Maynard Smith & Haigh 1974). Also, random sampling of a few parents as with artificial insemination may lead to fixation of genes unlinked to the gene under selection by chance. The selection schemes currently employed in cattle may make the fixation process particularly rapid. In practice, young bulls enter the progeny test scheme on a pedigree index computed by the BLUP-Animal Model (Henderson *et al.* 1959). The index is built by using the genetic value of relatives weighted by their relatedness with the candidate bull. Therefore, young bulls belonging to a family with good records are more likely to be included in the progeny test program. In this way the genetic pool of the group of parents of the next generation is dramatically reduced, even before genetic evaluation. After the progeny test, genetic indexes are computed with the same statistical procedure. Although the contribution of relatives has less weight here since records of the candidate (or that of its daughters) are considered as well, bulls in a "good" family still tend to have better indexes. Consequently, allelic variants are lost in an exponential way by the combination of selection and of preferential choice across families.

Increasing the selection pressure by the use of a lower number of sires per generation results in the reduction of the effective population size (*Ne*, see above) and the increase of inbreeding, which has short-term negative effects on productivity, particularly on reproductive traits. Hence it is not surprising that in highly selected dairy cattle breeds, a

continuous and alarming decrease in fertility has been observed in the last 10 to 20 years in countries in which fertility traits are not sufficiently taken into consideration in the selection objectives (e.g. Lucy 2001). In addition, inbreeding can promote the emergence of new hereditary diseases, such as the "complex vertebral malformation" (Mahler *et al.* 2006), which have strong detrimental economic effects on farms.

Artificial insemination has also dramatically changed the sex ratio, particularly in dairy cattle breeding, since its introduction into current practice in the past century. The ratio has declined from 1 to 10-30 males/females to 1 to several hundred (Rabasa 1950). A very low sex ratio leads to a strong reduction of the effective population size, and thus to inbreeding.

The threats on local breeds with low population sizes

Socio-economic context

The major threats to livestock genetic diversity result from systemic, regional and global economic forces and changing agricultural practices. Intensification of production systems, including the wider availability of vaccines and therapeutics against endemic diseases, promotes the use of higher-production, less well-adapted genotypes. These facts, combined with the progressive abandonment of agriculture in marginal areas and the success of industrial breeding, have led farmers to partially or completely abandon a number of autochthonous breeds. The lack of application of methods for estimating the real economic value of these breeds, beside the value of meat, milk, and wool production, is also partially responsible for this trend (Roosen *et al.* 2005). As a consequence, many locally adapted populations have been greatly reduced, posing the new problems of genetic drift and inbreeding to their ranchers.

Management of small size populations

Data collected within the Econogene EU project on sheep and goat diversity in marginal areas indicates the presence of significant inbreeding in most of the breeds investigated despite the scarce use of reproductive technologies (Cañon *et al.* 2006; Peter *et al.* 2007). This is likely due to poor breeding management of frequently small herds. An insufficient rotation of bucks/rams across farms leads to partial isolation and fragmentation at the farm, and additionally, the breed level. Hence, in addition to

economic issues, and the disinterest of modern youth in agricultural careers, cultural barriers further increase the risk of loss of diversity in livestock species.

Populations with a limited number of individuals are particularly difficult to manage with the aim of maintaining an acceptable level of inbreeding. A strong social/economic network in the past allowed the exchange of parents as a source of "new blood" for restoring diversity within herds. Even during Roman times parents were actively traded and "foreign" parents were highly appreciated (Columella circa 60). Currently, several barriers to live animal trade are imposed to avoid the spread of highly infectious diseases (blue tongue, swine fever, etc.). Breeders therefore orientate their choice towards artificial insemination or parents from a few certified sources, increasing the likelihood of inbreeding. Breeders Associations could provide technical assistance to these breeders, but it is understandable that they pay more attention to high value breeds and large farms than to small size populations. The situation across Europe is however varied, with some non-profit organisations very active in sustaining small populations, such as the Rare Breeds Survival Trust in UK. The Italian Breeders Associations (a quasi non-profit organization) host herd books for smaller populations (e.g. Grigia, Burlina) and provide mating plans that avoid inbreeding. However, even such well-intentioned efforts cannot guarantee the long-term survival of all endangered breeds.

Threats to adaptation

Adaptive traits may be rapidly lost by poorly designed crossbreeding leading to dilution of local genetics by exotic germplasm. Crossbreeding to a more productive breed from elsewhere, most often a high production breed, is widespread and can destroy the specific features of an indigenous breed within a few generations. The case of tripanotolerant livestock breeds in West Africa represents a good example of local adaptation that might be disrupted by crossbreeding (Agyemang 2005). Recovery from such loss of distinctiveness can be extremely difficult, requiring many generations of backcrossing to purebred indigenous animals. In some cases recovery is impossible because no purebred animals remain to allow a backcrossing recovery program (for instance, there are so few pure breed Maremmana cattle remaining today in Central Italy, that even crosses are granted the label of certification of origin). A number of examples exist, particularly in developing countries, where indiscriminate repeated cross-breeding

quickly disrupted generations of natural and anthropic selection for adaptation to harsh environments.

Traits such as resistance to local infectious and parasitic diseases, adaptation to poor forage, homing and gregarious behaviour, which represent key traits for the survival and management of herds in extensive farming, can be rapidly lost and difficult to rescue. An example of this effect can be found in Corsica, where local goats, when crossed to Alpine or Saanen breeds loose their gregarious and homing behaviour and get lost in the mountains where they are raised in free range. Another example is the Red Maasai sheep in Kenya, renowned for its hardiness and disease resistance, especially its resistance to gastrointestinal parasites (Baker et al. 1998). In the mid 1970's a subsidised dissemination program for Dorper rams was established in Kenya. Widespread indiscriminate crossbreeding followed. No instructions were supplied to farmers about how to maintain a continuous crossbreeding program and many farmers continued crossing their flocks to Dorpers, which subsequently proved unsuitable in many production areas (Consultative Group on International Agricultural Research Science Council 2005).

Geographic confinement

When the traditional rearing area is geographically limited, an additional risk is represented by highly contagious infectious diseases that may wipe out an entire population if back-ups do not exist elsewhere. This was the case of the Herdwick sheep breed in UK, almost exterminated recently by the foot and mouth disease epidemics in 2001 (Alderson 2001).

Several methods are proposed for conservation of farm animal genetic resources. They may be *in vitro,* through the cryo-preservation of animal gametes, embryos and tissues or *in vivo*, by conserving animal flocks *ex-situ,* that is outside their place of origin, for example in experimental farms, or *in situ*, that is within their natural environmental and socio-economic context. When the conservation of adaptive traits in a changing environment is the actual aim, *in situ* conservation is the best option.

Conclusion

Domestic animals are currently losing genetic diversity through many mechanisms. First, the highly productive breeds have recently been intensively selected for production

traits, without enough emphasis on the preservation of the overall genetic diversity. Many breeds in developed countries suffer from a very low effective population size despite their total number of individuals. The strong decrease in fertility of the Holstein cattle, as well as the recent emergence of new hereditary diseases, is a sign that inbreeding is becoming a serious threat in the short term. Second, autochthonous breeds in marginal areas are also seriously endangered. Farmers are often obliged to abandon their traditional breeds and to raise more competitive industrial breeds. As a consequence, many locally adapted breeds have already disappeared (Table 5.1). Furthermore, even in less developed countries, the introgression of genes from industrial breeds seriously compromises the long-term persistence of genetic resources in locally well-adapted breeds.

Many parallels can be found in issues related to threats and conservation of domestic and wild animal species. One of the most problematic threats to wild populations is the fragmentation due to human activity (Frankham *et al.* 2002). Habitat fragmentation induces the risk of excessive genetic drift and inbreeding in isolated populations. In domestic species, fragmentation is mainly due to human intervention that blocks gene flow across populations by keeping breeds as separate breeding units. In non-industrial breeds the diffused cultural inability to properly manage small size populations may lead to fragmentation and isolation even at the farm level.

In conservation biology, it is well known that the long-term viability of populations is directly linked to its effective population size. A reduction of the effective population size to below 50 seriously compromises the short-term survival of a wild population. This problem is exacerbated in industrial domestic breeds.

The real value of biodiversity is difficult to assess. This is true for wild species (e.g. Myers 1996), but also for domestic animals. Most of the difficulties in preserving the diversity of domestic animals are due to a short-term evaluation of the economic value that promotes the exclusive use of industrial breeds. Furthermore, preservation of genetic resources in domestic animals does not have the same image for the public as preserving the giant panda or whales. Domestic animals have been selected and modified by humans. They do not bear the same "natural" perception that wild species have for the public, despite being our food. This is a paradox, because our future will undoubtedly be linked to our ability to produce food from domestic animals. The fact that domestic animals are numerous, and that we have full control on their reproduction make it difficult to explain that some breeds are endangered and that we are losing valuable genetic resources.

In light of the current loss of genetic diversity in farm animals, it is extremely important to take measures that promote a sustainable management of these genetic resources. These measures must prioritize the *in situ* preservation of endangered breeds, and selection programs that will restore the genetic diversity in industrial breeds. *Ex situ* conservation is not suitable, as it relaxes the traditional selection pressures and would not allow the preservation of the genetic resources of interest. In the same way, cryo-conservation should only represent a very short-term strategy in case of emergency. The situation is exacerbated by the fact that we do not know which feature will be useful to exploit in the future, and which breed carries this feature today.

Beside the sustainable management of domestic species themselves, it is also extremely important to take care of the wild relatives and of the wild ancestors when they still exist. The wild ancestor of cattle is already extinct, and the closest wild relatives are vulnerable (*Bos frontalis*), endangered (*B. javanicus*), or critically endangered (*B. sauveli*); the putative wild ancestors of sheep and goats are all vulnerable or endangered (according to IUCN classification).

Concerning less productive breeds, the price of their products should take into account their value as storage of unique genetic diversity. The public should be made aware of this before any strategies for the sustainable management of livestock genetic resources are implemented. Therefore, in opposition to the rules of the global market, subsidies should be given to help farmers who contribute to the preservation of genetic resources in marginal or rare breeds. The Doha agreement (World Trade Organisation 2001) took this issue partially into consideration in permitting state subsidies for typical agricultural products. However this decision was only taken because of the marginal volume of this niche in comparison to the overall market.

Although cattle, sheep, and goats cannot be considered as endangered species according to the number of individuals, it is clear that many breeds are highly endangered, and that we are losing genetic resources. In a few decades, we might lose most of the highly valuable genetic resources that humanity has gradually selected over the past 10,000 years. Despite many conservation programs implemented by the FAO, the conservation of many locally adapted breeds opposes the short-term economic profit. Sadly, the erosion of livestock genetic resources is still continuing, and the same observation has also been made for crops (Esquinas-Alcazar 2005).

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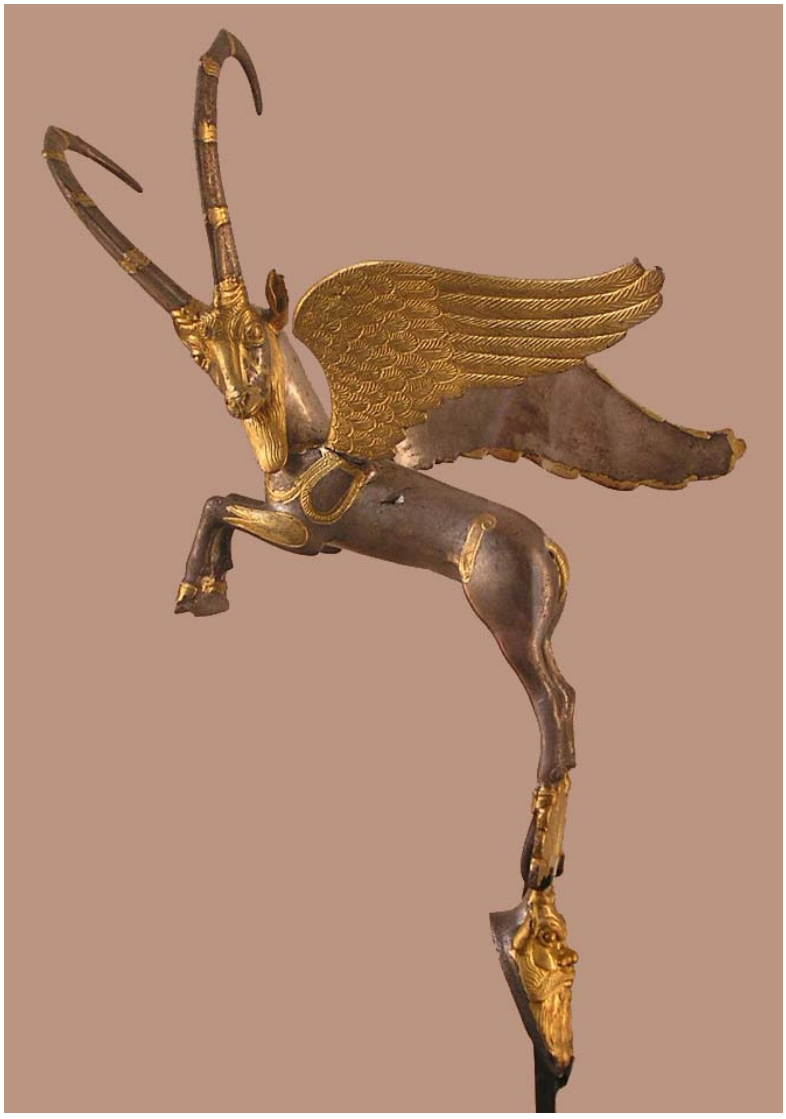
Discussion and Conclusion



Discussion and Conclusion

Since the beginning of the domestication, demographic processes, mutations, genetic drift, local adaptation and selection of breeds have modelled the genetic diversity of domestic populations. Therefore, understanding the population genetics of the domestic animals and of their wild progenitors is an essential prerequisite for the comprehension of the history of domestication, but also for designing conservation genetics programs. This is especially the case for the goat (*Capra hircus*) which was one of the first domesticated ungulates in Fertile Crescent more than 10,000 years ago. Thus, for investigating the evolutionary history and domestication process of this species, we studied the present genetic diversity of goat and of its wild progenitor (*C. aegagrus*).

We first provided a standard method for identifying the current genetic diversity of the goat at a worldwide scale. Thanks to this method and to a large-scale sampling, we were able to establish a clear nomenclature of the goat mtDNA haplogroups and also to assess the pertinence of defining new haplogroups. This survey involved the analysis of 2430 goats mtDNA sequences, including 946 new individuals coming from areas not often studied until now, especially from the Fertile Crescent. The analysis concerned the first hyper-variable fragment of the control region of the mtDNA. This fragment is extremely diverse, as attested by the 1540 haplotypes found out of the 2430 individuals analyzed. We found a large genetic diversity within 5 of the 6 haplogroups defined. However, the diversity is mainly distributed among goat haplogroups within the geographical areas. This weak phylogeographic structure of domestic goat probably results from the ubiquity of the A haplogroup which is strongly dominating (more than 90% of the individuals) and also from the broad distribution of the other haplogroups, which might be related to the human migrations.

But, even with a huge data set (2430 worldwide distributed individuals), it remains difficult to understand the domestication history by the genetic analysis of domestic goats on its own. First, it is difficult to estimate accurately if the demographic expansion came before or after the time of domestication. Second, it remains difficult to identify the domestication centre(s). A gradient of variability is expected to come out from the domestication centre(s), but the low phylogeographic structure of goats does not allow identifying such a pattern. Third, the measurement of the genetic diversity of goat by itself does not allow testing precisely the occurrence of a bottleneck at the time of domestication. The study of bezoars together with goats brought new information that

allows to reconstitute the history of domestication and to fully understand its process. New information came from the locations of wild haplotypes close to domestics, from the comparison between mtDNA and nuclear DNA, and from the comparison of the past demography of the wilds close to domestics compared to other bezoars. These new data, based on an extensive sampling (of 487 modern bezoars from 43 localities covering most of the distribution range) lead to a new two-step scenario for goat domestication. The first step of this scenario corresponds to an early phase of sustainable management of wild herds by humans, coming before the effective domestication. During this pre-domestication phase, some wild flocks of ancient bezoars have undergone a demographic expansion that is still detectable today. The estimate of parameters characterizing the demographic history of the populations from the genetic data shows significantly higher population growth rate at the bezoars bearing haplotypes close to domestic goats. Following pre-domestication, the second step is the effective domestication consisting in the capture of bezoars from the managed herds. The current geographic distribution of bezoars genetically close-to-domestics, encompasses a large area that includes Eastern Anatolia, the whole Zagros, the Central Iranian Plateau, and Northeastern Iran. This is in favour of a large-scale phenomenon, both during the pre-domestictaion and the domestication phases. The domestication of goats has also been a large-scale event at on a genetic point of view. The combined analysis of mtDNA and nuclear DNA polymorphism, for bezoars and domestic goats, demonstrated that a large genetic diversity, corresponding to a large number of mtDNA haplotypes, was captured at the initial step of the effective domestication. The first domesticated goats were able to capture most of the genetic diversity of their wild ancestors and clearly, goats do not fit with the bottleneck domestication paradigm. This scenario is very different from previous models, which call for restricted domestication centres and population bottlenecks.

Perspectives

Fully understanding the evolutionary history of domestic goats would also require the use of nuclear markers. For example, our study confirmed that more than 77 % of the mtDNA variation is found within goat breeds and that nearly 25% of the breeds are composed of at least 2 haplogroups. This is in accordance with the recent fragmentation of local goat populations into discrete breeds about 200 years ago, under strong selection pressures on a few phenotypic traits. This structure can be seen on nuclear markers linked to the selected parts of the genome. This kind of study can be important, especially because of the critical situation of several breeds. Moreover, sequencing many nuclear genes would give a huge amount of information that could lead to estimate accurately the expansion times of bezoars genetically close-to-domestics and goats. Such data would allow testing the occurrence of a pre-domestication phase, which would involve an expansion of bezoars before that of goats.

We also propose the study of ancient goat samples from archaeological sites. Comparing the modern and ancient genetic diversity with different molecular markers can help determining the differentiation between them, and then can lead to identify the causative mutations for phenotypic variation. This will allow to trace gene selection and the spread of economically important alleles during domestication.

Finally, we propose to test if such a large-scale scenario without bottlenecks that we found in goat is also applicable to other domestic animals. Is the absence of bottlenecks during the domestication process a prerequisite for a successful and sustainable domestication?

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Annex

Review of archaeozoological data for the earliest goat domestication based on Marjan Mashkour and Jean-Denis Vigne studies

The earliest archaeozoological evidences of goat domestication are located in Eastern Anatolia (high valleys of the Euphrates and Tigris rivers) and in the Central Zagros mountains (Figure 4.2a). Domestication in the first one occurred five to ten centuries earlier than in the second one (Figure A1). Archaeology is still unable to tell wether the Zagros center of goat domestication has been influenced by the Anatolian center or if it emerged by itself, but it clearly attests important cultural differences between the two regions (Aurenche & Kozlowski 1999; Cauvin 2000), which suggest weak to no cultural exchanges between them before the end of the prepottery Neolithic.

A third, but much younger center for goat domestication, is currently accepted for the eastern footlands of the Balutchistan mountains (Pakistan), at the western boundary of the Lower Indus plain. There, the long stratigraphy of the site Mehrgarh suggested management/domestication of goats as early as the earliest pre-pottery Neolithic phase of the site, ca. 8200-7500 cal. B.P., perhaps a bit before sheep and cattle domestication (Meadow 1979; Meadow 1981; Meadow 1996).

Eastern Anatolian area

In the Eastern Anatolian area, archaeology detected five main steps in the early neolithisation process:

- Natufian-Khiamian periods (14,000-11,000 cal. B.P.): like they did in the Southern Levant (Bar-Yosef & Valla 1991; Valla 2000), some of the human groups of Eastern Anatolia became sedentary, in small villages with round houses made out of stone and mud (Cauvin 2000). These small groups of hunters-gatherers achieved their sedentary lifeway by exploiting a broad spectrum of plants and animals. According to archaeozoological data from sites such as Mureybeth, large game was mainly composed of gazelle (*Gazella subgutturosa*), wild ass (*Equus hemionus*), aurochs (*Bos primigenius*) and, in the highlands, wild sheep (*Ovis orientalis*) and wild goat (*Capra aegagrus*) (Cauvin *et al.* 1998; Gourichon 2004).
- Pre-Pottery Neolithic A (PPNA) and beginning of the early Pre-Pottery Neolithic B (PPNB) periods (11,000-10,500 cal. B.P.): villages are much larger and quadrangular stone houses are organised around large common semi-buried round houses (e. g. Jerf

El Ahmar, Stordeur 2000). Large collective sites with monumental art such as Göbekli (Schmidt 2002; Peters & Schmidt 2004) indicate high level of social organisation. These well-organised villagers practiced predomestic agriculture (Tanno & Willcox 2005). They were however still hunters in a similar way as during the previous period (Peters *et al.* 2005), though Rosenberg et al. (1995) claimed a questionable PPNA sheep, goat and pig management at Hallan Çemi.

- In the course of the early PPNB, ca. 10,500 cal. B.P.: Peters et al. (Peters *et al.* 2005) detected clear changes in the culling strategy and slight decrease of size for both sheep and goat in the earliest layers at Nevalı Çori, a large prepottery village in the upper Euphrates valley. This is the earliest known evidence of goat domestication in the world. It is however possible that predomestic or early domestic goat have existed on other sites of the same area, such as Çayönü, where archaeological data strongly suggested that sheep, goat, pig and cattle domestication begun during the phase dated to ca. 9200-9100 cal. B.P. ("Grill Building" phase) but where Hongo and Meadow (2000) also noticed an increase of the importance of caprines in the diet a bit earlier, ca. 9300-9200 cal. B.P.
- Starting from the end of the early PPNB and during the Middle PPNB (10,300-9600 cal. B.P.), villages get larger and much well organised, sometimes with very well standardised house organisations (i.e. Halula, Molist Montaña 1991). Goat bones were found in numerous of them, out of the natural distribution area of the bezoar, testifying frequent transfers of small flocks of managed / domestic animals. The Cypriot site of Shillourokambos gave both the earliest and the most distant evidence of these transfers: goat has no native ancestor on the island and goat bones have been found in well isolated layers or deep wells dated to 10,400-10,200 cal. B.P. (Vigne *et al.* 2000); however, these goats rapidly ferralized and, between 10,000 and 9,500 cal. B.P., they were mostly hunted by the villagers of Shillourokambos, who however husbanded sheep, pig, and probably cattle (Vigne *et al.* 2003). Approximately at the same date, goat bones are also found at Aswad (near Damascus) in a plain area where wild goats probably did not live; they are interpreted as resulting from the transfer of early domestic goat from Anatolia (Helmer & Gourichon. in press). Starting from ca. 9,800-9,700 cal. B.P., domestic goat are found at two other large Middle PPNB sites out of the original area located in the Middle Euphrates valley: Halula (Saña Seguí 1999) and Abu Hureyra (Legge 1996; Moore *et al.* 2000). It is also present more westerly, at Aşıklı (Central Anatolia; Vigne & Buitenhuis 1999), and more easterly, at Nemrik

(Northern Iraq, Koslowski 1989-99). In these two last sites however, local wild bezoar pre-existed, and the question of weather they were locally domesticated or transferred from other domestication center(s) remains open (orange squares on Figure 4.2a). All through this period, hunting continued to provide the main part of the meat subsistence, which leads Helmer and Vigne (in press) to speak of stock breeding cultivators-hunters. Size decrease and bone modifications due to domestication are undetectable (Shillourokambos; Vigne *et al.* 2000, Vigne *et al.* 2003) or weak (Saña Seguí 1999), so that they can only result from hormonal modifications due to stock keeping (Zohary 1998), without any clear and deliberate oriented human selection (Helmer and Vigne, in press; Vigne, in press).

- Starting from the Late PPNB (ca.9500 cal. B.P.), Neolithic villages still grew in size and organisation. Domesticates then became the most important part of the meat (Helmer & Vigne, in press). In the same time, important morphological modifications appeared, which should result from oriented human selective pressures (Zohary 1998). For goats, this is the time of the first very twisted male and very reduced female horncores (Clutton-Brock 1981).

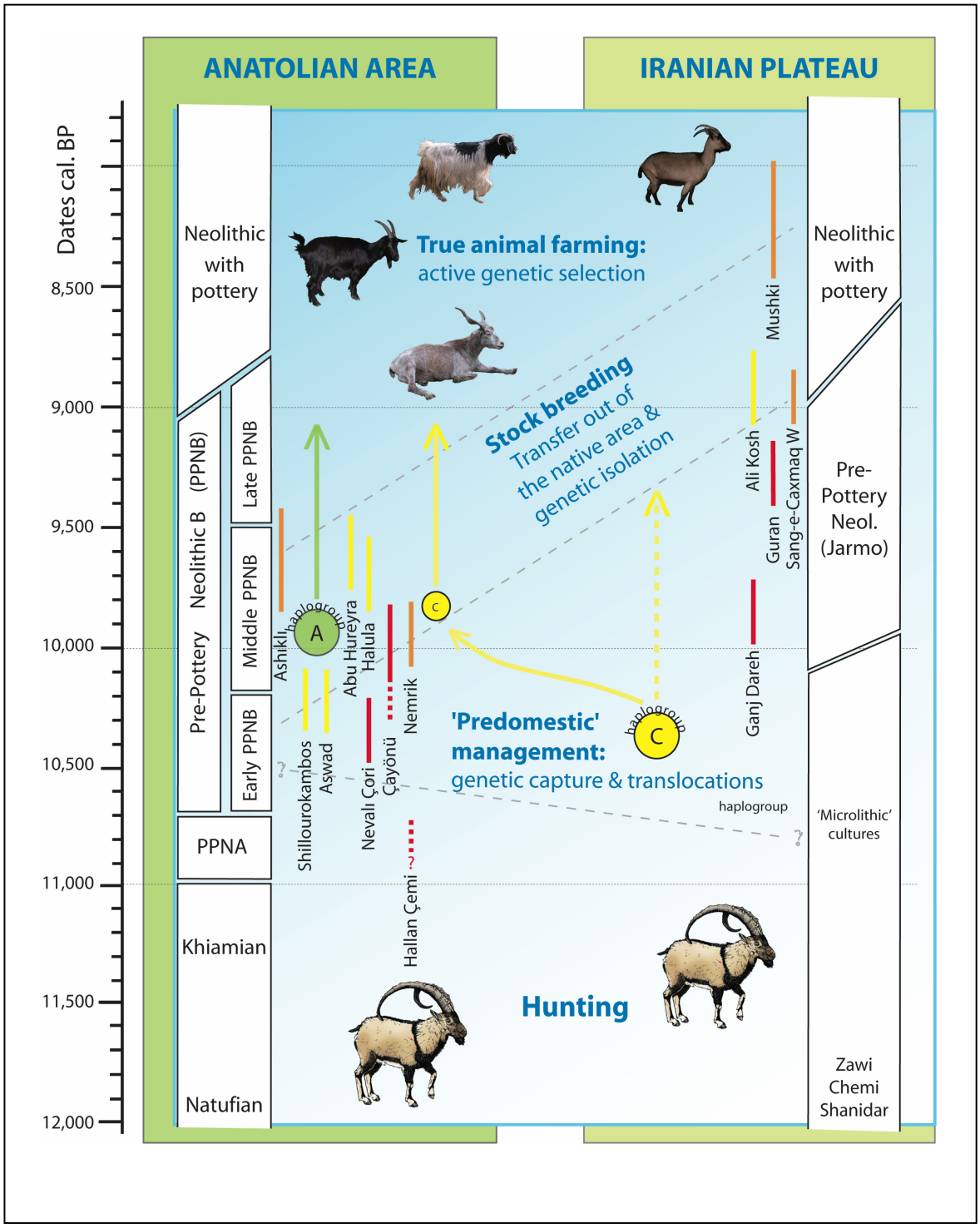

Figure A1. Proposal for a chronological succession of the different phases of goat domestication in the two main cradles of domestication, Eastern Anatolia (left) and Zagros (right). Evidences of effective domestication appeared slightly later in the second one. Vertical segments summarize, for the sites mentioned in Figure 4.2A, the dates of the earliest evidence of local goat domestication (red), the dates of either local domestication or transfer of goats (orange) and the dates of earliest appearance out of the original area of the bezoar (yellow) PPNA: Pre-Pottery Neolithic A , PPNB: Pre-Pottery Neolithic B.

Iranian Plateau

Contrary to Eastern Anatolia, domestication process remains puzzled on the Iranian Plateau, certainly due to the scarcity of archaeozoological studies. The Easter fringe of the Mesopotamian valleys, the Zagros mountains and specifically their central region were suspected as critical places for the history of ungulates domestication (Braidwood 1961; Perkins 1961; Perkins 1964; Hole & Flannery 1969). Early goat domestication, more specifically, was documented by key archaeological sites of the central Zagros, in the Kermanshah region (Bökönyi 1977; Hesse 1978; Uerpmann 1979; Bar-Yosef & Meadow 1995).

However, M. Zeder (Zeder 1999; Zeder 2000; Zeder 2001; Zeder 2005; Zeder *et al.* 2006) recently reinvestigated this question in the Zagros using previously studied archaeozoological Middle Paleolithic to the Neolithic collections, by the way of metrical and demographic studies and of radiocarbon dating. Analyzing modern bezoars and goats of the Zagros, she questioned the correlation between domestication and size decrease, and strengthened the necessity of first relying on demographic profiles for detecting early domestication. She evidenced early domestication without any size modification in the central Zagros, at Ganj Dareh, dating to 9,900-9,700 cal. B.P., then at Tapeh Guran (9,500-9,200 cal. B.P.), two pre-pottery Neolithic sites. She also evidenced early transportation of non-modified domestic goat to the western Zagros lowlands, at Ali Kosh, dating to ca. 9,000 cal. B.P.

More recently, new evidence came from animal bone assemblages in central and southern Zagros (namely Tal-i-Mushki, Fars, 8,000-8,500 cal. B.P., Mashkour *et al*. 2006) and in northeastern Iran, farther to the East. There, in southeastern Alborz, the prepottery Neolithic western mount at Sang-e-Caxmaq (near Shahroud, Masuda 1974) (near Shahroud, Masuda 1974), has been dated to [9059-8711] cal. B.P. (UB-7157: 7997±42 B.P., level 4) and to [9047-8699] cal. B.P. (UB-7158: 7971±42 B.P., level 1; Mashkour & Vigne, unpublished data). Preliminary metric analyses of bones evidenced a small size with reference to early Holocene bezoar at Asiab (dated to 11,000-10,000 cal. B.P.; Zeder 2005), and early goats at Ganj Dareh (Figure A2). We can conclude that the size of the goat at Sang-e-Caxmaq was much smaller as the size of the wild bezoar which lived in this area at that time, because the latter should have themselves been larger than the wild goats of the Zagros (lower altitude and latitude). In addition, the size of the Sang-e-Caxmaq's

goats is very similar to the one of the fully domestic goats at Sarab (dated to 9,000-8,000 cal. B.P.; Zeder 2005). Either due to a very high proportion of adult females or to a strong size decrease with reference to the wild, the small size of goats at Sang-e-Caxmaq clearly evidence domestication. These preliminary data indicate that goat domestication in this area, i.e. ca. 1000 km eastern far from the Zagros center of goat pre-domestication, begun less than 500 years later than in the Zagros area. This is a very early date with reference to Ali Kosh, where domestic goats are attested approximately at the same dates as at Sang-e-Caxmaq, but which is located much nearer from the Zagros domestication center. Whether the birth of goat domestication in the Sang-e-Caxmaq area resulted from a rapid spread of domestic goat from the Zagros toward the East or from an independent domestication event of local bezoars remains an open question for archaeologists.

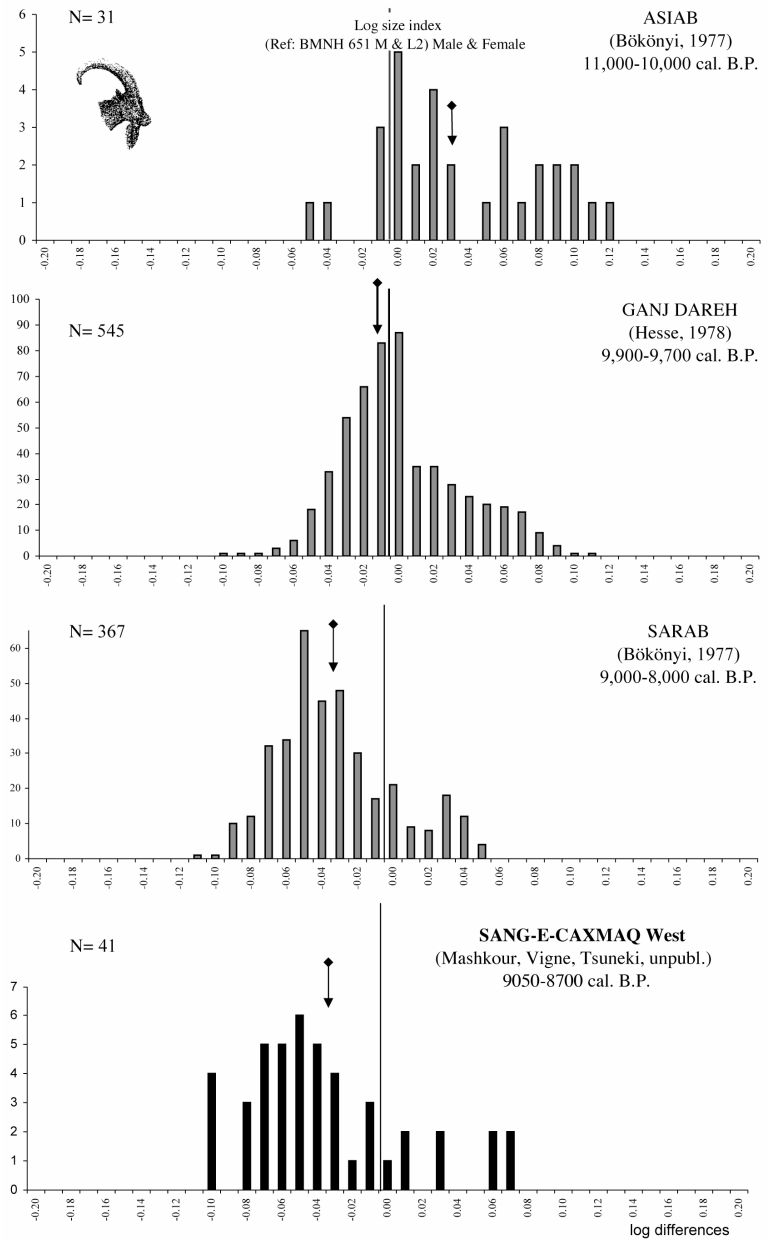

Figure A2. Log size index of the Sang-e-Caxmaq goat compared to those at three archaeological sites in the Central Zagros.

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Résumé

La chèvre (*Capra hircus*) est l'un des premiers ongulés domestiqués il y a plus de 10 000 ans dans le croissant fertile. L'histoire de la domestication a été abordée par l'analyse comparée de la diversité génétique des chèvres domestiques et de celle de son ancêtre sauvage (*Capra aegagrus*). Nous avons tout d'abord mis au point une méthode standard permettant d'établir une nomenclature claire des haplogroupes mitochondriaux, et aussi de définir de nouveaux haplogroupes lorsque cela s'avère pertinent. Cette méthode a été utilisée pour analyser 2430 séquences d'ADN mitochondrial (fragment HV1 de la région de contrôle), incluant 946 nouveaux échantillons issus de régions très peu étudiées jusqu'ici (notamment le Croissant Fertile). Les haplogroupes mitochondriaux présentent une forte diversité génétique qui est essentiellement distribuée entre haplogroupes au sein des régions géographiques. Même avec un jeu de donnée aussi important que celui-ci, il est très difficile de comprendre l'histoire de la domestication en se basant uniquement sur l'analyse des animaux domestiques. L'étude conjointe de la diversité des chèvres et de leurs ancêtres sauvages (les aegagres) ont apporté les informations permettant de reconstituer l'histoire de la domestication. Ces données ont été acquises à partir de 487 aegagres issus de 43 localités recouvrant l'ensemble de l'aire de répartition de l'espèce. Chez les 308 aegagres génétiquement proches des chèvres, nous avons trouvé la signature d'une croissance démographique plus forte que chez les autres aegagres. Cela suggère un nouveau scénario de domestication de la chèvre en deux étapes. La domestication *sensu stricto* aurait été précédée d'une phase de gestion des troupeaux sauvages par l'homme (la pré-domestication). Ces processus se sont déroulés sur une vaste zone comprenant l'Est de l'Anatolie, l'ensemble du Zagros, le Plateau Iranien Central et le Nord Est de l'Iran, où les aegagres génétiquement proches des chèvres sont toujours présents. L'analyse comparée de la diversité nucléaire et mitochondriale chez les chèvres et les aegagres démontre qu'une grande partie de la diversité génétique sauvage a été capturée par les domestiques. Il n'y a donc pas eu de goulot d'étranglement au moment de la domestication de la chèvre. Ce scénario est très différent des modèles précédents qui mettaient en avant des processus à échelle réduite, avec des centres de domestication très localisés et une forte réduction de diversité génétique.

Abstract

The goat (*Capra hircus*) was one of the first domesticated ungulates in Fertile Crescent more than 10,000 years ago. For investigating the evolutionary history and domestication process of this species, we studied its present genetic diversity and that of its wild progenitor, the bezoar (*Capra aegagrus*). Initially, the study of 2430 individuals from all over the old world allowed us to characterize the genetic diversity of domestic goats. This study included 946 new individuals from regions poorly studied until now, mainly the Fertile Crescent. The analysis concerned the HVI segment of the control region of the mtDNA. This large-scale study allowed to establish a clear nomenclature of the goat maternal haplogroups and also to assess the pertinence of defining new haplogroups. We found a large genetic diversity that was mainly distributed among goat haplogroups within geographical areas. However, even with such a huge data set, it remains difficult to understand the domestication history by the genetic analysis of domestic goats on its own. Therefore, to fully understand the domestication process, we compared the polymorphism of 487 modern bezoars from 43 localities covering most of their distribution areas to that of the 2430 goats. Based on mtDNA data, we found that 308 bezoars were close relatives to the six goat mtDNA haplogroups. They showed a higher population growth rate than other bezoars. This data supports a new two-step large-scale domestication scenario for goats. After an early phase of sustainable management of wild herds by humans (pre-domestication phase), the effective domestication took place over a large area. This area included Eastern Anatolia, the whole Zagros, the Central Iranian Plateau and the North-Eastern of Iran where wilds close-to-domestics are still present. The combined analysis of mtDNA and nuclear DNA polymorphisms for bezoars and domestic goats, demonstrated that a large genetic diversity, corresponding to a large number of mtDNA haplotypes, was captured at the initial step of the effective domestication. The first domesticated goats were able to capture most of the genetic diversity of their wild ancestors and clearly, the goats do not fit the bottleneck domestication paradigm. This scenario is very different from previous models, which call for restricted domestication centres and population bottlenecks.