Insights from evolutionary history and population genetics for domestic and wildlife conservation
– cases of the Old World camelids and cheetahs –

Evolutionsgeschichtliche und populationsgenetische Aspekte

für die Erhaltung von Wild- und Haustieren

- ein Beispiel von Altweltkamelen und Geparden -

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Cheetahs sent by the King of Oudh to accompany the Governor General

From a drawing by Emily Eden *c.* 1837. Published in *The End of the Trail* by Divyabhanusinh; Banyan Books, New Delhi, India. (1995, p 87)

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[*] Le Gehilfe – in Léonard le Génie ©; Bob de Groot; ed. Dargaud©

Declarations

I confirm that I have followed the rules of scientific good practice in all respects.

All sampling was done in the respect of the ethics and animal care legislations.
Samples were exported and imported following the legislation defined by Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) with permits in due form. When required, sanitary import authorizations were obtained from the Federal Ministry of Health, Austria (Bundesministerium für Gesundheit).

Contributions

Some results of this monograph thesis have already been submitted to peer-reviewed journals.

1. Phylogeography, genetic structure and population divergence time of cheetahs in Africa and Asia: evidence for long-term geographic isolates (2010) Molecular Ecology, 20 (4): 706–724.

P. Charruau: performance of labwork and analytical studies in the different institutions, interpretation of results, drafting and writing of the manuscript

C. Fernandes, P. Orozco-Terwengel: contribution to the statistical analyses (*e.g.* IMa) and interpretation of results

J. Peters: provided the archaeo-zoological materials and interpretations

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P. Vercammen: sample collection for Northern East Africa

C. Schlötterer: population genetics expertise and discussion of results

A. Kotze: supervision of South African sample collection and molecular analysis in the NZG facility

E.-M. Geigl, T. Grange: supervision ancient DNA analysis in the IJM facility

C. Walzer: conception of the overall project idea, coordination of the sample collection

P.A. Burger: design of the study, performance of analytical work, writing of the manuscript, correspondence with the reviewers

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**both authors contributed equally to the work*

L. Boast: sampling and contribution to the discussion

A. Kotze: design of the project and supervision

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**both authors contributed equally to the work*

A. Mohammad Abdussamad: collection of the Nigerian samples, performance of the labwork.

J. Peters: archaeo-zoological expertise, editing of the manuscript

B. Faye: coordination of the sampling in North Africa and Southern Asia, expertise in camel husbandry and history

O. Hanotte: supervision of the project, contribute to the discussion on domestication, editing of the manuscript

P.A. Burger: design of the study, supervision of the project, writing of the manuscript

ABSTRACT IN ENGLISH

Conservation of biodiversity aspires the protection of the long and multifarious evolutionary heritage that is threatened today by the rapid human demographic development and unsustainable handling of the biological resources. If biodiversity preservation is often associated with ecology research, conservation genetics aims maintaining the today threatened genetic variation. Contrary to the widespread opinion, not only wildlife is concerned by genetic depletion. Indeed, domestication is inclined to increase the livestock headcount and the range of these species, as breeding organizations tend to homogenize the genetic pool in order to spread and maintain traits of economical interest in the global population. However, the preservation of wildlife and domestic diversity for the future will require sustaining plasticity and potential of adaptation to face global climate change and disease emergence. Success of conservation genetics' projects relies on the enhancement of knowledge about the current genetic diversity and its distribution and even more on the investigation of the evolutionary history that has shaped this variation. This thesis aimed to illustrate the two different aspects of conservation genetics; the evolutionary history and population genetic principles were investigated in two wild species, namely the cheetah (*Acinonyx jubatus*) and the wild camel (*Camelus ferus*) as well as in the two domestic forms, dromedary (*Camelus dromedarius*) and Bactrian camel (*Camelus bactrianus*). The results of these conservation genetics projects have already facilitated the elaboration of specific management plans by renowned international organizations.

ABSTRACT IN GERMAN

Mit dem Schutz von Biodiversität streben wir vor allem die Bewahrung unseres weltweiten Evolutionserbes an, das heute von wachsender Bevölkerung und verantwortungslosem Umgang mit Ressourcen immer mehr bedroht wird. Biodiversität wird oft alleinig mit dem Erhalt von ökologischer Vielfalt in Verbindung gebracht wird. Das Fachgebiet „Conservation Gentics" jedoch zielt ganz spezifisch auf die Erhaltung der genetischen Vielfalt in den unterschiedlichen Ökosystemen. Im Gegensatz zu einer weitverbreiteten Annahme sind nicht nur Wildtierarten von genetischer Verarmung bedroht. Tatsächlich steht bei der Domestikation von Haustieren die Züchtung und rasche Verbreitung bevorzugter (Leistungs-) Merkmale im Vordergrund, und damit einhergehend eine Vereinheitlichung des Genpools der globalen Population. Die Bewahrung der genetischen Vielfalt von Wild- und Haustieren ist unbedingt erforderlich für das Potential, sich an wechselnde Umweltbedingungen (Klimaänderung, neue Krankheiten) anzupassen. Somit liegt der Erfolg von Arterhaltungsprojekten in den umfangreichen Erkenntnissen über genetische Diversität und deren Verteilung (Populationsstrukturen), sowie in der Evolutionsgeschichte, die zu dieser modernen Vielfalt geführt hat. Diese PhD Arbeit hat es sich zum Ziel gesetzt, zwei unterschiedliche Aspekte von 'Conservation Genetics' zu beleuchten: die Evolutionsgeschichte und populationsgenetische Prinzipien am Beispiel von zwei Wildtierspezies, Gepard (*Acinonyx jubatus*) und Wildkamel (*Camelus ferus*), sowie der domestizierten Formen, Dromedar (*Camelus dromedarius*) and Trampeltier (*Camelus bactrianus*). Die Ergebnisse dieser PhD Arbeit wurden bereits erfolgreich in spezifischen Managementplänen renommierter Organisationen umgesetzt.

1. Conservation Biology

"Investigate the past and understand the present in order to have effective actions for the future"; this could be one of the credos for conservation. More than ever, species are confronted with changing environments. Their survival is continually challenged and can be ensured only by their capacity to adapt. Genetic variation is the raw material of evolution and consequently of adaptation. Regarding the major anthropogenic extinction crisis we are going through, loss of diversity is of great concern [1]. Conservation can be viewed as an attempt to protect this diversity, which has been produced through long evolutionary processes over millions of years [2]. Three levels of diversity are commonly recognized: (i) the biodiversity, that encompasses all the different habitats, biological communities, and ecological processes, as well as the variation within individual ecosystems; (ii) the species diversity, that considers all the different species and their phylogenetic relationships; and (iii) the genetic diversity, which includes all the genes and their variability in all living individuals and populations [3]. An effective conservation project requires a balanced approach taking into account the diversity at these different levels.

While biodiversity conservation is tied closely to ecology, many of the basic notions required for conservation of species and genetic diversities can be investigated using evolutionary and population genetic approaches [4].

2. When conservation encounters population genetics and evolutionary principles

> *"Whether our concern is the wild relatives of cultivated plants or wild animals, the conservationist is faced with the ultimate sampling problem – how to preserve genetic variability and evolutionary flexibility in the face of diminishing space and with very limited resources. Inevitably we are concerned with the genetics and evolution of small populations and with establishing practical guidelines for the practicing conservation biologist."*
>
> Sir Otto H. Frankel & Michael E. Soulé (1981, p. 31)

2.1. Concept of effective population size

As it unfortunately will be impossible to protect all the threatened biological diversity from extinction, conservation genetics aims to find an optimum between the number of species/individuals and the amount of evolutionary distinctiveness and genetic diversity to preserve [4]. At the species diversity level, projects of conservation prioritization, such as the 'EDGE of Existence' program[1], focus specifically on threatened species that represent a significant amount of unique evolutionary history. At the genetic diversity level, this 'optimization concept' is included in the complex but basic notion of population genetics, namely the effective population size (N_e; [5]).

N_e describes an ideal population which (i) counts as many males as females who are able to reproduce, (ii) experiences random mating between its individuals with an equal contribution of all their gametes to the next generation and (iii) maintains constant the number of breeding individuals from one generation to the next (Wright-Fisher assumptions). If all the above assumptions hold, N_e will equal the census size (N_c; head count size of a population). Generation after generation, this ideal number of individuals will carry as much genetic variation as the actual population [5]. Any forces that cause deviation from the above assumptions will reduce N_e, and consequently, the genetic diversity. In practice, N_c is generally higher that N_e [6], as all natural populations violate at least one of the assumptions. Fluctuations of N_e will then not guarantee the preservation of genetic diversity. Whereas endangered species are characterized by a continual population decline, conservation genetics projects should ideally aim for keeping N_e as large as possible, regardless of the census size.

2.2. Causes and consequences of reduced population size in the context of conservation

The level of genetic variation follows the same dynamic as N_e. Since all populations are prone to evolutionary forces that act on their N_e and shape their genetic diversity, in conservation, genetic drift is of particular relevance. Indeed, genetic drift can be seen as a random sampling of the gametes that contribute to the next generation and consequently

[1] EDGE (Evolutionary Distinct and Globally Endangered) is a program by the Zoological Society of London (ZSL). www.edgeofexistence.org

as a change in allele frequency from one generation to the next [5]. Although we cannot predict the direction of change in allele frequencies (towards loss or fixation) due to stochastic processes, in general, the effect of genetic drift is bigger in smaller populations. Attention to populations with small N_e is therefore of importance in conservation, as the magnitude of the random process of genetic drift is higher and by consequent increases the probability of loss of diversity [7]. Epidemics, drastic changes between the climate periods, over-exploitation, and other anthropogenic factors are often responsible for demographic contractions, and thus, for fluctuations of N_e and of the genetic diversity. Such events are defined as bottlenecks, conveying the idea of an episode during which only few individuals (few alleles) have survived to continue the existence of a population [4]. Founding a new isolated population with a small number of individuals ('founder effect') can also be considered as a severe bottleneck. Inbreeding is probably one of the earliest observations in population genetics ([8] and [9] reviewed by [10]; [11]) and is widely accepted as a major threat for biodiversity. Small populations are particularly sensitive to inbreeding (illustrated and reviewed by [10]) as the probability of mating between related individuals or gametes identical by descent (IBD) increases. This leads to the homogenization of the diversity and a decrease of heterozygosity [5,12]. Via this process, the probability of fixation and expression of deleterious alleles increases and causes a so-called 'inbreeding depression' (reduction of the reproductive success and of the viability of the individual).

Destruction of habitats and ecosystems and establishment of anthropogenic barriers (dams, roads, etc.) are also one of the main concerns in conservation genetics, as population fragmentation has consequences at the genetic level [13]. Compared to a single large panmictic population, meta-population structure presents a smaller N_e in each of its subdivisions (demes), which evolve and respond to drift in separate ways [14,15]. Additionally, in a geographically structured and isolated network of populations, exchange of individuals and random mating are reduced, which results in a diminution of the heterozygosity within each of the demes due to inbreeding.

On the other hand, genetic differentiation between populations can also be the consequences of directional selective processes. In the context of heterogeneous

environmental conditions and pressures, the probability of surviving and passing their alleles to the next generation (fitness) may fluctuate between the individuals (natural selection). The different rates of success of the individuals may results in a directional success of better-adapted genotypes to a particular environment (local adaptation) and consequently in spatial structuring of the genetic diversity. However, in small populations, the effects of natural selection are often blurred by genetic drift (reviewed by [16]).

2.3. Counterbalance of stochastic and deterministic pressures in the view of conservation

Contribution of new alleles contends for the loss of genetic diversity. In practice, it is applied through management tools, such as population reinforcement (the 'import' of new individuals) or establishments of corridors between subpopulations (demes). In population genetics this is encompassed in the concept of migration also called gene flow. Migration is a way to increase population size and to reduce the heterogeneity in the allele frequencies and the kinship coefficient (expected percentage of homozygosity arising from alleles identical by descent). Gene flow thus acts as genetic rescue of the populations from extinction [17]. In a metapopulation system, gene flow brings genetic homogeneity between the different demes and subsequently balances the effect of the genetic drift that tends towards genetic heterogeneity of the subpopulations due to the random process. On the other hand, gene flow may also limit local adaptation [18].

3. Which species are of concern for conservation genetics?

Commonly, conservation evokes the image of endangered wildlife. One of the main authorities in conservation, the International Union for Conservation of Nature and Natural Resources (IUCN), categorizes a species as 'Critically Endangered', 'Endangered' or 'Vulnerable to extinction', when its effective population size falls below 50, 250 and 1000, respectively [19]. These criteria, however, do not apply exclusively for wild and rare species. Loss of genetic diversity equally affects populations that are already under human management. Indeed, if domestication tends to increase the census size of

population and the range of the species, the effective population size might be extremely reduced due to the breeding organization and to the pursuit of increasing productivity [20]. In addition to all the stochastic processes that shape genetic structure of small N_e populations, in the case of domestic species, genetic diversity is extremely sensitive to directional evolutionary forces. In the interest of the breeders, artificial selection acts preferentially on alleles with large phenotypic effects (*e.g.* in dogs; [21]). Because of the economic and/or esthetic interests of this allele, the preferred allele is maintained/fixed in the population by extensive breeding of its (related) carriers, and at the same time increases inbreeding depression. Sustainable livestock management for the future will require maintaining plasticity and the potential for adaptation to face global climate change and disease emergence.

4. 'Made-to-measure' conservation projects

Conservation genetics aims to assist management decisions by providing a profound knowledge of the phylogeography (evolutionary history and biogeography) of the species of interest. Indeed, the lack of information about the contribution of populations to the genetic diversity of a species and about the evolutionary forces that lead to its pattern could cause the failure of a conservation program. Depending on the species, similar actions may have antagonist effects to the anticipated one. For example, a classic conservation approach often aims at connecting populations in order to limit genetic depletion. However, in the case of ecologically mediated population structure, local adaptation might be lost via individual translocation but also may generate an outbreeding depression (reduced fitness of the hybrids between locally adapted and translocated individuals). Conversely, if the fitness of the hybrids is not reduced but increased, this hybrid vigor will, after several generations, lead to the genetic swamping of the unique diversity that was initially the focus of the conservation project. Consequently, decisions about the establishment of gene flow between populations should be measured and take into account the specificity of each population as well as the cost-benefit (cost: outbreeding depression or hybrid vigor; benefit: reduction of inbreeding depression and genetic drift) that such action will have on the population's fitness [22].

5. Challenges and aims of the PhD project

"Investigate the past and understand the present in order to have effective actions for the future."

The challenge of this PhD project is in the investigation of the current genetic diversity distribution and of the evolutionary history of four different species. Regarding the threats that act on the genetic diversity and based on the definition of 'endangered species', principles of conservation genetics were applied to two wild species, namely the cheetah (*Acinonyx jubatus*) and the wild camel (*Camelus ferus*) as well as to two domestic species, the dromedary (*Camelus dromedarius)* and the Bactrian camel (*Camelus bactrianus*). These genetic investigations were done prior to management decisions carried out by international organizations (IUCN, FAO, WWF, Mongolian Academy of Sciences, WCPF, Panthera).

5.1. The African and Asiatic cheetahs

Acinonyx jubatus is the last representative of its genus. As the emblematic sprinter cat of the African and Asiatic continents, the species is well known among conservationists. Since the 1980s the cheetah is mentioned in genetic textbooks as the example of a species that had undergone a severe bottleneck and suffered from inbreeding depression [23,24,25,26,27]. This demographic event was assumed to have taken place at the end of the Pleistocene causing a drastic loss of diversity and consequently a high genetic similarity of the animals [25,28]. Further studies carried out on the Southern African subspecies hypothesized that the observed lack of diversity might be the cause of decreased reproduction, cub survival, and high disease susceptibility [23,26,29]. However, field observations and studies did not corroborate this theory and suggested anthropogenic pressures to be the main cause of the cheetah population decline [30,31,32]. With a census unlikely to exceed 12 000 individuals including the captive population [32,33], the cheetah is registered in the red list of the IUCN as "Vulnerable to extinction". Five cheetah subspecies have been described based on geographic criteria, namely *A. j. jubatus* in Southern Africa, *A. j. raneyi* in the Tanzanian and Kenyan plains, *A. j. soemmeringii* in Northern East Africa, *A. j. heckii* in Western Africa and *A. j. venaticus*

from northern Africa to the Indian subcontinent [34]. Only two of these subspecies, *A. j. venaticus* and *A. j. heckii*, were assigned as “critically endangered”. No genetic investigation had been carried out on these five subspecies, which were already implicitly used as conservation units for management programs [32].

Using the first comprehensive sample set covering four of the five geographic populations (except West Africa, presumably *A. j. heckii*), I aimed to investigate the global genetic diversity of the cheetah. The idea was to validate the subspecies classification with genetic data. I also intended to estimate the time of divergence between these populations. As it was assumed that all species suffered from a drastic bottleneck 10 000 years ago, I expected weak population structure and low genetic diversity.

While it is unclear if Asiatic populations ever reached the density of their African counterparts, historical records report large numbers of cheetahs in Asia until the nineteenth century. During the Middle Ages and early Modern Times, Mughal emperors, in particular Akbar the Great (1556–1605), were known to keep thousands of cheetahs as hunting aids [35,36,37,38]. This practice spread to Europe [39] and Southwest Asia [36,40] until cheetahs became rare, which led to regular imports of individuals from East Africa [35,37] into India during the European colonial era. Until now, only sub-Saharan populations [30,41,42,43,44] and a few Algerian individuals [45] have been investigated using genetic markers. Accordingly, comprehensive data regarding the relationships among all African subspecies and between African and Asiatic cheetah populations were lacking.

In parallel of the investigation of the phylogeography, genetic structure and evolutionary history of cheetahs from most extant and recently extinct populations in Africa and Asia, I gave particular attention to the Asiatic cheetah, as it is critically endangered and restricted to a small remnant population in Iran with possibly a few individuals in Pakistan [46] and Afghanistan [47]. Asiatic cheetahs are known to occur in 13 sites in central and northern Iran where the total population is estimated at 70–110 [46,48]. Widespread poaching of the cheetah’s prey base and persecution by local livestock herders are the main causes of the cheetah’s recent decline and, together with road

accidents, are likely the limiting factors to their recovery today [48,49]. Historical records of extinction in the Arabian Peninsula indicate that this population became progressively and ultimately isolated from any potential link to Africa between approximately 1950 and 1980 [50]. However, it was unclear if demographic and genetic exchange between African and Asiatic cheetahs occurred prior to this recent anthropogenic isolation. To investigate these questions, I aimed to apply palaeogenetic analyses to compare extinct and extant Asiatic cheetahs with the major African populations. The identification of taxonomic and populations units, and understanding their evolutionary relationships, is essential for the conservation of biological diversity [2]. Within species, preservation of genetically distinct local populations maintains evolutionary processes and potential and minimizes extinction risks [51].

A recent study from Castro-Prieto et al. [52] showed that despite low levels of MHC diversity, even so similar to other mammalian species, there is little evidence of genetic detrimental effects to the immunocompetency or reproduction in wild cheetah populations [52,53]. In addition, in the first part of my study I revealed a higher genetic variation among modern-day cheetah populations than previously thought and I identified the investigated populations as long-term geographic isolates. All these new results emphasize once more anthropogenic pressures as causes of cheetah population decline. Botswana hosts the second largest free ranging cheetah population with approximately 1800 individuals [54,55]. Habitat deterioration due to livestock overgrazing is more than ever of concern [55]. Botswana cheetahs are threatened by the reduction of sustainable habitats as animals are widely dispersed with a continuous range across the country, and all the more as they are often found at higher densities outside of protected areas [55,56]. In those areas, cheetahs incur lower competition from larger predators such as lion (*Panthera leo*) and spotted hyena (*Crocuta crocuta*), but are often in conflict with livestock farmers [55]. To enhance the knowledge on the population in the view of conservation management, together with the National Zoological Garden's research team, we combined behavioral and genetic approaches to explore social and genetic groupings of cheetahs in Botswana. On the unrelated animals I quantified patterns of genetic variation and differentiation within and between cheetahs from different locations. As

cheetah movements in Botswana are not restricted by recognizable geographic barriers, I expected little or no genetic sub-structuring among populations.

5.2. The Old World camelids

Member of the Tylopoda order, *Camelidae* family is divided into two tribes: the *Lamini* (llama, alpaca, vicuña, guanaco) exclusively in the New World continents and the *Camelini* (*Camelus sp.*) from the Old World. Although the biological species concept [57] fails to define the species within the genus *Camelus*, the latter contains three interfertile species: *C. domedarius*, the dromedary or one-humped camel, *C. bactrianus*, the Bactrian or two-humped camel, and *C. ferus*[2], the only wild camel species remaining on the Eurasian continent.

5.2.1. Domestic camel biodiversity

Domestic plants and animals represent a paradox in terms of genetic diversity. Their evolutionary history since the divergence from their wild relatives had been entirely under human control. Domestication is increasingly being recognized as a dynamic process over time during which environmental, biological and cultural variables interact and gradually or rapidly alter the behavior and genetics of the animals involved [59,60].
Dromedaries and Bactrian camels were among the last domesticated livestock *circa* 3000-5000 years ago (late Bronze and Iron ages; [61,62]). Both species played a key-role in transport of goods and people along historical trading routes like the mythic silk, incense and salt routes. These two species were then major drivers of the expansion of emblematic ancient civilizations like the Persians and Arabs across arid or semi-desert regions [63]. Today, a number of rural and nomadic societies in Northeastern Africa and in Central and East Asia still depend on the camels in terms of transportation and milk, meat, and wool production [63]. Both species offer unique and sustainable opportunities for livestock production in marginal agro-ecological zones, in a world increasingly under the challenge of climatic changes [64]. Comprehensive studies based on sampling over

[2] the naming of the wild camel follows the ruling by the International commission on Zoology Nomenclature (ICZN; 58) which fixes the first available specific name based on a wild population.

the global range are needed to establish basic knowledge about the genetic diversity and the evolutionary history of these two promising livestock species.

Known as the 'ship of the desert' [63], the dromedary allowed the transportation of people and goods (*e.g.* salt and incense) over long distances connecting the Indian Ocean with the Mediterranean Sea (Fig. 1). In this respect the dromedary has outperformed all other domestic mammals, including the donkey. Furthermore, recent zoo-technical improvements have aroused renewed interest into its productivity traits in a context of advancing desertification and global climatic change. [64].

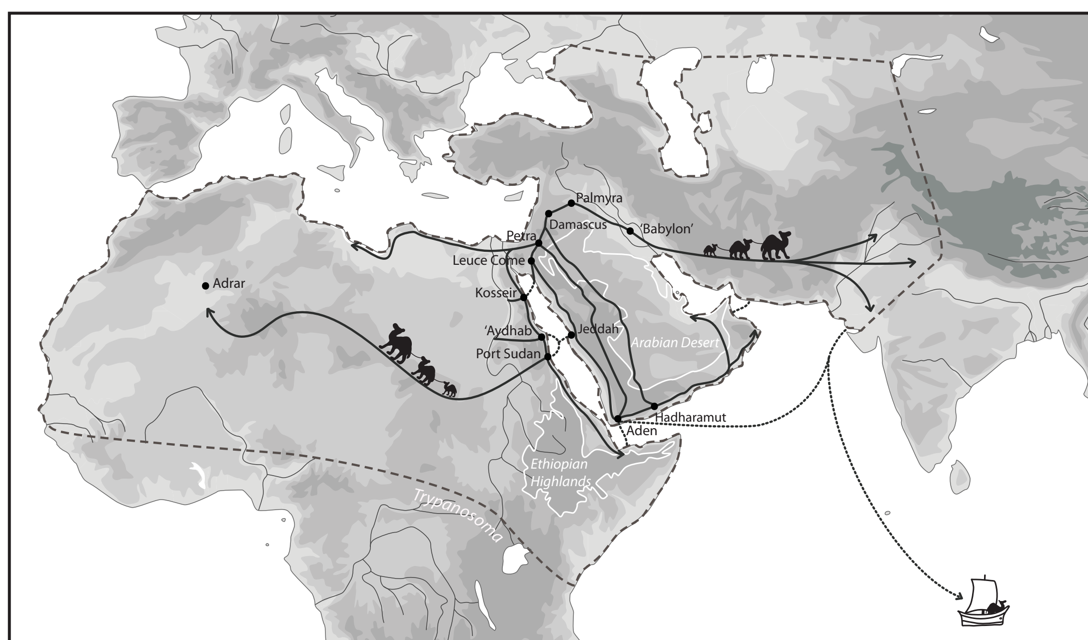

Fig. 1. Historical trading and dromedary caravan routes according to descriptions from Bulliet [63] and Heiss [65]. Solid and dotted lines represent land- and sea-trading roads respectively. The historical repartition of domestic dromedaries was depicted with dashed lines. It is bordered to the south by areas infested with trypanosomia. Geographical barriers as Ethiopian Highlands and Arabian Desert are surrounded by white lines. Physical background map was retrieved from www.freemap.jp. **Land routes** – From Aden to North Arabian Peninsula – the Incense Road: 1 - al tariq Tihama: Tihama road (coastal plains); 2 – al tariq al jibal: highland road; 3 - al tariq al sufla: lower road, via eastern Arabian Desert. 4 - From Hadharamut to the east coast of the Arabian Peninsula. 5 - North Arabian Peninsula to Egypt via the Sinai. 6 - Red Sea costal road from Port Sudan to the Horn of Africa. 7 - Trading route between the Nile river to Myos Hormos (near today's Kosseir) via Leuce Come until Petra and Damascus. 8 - Trading route between the Nile river and 'Aydhab. 9 - Trans-Saharan route connecting major centres of southern Saharan rock art (Darfur (western Sudan); Ennedi and Tibesti (Chad); Tassili and Ahaggar (Algeria)) to Adrar (Algeria) and linking these regions with the upper Nile valley. 10 - Route along the Mediterranean coast. 11 - Silk Road (schematic presentation of a historical network of trading routes). **Sea routes** – a - South Arabian Peninsula (Hadharamut, Aden) to the Horn of Africa ('Land of Punt'). b - Jiddah to 'Aydhab / Port Sudan. c - Gulf of Oman to Iran. d - Spice Route

between South Arabian Peninsula (Aden) and Indian subcontinent. f - export of camels from Pakistan into Australia starting in the 1860s.

In contrast to other livestock species, the domestication of the Old World camelids (*Camelini*) has not been investigated in detail. Genetic exchanges with the wild ancestor were essential during the initial phase of domestication but the practice probably receded with the intensification of breeding to avoid less desirable wild-type behavioral, physiological or morphological traits. The high mitochondrial DNA diversity in ungulate species such as goat, horse and cattle has been interpreted as a sign of recurrent introgression during the early stage of domestication [66,67,68]. The dromedary may be particularly informative in this respect. After the Pleistocene, the ancestor of the domestic one-humped camel was geographically restricted to the coastline of the Arabian Peninsula [69], a rather small geographic area compared to that available to the wild relatives of other domesticates. Archaeological evidence suggests that the domestication process of the dromedary started relatively recently during the Iron Age I Period dating to *c*. 1400 to 900 Before Common Era (BCE) [61,70,71,72]. The transition from hunting to husbandry was deduced from the archaeological context and the occurrence of individuals significantly smaller in size than the wild one-humped camels hunted in mangrove habitats during the Bronze Age. This coincides with a continuous decline of the wild dromedaries, which in contrast to the wild ancestors of most other livestock probably did not survive the start of the Common Era [61,71,72,73]. The dispersion of the domestic dromedary outside the Arabian Peninsula was extensive. They arrived on the African continent and Mesopotamia as early as the Persian Period (525 – 404 BCE) [63,74]. The species was rapidly adopted and fulfilled its role up to the 20th century, with camel caravans including thousands of pack animals [65,75].

From ancestral pastoralism to modern farming practice, the agricultural biodiversity has been shaped by humans, which resulted in a multitude of breeds. Each of them provides the domestic species with its own genetic diversity, while it carries an extremely reduced genetic variation due to the selective pressures and controlled breeding imposed by humans. This uniformity brings valuable subsistence and economic resources that can be negated in case of virulent epizootic or drastic environmental changes [76]. Effective

management of farm resources will therefore require a better understanding of the current genetic diversity distribution of these species and of the evolutionary history that led to this pattern. Unfortunately, the world livestock diversity is currently shrinking [76]. In addition to the loss of unique adaptive traits it is also a part of the species variation that disappears. On the other hand, structuring can also be linked to breed organization. Indeed, livestock are usually characterized by a low genetic diversity within breeds due to the will of the breeders to increase the productivity and maintain certain phenotypic traits. Extensive breeding of the phenotype carriers may lead quickly to a shared and reduced diversity, which would be detected at the genetic level as structuring. Dromedary breeds have been described according to color and body criteria [77], but mainly according to the breeder tribes they belong to. If the traditional husbandry is slowly moving toward dairy and meat breeding systems, the main advantage of the dromedary remains its usage as a multi-purpose livestock. Consequently I did not expect to observe any structuring according to phenotypic traits, as it is unlikely that an artificial selection signal overtook the one from the intensive gene flow.

During my PhD project I aimed to unravel the demographic history of the dromedary across the whole distribution through the analysis of nuclear and mitochondrial diversity. My results shed new light on the ancestral population structure and variation captured during domestication. Together with my collaborators from Nottingham University, we provided a unique insight into the human-mediated dispersion of the species across the Old World. This deepens the general understanding on the distribution of genetic diversity in modern dromedaries, a pre-requisite to the sustainable conservation and utilization of the economic, ecological and cultural values of this unique domesticate

5.2.2. Wild camel diversity

Camelus ferus had been considered as the potential ancestor of the domestic Bactrian camels or even more rarely as feral animals ([62] and *ref. therein*). Today the wild camel survives in only four areas worldwide: the western Gobi Desert (Great Gobi A Strictly Protected Area, south-western Mongolia) Gansu Gobi, Lop Nur and Taklamakan desert (China) [78,79,80]. With a global census of less than 1000 individuals [80], the wild camels are considered as ‘Critically Endangered’, nearing extinction since 2002 [78].

Based on genetic analyses (mitochondrial data) the extant wild camels are unlikely to be the direct ancestors of their domestic relatives. With a divergence estimated about 0.6-0.8 million years ago with its closest relatives [81,82], the current wild camel populations are the last representatives of a unique evolutionary history. This has been considered in the EDGE program[1], which prioritizes the wild camel as the 13th most endangered species, before the emblematic Javan rhinoceros (*Rhinoceros sondaicus* – 14th), giant panda (*Ailuropoda melanoleuca* – 19th) and cheetah (*Acinonyx jubatus* – 355th). In addition to the threat of inbreeding depression and anthropogenic pressures due to habitat destructions and livestock competition, *C. ferus*' uniqueness is menaced by the absence of geographic and reproductive barriers with *C. bactrianus*. To assist management projects in Mongolia and China, using non-invasively collected samples, I investigated the genetic diversity of the wild camels and their level of admixture with their domestic relatives.

5.3. Aims of the PhD project

During this project, for each of the four species I aimed to:

1. investigate the genetic structure and the origin of the genetic variation
2. determine the evolutionary history and phylogeography of the species
3. confirm or deny their taxonomic classification (species, subspecies, breed)
4. assist conservation projects and managements

MATERIAL AND METHODS

1. Sample collection

Working with threatened species involves additional constraints in the sampling. The scarcity of the individuals and the anthropogenic stress from handling promote the usage of non-invasively collected samples. This biological material is mainly collected in the form of hair (*e.g.* collected from the bushes around water points) or feces. Non-invasively collected samples might remain a good solution even for captive species, as the sampling does not require any veterinarian care. Furthermore, in the case of sample export, hair material presents the advantages of being a limited vector for disease and virus and can be cleared of parasites; therefore non-invasively collected hair represents a conservative way of sampling, limiting stress of the animal and disease dispersion. In addition, when a species has been through a local extinction of some of its populations, museum and archaeological collections are potentially precious sources of material.

The modern samples of my study were collected non-invasively (hair and feces), during routine veterinary treatment (blood and saliva), or post mortem (skin biopsie). All samples were exported/imported with the necessary permits in place.

1.1. Cheetah project

For the investigation of the cheetah subspecies, I collected/received a total of 94 cheetah samples from all over the species range. The detail list is given in Table S1. Among this comprehensive sample-set I counted four osseous remains from two putative Asiatic cheetahs. They had been collected from the archaeological sites of Bastam and Tahkt-e Suleyman in the Province of West Azerbaijan, Northwest Iran. Bastam is situated ~50 km north of the city of Khvoy, close to the Turkish border at an altitude of 1300m. First inhabited in Urartian times and destroyed by a fire c. 650 BCE (Before Common Era), Bastam was reoccupied during the Median and Persian period (550–330 BCE) and finally in mediaeval times. Archaeological excavations in the 1970s produced a large faunal assemblage (n = 26 987) [83,84]. From a mediaeval context (9th–15th century CE), a complete Os metatarsale IV was recovered. Originally described as a wolf metatarsal

[83,84], the specimen was re-identified after a thorough comparison with fourth metatarsal bones of modern *Acinonyx jubatus*. The site of Tahkt-e Suleyman (lit. 'Throne of Salomon') lies midway between Urmia and Hamadan, about 30 km north of the town of Takab at an altitude of ~ 2000 m. Archaeological excavations carried out in the 1960s revealed Achaemenid / Persian, Parthian, Sassanid and mediaeval inhabitation, and produced a faunal assemblage of ~ 4000 bones. Kolb in 1972 [85] assigned a mandible, a cervical vertebra, and left and right coxal bones to *A. jubatus*, based on morphological criteria. The presence of post-cranial fragments is strongly indicative of a local origin of the animal(s) and not of an individual whose pelt had been traded into the site. The mandible, vertebra and one coxa from the site of Tahkt-e Suleyman, as well as the metatarsus from Bastam, were subjected to palaeogenetic analysis. All cheetah bones date to the 9th and/or 10th centuries CE. These two samples represented a unique opportunity for the investigation of the Asiatic genetic diversity at the medieval time.

For the study of the social and genetic structures of the Botswana cheetah population, a total of 69 blood samples were collected from wild-caught cheetahs throughout the distribution range in Botswana. Cheetah sampling across Botswana is represented in Fig.2. The sample-set included eight family groups, six coalitions, two orphan groups and 17 lone animals (Table S2). None of the sampled cheetahs had been part of a relocation program prior to this study. In addition, blood samples were collected from four male cheetahs that originated from the wild, but are currently held in captivity (coalition 2).

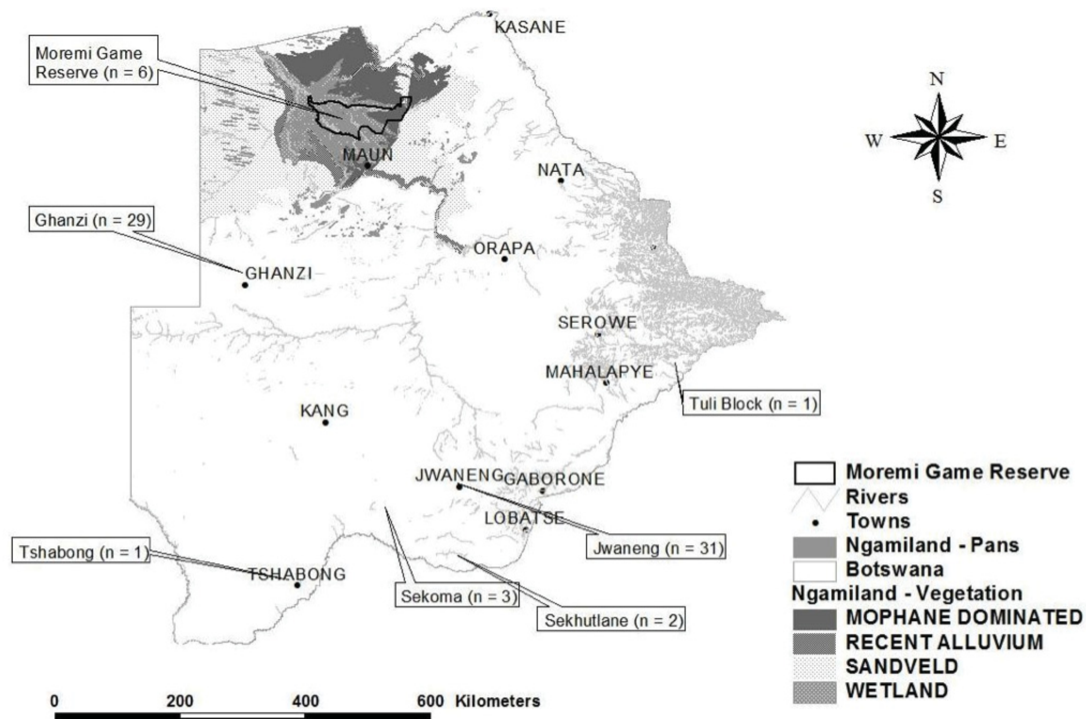

Fig. 2. Cheetah sampling sites across Botswana

1.2. Old World Camelids

For the investigation of the dromedary diversity distribution and the history that led to this pattern I screened dromedaries originating from 20 countries and representative of the species range. Thanks to a collaboration with Nottingham University UK and King Faisal University SA, more than 1000 dromedaries have been sampled and genetically investigated. Based on geographical barriers, *e.g.* the Red Sea, the Arabian Desert and the Ethiopian highlands (Fig. 1), the samples were grouped into five geographical regions: Horn of Africa (HAF: Somalia, Ethiopia, Kenya; n=170), Sahara (SHR: Sudan, Chad, Niger, Algeria, Tunisia, Libya; n=227), North Arabian Peninsula (NAP: Sinai - Egypt, Jordan, Syria, northern Saudi Arabia; n=331), South Arabian Peninsula (SAP: southern Saudi Arabia, Yemen, Oman, United Arab Emirates; n=170), and Southern Asia (SAS: Iran, Pakistan, India, Australia; n=150). From the 1860s to the 1920s about 20 000 camels were imported to Australia from north-west regions of the Indian subcontinent [64,86]. For this reason, and as confirmed by my population structure analysis, I included Australian dromedaries with the Southern Asia population. The complete list of samples is given in Table S3.

To determine the existence of hybrids in the extant *Camelus ferus*, two out of the three remaining wild camel populations in Mongolia (Gobi Strictly Protected Area “A”) and China (Xinjiang Lop Nur Wild Camel National Nature Reserve) were sampled (Fig. 3). I proceeded successfully 55 Mongolian and 25 Chinese samples. In order to compare their genetic profiles with the ones obtained from their domestic relatives, I got access to more than 160 Bactrian camel samples from Iran, Kazakhstan, Mongolia, China and European zoos.

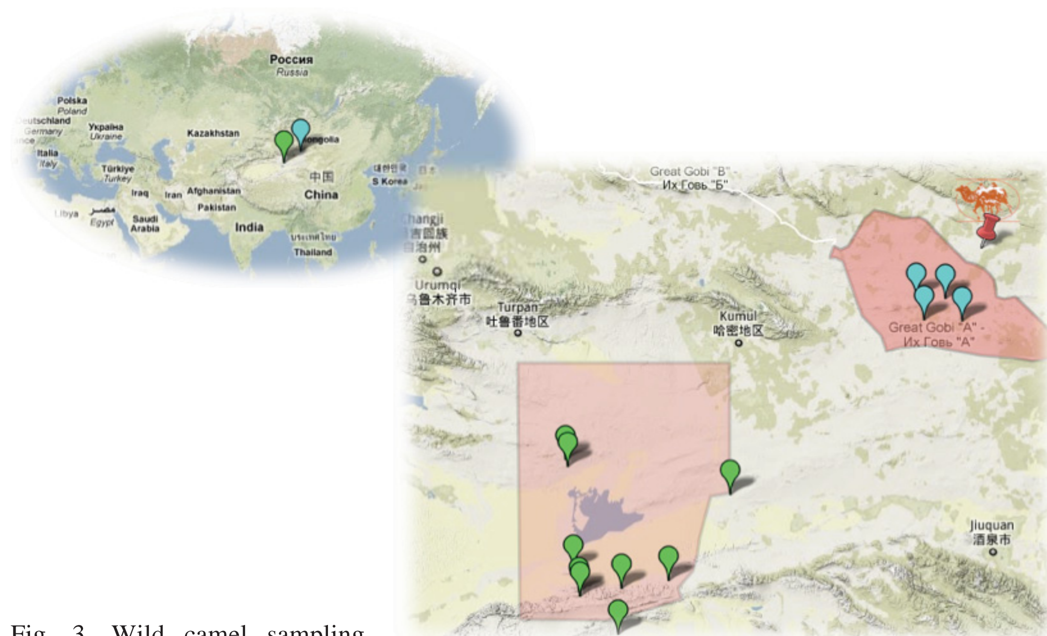

Fig. 3. Wild camel sampling sites with two of the three remaining populations. Gobi Strictly Protected Area “A” sample locations are marked in turquoise and Xinjiang Lop Nur are marked with green tags. The red pin indicates the breeding centre of Zakhing Us, where semi-captive wild camels are kept during mating season. The Mongolian and Chinese national reserves and protected areas where wild camels occurred are shaded in red. © Google Map © 2011.

2. DNA extraction

2.1. Modern DNA

Genomic DNA was extracted from blood and saliva stored on FTA® cards (Whatman) at room temperature, EDTA blood and hair samples. DNA extraction from the biological material stored on FTA cards were carried out with FTA® Purification

Reagent (Whatman) following manufacturer's instructions. Hair samples were digested with a modified lysis buffer [87] and DNA extractions were proceeded using DNeasy Tissue Kit (Qiagen). Genomic DNA was isolated from EDTA blood and tissue with the DNeasy Tissue Kit (Qiagen) and the NucleoSpin®-Tissue Kit (Macherey-Nagel) according to the manufacturers protocols. Faeces were processed, following a two-step storage protocol [88], with the QIAamp DNA Stool Mini Kit (Qiagen). Negative controls were performed in every set of extractions.

2.2. Historical and ancient DNA

Hides and skeletons from museum collections might contain DNA of sufficient quality and therefore give access to a currently extinct diversity. This is also the case with archaeo-zoological remains; in ideal environmental conditions, DNA can be preserved in bone matrix over several thousand years and reveals ancestral diversity information. However non-invasive, museum and archaeo-zoological sampling are greatly subjected to DNA degradation due to the presence of degrading enzymes, including nuclease in some tissue or bone mineralization. The preservation of the samples in non-adapted pH environments, the usage of tanning chemicals, and exposure to UV light usually aggravate the DNA degradation.

I performed all the ancient DNA (aDNA) extractions from mediaeval cheetah specimens in highly contained laboratories of the palaeogenetic core facility at the Institute Jacques Monod, Paris. The superficial layer of the small bone fragments was removed and samples were ground to a fine powder in a freezer mill (Freezer Mill-6750; Spex Certiprep). The bone powder (180 mg) was incubated (37 °C; 48 h) in extraction buffer (0.5 M EDTA pH 8.0; 0.25 M sodium phosphate buffer pH 8.0; 1 mM ß-Mercapto-ethanol). The extract was purified according to an improved protocol using the QIAquick gel extraction kit (Qiagen). Museum skin pieces were incubated twice (24 h) in TE buffer to remove potential enzyme inhibitors (Johnson et al. 2004). Complete enzyme digestion was carried out in an improved lysis buffer [100 mM Tris–HCl pH 8.0; 100 mM NaCl; 3 mM CaCl2; 2% N-lauroyl-sarcosyl (NLS); 40 mM DTT; 5 mM PTB (N-phenacyl-

thiazolium- bromide [89] in 10 mM phosphate buffer); 340 μg proteinase K] [87]. After 24 h one-eighths of an Inhibitex pill (Qiagen) was added to the samples, which had extensively undergone a tanning process. Maxilloturbinate bone shreds [90] were ground and the bone powder was incubated (56 °C; 48 h) in lysis buffer (0.5 M EDTA pH 8.0; 0.25 M sodium phosphate buffer pH 8.0; 1 mM ß- Mercapto-ethanol; 2% NLS; 340 μg proteinase K). DNA extraction was performed with commercial kits (Qiagen) in the presence of negative controls. I carried out two independent extractions for the mediaeval bones, as well as for the other samples where sufficient material (*i.e.* museum specimen) was available.

3. Marker-selection and DNA amplification

Due to the high copy numbers present in one animal cell, mitochondrial DNA (mtDNA) is more likely to be preserved and consequently captured during PCR in comparison with nuclear DNA (nDNA). MtDNA molecules are therefore the dominant targets for ancient DNA (aDNA) analysis [67,91]. Moreover the availability of mitogenome sequences in public databases (*e.g.* GenBank) allows us to design specific primers, which reduce the risk of cross amplification. In addition to the degradation factors, amplification via PCR can be unsuccessful due to the presence of inhibitors in the genomic DNA extract and/or the rarity of template molecules[3]. In the case of nDNA, the preservation is more problematic. Microsatellite analyses need to be performed with extra attention given to the problem of null-allele and dropout [92,93].

3.1. MtDNA marker

3.1.1. Modern and historical DNA sequencing.

To screen the maternal genetic diversity of the cheetah across its species range, I sequenced a total of 62 modern and 16 historical cheetah PCR products for parts of MT-ND5 [nt 12657–13087; numbering according to GenBank (Accession no. GI:38349475.1)], cytochrome b (MT-CB; nt 15940–16173) and MT-CR without repetitive sequences (nt 16333–16487 and nt 16811–16876) [94], resulting in a 915-bp

[3] ancient DNA extract concentration is often measured in femtogram (10^{-15}g) or picogram (10^{-12}g); shed hair 1-12ng/mL; plugged hair concentration 1-750ng/mL; saliva 5000ng/mL; blood 30,000ng/mL

concatenated mitochondrial fragment. The last 29 bp of the tRNA Leucine ($tRNA^{Leu}$; nt 12628–12656) were analyzed to ensure the correct amplification of a 3-bp indel mutation at the third and fourth codons of MT-ND5. In parallel I sequenced one *Puma concolor* for the same fraction of mtDNA.

I sequenced more than 580 dromedaries for a continuous fragment of mtDNA (867 bp; nt15112 - nt15978; numbering according GenBank NC009849.1) including part of the cytochrome B (Cyt-B, 184 bp), $tRNA^{Thr}$ and $tRNA^{Pro}$ ($tRNA^{(Thr+Pro)}$, 134 bp) and partial control region (CR, 549 bp) until the short tandem repeat. In collaboration with Nottingham University we combined a total of 662 animals from well-informed origin for further analyses.

For inference of potential maternal hybridization, I sequenced the equivalent mtDNA fragment that the dromedary (orthologue region) from my wild and Bactrian camel samples (803 bp; nt15120 - nt15922; numbering according GenBank NC009629.2).

For all the four species, after purification of the PCR products by enzymatic reaction (ExoI-FastAP; Fermentas) and quantification, I performed the sequencing in both directions using MegaBACE 500 sequencer (GE Healthcare) and BigDye chemistry (GE Healthcare).

3.1.2. Quantitative real-time PCR and sequencing of mediaeval cheetah specimens.

I amplified fragments of 139 base pairs (bp), including 14 informative polymorphisms in NADH-dehydrogenase subunit 5 (MT-ND5) and control region (MT-CR) (Table 1), from two mediaeval and 14 highly degraded museum specimens using UNG-coupled quantitative real-time polymerase chain reaction (UQPCR) [95] with the LightCycler® FastStart DNA MasterPLUS SYBR Green I mix (Roche Diagnostics GmbH).

Amplicons	nt	*A. j. venaticus*	*A. j. jubatus*	*A. j. soemmeringii*	North Africa population	*A. j. raineyi*
MT-ND5	12665–12667	ATC	ATC	—	ATC	ATC
	12679	T/C	C	C	C	C
	12698	C	C	**A**	C	C
	12707	A	A	A	**G**	A
MT-CR1	16448	**T**	C	C	C	C
	16454	T	T	T	T	C/T
	16473	T	T	**C**	T	T
	16474	A	G	G	A	G
MT-CR3	16817	T	T	T	C	C/T
	16818	A	A	G/A	A	A
	16831	A	A	A	A	G/A
	16854	A	A	A	A	G/A

Table 1. Informative sites screened in the 139-bp mtDNA concatenated fragment. The sites were deducted from the sequencing of modern cheetahs for the long mtDNA fragment. nt: nucleotide position (GenBank Accession no. GI:38349475.1); MT-ND5: mitochondrial NADH-dehydrogenase subunit 5; MT-CR: mitochondrial control region. Diagnostic nucleotide polymorphisms are highlighted in bold. *A. j. venaticus* (*Acinonyx jubatus venaticus*) refers to the Southwest Asian cheetah population.

Briefly, to minimize carry-over contamination, I replaced dTTP by dUTP in the PCR mix and performed a digestion with uracil-N-glycosylase (UNG) prior to each PCR to cleave any contaminating PCR products originating from previous PCR steps. At the same time, this step also cleaves the main diagenetic lesions, deaminated cytosine, thus increasing the reliability of the obtained sequences. Amplifications were carried out in individual glass capillaries. I performed quantification of initial target molecules for each PCR using a titration curve established with a homologous reference (DNA from a Namibian lineage specimen, *A. j. jubatus*) according to Pruvost et al. [95,96]. The inhibition of the polymerase by the aDNA extracts was quantified taking into consideration three parameters: (i) delay of the threshold value Ct (crossing point at threshold), (ii) the kinetics of the synthesis of the PCR product, and (iii) the efficiency of the PCR. I adjusted the quantity of aDNA extract amplified by PCR according to the results of the inhibition tests to minimize interference of the inhibitors with the PCR. I characterized of the PCR products by analyzing the fusion temperature (Tm) using the Lightcycler® and via electrophoresis in a 10% polyacrylamide gel. I performed multiple PCR amplifications on each independent extract. PCR products of the expected Tm and size in the gel were purified using the QIAquick PCR purification kit (Qiagen) and sequenced in both directions by Eurofins MWG GmbH (Ebersberg, Germany). For each ancient sample I performed two independent extractions separated in time. I amplified each extract using

several primers and obtained each PCR product at least twice. I compared all the obtained sequences to the reference mitogenome of *Acinonyx jubatus* [Accession number GI:38349475.1]. The same haplotypic sequences were obtained from the two different bones (mandible and vertebra) from Tahkt-e Suleyman indicating that they likely belonged to one individual, a result that is not contradicting the palaeontological determination.

3.2. Nuclear microsatellite markers

Cheetah genotypes were obtained from 60 modern and seven historical samples at 20 microsatellite loci (FCA005, FCA008, FCA014, FCA026, FCA069, FCA078, FCA085, FCA096, FCA097, FCA105, FCA126, FCA133, FCA171, FCA212, FCA214, FCA220, FCA224, FCA230, FCA247, FCA310) developed in *Felis catus* [97] and tested on cheetahs [30,43,98]. I performed the Southern African sample analyses at the Centre for Conservation Science of the National Zoological Gardens in Pretoria using an ABI 3130 sequencer (Applied Biosystems Inc.). I determined the genotypes of all other samples with the MegaBACE 500 at the Vetmeduni, Vienna. At least three independent genotype results were produced for each locus and each individual. Two defined standard individuals were run in each genotyping series. Electropherograms were evaluated using the softwares GeneMapper v3.1 (Applied Biosystems) and MegaBACE Genetic Profiler v2.2 (GE Healthcare), respectively. Results from the loci FCA078 and FCA096 were removed because of the insufficient quality of the electropherograms despite multiple reiterations.

Botswana individual profiles were obtained for a subset of 14 microsatellite loci (FCA005, FCA008, FCA014, FCA026, FCA069, FCA085, FCA096, FCA097, FCA105, FCA126, FCA171, FCA212, FCA214, FCA310). Based on size range and fluorescent dye of the markers, PCR products were pooled and analyzed on an ABI 3130 Genetic Analyzer. At each locus, allele sizes were calculated by comparison with 500-LIZ® (Applied Biosystem Inc.). One standard individual was run in each genotyping series, in

parallel with negative controls. Data were collected and analyzed using GeneScan® 1.2.2-1 and Genotyper® 3.1 (Applied Biosystem Inc.).

Autosomal genotypes were obtained for 970 dromedaries from 18 microsatellite loci selected according to joint Food and Agricultural Organization of the United Nations (FAO) and International Society for Animal Genetics (ISAG) recommendations (CMS09, CMS13, CMS15, CMS17, CMS18, CMS25, CMS50, CMS121 [99]; CVRL01*, CVRL04*, CVRL05*, CVRL06*, CVRL08 (*modified from [100]); LCA66 [101]; VOLP10, VOLP32 [102]; and YWLL44, YWLL59 [103]) [104]. Profiles from CMS17 were not included in the analysis, as this marker developed for Bactrian camel (*C. bactrianus*) was found monomorphic in the 970 genotyped dromedaries. Additional 20 Bactrian camel genotypes were obtained to confirm the absence of introgression between the two species. I performed the genotyping of the samples from AU, BD, DZ, EG, ET, JO, IR, KE, LY, NE, PK, SO, SD, SY, TD, TN, and YE[4] (Table S3) using the MegaBACE 500 sequencer. Additional genotyping was performed in Sheffield University using the ABI 3730 (Applied Biosytems; samples from AE, AU, KE, OM, SO, SD, SA). In each of the genotyping series, in parallel with negative controls, two individuals shared between the two institutions were run as standard. I combined and standardized of both datasets based on an additional overlapping subset of five samples typed in both facilities. Electropherograms were evaluated using GeneMapper 3.7 (Applied Biosystems) and MegaBACE Genetic Profiler 2.2 (GE Healthcare), respectively.

To investigate the genetic diversity of the wild camels and their level of admixture with their domestic relatives, I genotyped successfully 66 Mongolian and 24 Chinese wild camels and more than 160 Bactrian camels with a selection of 19 microsatellite markers (CVRL07 [100], KS01, KS02, KS03, KS04, KS05, KS06, KS07, KS08, KS09, KS10 [105], LCA65 [101], VOLP08, VOLP010, VOLP32, VOLP059 [102], YWLL29, YWLL36, YWLL38 [103]).

[4] Country codes following ISO 3166-Alpha 2

4. Mitochondrial and nuclear DNA data analysis

4.1. Investigation of the genetic variation and structure

4.1.1. At the mitochondrial level

Mitochondrial sequences were aligned with CODONCODE ALIGNER 3.7.1 (Codon Code Corporation). Unique and novel mitochondrial sequenced were deposited in GenBank (Accession nos puma, GU984641; cheetah, GU984642 – GU984735; dromedary, JX946206 – JX946273). A new polymorphism was considered as authentic when it was displayed in at least three independent sequences.

Mitochondrial haplotype (H_d) and nucleotide diversities like π (average number of pairwise differences) [106] and θ_S (based on the number of segregating sites) [107] were computed in ARLEQUIN 3.5 [108] using the best-fit evolutionary models (see § *4.2.1.*) for both global and geographical populations for each of the four species.

To infer the levels of genetic differentiation between different pre-defined geographical populations I performed Analysis of Molecular Variance (AMOVA) and calculated mitochondrial pairwise ϕ_{ST} with ARLEQUIN 3.5. Mitochondrial pairwise genetic distances can be graphically represented in non-metric multidimensional scaling (NMDS) plots using the R "vegan" package [109]. Without using any prior information about the location of the samples (without loc-prior), I investigated whether genetic clustering solutions reflected the geographically defined populations. For the different mitochondrial data sets, I applied a Bayesian Analysis for Population Structuring implemented in BAPS 5.2 using the 'clustering of linked loci' model [110]. In this method, the number of populations is treated as unknown parameter and is directly inferred from the data set without defining a prior estimate. I specified prior upper bound values for the number of clusters in the data (*i.e.* 2-10) and performed 5 independent runs for each value. In all iterations the clustering solutions of the individuals were identical.

4.1.2. At the nuclear level

For each of the nuclear loci I estimated the number of alleles (n_A), observed (H_O) and expected (H_E) heterozygosities, deviation from Hardy-Weinberg equilibrium (HWE)

proportions, polymorphic information content (PIC) and null allele frequencies using CERVUS 3.0.3 [111].

For the geographically defined populations, expected and observed heterozygosities (H_E and H_O), total (TNA) and mean number of alleles (MNA) were calculated in MICROSATELLITE TOOLKIT [112]. Average polymorphisms and allele frequencies were estimated with MSAnalyzer 4.05 [113].

To compare allele diversity between populations, I assessed population allelic richness (*Ar*) accounting for differences in sample size with FSTAT 2.9.3.2 [114]. Inbreeding coefficients (F_{IS}) for each population were calculated using GENETIX 4.05.2 [115]. Statistical significance for mean H_E and *Ar* were tested with the Wilcoxon rank-sum test using R version 2.10.1 [109].

An analysis of molecular variance (AMOVA) was performed to determine the proportion of genetic variance explained by the differences within and between the pre-defined populations. AMOVA calculations were performed in ARLEQUIN 3.5 and significance levels were obtained with 10 000 permutations. Nuclear pairwise F_{ST} were estimated in MSAnalyser 4.05 [113], which corrects for multiple testing. They can also be graphically represented in non-metric multidimensional scaling (NMDS) plots.

Without giving any information about the sample origin, two complementary clustering approaches were used to assess genetic differentiation among subspecies/ populations. First, I investigated the population structure at the nuclear level and performed admixture analysis using the Bayesian approach for multi-locus data implemented in BAPS and in STRUCTURE [116]. In BAPS for the microsatellite data I used the model ‘clustering of individuals’. I further performed the admixture analysis based on the results of the mixture clustering of the data using 500 iterations and a number of 1000 reference individuals per population, each with 10 reiterations. In STRUCTURE I used a mixed ancestry admixture model, which assumes that each individual derived its ancestry from 1 to K populations. Individuals were clustered

minimizing departure from Hardy-Weinberg proportions and linkage (gametic) disequilibrium within the K populations. Each population will be characterized by an (unknown) allele frequency for each locus. Structure was run for 10 repetitions of 50 000 iterations each, with a burn-in period of 10 000 iterations. K value inference was conducted from 2 to 15 in order to estimate the true number of populations. BAPS provides automatically the best clustering solution according to the posterior probability (PP). In STRUCTURE I determined the best clustering solution by calculating DeltaK = mean(|L''(K)|)/sd(L(K)) [117] in STRUCTURE HARVESTER [118]. STRUCTURE figures were displayed and edited using DISTRUCT 1.1 [119]. Second, I estimated the degree of population structure applying the multidimensional factorial correspondence analysis (FCA) in GENETIX. The approach portrays the relationship between individuals or populations based on the detection of the best linear combination of allele frequencies. Finally, I examined the evolutionary circumstances of dispersion and gene flow among the five geographically defined populations based on microsatellites and calculated the effective number of migrants (*Nm*) exchanged per generation between two geographic regions (Wright's island model [120]; $Nm = (1-F_{ST})/4F_{ST}$) as implemented in GENETIX.

For the specific question of hybridization between wild and domestic Bactrian camels I tested the significance of the observed admixture (mix ancestry or recent migration) on the wild camel profiles. In STRUCTURE I used the model with prior population information ($g^{(i)}$: geographic sampling location) and set v = 0.001 – 0.05, the probability that an individual is a migrant to the population $g^{(i)}$ or has an immigrant ancestor in the last G = 3 generations.

4.2. Investigation of the evolutionary history

4.2.1. Phylogeny reconstruction

To infer a phylogeny in my four comprehensive species mtDNA data sets, I constructed Median-joining networks using Network 4.5 with adapted settings following the software instructions (transition / transversion ration; maximum of mismatch distribution: ε; Bandelt et al. 1999). Additionally, I used Maximum Likelihood and Bayesian statistical approaches. Both methods required an evolutionary model for the nucleotide substitution.

Selection of the best-fit model to the different sequence sets was done in jModelTest v0.1.1 [121] using Akaike Information Criterion (AIC) with correction for small sample size (AICc) [122]. I applied the ML method implemented in PHYML 2.4.4 [123]. The support of internal branches was evaluated with 1000 nonparametric bootstrap iterations. In addition, I inferred the phylogenetic relationship among mtDNA haplotypes with MRBAYES 3.2.1 [124,125] using two independent Markov Chain Monte Carlo (MCMC) runs for 1.1 millions generations each. Trees were sampled every 1000 generations; the first 25% of these were discarded as burn-in.

To infer the nuclear phylogeny I generated neighbor-joining (NJ) trees based on the proportion of shared alleles between individuals (D_{PS}) with the software PHYLIP 3.69 [126], visualized in FigTree v1.3.1. [127] and edited in Adobe® Illustrator® CS4 14.0.0 (Adobe System Inc.). The D_{PS} [128] was estimated with MSAnalyser 4.05.

4.2.2. Divergence time

The estimation of divergence time requires calibration points that approximate the divergence between an outgroup and the clade of interest; usually these time inferences require the assumption of a constant mutation rate (μ) over time and across taxa. Therefore, I tested the null hypothesis of a constant evolutionary rate with the molecular clock test implemented in TREEPUZZLE 5.2 [129]. I used a data subset composed of one sequence per haplotype to reduce the number of parameters and put as starting tree a ML tree rooted with an outgroup (*Puma concolor* for the cheetah and *C. bactrianus* for the dromedary). For both species, the log-likelihood of the more complex model was not significantly increased with respect to the simpler model (P-value > 0.05), supporting the assumption of a molecular clock [130]. However I noted that the assumption of a constant rate of change among the camelids had been rejected previously [131]. For this reason I performed an additional molecular clock test in PAML 4.6 [132] using a mid-point rooted starting tree obtained from the 68 dromedary haplotypes without outgroup. I used FIGTREE 1.3 [127] to define the mid-point root from a consensus unrooted ML tree built in PHYML. In both approaches I could not reject the molecular-clock hypothesis at a

significance level of 5% (rooted tree: df = 67, $\Delta = 71.30 < \chi^2_{\alpha=0.05} = 87.11$; unrooted tree: df = 66, $\Delta = 57.58 < \chi^2_{\alpha=0.05} = 85.97$).

Failure to reject the molecular clock hypothesis allowed me to estimate the divergence time based on the relationship between genetic distance and time, $D = 2\mu T$.
Previous estimates of the divergence between the one- and two-humped camels gave a rather large time frame of 3 to 8 Mya [131,133]. Computation of D were performed in ARLEQUIN using the net number of nucleotides between populations (D_A) [134] and the coalescent method (tau), which accounts for the effects of bottleneck and unequal sizes of the derived populations [135]. Between the dromedary clade and the Bactrian camel sequence, I measured the genetic distances as $D_A = 268.25$ and tau = 258.08. Assuming that the one- and two-humped camel lineages split 8 Mya, μ ranged from 0.0193 to 0.0186 substitutions per site per million years; with a 3-Mya calibration time, μ varied between 0.0514 and 0.0495 sub/site/Myr. Using BEASTv1.7.2, inference of the divergence time and the changes in the female effective population size (N_e) through time (Bayesian Skyline plot) within the dromedary haplotypic dataset failed. Sampling of the priors revealed the lack of information encompassed in the data and therefore the non-validity of the analysis.

Given an estimated cheetah–puma divergence at 4.92 Ma (95% CI = 3.86– 6.92) [136], the substitution rate was inferred using the formula $d = 2\mu T$, where d is the genetic distance. The 3-bp deletion (nt12665 – nt12667) was considered as a single indel event in all subsequent analysis. For the computation of d_{xy}, I used the software MEGA 4.0 [137], which allows for rate heterogeneity among lineages, and the Tamura–Nei substitution model [138] with $\Gamma = 0.118$ (parameter selected by the AIC with correction for small sample size; AICc) as selected by TREEFINDER [139]. The estimated d_{xy} was 0.567 (SD ± 0.175), which translates into a substitution rate of $5.76 \cdot 10^{-8}$ sub/site/yr (95% CI = $1.57 \cdot 10^{-8}$– $1.19 \cdot 10^{-7}$). I also estimated the divergence times between Asiatic (*A. j. venaticus*) and Southern African (*A. j. jubatus*) cheetahs and between Northern-East (*A. j. soemmeringii*) and Southern African cheetahs using D_A and tau. Additionally, these divergence times were estimated using IMa [140]. This program implements a

coalescent-based isolation with migration model that can be applied to genetic data drawn from a pair of closely related populations or species [141] to infer six demographic parameters [population sizes of the extant as well as the ancestor population, migration rates (m1, m2) per gene in both directions, and time (t) since divergence]. After preliminary runs to optimize settings, four replicate simulations were run. Estimates were generated under the HKY model. Simulations used 10 Markov chains, with 45 chain swap attempts per step, and were run for 20 million steps discarding the first 1 million steps as 'burn-in'. Genealogies were sampled every 100 steps. Convergence of the simulations was assessed by comparison of their marginal parameter distributions across independent replicate runs. Saved genealogies were used to estimate the joint marginal distribution of t (the estimator of population divergence time) from an evenly spaced sample of 200 000 trees. To convert coalescent times to years before present, I used the substitution rate estimated above ($5.76 \cdot 10^{-8}$ sub/site/yr) and a generation time of 6 years [142]. 'Nested models' [140] were also examined and compared to the full six-parameter model using log-likelihood ratio tests. For comparison with previous divergence time estimates between cheetah subspecies based on microsatellite data [98], I estimated the timing of the splits between Asiatic and African subspecies (*A. j. venaticus* and *A. j. jubatus*) and among African cheetahs (*A. j. soemmeringii* and *A. j. jubatus*) using the $(\delta\mu)^2$ genetic distance (measured in MSA) and the equation $(\delta\mu)^2 = 2\mu G$ (μ = mutation rate; G = generations) [143]. I applied two estimates of mutation rate for microsatellite loci in humans ($5.6 \cdot 10^{-4}$ and $2.05 \cdot 10^{-3}$), which were previously used by Driscoll et al. [98], and an additional estimate for the average microsatellite mutation rate in mammals ($2.05 \cdot 10^{-4}$; [144]) that has been employed in several studies on other felid species [145,146,147]. Furthermore, to estimate the divergence times among African populations and between Asiatic and African cheetahs, I used the stepwise-weighted genetic distance (D_{SW}) [148] and the equation from Calabrese et al. [149]: $D_{SW} = \sqrt{(2/\pi)} \cdot \sqrt{(2\beta\tau + 4\beta N_e)} - 4\beta\omega N_e / \sqrt{(8\beta N_e + 1)}$, where π is a constant; β, mutation rate; τ time in generations; N_e, effective population size calculated under the SMM and inferred from the expected heterozygosity [150]. The stepwise weighted genetic distance (D_{SW}) was calculated with Populations 1.2.30 [151].

4.2.3. Past demography

In each of the cheetah populations for which I managed to collect enough nuclear data, I looked for evidence of a decline in their effective population sizes using the program Bottleneck 1.2.0.2 [152]. I performed the evaluation using the stepwise mutation (SMM) and two-phase (TPM) models of microsatellite evolution. The significance of the tests was assessed using Wilcoxon sign-rank test, which is the most appropriate test when fewer than 20 microsatellite loci are used [152].

For the dromedary population I searched for population expansion in the context of domestication in the mitochondrial data and performed neutrality tests in ARLEQUIN, namely mismatch distribution, Tajima's D and Fu's F_S, which has been shown to be especially sensitive to population expansion [153]. Assuming a constant mutation rate, the pairwise differences of a population that underwent sudden expansion are distributed according a Poisson distribution [154]. To test the goodness of fit of a Poisson distribution to the observed pairwise differences between the haplotypes, I compared the empirical log-likelihood values with the ones obtained for 1000 simulated Poisson distributions (with parameter lambda $\lambda_{simulation} = \lambda_{empirical}$). In the cases where the data fit a Poisson distribution, the single parameter of the empirical Poisson distribution, lambda (λ), is an estimate of the rate of mutation (μ) occurring in a period of time (t in generation); consequently, I inferred μ with the formula $\lambda = 2\mu t$. To test for population expansion in the multi-locus nuclear data set I used the Excel Macro program Kgtests [155]. Similar to the mismatch distribution for DNA sequences, the k-test compares the observed allele length distribution at each microsatellite locus with an expected distribution. This distribution will be multimodal in the presence of a constant-sized population but will display a single mode in case of population expansion [156]. The g-test is a statistical comparison of the observed allele size variance with a theoretical length variance under the assumption of constant population size. The k- and g-tests relay on a simple stepwise model and assume no population substructure.

RESULTS

1. Phylogeography, genetic structure and population divergence time of cheetahs in Africa and Asia: evidence for long-term geographic isolates

1.1. Genetic variation and population structure analysis

I screened 94 Asiatic and African cheetahs by combining data from 62 modern, 30 historical and 2 zooarchaeological specimens (Table S1). Three mtDNA regions (MT-ND5, MT-CB, MT-CR; partial sequences), corresponding to a total of 915 bp were sequenced from all modern and 16 well-preserved historical specimens. I identified 29 polymorphic sites and one 3-bp deletion resulting in 18 haplotypes (H_d = 0.909, SD = 0.013; p = 0.00659, SD = 0.00351). The highest numbers of polymorphic sites (n = 7) were detected within cheetahs originating from Southern Africa and East Africa, respectively, whereas Northern-East African and Asiatic cheetahs showed lower amounts of mitochondrial polymorphism (n = 3 and n = 2, respectively). A similar pattern was observed for haplotype (H_d) and nucleotide diversities (π) (Table 2).

	mtDNA (915 bp)				
Population	No. cheetahs (mtDNA/µsat*)	No. haplotypes	No. variable sites	Haplotype diversity (SE)	π (SE)
Total	78/60	18	29 + 1 indel	0.909 (0.013)	0.00659 (0.00352)
S-West Asia	11/8	3	2	0.345 (0.172)	0.00040 (0.00047)
N-East Africa	26/25	3	3	0.551 (0.048)	0.00073 (0.00064)
Southern Africa	29/27	8	7	0.828 (0.046)	0.00197 (0.00130)
East Africa	11/0	3	7	0.636 (0.090)	0.00381 (0.00237)
North Africa	1/0	1	0	—	—
	µsat (18 loci)				
	% Polymorphic loci	Total no. alleles	Average no. allele/locus (SE)	% Private alleles	H_E
	100	145	8.06 (1.39)	31.72	0.766
	88.9	42	2.33 (1.03)	7.14	0.397
	100	107	5.94 (1.70)	14.95	0.674
	100	111	6.17 (1.38)	24.32	0.698
	—	—	—	—	—
	—	—	—	—	—

Table 2. Genetic variation in cheetahs inferred from mitochondrial DNA (mtDNA) and nuclear DNA (µsat) data. *Nuclear genetic variation was assessed only among the extant populations

For the palaeogenetic analyses, I selected three diagnostic regions (139 bp) containing 14 informative sites (Table 1). These sites faithfully recovered the partitioning into haplogroups observed in the 915-bp data set. I successfully amplified these regions in mediaeval A. jubatus specimens from two archaeological sites in Iran, Bastam (metatarsal

bone) and Tahkt-e Suleyman (vertebra, mandible). These samples represent the few cheetah bones hitherto discovered in archaeological excavations in Southwest Asia. In addition, I amplified these diagnostic regions in 14 highly degraded DNA samples originating from countries where cheetahs are now extinct (e.g. India) or close to extinction. All replicates of the sequences retrieved from the independent extracts were identical. I used haplotype network analysis and BAPS to infer the relationships between the different mtDNA haplotypes. In both median-joining networks (Fig. 4b: 139 bp and Fig. 4c: 915 bp), a star-shaped radiation stemming from a Southern African haplogroup corresponding to the subspecies *A. j. jubatus* can be observed. The East African cheetahs, described as *A. j. raineyi*, emerged in two different branches from the central haplotype. Although none of the East African cheetahs shared a common haplotype with the Southern African individuals, one haplotype comprising Tanzanian and Kenyan cheetahs (defined by nt 16817; Fig. 4b) clustered together with Southern African cheetahs in the BAPS analysis [posterior probability (PP) = 1; Fig. 5a]. Another sub-Saharan cheetah haplogroup was defined (Fig 5a) corresponding to the Northern-East African subspecies *A. j. soemmeringii*. I observed a monophyletic clustering for this haplogroup in the ML tree (915 bp) with a bootstrap support of 99% (1000 iterations; not shown). Two more haplogroups were recovered (Fig. 4b) in samples from different parts of a range (North Africa and Southwest Asia) that had previously been considered to harbor the same subspecies *A. j. venaticus* [34,157]. The partitioning of these cheetahs into two distinct clusters was also confirmed by BAPS (Fig. 5a). One of these clusters encompassed animals from Western Sahara, Algeria, Libya and western Egypt (Libyan Desert) [158].

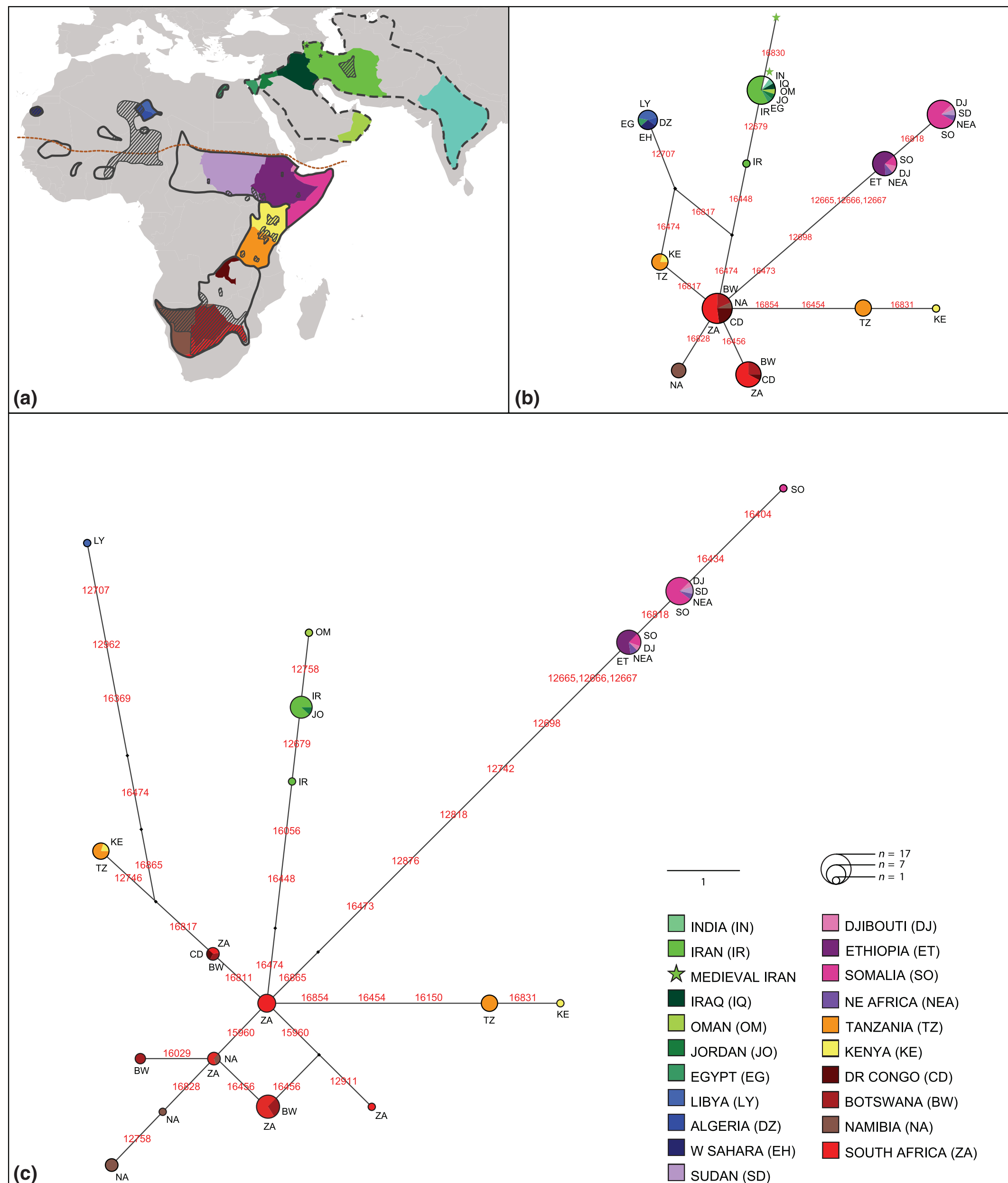

Fig. 4. Median-joining (MJ) networks showing phylogeographic structure in African and Asiatic cheetahs. (a) Geographical distribution of the cheetah subspecies and sample repartition. Solid and dashed lines represent the historical distributions of the African and Asiatic cheetah subspecies, respectively [34,38]. Hatched fields correspond to current cheetah populations [32]. The different color shades refer to the screened cheetah subspecies, *Acinonyx jubatus jubatus* (red), *A. j. raineyi* (yellow), *A. j. soemmeringii* (purple), *A. j. venaticus* (green), and to the North African cheetah population (blue). Stars indicate the archaeological sites of Bastam and Takht-e Suleyman, Iran. The dotted line represents the southern boundary of the Sahara. The background map was retrieved from http://www.planiglobe.com (accessed 14 January 2010). (b) MJ-network based on the 139-bp concatenated mitochondrial sequence alignment of 94 samples. (c) MJ network based on the 915-bp concatenated mitochondrial fragment obtained from 62 modern and 16 historical cheetah samples. The consensus networks of all the shortest trees are shown. The specimens included are colour-coded according to their geographical origins (country codes following ISO 3166-Alpha 2). Small black squares represent median vectors, which correspond to either homoplasies or missing haplotypes. Red

numbers above lines refer to nucleotide mutations separating the haplotypes [numbering according to GenBank (Accession no. GI:38349475.1)]. Positions 12665–12667 correspond to a 3-bp indel in MT-ND5, which we parsimoniously considered as a single evolutionary event. Exact positions of the concatenated mitochondrial fragments are given in Table S4.

The other cluster contained three Asiatic haplotypes represented by the current, historic and mediaeval Iranian cheetah samples as well as by museum specimens from India, Oman, Iraq and Jordan (Fig. 4b). In addition, one sample collected by Theodor von Heuglin in eastern Egypt (Table S1) clustered with this Asiatic haplogroup (Figs 4b and 5a). An exact test of population differentiation based on haplotype frequencies resulted in significant differences ($P < 0.05$) between all African and Asiatic clusters as defined by the Bayesian structure analysis (Fig. 5a). The population pairwise genetic distances (F_{ST}) among these clusters ranged from 0.724 to 0.930 (within Africa) and 0.818–0.958 (Southwest Asia vs. African populations; Table 3). Comparing the F_{ST} values among the African clusters with those calculated between Asiatic and African populations, no significant differences were detected ($P = 0.246$; Wilcoxon rank-sum test corrected for multiple testing).

	S-West Asia	N-East Africa	Southern Africa	East Africa	North Africa
S-West Asia	—	0.295	0.305	na	na
N-East Africa	0.930/0.947	—	0.170	na	na
Southern Africa	0.818/0.689	0.772/0.806	—	na	na
East Africa	0.951/0.951	0.901/0.939	0.724/0.613	—	na
North Africa	0.958/na	0.930/na	0.796/na	0.972/na	—

Table 3. Population pairwise distances based on the concatenated mitochondrial sequence (below the diagonal: F_{ST}; 139 bp; n = 94 / 915 bp; n = 78) and 18 polymorphic microsatellite loci (above the diagonal: F_{ST}; n = 60). All F_{ST} P-values are significant ($P < 0.0001$). na, not applicable. Populations were defined according BAPS and FCA clustering.

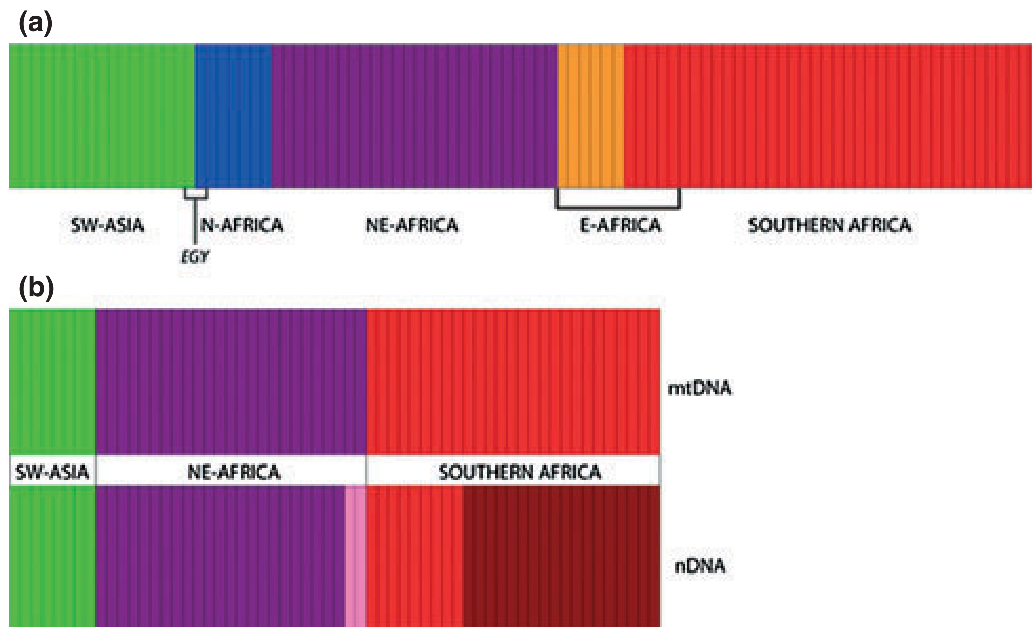

Fig. 5. Bayesian analysis of population structure (BAPS) of African and Asiatic cheetahs. (a) Clustering based on a 139-bp mitochondrial concatenated fragment of 94 cheetahs. Individuals (represented by single bars) are assigned to five distinct clusters (posterior probability, PP = 1). (b) Clustering based on a 915-bp mitochondrial fragment and 18 microsatellite loci using 60 modern cheetahs. Extant cheetahs are assigned to three (PP = 0.999) and five (admixture analysis; PP = 0.999) clusters using mitochondrial (mtDNA) and nuclear DNA (nDNA), respectively. SW-ASIA, Southwest Asia; N-AFRICA, North Africa; EGY, Egypt; NE-AFRICA, Northern- East Africa; E-AFRICA, East Africa; S-AFRICA, Southern Africa.

In addition to the mitochondrial sequences, I analyzed 18 polymorphic microsatellite loci. Using solely modern samples, I assessed the genetic variation among the extant populations according to the clustering solutions with BAPS [mtDNA 915 bp, PP = 1; nuclear DNA (nDNA), PP = 1; Fig. 5b]. The three clusters obtained with mtDNA reflected the geographical distributions of the described subspecies *A. j. jubatus*, *A. j. soemmerringii* and *A. j. venaticus*. At the nuclear level I could define two additional clusters, which represent substructuring within the Southern and Northern-East African subspecies, respectively. I obtained similar clustering results when I visualized the phylogenetic relationship of the individual genotypes in a three-dimensional FCA (Fig. 6).

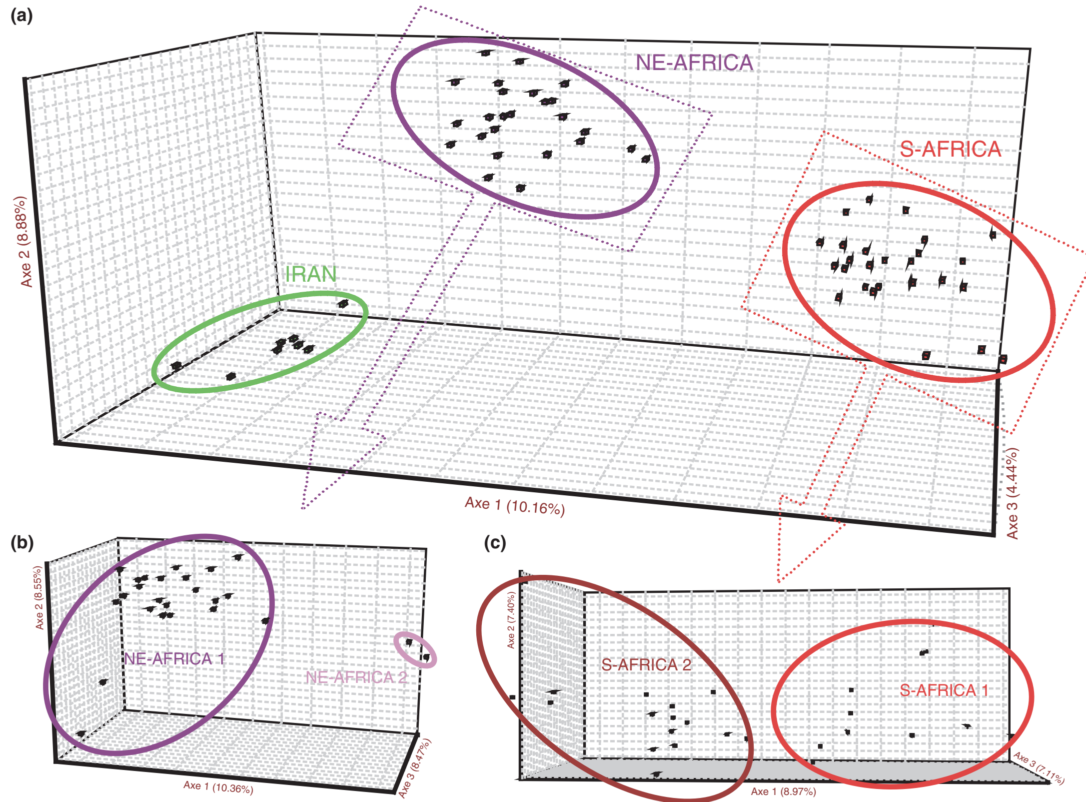

Fig. 6. Three-dimensional factorial correspondence analyses (FCA) of African and Asiatic cheetahs based on 18 microsatellite loci. (a) The population structuring of 60 individuals in three clusters corresponding to their geographical origin is shown. The axes 1–4 explain 27.4% of the variation among the populations. (b, c) FCA graphs considering independently the Southern (n = 27) and Northern-East African (n = 25) cheetah populations. The subclustering within each population reflects the clusters defined with BAPS (Fig. 5b).

The results from the admixture analysis based on 500 simulations from posterior allele frequencies revealed no admixture (all *P*-values = 1; Fig. 5b) and therefore no evidence of past or present gene flow. The Iranian cheetahs (H_E = 0.397) were significantly less variable than the Northern-East (H_E = 0.674) and Southern African (H_E = 0.698) populations (P < 0.001; Wilcoxon rank-sum test corrected for multiple testing). I detected a significant number of loci with heterozygosity excess under the SMM and TPM models, which is consistent with a recent effective population size decline in the Iranian cheetahs. By contrast, no significant signature of a bottleneck was visible in the Southern and Northern-East African populations (Table 4).

	***P*-value (SMM)**	***P*-value (TPM)**
S-West Asia	0.0133	0.0107
N-East Africa	0.8769	0.1733
Southern Africa	0.9700	0.2475

Table 4. Significance of tests for heterozygosity excess assessed using a Wilcoxon sign-rank test under the SMM and TPM model implemented in Bottleneck 1.2.0.2

The population pairwise F_{ST} / R_{ST} values showed significant differentiation between the three populations (P < 0.0001; Tables 3 and 5) and the AMOVA results indicated that 22.7% of the total variation occurred among the different populations / subspecies.

	N-East Africa (n=25)	Southern Africa (n=27)
S-West Asia (n=8)	0.216	0.455
N-East Africa	_-	0.226

Table 5. Population pairwise distances R_{ST} based on 18 polymorphic microsatellite loci. R_{ST} were calculated in ARLEQUIN 3.5. R_{ST} p-values are significant (p < 0.0001). Populations were defined according BAPS and FCA clustering.

In a NJ tree (Fig. 7a), the bootstrap support for the branch assembling all modern Asiatic cheetahs was 100% (100 iterations). As all specimen of the East African subspecies *A. j. raineyi* were collected from museum or non-invasively (Table S1), their DNA qualities were not sufficient to retrieve consistent and reliable information over all loci. However, I could obtain nuclear data for seven historical samples (#9, 10, 11, 19, 48, 89, 90; Table S1). When these samples were added to the NJ tree analysis (Fig. 7b) the branch leading to all Southwest Asian samples, which cluster separately from the African individuals (including Libya), had a bootstrap support of 72%.

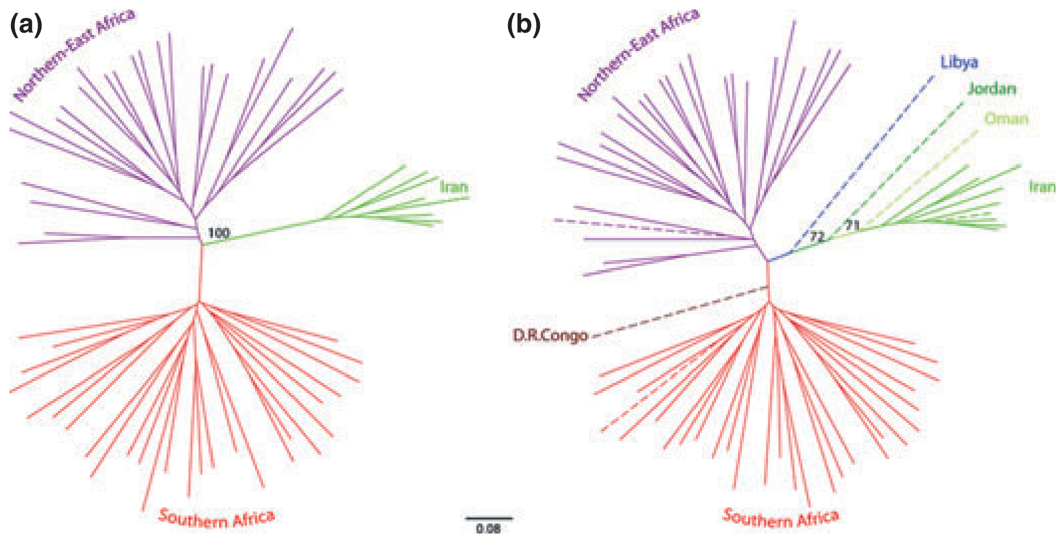

Fig. 7. Neighbor-joining (NJ) trees displaying African and Asiatic cheetahs in independent branches. The NJ trees are based on the proportion of shared alleles (D_{PS}) between individuals using 18 microsatellite loci amplified (a) in 60 modern (b) plus additional seven historical cheetah samples. Modern (solid lines) and historical (dashed lines) samples are color-coded according their geographical origin. Only bootstrap values (100 reiterations) above 70% are displayed.

1.2. Estimation of the divergence time

I estimated the divergence time, first between Asiatic and Southern African cheetahs, which correspond to the central haplogroup in the mtDNA network, and within Africa, between the best-sampled subspecies *A. j. soemmeringii* and *A. j. jubatus*. Based on the mitochondrial 915-bp fragment, the D_A (4.412) between *A. j. venaticus* and *A. j. jubatus* was translated into a population split at 41 900 ya (95% CI = 20 300–153 800). Following Gaggiotti & Excoffier [135], the divergence between these two populations was estimated at 32 170 ya (95% CI = 15 570–118 020). The divergence time between the African subspecies *A. j. soemmeringii* and *A. j. jubatus* was calculated at 66 500 ya (95% CI = 32 200–244 000) and 55 085 ya (95% CI = 26 660–202 100) using D_A (6.996) and the method of Gaggiotti & Excoffier [135], respectively. The demographic modelling with IMa suggested a split between *A. j. venaticus* and *A. j. jubatus* at 44 403 ya (90% HPD = 27 420–379 222) and between *A. j. soemmeringii* and *A. j. jubatus* at 72 296 ya (90% HPD = 43 928–379 317). The upper bound for the credibility interval is not informative, as it critically depends on the assumed prior for the maximum value of t when the curve slowly decreases to zero after the mode of t. The log-likelihood ratio tests did not reject

models with m1 = m2 = 0, which are appropriate for studying the divergence of populations under allopatry [159]. Hence, by setting migration rates to zero, I applied a conventional isolation model [160]. The splits *A. j. venaticus / A. j. jubatus* and *A. j. jubatus* / *A. j. soemmeringii* were then estimated at 42 120 ya (90% HPD = 16 295–83 677) and 66 698 ya (90% HPD = 24 067–117 615), respectively.

Using the microsatellite $(\delta\mu)^2$ and two human microsatellite mutation rates ($2.05 \cdot 10^{-3}$ and $5.6 \cdot 10^{-4}$) employed by Driscoll et al. [98], I estimated the split between *A. j. venaticus* and *A. j. jubatus* at 6700 and 24 700 ya, respectively. Using an average mammalian microsatellite mutation rate ($2.05 \cdot 10^{-4}$; [144]), I estimated this divergence at 67 400 ya. The divergence time between *A. j. soemmeringii* and *A. j. jubatus*, using the fastest (human) microsatellite mutation rate, was 3200 ya but rose to 32 400 ya when applying the average mammalian mutation rate. To compare these estimates with another distance method, I used the stepwise-weighted genetic distance D_{SW}, which is based on the allele frequency differences among populations [148]. Applying again the two human microsatellite mutation rates and the average mammalian mutation rate, and following Calabrese et al. [149], I calculated the divergence time between Iranian and Southern African cheetahs at 4700, 17 300 and 47 200 ya, respectively. The fastest mutation rate translated into a divergence time estimate among the African subspecies *A. j. soemmeringii* and *A. j. jubatus* of 1600 ya whereas it reached the value of 15 600 ya using the average mammalian mutation rate.

2. Genetic diversity and population structure of free-ranging cheetahs in Botswana

Of the 73 samples cheetahs, 32 were unrelated animals according their genetic profile. The subsequent analyses were performed on a subset encompassing only unrelated individuals: 14 cheetahs from Ghanzi, 4 from the Moremi Game reserve, 8 from Jwaneng, 3 from Sekoma and a unique individual for Sekhutlane, Tshabong, and Tuli, respectively (Table S2). None of the loci deviated from Hardy-Weinberg equilibrium proportion. The average expected heterozygosity (H_E) was 0.620 and within the different geographic populations H_E values ranged from 0.549 to 0.653 (Table 6).

Population[a]	No. of unrelated samples	Total no. of alleles	Mean no. of alleles /locus	% of private alleles	Allelic Richness[b]	H_E	H_O
Moremi[c]	4	40	2.86	12.50	2.59	0.5493	0.4524
Ghanzi	14	68	4.86	13.24	3.02	0.6532	0.6085
Jwaneng	8	55	3.93	1.82	2.73	0.5792	0.6492
Sekoma	3	37	2.71	2.70	2.71	0.5691	0.6428
Total	32	78	5.57	20.51	2.91	0.6201	0.5808

Table 6. Heterozygosity values and average number of alleles per locus of four cheetah populations from Botswana[a] based on14 microsatellite loci. [a]Populations from Sekhutlane, Tshabong and Tuli were represented by only one individual each and therefore were not included into the analysis. [b] The allelic richness was calculated based on a minimum of three diploid individuals per population. [c]The Moremi population had five unrelated individuals, however, # C6 was not included in the analysis as only 56% of its genotype profile was complete.

Using STRUCTURE, all animals were assigned to one unique cluster (K=1). This clustering result indicates that all the unrelated cheetahs were theoretically derived from one ancestral population. Supporting evidences was deducted from the AMOVA analysis as 93% of the variation was shared among the different localities. The low genetic distance measured between the two largest sampled populations (Ghanzi *vs* Jwaneng $F_{ST} = 0.035$; $R_{ST} = 0.068$; $p < 0.05$; Table 7) indicated as well a weak sub-structuring of the diversity. Interestingly, the Moremi population appeared as a 'distinct' group compared with the neighboring Ghanzi cheetahs (Fig. 2 and 8; Table 7).

F_{ST} / R_{ST}	Moremi (n=4)	Ghanzi (n=14)	Jwaneng (n=8)	Sekoma (n=3)
Moremi	-	0.079*	0.000	0.052
Ghanzi	0.085*	-	0.068*	0.119*
Jwaneng	0.083*	0.035*	-	0.000
Sekoma	0.033	0.000	0.000	-

Table 7: Genetic distances F_{ST} (below diagonal) and R_{ST} (above diagonal). * Significant values (p-value < 0.05). Populations from Sekhutlane, Tshabong and Tuli were represented by only one individual each and therefore were not included into the analysis.

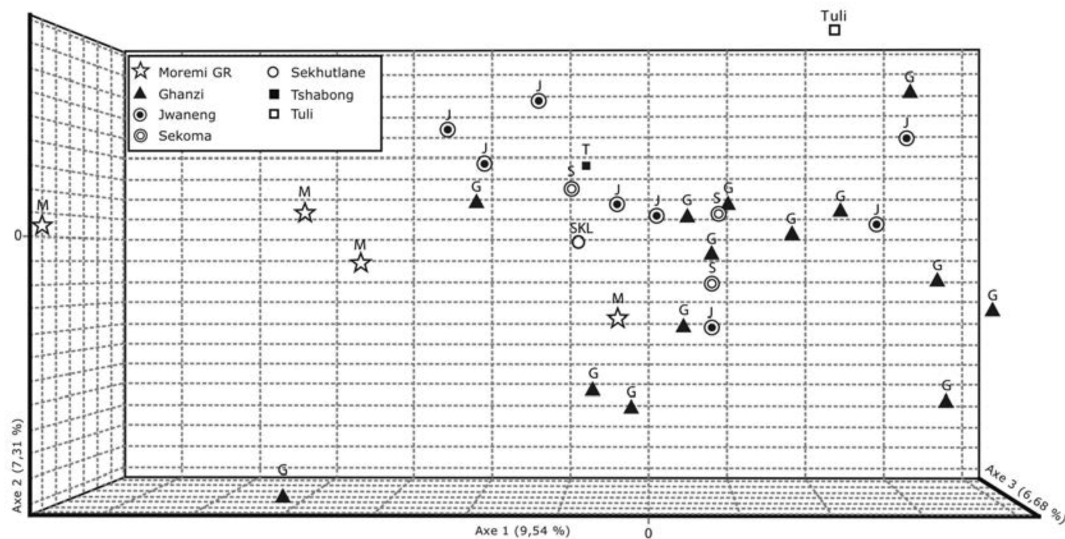

Fig. 8. Factorial Correspondence Analysis (FCA) of 32 unrelated individuals based on 14 microsatellite loci. M: Moremi Game Reserve (n = 4); G: Ghanzi (n = 14); J: Jwaneng (n = 8); S: Sekoma (n = 3); SKL: Sekhutlane (n = 1); T: Tshabong (n = 1); Tuli: Tuli (n = 1).

3. Dynamics of domestication and trading revealed by the global genetic diversity of the dromedary

3.1. Lack of genetic signal to identify domestication origin(s)

Examining the present diversity and its distribution I expect to gain insight into the past, as domestic populations close to the putative centre(s) of origin can be assumed to retain higher levels of ancestral polymorphism, in the absence of recurrent introgression outside the area(s) of domestication [161]. Negative correlation between genetic diversity and the geographic distance from the place of origin has been observed in numerous livestock species, *e.g.* cattle [161,162], sheep [163,164] and goats [165]. In the case of the dromedary, zooarchaeological studies suggest that domestication took place in the coastal southeast Arabian Peninsula [61,70,71,73]. Prior to the introduction of domestic camels, there had been no representatives of *Camelus* on the African continent since the Late Pleistocene and no validated archaeological evidence for the occurrence of wild dromedaries during the Holocene has been found outside the Arabian Peninsula [69,70]. I would thus expect the camel populations from the Arabian subcontinent to display the highest level of diversity and variation. To examine this expectation and to provide additional information to that resulting from studies focused on region- or country-

specific diversity (*e.g.* [166,167,168,169,170,171,172], I combined two comprehensive datasets encompassing nuclear and mitochondrial profiles of 970 and 662 dromedaries, respectively, from the species' entire range. I grouped the sampled individuals into five geographically distinct populations: Horn of Africa (HAF), Sahara (SHR), north (NAP) and south Arabian Peninsula (SAP) and Southern Asia (SAS) (Table S3).

Considering the global population, both nuclear heterozygosity (H_E = 0.630 ± 0.044) and allelic richness (*Ar* = 7.31), corrected for uneven sample size, corresponded to the variation reported in previous studies (*e.g.* [166,167,168,172] and were comparable to my local estimates (H_E = 0.580-0.633; Table 8). This indicates shared diversity over the complete species range. At the mitochondrial level, I detected 68 haplotypes with haplotype diversities (H_d) that were slightly lower (0.68-0.79; overall: 0.74; Table 8) than the estimates for different populations of vicuña (0.72-0.90; overall: 0.76) [173] and domestic Bactrian camels (overall: 0.77) [82]. Nuclear and mitochondrial AMOVA analyses revealed that more than 90% (93.01% and 95.28%, respectively) of the variation was distributed among the different dromedary populations reflecting high levels of shared diversity and little substructure.

	mtDNA (867 bp)						
Pop	No. drom.	Haplotypes	Var. sites	H_d	π	*k*	θ_S
HAF	74	15	16	0.793 (0.028)	0.0059 (0.0032)	5.118 (2.510)	3.282 (1.150)
SHR	203	23	22	0.682 (0.035)	0.0031 (0.0018)	2.661 (1.425)	3.736 (1.112)
NAP	183	29	23	0.754 (0.030)	0.0029 (0.0017)	2.506 (1.357)	3.977 (1.181)
SAP	77	22	20	0.756 (0.050)	0.0043 (0.0024)	3.723 (1.901)	4.070 (1.350)
SAS	125	22	19	0.711 (0.042)	0.0029 (0.0017)	2.502 (1.358)	3.518 (1.129)
Total	**662**	**68**	**45**	**0.744 (0.017)**	**0.0036 (0.0021)**	**3.097 (1.611)**	**6.363 (1.470)**
	Microsatellite (17 loci)						
Pop	No. drom.	TNA	MNA/locus	*Ar*	H_E	H_O	F_{IS}
HAF	160	97	5.71 (3.48)	5.54	0.580 (0.043)	0.532 (0.010)	0.082*
SHR	207	128	7.53 (5.04)	7.15	0.631 (0.042)	0.598 (0.008)	0.054*
NAP	317	135	7.94 (5.13)	7.01	0.633 (0.043)	0.605 (0.007)	0.044*
SAP	141	115	6.76 (4.59)	6.72	0.604 (0.050)	0.549 (0.010)	0.091*
SAS	145	121	7.12 (4.87)	7.06	0.617 (0.048)	0.560 (0.010)	0.092*
Total	**970**	**158**	**9.29 (5.45)**	**7.31**	**0.630 (0.044)**	**0.577 (0.004)**	**0.085***

Table 8. Genetic diversity of dromedaries grouped in five geographical populations inferred from mitochondrial and microsatellite data. Standard deviation values are indicated within brackets. Var. sites: variable sites. TNA: total number of alleles. MNA/locus: mean number of alleles per locus. *Ar*: allelic richness per locus and population based on minimum sample size of 131 diploid individuals. HAF: Horn of Africa; SHR: Sahara; NAP: North Arabian Peninsula; SAP: South Arabian Peninsula; SAS: Southern Asia. *p-value <0.001.

While the amount of heterozygosity and allelic richness did not differ significantly among SHR, NAP, SAP and SAS populations ($P > 0.05$ after Bonferroni corrections; Wilcoxon-Rank-Sum test), the HAF individuals exhibited the lowest nuclear diversity in terms of H_E (0.580 ± 0.043) and *Ar* (5.54; Table 8). At the mitochondrial level, the highest theta values (θ_S) were measured in NAP (3.977 ± 1.181) and SAP (4.070 ± 1.350). However, H_d, π (nucleotide diversity) and *k* (mean number of pairwise nucleotide differences) were higher in HAF (0.793; 0.0059; 5.118, respectively), exceeding even slightly the estimates for the populations in the Arabian Peninsula (NAP, SAP; Table 8). The elevated values of H_d, π and *k* could, in principle, also be explained by an unaccounted cryptic population structure in the HAF samples [174]. Hence, the higher polymorphism observed in HAF might result from the admixture of different gene pools rather than reflecting a large fraction of (retained) ancestral diversity. In fact, I detected the presence of two mitochondrial lineages (L1 and L2) that encompass all 68-dromedary haplotypes (Fig. 9a). While these two lineages could not be assigned to specific geographical areas, 85% of all investigated dromedaries pertained to L2. Notably, the HAF population exhibits the most balanced ratio between the two lineages (L1: 38%, L2: 62%; Fig. 9). This might be a consequence of a random founder effect or could result from multiple gene influx subsequent to the introduction of camels into the Horn of Africa.

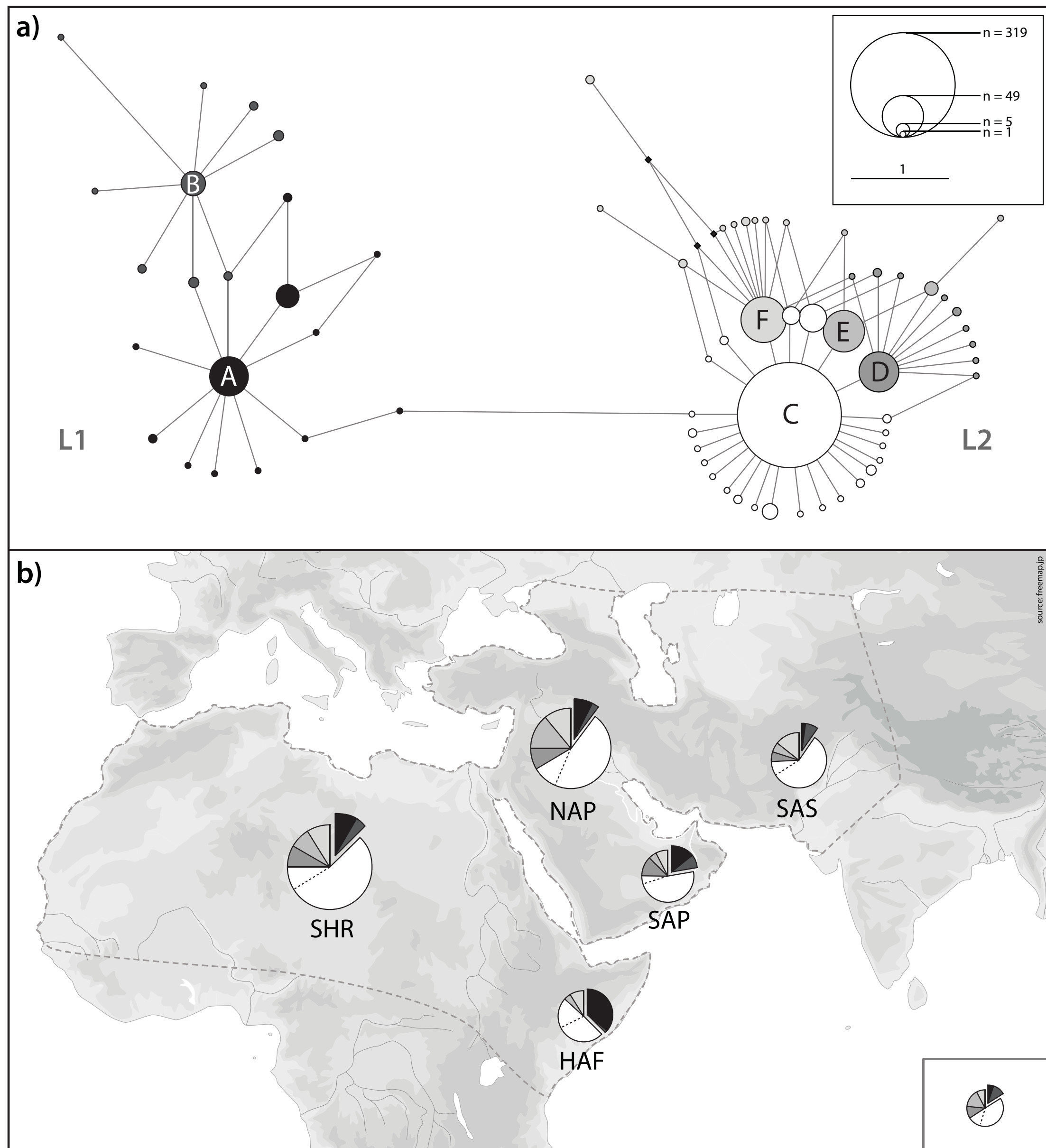

Fig. 9. Mitochondrial haplogroup repartition over the global range retrieved from 662 dromedaries. The haplogroups centered in A to F are coloured according to the Bayesian (BAPS) clustering solution (K=6). Circles are proportional to the sample size. a) The median-joining network displays the 68 haplotypes grouped into two maternal lineages L1 and L2. The consensus network of all shortest trees is shown. Small black squares represent median vectors, which correspond to either missing haplotypes or homoplasies. Branch lengths are proportional to the number of mutations. b) Geographical representation of the Bayesian clustering across the range. The dromedary species range is delimited by a dashed line. The proportion of haplotypes emerging from C that formed a separate cluster (K=7) is depicted with a dashed line within the white pie-section representing the merged haplogroup (K=6). The chart in the bottom right-hand corner represents the Australian dromedary population (n = 38). The sample sizes of the distinctive regions are given in Table 8.

3.2. Globalization of dromedary diversity by cross-continental trading

Previous studies have reported few differentiations among camel populations [166,168,172]. Significant differences were found only when the pairwise comparisons included populations termed as 'African' although they actually originated from the Horn of Africa. These results are consistent with the global population structure observed in my study and are reflected in the highest genetic differentiation (F_{ST}, ϕ_{ST}; Table 9), as well as in the lowest effective number of migrants (*Nm*) exchanged between HAF and the four other populations (Table 10).

F_{ST} / ϕ_{ST}	HAF	SHR	NAP	SAP	SAS
HAF	-	0.040***	0.045***	0.051***	0.062***
SHR	0.134***	-	0.006***	0.017***	0.018***
NAP	0.148***	0.000	-	0.018***	0.013***
SAP	0.038	0.021	0.029*	-	0.021***
SAS	0.131***	0.001	0.000	0.022*	-

Table 9. Population pairwise distances based on the 867-bp mtDNA sequences (ϕ_{ST}; below diagonal) and 17 microsatellite loci (F_{ST}; above diagonal). Distances between the five populations were graphically represented in non-metric multidimensional scaling plots (NMDS; Fig. S2). ****P*-value < 0.001; **P*-value < 0.05.

Nm	HAF	SHR	NAP	SAP
HAF	-			
SHR	6.00	-		
NAP	5.30	38.73	-	
SAP	4.67	14.76	13.30	-
SAS	3.99	14.21	16.21	13.77

Table 10. Effective number of migrants (*Nm*) between five geographically defined populations based on the nuclear pairwise F_{ST} distances (Table 2).

Almost no genetic differentiation (F_{ST}, ϕ_{ST}; Table 9) between SHR and NAP populations was found, implying ongoing gene flow since historical times (Table 10). Likewise, no correspondence between geographical and genetic distances (F_{ST}, ϕ_{ST}) was detected as displayed in the non-metric multidimensional scaling plots (Fig. 10).

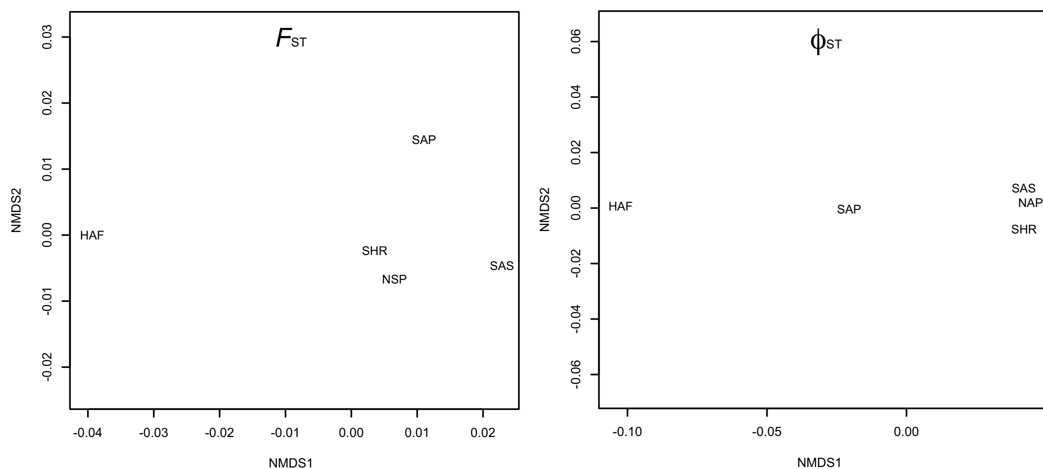

Fig. 10. Non-metric multidimensional scaling (NMDS) plots based on nuclear (F_{ST}) and mtDNA (ϕ_{ST}) genetic distance matrices measured between the five geographically defined dromedary populations.

Without using any prior information about the geographic origin of the dromedary samples, I performed Bayesian clustering analyses on the mitochondrial and nuclear datasets independently. For the set of 662 sequences, BAPS analysis revealed seven haplogroups as the best clustering solution (posterior probability, PP = 0.884). By merging into a unique haplogroup two clusters consisting of the single haplotype C and its satellites (one mutational step away from C; Fig. 9a), respectively, resulted in the second best partitioning solution of six clusters (PP = 0.12). No geographic pattern was revealed as all mitochondrial haplogroups were represented over the entire species range (Fig. 9b), while nuclear data suggested geographical clustering to some degree. From a theoretical number of two ancestral dromedary populations onwards, HAF nuclear profiles clustered independently from the rest of the individuals (Fig. 11).

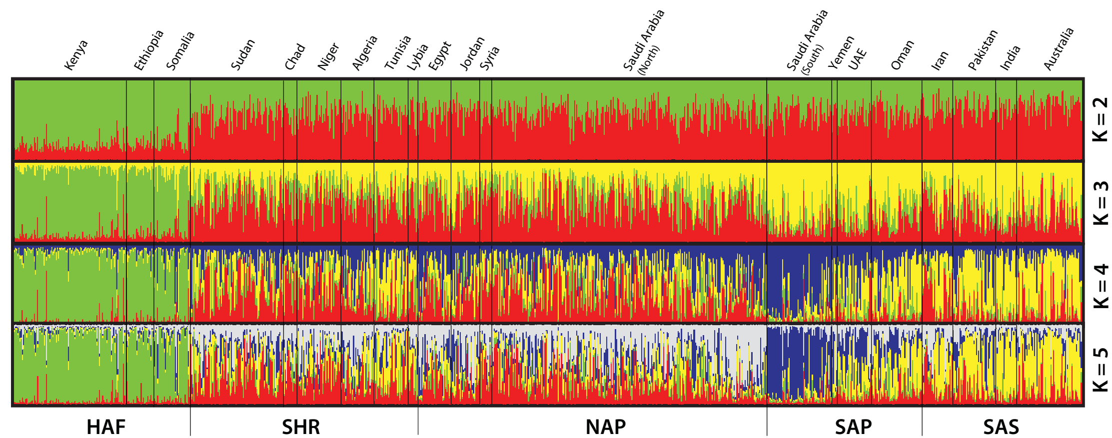

Fig. 11. Individual assignment plot of 970 dromedaries from 20 countries (STRUCTURE). The theoretical number of ancestral populations (K) was set from 2 to 5. Analyses were run without any loc-prior. The optimal clustering solution determined with DeltaK is reported in Table 11. The sample sizes of the distinctive regions and countries are presented in Tables 8 and S3.

Increasing the number of ancestral populations to three enabled the differentiation of some individuals of SAP and SAS (including Australian camels) from the SHR and NAP populations. With K = 4, I could distinguish an additional cluster within the SAP population, to which camels (Awardi, Awarik; Table S3) from an isolated mountainous region in Saudi Arabia belonged. Higher values of K increased the level of admixture but did not define deeper geographically or biologically meaningful substructuring. It is worth noting that the optimal number of clusters (DeltaK; Table 11) was obtained for K = 2, which differentiated HAF individuals from the rest of the global population (Fig. 11).

	K = 2		K = 3			K = 4				K = 5				
DeltaK	85.776368		6.470764			2.884892				0.260829				
Clusters	1	2	1	2	3	1	2	3	4	1	2	3	4	5
HAF	0.803	0.197	0.796	0.098	0.106	0.791	0.07	0.057	0.081	0.78	0.049	0.043	0.057	0.069
SHR	0.428	0.572	0.2	0.466	0.334	0.122	0.401	0.265	0.211	0.091	0.343	0.203	0.136	0.227
NAP	0.417	0.583	0.188	0.433	0.379	0.107	0.384	0.223	0.286	0.074	0.271	0.156	0.163	0.336
SAP	0.416	0.584	0.176	0.263	0.561	0.096	0.125	0.307	0.472	0.067	0.098	0.226	0.477	0.133
SAS	0.342	0.658	0.127	0.462	0.412	0.063	0.228	0.542	0.168	0.042	0.192	0.495	0.14	0.132

Table 11. Proportion of membership of each geographically pre-defined population for each of the K cluster solutions (Fig. 11). Colors refer to the cluster solutions of Fig. 2. The most predominant cluster in each pre-defined population was shaded with grey. Values of DeltaK criterion were calculated according Evanno *et al.* [117] using four independent STRUCTURE iterations for each of the K values (the outputs of one of these four iterations are plotted in Fig. 11). The highest DeltaK value was found at K = 2.

Similar results were retrieved with three-dimensional factorial component analysis (FCA) as the first two axes distinctly separated the HAF profiles (Fig. 12). The F_{IS} values (Table 8) indicate that the clustering did not result from strong inbreeding in any of the regions, including HAF.

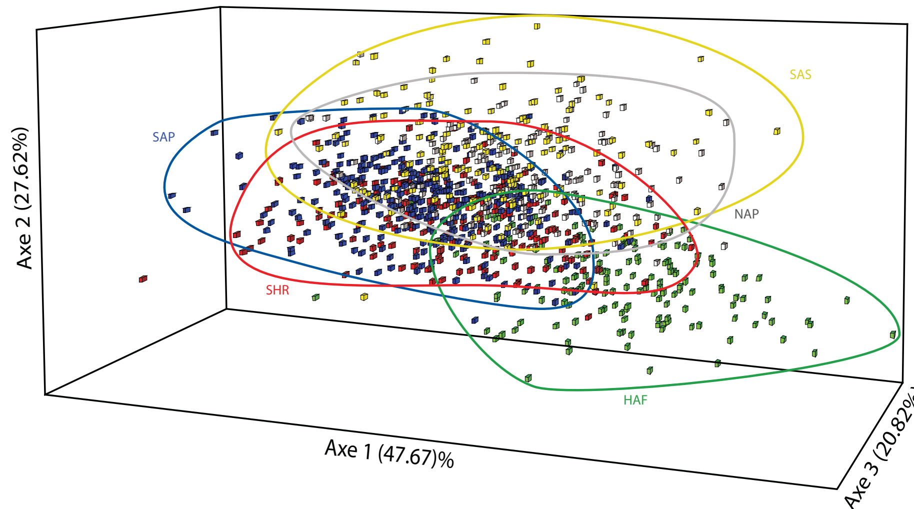

Fig. 12. Factorial correspondence analysis (FCA) of 970 dromedaries. Squares represent individual profiles and are coloured according to sampling locations (HAF: green, SHR: red, NAP: grey, SAP: blue, SAS: yellow). The first three axes represent 96.11% of the total genetic variation.

3.3. Domestication dynamics

Archaeozoological findings suggest that dromedary domestication started *circa* 3000 years ago, as the first evidence for the domestic form dates *c.* 1400 to 900 BCE [61,70,71]. I searched for this major change in the demographic history of the dromedary using phylogenetic approaches. Independently of the methods (MJN, Maximum Likelihood and Bayesian) I observed the grouping of the 68 haplotypes into two distinct lineages, L1 and L2 (Fig. 9a and 13).

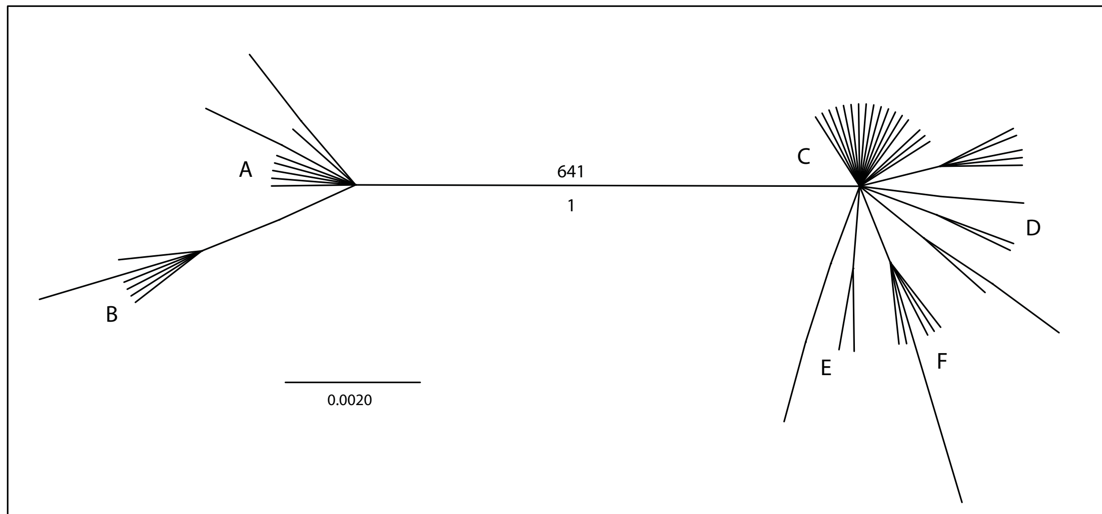

Fig. 13. Unrooted phylogenetic tree of 68 dromedary haplotypes constructed by Maximum Likelihood (ML) analysis. Numbers above branches represent bootstrap supports out of 1000 iterations using PhyML, whereas values below branches show posterior probabilities (PP) obtained with MRBAYES. Only bootstrap values above 60% and PP above 0.90 are displayed. A to F nomenclatures refer to the main haplotypes representative of the six BAPS clusters (Fig. 9).

I investigated whether the split between L1 and L2 might coincide with the time of domestication. Assuming that the one- and two-humped camel lineages split 3 to 8 Mya [131,133], the time to the most recent common ancestor (TMRCA) of L1 and L2 was then estimated at 85 000 and 235 700 ya based on the genetic distance D_A = 7.606, and at 70 000 and 194 000 ya using the distance tau = 6.272. These estimates clearly predate the period for domestication of the dromedary, towards the end of the Iron Age I Period [61,70,71,73]. Consequently, the fact that the two lineages are still present today indicates that multiple (at least two) wild maternal lines were domesticated.

In the context of domestication, molecular signals of sudden expansion are often interpreted as population growth and/ or diffusion of domesticates across a wider geographic range [175]. Looking explicitly for signals of global population growth, the *k*-test (intra-locus variation) over all loci failed to detect population expansion, as allele distributions were not significantly different from multimodal distribution (P = 0.801) despite the fact that seven of the 17 loci showed a negative *k*. The *g*-test (inter-locus variation) also failed to support a population history involving expansion: its value was large and non-significant (g = 1.468). Further tests for demographical changes, such as Bottleneck [152], did not yield statistically significant results. However, from the global

mtDNA profiles I measured negative values of Tajima's D (-1.676; $P = 0.021$) and Fu's F_S (-26.020; $P = 0.000$), which in the absence of selection could indicate past demographic expansion. Subsequently I investigated signals of population expansion in the timeframe of dromedary domestication. From the MJN (Fig. 9a) and the phylogram (Fig. 13) I distinguished six haplogroups corresponding to the BAPS clustering solution of K = 6 (Fig. 9). Within the ancestral lineage L1, two haplogroups were centered on the haplotypes A and B; while in L2 four grouped around the haplotypes C, D, E and F (Fig. 9a). The topology of these six haplotypes at high frequency, from which singletons dispersed in a star-like shape of one- or two-step mutations, and the uniformity of the external branch lengths suggest population expansion. I postulated that the entire diversity within the lineages L1 and L2 was generated since the time of domestication (strong bottleneck). Hence, I evaluated the assumption of expansion by testing whether the number of substitutions on the external branches followed a Poisson distribution [154]. When I assumed that the initial pool of domesticated camels consisted of individuals representative of the most frequent mitochondrial haplotypes, A for L1 and C for L2, the distributions of the substitutions were not significantly different from a Poisson distribution ($P > 0.05$). Using the relationship between λ (unique parameter of the Poisson distribution), mutation rate and time ($\lambda = \mu t$) and assuming that domestication commenced t = 600 generations ago (*c.* 3000 y with a generation time of 5 y), I estimated μ. To reach the amount of diversity detected in the first lineage with haplotype A as a starting point would demand at least $\mu_{(A)} = 0.61$ sub/site/Myr. Similarly, starting from haplotype C the mutation rate required to generate the diversity observed in L2 ($\mu_{(C)}$) was estimated to be 0.44 sub/site/Myr. If I instead assumed that the initial pool was formed from both most frequent haplotypes A and C, I calculated $\mu_{(A+C)} = 0.22$ sub/site/Myr. Such levels of mitochondrial mutation rates are highly unlikely [176]. I therefore rejected the model where the early diversity consisted only of the A and C haplotypes and assumed a higher amount of initial variation. I considered separately the two (A, B) and four (C, D, E, F) haplotypes, as the starting pools of diversity in lineages L1 and L2, respectively. As I could not reject population expansion ($P > 0.05$), $\mu_{(A+B)}$ was estimated at 0.17 sub/site/Myr and $\mu_{(C+D+E+F)}$ at 0.07 sub/site/Myr. Assuming one unique wild source

population consisting of all the six haplotypes, I calculated $\mu_{(A+B+C+D+E+F)}$ = 0.08 sub/site/Myr. Consequently, the presence of six or more frequent haplotypes was required to yield reasonable estimations of the mutation rate [176].

4. Hybridization in Old World camelids: case of the last wild camels (Camelus ferus)

Since it is commonly accepted that the wild camel has its own evolutionary history, there is important concern about hybridization in the last wild camel populations. With this survey I aimed to detect hybridization occurrence within two Strictly Protected Areas (SPA), Gobi SPA-A (Mongolia) and Lop Nur Camel Reserve (China), places where no domestic camel should be found. Therefore close to 150 samples have been collected non-invasively. This sampling approach made the genetic investigation extremely difficult and sensitive to typing errors. Ninety mtDNA sequences (66 Mongolian and 24 Chinese) have been successfully amplified. I sequenced the equivalent mtDNA fragment for close to 160 domestic Bactrian camels. At the mtDNA level already 5 Mongolian and 8 Chinese samples collected in the protected areas showed domestic haplotypes. For these samples I then needed to determine if they were maternal hybrids (domestic mother with wild bull) or if they were free-ranging domestic animals in the SPA. To answer this question but also to detect potential paternal hybrids, I used 19 microsatellite-marker and obtained reliable results for only 40 individuals (9 from China and 31 from Mongolia). First of all, the 40 profiles were tested with a capture/recapture approach (Dropout). I then obtained the genetic evidence that all profiles obtained from hair samples collected on bushes corresponded to 40 different animals. Unfortunately only five out of the 13 “doubtful” individuals provided reliable profiles and could then be incorporated in the subsequent analysis. The STRUCTURE result comparing domestic to wild profiles is illustrated on Fig. 14, where the blue cluster represents the wild samples. It is interesting to note that even with a large K, the investigated wild camels, despite their origin from two different locations, clustered always as a single population.

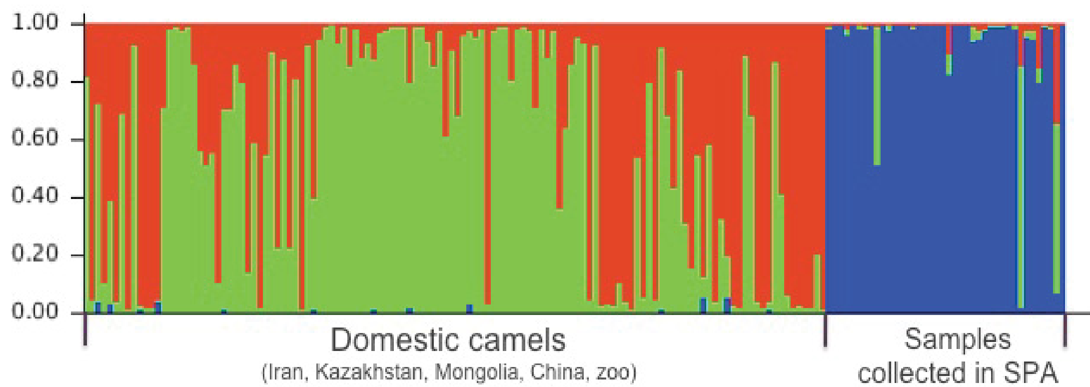

Fig. 14. Admixture structure plot for K=3. Bactrian camels (n= 125) are grouped into the two first clusters (green and red) isolated from the wild camels (blue cluster; n=40). Five samples collected in Strictly Protected Areas (SPA) displayed common alleles with the Bactrian populations.

Among the wild cluster, five individuals displayed admixture with domestic genome (fraction of green and/ or red; WC8, WC117, WC182, WC187 and WC194). Among these five profiles, two displayed wild mt-sequences (WC8 and WC117) and three were typed for domestic mt-haplotype (WC182, WC187 and WC194). In addition, I obtained reliable nuclear profiles for two individuals collected in the protected areas that displayed domestic mt-haplotypes (WC154 and WC 185). I expected these two camels to share a fraction of their genome with the domestic Bactrian cluster (green and/ or red) but surprisingly both of them displayed a wild nuclear profile (blue). These results are summarized in Table 12.

Label	%missing	Fraction of Bac. Gen.	Fraction of Wild Gen.	mtDNA
WC8	5	0.492 (0.299,0.695)	0.501 (0.303,0.699)	wild
WC117	0	0.158(0.000,0.429)	0.842 (0.570,1.000)	wild
WC154	26	0.026 (0.000,0.165)	0.974 (0.826,1.000)	dom.
WC182	5	0.977 (0.846,1.000)	0.023 (0.000,0.150)	dom.
WC185	5	0.016 (0.000,0.108)	0.984 (0.889,1.000)	dom.
WC187	15	0.136 (0.000,0.377)	0.864 (0.661,1.000)	dom.
WC194	5	0.966 (0.784,1.000)	0.034 (0.000,0.213)	dom.

Table 12. The level of admixture of the Bactrian and wild camels observed in the Fig. 14

I checked the significance of admixture as well as the informative power of the selected nuclear marker set (Table 13).

Label	Pop origin	Poss. source	v	No Imm.	Imm.	Imm. par.	Imm. gd par.	Imm. 3gen. ago	Significance
WC8	Wild	Bac	0.05	0.000	0.669	0.321	0.010	0.000	***
			0.001	0.000	0.000	0.686	0.305	0.009	***
WC117	Wild	Bac	0.1	0.846	0.000	0.000	0.036	0.117	ns
			0.05	0.934	0.000	0.000	0.015	0.051	ns
			0.001	0.999	0.000	0.000	0.000	0.001	ns
WC182	Wild	Bac	0.05	0.000	1.000	0.000	0.000	0.000	***
			0.001	0.000	1.000	0.000	0.000	0.000	***
WC187	Wild	Bac	0.1	0.693	0.000	0.000	0.041	0.262	ns
			0.05	0.841	0.000	0.000	0.021	0.137	ns
			0.001	0.997	0.000	0.000	0.000	0.003	ns
WC194	Wild	Bac	0.05	0.000	1.000	0.000	0.000	0.000	***
			0.001	0.000	1.000	0.000	0.000	0.000	***

Table 13. Testing whether particular individuals are immigrants or have recent immigrant ancestors. v = 0.001 – 0.05, the probability that an individual is a migrant to the population $g^{(i)}$ or has an immigrant ancestor in the last G = 3 generations.

WC8 is a real F1 hybrid (offspring of a wild mother and a domestic bull; sir: immigrant parent). WC182 and WC194 are actually two domestic camels free ranging in the SPA (immigrants). For WC117 and WC187 it seems that the set of microsatellites does not provide enough information to disentangle noise from real migration older than one generation backward (parents). For WC154 and WC185, their genetic profiles (domestic mt-haplotype and wild nuclear profile) could be explained by the occurrence of a domestic female in their maternal lineage ancestry. However the statistical power of the microsatellite set is too weak to test this assumption. In conclusion with the present set of markers I can affirm that domestic animals occur within the borders of the Lop Nur camel reserve (China) as well as hybridization exists within the wild Mongolian population.

The major concern of conservation genetics is not a question of census but it is mainly about the decrease of variation within a species or population. During this thesis, I carried out different projects representing two complementary considerations in conservation genetics: endangered domestic and wildlife diversities. In my projects it was essential to first investigate the current levels of genetic diversity in the global populations in order to infer the evolutionary history of the studied species and to understand the processes and contexts that over time shaped the variation that we observe today. Some results of this PhD project were already implemented in decision-making processes on wildlife conservation (reintroduction of the cheetah in India [177]; wild camel conservation plan [80]).

1. Cheetah project

1.1. Phylogeography of the four of the five cheetah subspecies

1.1.1. A not so genetically depauperate species

I investigated the genetic diversity and divergence within and between African and Asiatic cheetahs based on mtDNA and microsatellite data of 94 samples including two mediaeval cheetah bones (9th–10th century CE). In general, my data show that there is a higher genetic variation in the current global cheetah population than previously described [23,27,178]. This is due mainly to the fact that I included populations that had never been investigated before. The overall amount of mtDNA nucleotide diversity (π) of 0.66% in cheetahs was higher than observed in tigers (0.18%; [179]) and pumas (0.32%; [180]), similar to jaguars (0.77%; [181]), and lower than in leopards (1.21%; [182]). The total nuclear (microsatellite) diversity (H_E = 0.766) is comparable with that of other outbred felid species [98,180,181,182]. This might be explained by my use of highly polymorphic markers (all loci were polymorphic), therefore I also compared a set of 15 nuclear microsatellite loci applied in surveys of cheetahs (this study and [98]), domestic cats, pumas and lions (supplemental table 3 in [98]), and I found similar genetic

diversities (H_E values ranging from 0.681 to 0.777; Table 14) in the four felid species.

15 overlapping loci		Average number Allele/Locus (SE)	H_e
Cheetahs			
Driscoll *et al.* (2002)*			
	Acinonyx jubatus (all)	7.067 (1.534)	0.758
	A.j.jubatus (n=20)	5.533 (1.060)	0.711
	A.j.raineyi (n=10)	5.067 (1.223)	0.678
Marker *et al.* (2008)**			
	A.j.jubatus (n=89)	6.857 (1.351)	n.a.
current study*			
	Acinonyx jubatus (all)	8.267 (1.438)	0.777
	A.j.jubatus (n=27)	6.467 (1.598)	0.687
	A.j.soemmeringii (n=25)	5.933 (1.486)	0.692
	A.j.venaticus (n=8)	2.333 (1.047)	0.402
Domestic cats (Driscoll *et al.*; 2002)*			
	Felis catus (n=10)	5.867 (2.031)	0.704
Lions (Driscoll *et al.*; 2002) *			
	Panthera leo (n=60)	6.467 (2.356)	0.681
Pumas (Driscoll *et al.*; 2002)*			
	Puma concolor (n=30)	7.733 (1.751)	0.695

Table 14. Comparisons of average numbers of alleles per locus and expected heterozygosities calculated from 15 microsatellite loci overlapping in four different felid species. * 15 loci: FCA005, FCA008, FCA014, FCA026, FCA069, FCA085, FCA097, FCA105, FCA126, FCA133, FCA212, FCA224, FCA230, FCA247, FCA310. **14 loci (without FCA005).

The H_E levels in the investigated Southern and Northern-East African cheetah populations (Table 2) were similar to Namibian cheetahs (0.640–0.708) and higher than in the Serengeti population (0.599) [30]. The lower H_E (0.397) observed in the Iranian cheetahs might be the consequence of ancestral population divergence or a recent bottleneck, as I found significant evidence for a recent effective population size reduction in this population (Table 4).

1.1.2. When genetics supports classical taxonomy (or not!)

Within the African samples, I recovered the previously described relationship between the sub-Saharan cheetah subspecies *A. j. raineyi* and *A. j. jubatus* [44,98]. The clustering

of some Tanzanian and Kenyan animals together with Southern African cheetahs in the mtDNA BAPS analysis (Fig. 5a) suggests a population in East Africa that might be derived from relatively recent re-colonization events as observed in lions [183]. This should be investigated combining mtDNA and nDNA data obtained from additional samples of East African cheetahs. At the nuclear level, I observed substructuring in the Northern-East African and Southern African subspecies (Figs 5b and 6) into two sub-populations, which did not correlate with the geographical origin of the individuals. Weak population structure within the South African cheetahs [43] and a panmictic Namibian population [30] have been reported previously. Remarkably, the Northern-East African cheetahs were highly differentiated (nuclear F_{ST} = 0.170) from the Southern African individuals and clustered independently (Figs 5 and 6) and monophyletic. Between the African and Asiatic subspecies, I also discovered great differentiation at both nuclear and mitochondrial levels (Table 3). Similar levels of population ⁄ subspecies differentiation were described in leopards [182], pumas [180] and lions [183]. I could not detect significantly higher differentiation (mitochondrial F_{ST}, also call ϕ_{ST}) between African and Asiatic cheetahs than among the African subspecies. This indicates deep phylogeographic structure not only between African and Asiatic cheetahs but also among the African cheetah populations.

It is well documented that imports of tamed hunting cheetahs from Northern-East [35] and East Africa [37] into India and the Arabian Peninsula were a regular occurrence during the European colonial era. Given the possibility of interbreeding with African escapees, Asiatic cheetahs were not expected to form a genetically distinct unit. However, hunting cheetahs were highly valued, and there are no known records of individuals (accidentally or intentionally) released into the wild [37]. Moreover, the species is notoriously difficult to breed in captivity. Except for a single litter born in Akbar's collection of many thousands of cheetahs the first documented captive birth was at the Philadelphia Zoo in 1956 [30,37]. Therefore, the possibility of a captive, hybrid Asiatic-African population as a source of escapees or releases is very low. In my study, I found no evidence of recent gene flow between these populations (Fig. 5b). In all analyses, including the ones with mediaeval Iranian samples, the Asiatic cheetahs constituted a

unique cluster (Figs 4–7) suggesting an apparent monophyly of the Asiatic lineage. Historical museum specimens from Iran, Iraq and India (#12, 15, 16; Table S1) that could not be distinguished by morphological characteristics from African specimens [37] were genetically confirmed as Asiatic individuals. The clustering results of the Asiatic cheetahs were of particular interest because this population has been proposed to form a single subspecies, *A. j. venaticus*, with North African cheetahs [34,184]. Notably, Egypt harbored two genetically distinct populations in the past, as I observed clustering of the two Egyptian samples in different haplogroups (Figs 4b and 5a). One now extinct population in eastern Egypt (Northern Sinai; [185,186]) could be represented by the historical sample collected by Theodor von Heuglin in the early 1850s, which clustered with samples from Southwest Asian countries (Jordan, Iran, Iraq and Oman). The other specimen collected in western Egypt (Libyan Desert; [158]) shared the same haplotype with cheetahs from North Africa and represented a population that might still exist today in the Libyan Desert [185,186]. I could not detect hybridization of Asiatic and African cheetahs in my study (Fig. 5). This suggests that palaeoclimatic constraints, ecological barriers and/or geographical features prevented past gene flow between the two putative populations of this part of Africa. Genetic separation is also supported by the nuclear NJ tree, as the branch leading to the Jordanian (and all Asiatic) samples, which cluster separately from the Libyan (and all other African) individuals, had a bootstrap support of 72% (Fig. 7b). The classification and taxonomy of North African cheetahs are still debated [34,157]. This population might be genetically contiguous with cheetahs from West Africa (Senegal to Niger), thus it is critical to further investigate current Egyptian and West African populations as suggested by Belbachir [157]. In the light of my results, the previous proposal of a single subspecies, *A. j. venaticus*, encompassing the Iranian cheetah and its North African congeners [34,184] is not supported.

1.1.3. Cheetahs and their famous bottleneck

In summary, my data based on palaeogenetic analyses demonstrate that the isolation between Asiatic and African cheetahs has existed for millennia. To date, divergence time between cheetahs has only been estimated among the (closely related; Figs 1 and 2)

African subspecies *A. j. jubatus* and *A. j. raineyi*. Using mtDNA (mtRFLP) and microsatellite distance data [$(\delta\mu)^2$], the divergence time had been estimated at 28 000–36 000 ya [27]and 4253 ya [98], respectively. The latter was inferred with mutation rates estimated from human microsatellite data (Driscoll et al. 2002). In general, time estimations based on microsatellite distance data can be challenging, particularly if no taxon-specific microsatellite evolution rates are available, as it is the case in felids. Also, it is important to take into account potential homoplasy of microsatellites [187,188,189] in the estimation of divergence time between ancient isolates, as some cheetah subspecies are suggested to be by my mtDNA divergence time estimates. In this study, I included two newly investigated subspecies (*A. j. soemmeringii* and *A. j. venaticus*) and an average mammalian microsatellite mutation rate previously applied in other felid species [145,146,147] to calculate the divergence times within and between African and Asiatic cheetahs. Depending on the genetic marker (mtDNA or nDNA), the nuclear genetic distance [$(\delta\mu)^2$ or D_{SW}] and the choice of the microsatellite mutation rate (human or average mammalian), I retrieved results differing by more than one order of magnitude. Large differences between mitochondrial and nuclear time estimates using human microsatellite rates have been previously observed in wild felids [27,183]. This could be explained by the fact that the genetic distances $(\delta\mu)^2$ and D_{SW} are considered to underestimate divergence [149,188,189]. In my data, I found higher genetic differentiation at microsatellite loci, as measured by F_{ST} values and genetic distances [$(\delta\mu)^2$ or D_{SW}], between *A. j. venaticus* and *A. j. jubatus* than between *A. j. soemmeringii* and *A. j. jubatus*. However, this might be due to a possible stochastic increase in divergence associated with a recent population bottleneck [190,191], which signature I could apparently detect in my data in *A. j. venaticus*. Choosing the average mammalian mutation rate and considering the mtDNA estimate, I can place the split between Asiatic and African cheetahs at 32 000–67 000 ya and within Africa, between *A. j. soemmeringii* and *A. j. jubatus*, at 16 000–72 000 ya. However, considering the substantial variation in divergence time estimates I acknowledge that decisions for the conservation of this endangered species should not be based on time estimates alone.

1.1.4. Implications for conservation

In this study, I re-visited the currently recognized cheetah subspecies [32,34] in light of the results retrieved from geographically defined populations. I verified the veracity of *A. j. venaticus* and *A. j. soemmeringii* based on recognizable phylogenetic partitioning (mitochondrial monophyly and significant divergence at nuclear loci; [192]) and absence of gene flow [193]. My study suggests a close relationship of *A. j. raineyi* with *A. j. jubatus*; however, minisatellite [27] and microsatellite variation [98] support the separation of these two sub-Saharan subspecies. I also clarified the western range limit of the critically endangered *A. j. venaticus* observing a historical range in contrast to recent accounts, which included North Africa [34]. The identification of a subspecies recognizes biological distinctiveness and should be sufficient as first-order systematic hypothesis when the aim of conservation is to preserve biological diversity [194]. As large-scale genomic information becomes available also for non-model species, adaptive genetic markers might be used to estimate diversification and adaptive genetic variation in subspecies/populations, in combination with supposedly neutrally evolving loci. It might also help to understand how populations can survive despite a low neutral genetic variation [195,196].

Although there is little evidence that inbreeding depression affects African cheetahs [197] and current threats to the species are primarily anthropogenic [30,38,48,49], the lower genetic diversity in the Iranian population is cause for concern in light of their critically low numbers [32,49]. Any further decline in Iranian cheetah numbers would require increasingly extreme conservation measures, including the consideration of supplemental introductions from Africa, similar to that required for the demographic rescue of Florida panthers [198,199,200]. However, contrary to the close geographic and genetic distances described in Texas and Florida panthers [199], I did not detect historical gene flow between African and Asiatic cheetahs (Fig. 5). In addition to the formidable logistical and financial obstacles arguing against introductions, my results emphasize the importance of preserving the genetic distinctiveness of the critically endangered Iranian cheetahs. That will also entail a stronger understanding of possible substructuring in the Iranian population. At least 10 cheetahs moving between known population centers have been

killed on roads since 2004 including most recently a female with two cubs in August 2010 (A. Jourabchian, unpublished data). Ongoing, rapid infrastructural development around some cheetah sub-populations in Iran will increase the likelihood of demographic and genetic fragmentation. These processes are currently poorly understood but are the focus of an ongoing multinational research effort led by Iranian biologists which has deployed GPS collars on cheetahs and is undertaking further analysis of genetic differences between cheetah subpopulations in Iran [49]. Most significantly, the government of Iran recently renewed its commitment to a major conservation effort of the species [201].

My results have particular implications for proposed reintroductions in the cheetah's former range in Asia, especially in India [202]. Such endeavors face massive challenges of habitat and prey availability but assuming these are overcome, the question of the founder's origin remains. The genetic distinctiveness of Asiatic cheetahs would argue that reintroduction efforts should attempt to use cheetahs from Iran. However, this population is critically endangered and cannot sustain removals. Both Southern and Northern-East African cheetahs would have sufficient genetic variability to be considered as independent source populations. Thus, the choice of the most promising source population should be based on ecological, behavioral and viability criteria with minimum taxonomic swamping. In any case, the current Iranian cheetahs will probably remain the only representatives of the subspecies *A. j. venaticus* in Asia for the foreseeable future.

Current conservation and management strategies are usually based on the recognition of the subspecies taxonomy. In the case of the cheetah this has rarely been considered, as cheetahs were found to have little genetic variation [44,178]. My data suggest this viewpoint to be valid for the two sub-Saharan subspecies *A. j. jubatus* and *A. j. raineyi*, which could not be entirely separated in the mitochondrial population structure analysis. However, I show that Northern-East African, Southern African and Asiatic cheetahs are long-term geographic isolates with independent evolutionary histories. Moreover, I demonstrate that the critically endangered Iranian cheetahs are an autochthonous, monophyletic population and the last representatives of the Asiatic cheetah. My data also support the view of an independent subspecies status for the cheetahs in North Africa.

This population may be genetically contiguous with those from West Africa (Senegal–Niger), historically classified as *A. j. hecki*, but additional sampling is required to resolve this issue [157]. Also, it will be important to survey adaptive genetic variation in the cheetah subspecies to better understand evolutionary differentiation caused by ecological adaptation. Based on my results, I can conclude that unique diversity remains in the cheetahs of Africa and Asia and that conservation of these populations, especially of the critically low numbering Iranian individuals, should rank high among felid conservation priorities.

1.2. Panmictic cheetah population in Botswana

In the light of the latter findings, I further investigated the Botswana cheetahs representing the second largest cheetah population in Africa, in collaboration with the National Zoological Gardens research team (Pretoria, South Africa). Within this comprehensive genetic survey on the Botswana population, I analyzed the population structure for the establishment of relevant conservation strategies in regard to the increased persecutions by livestock farmers, the depletion of their prey base, the fragmentation of the environment, and illegal trade that threaten this cheetah population.

1.2.1. Genetic diversity and population structure

The level of genetic diversity within Botswana (H_E = 0.620; Table 6) was comparable to populations from Namibia (0.640 - 0.708), the Serengeti in Tanzania (0.599), northern east (0.674) and southern Africa (0.698) [30,203]. Weak subdivision among the geographical cheetah populations suggests that gene flow occurs. Similar low genetic divergence was observed in Namibian cheetahs originating from seven geographic regions [30]. The authors indicated that increased gene flow in Namibian cheetahs might be due to translocation of cheetah from farm areas [30]. However, the number of cheetah translocations conducted in Botswana was low and rarely involved the movement of cheetahs across regions (*CCB pers comm.*). Cheetahs have large home ranges [204]; [205] and males have been shown to migrate far from their natal range (*CCB pers comm.*). Therefore the low genetic divergence and high levels of gene flow can be attributed to natural cheetah movements. Interestingly, the Moremi population appeared

as a ‘distinct’ group compared with the neighboring Ghanzi cheetahs (Fig. 8; Table 7). The Okavango delta (Fig. 2) might act as a potential natural barrier between these two populations. However, these results obtained from a limited sample set would require further investigations. Fieldwork with radio-collared animals is ongoing and, besides providing new samples, will explore the influence of the Okawango as a barrier for cheetah movements (Brokehuis *in prep.*).

1.2.2. Implication for conservation

In summary, genetic and behavioral data from this study offers a baseline for future studies and will contribute to the development of management strategies for cheetah conservation in Botswana. The absence of a strong genetic structuring is likely a consequence of substantial gene flow among cheetahs from the different regions and suggests that Botswana wild cheetahs can be managed as a single population. The persistence of genetic connectivity between cheetah populations in Botswana will depend critically on future minimized habitat degradation. Thus it is imperative that management strategies and policies incorporate knowledge in regards to land use and management and focus on maintenance and/or creation of corridors between cheetah populations to retain gene flow.

1.3. Outcome of the cheetah projects

Both cheetah projects already contributed to management decisions in the field and/or provided guidelines for future studies (*e.g.* isolation of the Okavango cheetahs; conservation program of the Iranian cheetah). Beyond, the publication in Molecular Ecology (2011) of my first project results highlighting the genetic singularity of each cheetah subspecies, was relayed to the general public via world-renowned media like the BBC [206] and USA Today [207]. This media coverage led my work to be cited in the Supreme Court of India as scientific reference against a project introducing Namibian cheetahs to India [177]. The initial reintroduction project relied on deductions made on the similarity of the cheetahs along their complete species range [202,208]. The petitioners gaining support from my work considered this governmental project as an

introduction of a new subspecies rather than a re-introduction of the previously existing cheetah subspecies in India, which would go against the IUCN guidelines.

2. Camelids project

2.1. Dromedary – a particular livestock species

Domestication is a gradual and complex process. While many questions about the genetic origin of the Bactrian camel and the dromedary remain to be resolved, with the surveys carried out during my PhD study, I gained much information about the process and dynamics of the dromedary domestication (*in prep* to be submitted in PNAS).

2.1.1. Origin of domestication vs globally shared diversity

I combined archeological knowledge with my genetic results obtained from a survey from the most comprehensive modern sample set covering the entire domestic species range. However, the fact that genetic diversity is shared across regions precludes firm conclusions about the possible center(s) of domestication based on the assumption of higher variation retained in the ancestral population(s). Instead my analysis suggests an extensive globalization of domestic dromedary diversity across its current distribution with a lower extent for the Horn of Africa. Most of the dromedary breeds' definitions reflect the breeder's tribes, while they are rarely based on color and body criteria [77]. Consequently I did not expect to observe structuring according to phenotypic traits. Indeed looking at the four other regions more closely, I observed little differences between Southern Asian dromedaries and those confined to Sahara, North and South Arabian Peninsula (Table 9), as reflected in the comparable amounts of gene exchange (Table 10). For a minimum number of four ancestral populations (K = 4), some dromedaries from Oman and the UAE showed admixture with the cluster containing Asian individuals (Fig. 11). These results illustrate the traditional use of trading roads and the cultural dialogue between the east coast of the southern Arabian Peninsula and Persia (today's Iran) across the Gulf of Oman (Fig. 1). A final interesting observation concerns the genetic make up of the Australian dromedary population. Although the animals were imported from a single geographic area [64,86], all of the mtDNA haplogroups (Fig. 9)

and similar levels of nuclear diversity (Fig. 11; Table 15) are represented in the current domestic and feral Australian camel population. This mirrors the fact that the extensive admixture and absence of phylogeographic structure in the dromedary population of the Old World was already accomplished by the middle 19th century.

	mtDNA (867 bp)						
Populations	No. drom.	Haplotypes	Var. sites	H_d	π	k	θ_S
Australia (AU)	38	11	13	0.814 (0.052)	0.0036 (0.0021)	3.153 (1.670)	3.094 (1.216)
Iran (IR)	30	12	15	0.717 (0.090)	0.0039 (0.0023)	3.396 (1.788)	3.786 (1.484)
Pakistan (PK)	38	7	8	0.588 (0.088)	0.0021 (0.0014)	1.793 (1.059)	1.904 (0.848)
India (BD)	19	3	2	0.632 (0.073)	0.0009 (0.0008)	0.804 (0.606)	0.572 (0.427)
Southern Asia	125	22	19	0.711 (0.042)	0.0029 (0.0017)	2.502 (1.358)	3.518 (1.129)
	Microsatellite (17 loci)						
Populations	No. drom.	TNA	MNA/locus	Ar	H_E	H_O	F_{IS}
Australia (AU)	59	99	5.82 (3.54)	1.60	0.604 (0.050)	0.544 (0.016)	0.100
Iran (IR)	28	98	5.76 (3.60)	1.61	0.616 (0.047)	0.574 (0.023)	0.070
Pakistan (PK)	39	99	5.82 (3.78)	1.62	0.617 (0.047)	0.561 (0.019)	0.092
India (BD)	19	81	4.76 (2.44)	1.57	0.574 (0.062)	0.588 (0.028)	-0.025
Southern Asia	145	121	7.12 (4.87)	1.62	0.617 (0.048)	0.560 (0.010)	0.092

Table 15. Genetic diversity of dromedaries of the Southern Asia region inferred from mitochondrial and 17 microsatellites data.

The lack of phylogeographic differentiation illustrates the globalization of diversity. I propose that the dromedary's role in cross-continental trade networks gave rise to intense sharing of genetic variation. The long-standing tradition of exploiting one-humped camels is characterized by the exchange, selling or mating of pack animals at ancient trading centers and caravanserais along the routes connecting the Arabian Peninsula with the Sahara and the Levant to the Far East, with northern Arabia as the crossroads (Fig. 1). This highlights the extensive back-and-forth movements as a unique feature of the dromedary as opposed to other livestock.

2.1.2. Introduction of Arabian camels to Africa

Independently of the genetic marker, HAF was identified as the most genetically distant and distinct population. This was clearly reflected in the STUCTURE results (Fig. 11), the highest genetic differentiation (Table 9, Fig. 10 and 12) and the lowest *Nm* values (Table 10). It contrasts thoroughly with the SHR population (*i.e.* Sudan), which shows close genetic affinity with all other regions, but to lower extent with its closest neighbor (*i.e.* Ethiopia, HAF), reflecting the geographical barriers and possibly different cultural

patterning in camel production between these two regions. These observations are also in agreement with zooarchaeological records, which state that dromedaries were introduced into north-eastern Africa as domesticated animals via the Sinai (Fig. 1), possibly starting during the Persian Period (525 – 404 BCE; [63,74] and intensifying in Roman times [209]. However, the first unequivocal evidence for the presence of camels in north-western Africa is much later and comes from archaeological levels dating to the late Classical/early Byzantine Period. In the lack of genetic and zooarchaeological evidence of distinct domestication event, my results indicate a particular genetic history for the dromedary population of the Horn of Africa. It shows that HAF was not as much affected as the other populations by the globalization of genetic diversity due to its isolation from the northern part of the continent by ecogeographical barriers, such as the Ethiopian Highlands and the Sudd or Bahr al Jabal in South Sudan. Moreover, many areas located around the Horn of Africa are infested with trypanosomosis, which must have been a major limitation to the expansion of camel husbandry as well (Fig. 1). In this context, there are only a couple of possible routes by which domestic camels could have entered the region, both of which involve a migration of dromedaries from the Arabian Peninsula. Arabian camels could have reached the Horn of Africa either directly across the Gulf of Aden or by travelling south along coastal roads in south-eastern Egypt and north-western Sudan (Fig. 1). A seaborne introduction appears more likely, as there is increasing evidence for the role of the southern Arabian Peninsula as a corridor between the African and Asian continents for the movements of crops and livestock [210], *e.g.* zebu cattle and fat-tailed sheep [211]. Additional evidence might come from socio-ethological observations; today's Horn of Africa camels are used largely for milk production rather than for riding and transportation and this could bear similarities with practices during the early stage of camel husbandry in south-east Arabia [63,70]. In any case, Arabian camels have been introduced to the African continent via at least two entry points. It is worth noting that the dromedary dung from the site of Qasr Ibrim in South Egypt dated around 740 BCE has been interpreted as indicative for an early introduction via the Horn of Africa [72]. However, in view of the ecogeographical barriers separating the lower Nile from its upper Basin, this is not very likely. A transfer across the Red Sea (Fig. 1) is

possible but 1st millennium BCE camel remains from coastal sites in south-eastern Egypt and north-western Sudan would be necessary to confirm this third potential route of camel imports into Africa.

2.1.3. Domestication scenarios

My data show that at least six female lines contributed to the current gene pool. It is worth noting that this amount of maternal diversity is similar to that observed for example in goats, cattle and donkeys [66,67,161,212,213].

Three scenarios can potentially explain the patterns of genetic diversity recorded here: at the time of domestication the initial gene pool was captured from *(i)* one unique and highly diverse wild dromedary population, *(ii)* two independent source populations, each represented by one of the two observed ancestral lineages, or *(iii)* a primary small population of domesticates, with subsequent recurrent introgression of wild lineage(s) into the early domesticated gene pool. As none of the two lineages can be linked to a geographical region, it is difficult to decide which scenario is the most likely. If the first one applies, my data would support an effective population size (N_e) of 10,000 to 27,000 females for the ancestral wild source population ($T = 2N_e(1- 1/k)$ in generations). Parallel to the present-day situation in the domestic form it can be assumed that wild dromedary populations were organized in harems; for this reason the total N_e might not have been very much larger. In contrast to Luikart et al. [66] who rejected the hypothesis of a single domestication event in *Capra* based on their estimated ancestral N_e, I regarded the above estimate as high but plausible and thus the first scenario as not improbable. On the other hand, multiple maternal origins were more likely in livestock domestication [175]. As displayed in the mismatch distribution, lineage L1 might have expanded earlier than L2 (Fig. S5). Even so, it cannot be decided which of the scenarios *(ii)* or *(iii)* applies, as I face difficulties disentangling the occurrence of independent domestication events from recurrent introgression of wild lineage(s) into the early domesticated gene pool. The poor knowledge of the Holocene distribution of wild one-humped camels on the Arabian Peninsula is a further limiting factor. To date, concentrations of bones indicative of larger camel herds have only been found in Neolithic to Bronze Age contexts on the eastern coast [61,73,214,215]. Isolated pre-Iron Age camel remains have also been identified in

the Southern Levant. However, the specimens turned out to be intrusive in the archaeological context or their ^{14}C-datings to be unreliable [72,216]. As for the Southern Arabian Peninsula, this region might indeed have sustained a wild population in prehistoric times, as mangrove habitats might have been present on the Omani and possibly Yemeni coasts. Although the archaeological record is too incomplete to detail the wild dromedary's distribution in Holocene times, it can be assumed that it was quite restricted compared to the ancestral range of other livestock species. The restricted distribution of the wild one-humped camel probably accounts for its demise less than a millennium after the appearance of the domestic form [61,73]. In this respect, palaeogenetic investigation of wild and early domestic camels could provide insights into the repartition of the ancestral diversity. It might also help in detecting early phylogeographic signal(s) prior to the intensive gene flow induced by human selection and large-scale trading. While poor DNA preservation in arid regions would pose a significant technical challenge the work, this approach would represent the only possibility to distinguish between the three scenarios proposed in this study.

The striking feature in the history of domestication of *Camelus dromedarius* is that the current gene pool stems from a surprisingly high initial diversity relative to the limited distribution of their wild ancestors. This contrasts with the histories of other livestock, where multiple populations were domesticated over large geographical areas and wild ancestors co-existed over an extended period of time allowing for recurrent introgression. My results make it likely that a significant part of the wild species' overall diversity contributed to the foundation of the genetic variation present today. This underlines the potential of the species to adapt sustainably and to face increasing desertification and climatic change.

2.1.4. Dromedary an endangered livestock?

In regard to conservation of the genetic diversity, no deep population structure has been detected. This reflects the traditional usage of the dromedary as a multipurpose livestock (absence of structuring in terms of 'breed' characterization) and as a beast of burden across the continents for centuries (absence of structuring due to massive gene flow between the populations). Unlike other livestock species highly concerned by genetic

depletion [20,76], the traditional dromedary husbandry seems to have fostered the genetic diversity inherited from the wild ancestors. There is however a reserved judgment about the global dromedary diversity. Husbandry may slowly move to an intensification of the production systems, racing camels are a particular case. They are part of a parallel trade economy and were not included in the study to avoid bias in the inference of evolutionary history. However with the development of embryo-transfer [217,218] and cryo-preservation of sperm [219], these priceless animals may face in few generations the same issues about inbred diversity that we encounter today in European cattle and sheep ([20] and *ref. therein*).

2.2. Hybridization of the last wild camels: a threat among others

The results achieved on wild and Bactrian camels had an immediate impact on conservation decisions. From the non-invasive survey, I detected the presence of domestic individuals in strictly protected areas. Among the 40 reliable individual profiles, two different samples presented levels of admixture similar to the one observed for hybrids issued of a backcrossing between a F1 and a wild camel. Unfortunately the set of markers used in this study was not powerful enough to support this assumption with a high confidence. The occurrence of a F1 hybrid was detected actually in the semi-captive herd of the Gobi A. Therefore this individual should be prevented to mate with a “real” wild camel. Even though this study revealed a low level of admixture in the wild herd, nevertheless it highlighted two aspects for the wild camel genetic diversity: first, the unique evolutionary history of the wild camel, and second, the process of hybridization as a potential threat for the wild diversity. These unpublished results (*in prep*) were I depresented to the Mongolian and international scientific communities. The fact that wild camel uniqueness might be jeopardized by the sympatry with its domestic relatives was a threat almost ignored from decision makers until then. During the National Conservation Strategy Workshop held in Mongolia, Oct. 2010, “preserving the genetic integrity of the wild camel” was included as a conservation priority to the draft of the Mongolian National Conservation Strategy for the wild camel and its desert habitat[5] [80]. In the view of this conservation plan, the Mongolian legislation on the hybrid husbandry has already

[5] The conservation strategy plan should be presented to the Mongolian Ministry of Nature, Environment and Tourism for official endorsement current 2012.

been strengthened, requiring the elimination of any hybrids among the domestic herds and inside the strictly protected areas. In addition, usage of these animals for racing purposes has been forbidden, reducing the economic interest of such beasts. However the severe repercussion of the habitat destruction on the extreme low census might lead to *Camelus ferus*' extinction before the wild genetic diversity becomes obsolete.

3. Limitations and perspectives of the projects

Choosing informative molecular markers is critical. Historically, the vast majority of genetic studies for wildlife conservation have been based on a limited range of markers, typically mtDNA and/or microsatellites. While these studies have provided some valuable insights [67,179,203,212], they are hampered by the limitations of the markers used. MtDNA, a well-established and convenient marker, provides information from only a single locus, while multiple independent samples are required to estimate population genetic parameters with statistical confidence [220]. Microsatellites may fill this requirement but their mutational mechanism remains poorly understood, which makes them hard to model (*e.g.* for phylogeny reconstruction). As a result, mtDNA and microsatellites have provided useful but limited information for evolutionary inference and conservation management. During the last ten years, the conservation genetics field has tried to turn to single nucleotide polymorphism (SNP) analysis [221]. SNPs have emerged as more suitable markers for investigating complex and/or recent demography due to their density, their equal distribution across the different parts of the genome, and their better understood mutational mechanisms. This approach was already much more in use for genetic investigation of livestock diversity [164,222]. In contrast to mtDNA and microsatellites, SNP surveys were limited to sister-species of model organisms for which genomes are at least partially sequenced (either genes of interest or full genomes). However this was not the case with both the cheetah, as *Acinonyx* is a monotypic genus, and the *Camelus* genus, which shows really large divergences between its different taxa.

Today the genetics field faces a technical revolution. Whole-genome sequencing becomes affordable for non-model species. The detection of specific markers spread along the entire genome provides us with sufficient statistical power for inferring complex

population genetics questions. Whereas this technology will not help to solve questions like the origin of the domestication, we can take advantage of these new developments to document potential gene regions and genes artificially selected for their economical interest. From a wildlife conservation genetics viewpoint, we will be able to investigate local adaptation by using a landscape genetic approach, a goal that was impossible to reach with mtDNA and microsatellites. For example in the case of the cheetahs, I observed that each of the subspecies presents its own diversity and diverged from each other at least 20 000 years ago. With the classical mtDNA/ microsatellite markers I had limited information to disentangle two of the scenarios that might have led to this pattern: (i) directional selection and local adaptation of each subspecies due to the heterogeneity of the environments, or (ii) drift independently affecting the relic populations resulting from deep changes of the paleo-climate during the Pleistocene. While drift randomly affects all loci distributed along the genome, natural selection shapes the genome in increasing the frequency of advantageous alleles and leads to quick fixation of the allele of interest. The effect of directional selection will be localized to a specific locus, which makes it difficult to detect among the three billions bases that compose mammalian genomes. There are similar limitations that prevent from detecting any signal of artificial selection in the context of domestication of the Old World camelids.

During the initial phase of my PhD project, none of these technologies were already applied to any of the species in the project. Even if I did not apply these new technologies, often called Next Generation Sequencing, directly to my research, groups and projects at the Institute of Population Genetics using these approaches surrounded me. I therefore benefited from their knowledge and learned from my colleagues. This has allowed me to complete a grant application for a post-doctoral project (Genomic investigation of the Asiatic wolf – PI: Prof. Robert Wayne; UCLA) dealing with conservation genomics – the future of this field.

4. Conservation, a multi-disciplinary field

Conservation genetics is not a goal in itself but a tool among others. Archeological, zootechnical[6], but also geographical knowledge were needed in the different projects for comprehensive interpretation of the genetic data. As we have seen in both cases of the wild camel and the Indian cheetah, conservation genetics' results might also be used as a way of raising awareness in decision makers and the general public. However conservation decisions on population management should not be restricted to genetics. For example, in the case of the Iranian cheetahs, the genetic variation was higher than expected and observed in other "critically endangered" felids (*e.g.* Florida panthers H_E ranging from 0.167 to 0.318; [199]). Nevertheless if the anthropogenic pressures cannot be reduced and if the population decline cannot be curbed, despite their genetic uniqueness, conservation projects might have to consider population reinforcement of the Iranian population in order to maintain the fragile equilibrium of the ecosystem. This decision should not be only involve geneticists, but should also take into account the results of scientific studies from other fields. The success of a conservation project will have more impact if it combines the results of diverse research disciplines such as genetics, ecology, ethology, physiology, natural resource and population management, but also ethics, education, law, social and political sciences.

[6] Science and technology of animal husbandry

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APPENDIX

Table S1. Details on the samples used in the cheetah phylogeography study

No.	ID	Type	Origin (time*)	Collection place
1	AJI 01	Faeces	Iran (IR)	IR
2	AJI 02	Faeces	IR	IR
3	AJI 03	Faeces	IR	IR
4	AJI M1A	Faeces	IR	IR
5	AJI M2A	Faeces	IR	IR
6	AJI T	Faeces	IR	IR
7	AJI 08	Faeces	IR	IR
8	AJI 11	Faeces	IR	IR
9	AJI 04	Museum tissue	IR	Sharjah, AE
10	HZM 2.26502	Hide	Oman (OM; 1977)	HZM, GB
11	ZMB 56122	Hide	Jordan (JO)	NHM Berlin, DE
12	BMNH ZD 1939.536	Hide	IR	NHM London, GB
13	SAPM-Gepard-1a-F6-Ba	Metatarsal bone	IR, Bastam (800–900 ce)	SAP Munich, DE
14	SAPM-Gepard-1b-TeS1	Mandible + vertebra	IR, Tahkt-e Suleyman (800–900 ce)	SAP Munich, DE
15	BMNH ZD 1943.56	Museum tissue	Iraq (IQ; 1928)	NHM London, GB
16	BMNH 32.4.7.1	Hide	India (IN; 1925)	NHM London, GB
17	SMNS 18941	Maxillot. bone	Egypt (EG; T. v.Heuglin; 1850s)	SMN Stuttgart, DE
18	SMF 58993	Hide	EG, Libyan Desert (1974)	SM Frankfurt, DE
19	NMW 12071	Hide	Libya (LY)	NHM Vienna, AT
20	NMW 12070	Hide	LY	NHM Vienna, AT
21	BMNH ZD 1957.312	Hide	LY (1955)	NHM London, GB
22	BMNH ZD 1939.1685	Museum tissue	Algeria (DZ)	NHM London, GB
23	ZMB 56277	Maxillot. bone	Western Sahara (EH)	NHM Berlin, DE
24	ZMB 42242	Hide	EH, Rio d'Oro	NHM Berlin, DE
25	ADJ 2	Hair	Ethiopia (ET), custom's seizure	DECAN, DJ
26	ADJ 3	Hair	ET, custom's seizure	DECAN, DJ
27	ADJ 4	Hair	ET, custom's seizure	DECAN, DJ
28	ADJ 5	Hair	ET, custom's seizure	DECAN, DJ
29	ADJ 6	Hair	ET, custom's seizure	DECAN, DJ
30	ADJ 8	Hair	Djibouti (DJ)	DECAN, DJ
31	#4421	Skin	Somalia (SO)	Sharjah, AE
32	#4499	Skin	SO	Sharjah, AE
33	#4500	Skin	SO	Sharjah, AE
34	#4203	Skin	SO	Sharjah, AE
35	#4208	Skin	SO	Sharjah, AE
36	#4202	Skin	SO	Sharjah, AE
37	#4223	Skin	SO	Sharjah, AE
38	#4205	Skin	SO	Sharjah, AE
39	#4229	Skin	SO	Sharjah, AE
40	#4228	Skin	SO	Sharjah, AE
41	#4206	Skin	SO	Sharjah, AE
42	#4201	Skin	SO	Sharjah, AE
43	#4418	Skin	SO	Sharjah, AE
44	#4222	Blood	SO	Sharjah, AE
45	#4216	Skin	SD	Sharjah, AE
46	LP4304	Hair	Northern-east Africa (N-E.A)	La Palmyre, FR
47	#4415	Skin	N-E.A	Sharjah, AE
48	SMNS 38432	Hide	DJ, custom's seizure (<1985)	SMN Stuttgart, DE

49	ADJ 1	Hair	ET, custom's seizure	DECAN, DJ
50	ADJ 7	Hair	ET, custom's seizure	DECAN, DJ
51	Claudia	Faeces	Kenya (KE)	DECAN, DJ
52	ZMB34306	Maxillot. bone	Tanzania (TZ)	MHN Berlin, DE
53	ZMB56287	Maxillot. bone	TZ	MHN Berlin, DE
54	ZMB56302	Maxillot. bone	TZ	MHN Berlin, DE
55	ZMB56306	Maxillot. bone	TZ	MHN Berlin, DE
56	ZMB56309	Maxillot. bone	TZ	MHN Berlin, DE
57	Tigger	Faeces	KE	DECAN, DJ
58	ZMB56128	Maxillot. bone	TZ	MHN Berlin, DE
59	ZMB56289	Maxillot. bone	TZ	MHN Berlin, DE
60	ZMB56293	Maxillot. bone	TZ	MHN Berlin, DE
61	ZMB56299	Maxillot. bone	TZ	MHN Berlin, DE
62	GACH 18/08	Blood	South Africa (ZA)	Pretoria NZG, ZA
63	GACH 23/06	Blood	ZA	Pretoria NZG, ZA
64	GACH 26/08	Blood	ZA	Pretoria NZG, ZA
65	GACH 33/08	Blood	ZA	Pretoria NZG, ZA
66	GACH 35/08	Blood	ZA	Pretoria NZG, ZA
67	GACH 38/08	Blood	ZA	Pretoria NZG, ZA
68	GACH 42/08	Blood	ZA	Pretoria NZG, ZA
69	GACH 44/08	Blood	ZA	Pretoria NZG, ZA
70	GACH 45/08	Blood	ZA	Pretoria NZG, ZA
71	#1463	Lung	Namibia (NA) descendant	La Palmyre, FR
72	#1557/NMSZ 2001.37	Muscle	NA	NMSZ, GB
73	S1571	Muscle	ZA descendant	Private owner, DE
74	1921	Muscle	NA descendant	Zoo Salzburg, AT
75	#3155/NMSZ 2000.151.2	Muscle	NA descendant	NMSZ, GB
76	#3240	Faeces	ZA descendant	Zoo Vienna, AT
77	GACH 34/08	Blood	ZA	Pretoria NZG, ZA
78	#3779/NMSZ 1999.221	Muscle	ZA descendant	NMSZ, GB
79	Douma	Muscle	ZA	Zoo Lunaret, FR
80	GACH 25/08	Blood	ZA	Pretoria NZG, ZA
81	GACH33	Blood	ZA	Pretoria NZG, ZA
82	GACH 01/08	Blood	Botswana (BW)	Pretoria NZG, ZA
83	GACH 02/08	Blood	BW	Pretoria NZG, ZA
84	GACH 11/08	Blood	BW	Pretoria NZG, ZA
85	GACH 12/08	Blood	BW	Pretoria NZG, ZA
86	GACH 15/08	Blood	BW	Pretoria NZG, ZA
87	GACH 16/08	Blood	BW	Pretoria NZG, ZA
88	#4268	Skin	NA	Sharjah, AE
89	#2486/ZFMK 2005.357	Hide	ZA, king cheetah	MHN Bonn, DE
90	RMCA 454	Maxillot. bone	D.R.Congo (CD)	RMCA, BE
91	RMCA 1236	Maxillot. bone	CD	RMCA, BE
92	RMCA 19237	Maxillot. bone	CD	RMCA, BE
93	RMCA 22347	Maxillot. bone	CD	RMCA, BE
94	RMCA 22390	Maxillot. bone	CD	RMCA, BE
95	*Puma concolor*	Blood	Unknown	Zoo Salzburg, AT

*Date of collection of historical samples, if available.

#: registration number in the international cheetah studbook; maxillot. bone: maxilloturbinate bone; museum tissue: dried tissue remaining on the skull; IR: Ariz & Bafq Protected Area, eastern Yazd province, Naybandan Wildlife Refuge south of Tabas, IR; Sarjah: Breeding Centre for Endangered Arabian Wildlife, Sharjah, AE; HZM:

Harrison Institute, Sevenoaks, GB; NHM: Natural History Museum; SAP: State Collection of Anthropology and Palaeoanatomy, Munich, DE; SMN: Museum of Natural Sciences, Stuttgart, DE; SMN: Naturmuseum Senckenberg, Frankfurt, DE; DECAN: DECAN rescue centre, Djibouti, DJ; La Palmyre: Parc zoologique de La Palmyre, FR; Zoo Lunaret: Parc Zoologique Henri de Lunaret, Montpellier, FR; NZG: National Zoological Gardens, Pretoria, ZA; NMSZ: National museum of Scotland, Edinburgh, GB; RMCA: Royal Museum of Central Africa, Tervuren, BE. Country codes following ISO 3166-Alpha 2.

Table S2: Summary of genetic relationships and social groups of wild caught Botswana cheetahs

ID no	Location caught	Sex	Age (months)	Social group[a]	Soc. group genetic. related	Genetic relationships	Genetic probability[c]
# 1[b]	Jwaneng	F	> 30 < 48	Family 1	Yes	Mother of # 5, 6, 7, 8, 9	1.000
# 5	Jwaneng	M	> 6 < 12	Family 1	Yes	Sibling of # 6, 7, 8, 9 / Offspring of # 1	1.000
# 6	Jwaneng	F	> 6 < 12	Family 1	Yes	Sibling of # 5, 7, 8, 9 / Offspring of # 1	1.000
# 7	Jwaneng	M	> 6 < 12	Family 1	Yes	Sibling of # 5, 6, 8, 9 / Offspring of # 1	1.000
# 8	Jwaneng	F	> 6 < 12	Family 1	Yes	Sibling of # 5, 6, 7, 9 / Offspring of # 1	1.000
# 9	Jwaneng	M	> 6 < 12	Family 1	Yes	Sibling of # 5, 6, 7, 8 / Offspring of # 1	1.000
# 22[b]	Jwaneng	F	> 48 < 96	Family 2	Yes	Mother of # 17, 18, 19, 20, 21	1.000
# 17	Jwaneng	M	> 12 < 18	Family 2	Yes	Sibling of # 18, 19, 20, 21 / Offspring of # 22	1.000
# 18	Jwaneng	M	> 12 < 18	Family 2	Yes	Sibling of # 17, 19, 20, 21 / Offspring of # 22	1.000
# 19	Jwaneng	F	> 12 < 18	Family 2	Yes	Sibling of # 17, 18, 20, 21 / Offspring of # 22	1.000
# 20	Jwaneng	M	> 12 < 18	Family 2	Yes	Sibling of # 17, 18, 19, 21 / Offspring of # 22	1.000
# 21	Jwaneng	M	> 12 < 18	Family 2	Yes	Sibling of # 17, 18, 19, 20 / Offspring of # 22	1.000
# 29[b]	Jwaneng	F	> 48 < 96	Family 3	Yes	Mother of # 28, 30	1.000
# 28	Jwaneng	F	> 12 < 18	Family 3	Yes	Sibling of # 30 / Offspring of # 29	1.000
# 30	Jwaneng	F	> 12 < 18	Family 3	Yes	Sibling of # 28 / Offspring of # 29	1.000
# 33[b]	Jwaneng	F	> 30 < 48	Family 4	Yes	Mother of # 49, 50, 51, 52	1.000
# 49	Jwaneng	F	> 12 < 18	Family 4	Yes	Sibling of # 50, 51, 52 / Offspring of # 33	1.000
# 50	Jwaneng	M	> 12 < 18	Family 4	Yes	Sibling of # 49, 51, 52 / Offspring of # 33	1.000
# 51	Jwaneng	M	> 12 < 18	Family 4	Yes	Sibling of # 49, 50, 52 / Offspring of # 33	1.000
# 52	Jwaneng	F	> 12 < 18	Family 4	Yes	Sibling of # 49, 50, 51 / Offspring of # 33	1.000
# 37[b]	Jwaneng	F	> 48 < 96	Family 5	Yes	Mother of # 34, 35, 36, 38	1.000
# 34	Jwaneng	M	> 0 < 6	Family 5	Yes	Sibling of # 35, 36, 38 / Offspring of # 37	1.000
# 35	Jwaneng	M	> 0 < 6	Family 5	Yes	Sibling of # 34, 36, 38 / Offspring of # 37	1.000
# 36	Jwaneng	F	> 0 < 6	Family 5	Yes	Sibling of # 34, 35, 38 / Offspring of # 37	1.000
# 38	Jwaneng	F	> 0 < 6	Family 5	Yes	Sibling of # 34, 35, 36 / Offspring of # 37	1.000
# 39[b]	Ghanzi	F	> 48 < 96	Family 6	Yes	Mother of # 41, 42	1.000
# 41	Ghanzi	F	> 18 < 30	Family 6	Yes	Sibling of # 42 / Offspring of # 39 and 43	1.000
# 42	Ghanzi	F	> 18 < 30	Family 6	Yes	Sibling of # 41 / Offspring of # 39 and 43	1.000
# 58[b]	Ghanzi	F	> 48 < 96	Family 7	Yes	Mother of # 55, 56, 57, 59, 60	1.000
# 55	Ghanzi	M	> 6 < 12	Family 7	Yes	Sibling of # 56, 57, 59, 60 / Offspring of # 58	1.000
# 56	Ghanzi	M	> 6 < 12	Family 7	Yes	Sibling of # 55, 57, 59, 60 / Offspring of # 58	1.000
# 57	Ghanzi	F	> 6 < 12	Family 7	Yes	Sibling of # 55, 56, 59, 60 / Offspring of # 58	1.000
# 59	Ghanzi	F	> 6 < 12	Family 7	Yes	Sibling of # 55, 56, 57, 60 / Offspring of # 58	1.000
# 60	Ghanzi	M	> 6 < 12	Family 7	Yes	Sibling of # 55, 56, 57, 59 / Offspring of # 58	1.000
# C10[b]	Moremi GR	F	> 48 < 96	Family 8	Yes	Mother of # C1	1.000

# C1	Moremi GR	F	> 18 < 30	Family 8	Yes	Offspring of # C10	1.000
# 64[b]	Ghanzi	F	> 48 < 96	Lone 1	Yes	None	N/A
WD7[b]	Ghanzi	M	> 12 < 18	Lone 2	Yes	None	N/A
# 23	Ghanzi	M	> 0 < 6	Lone 3	N/A	Distantly related to # 44 (could be cousins)	0.351
# 26[b]	Ghanzi	M	> 6 < 12	Lone 4	Yes	None	N/A
# 27	Ghanzi	M	> 48 < 96	Lone 5	N/A	Distantly related to # 46	0.547
						Distantly related to # 53	0.470
# 40	Ghanzi	M	> 0 < 6	Lone 6	N/A	Offspring of # 43	0.973
# 43[b]	Ghanzi	M	> 96 < 144	Lone 7	N/A	Father of # 40	0.973
						Father of # 41 and 42	1.000
# 44[b]	Ghanzi	M	> 30 < 48	Lone 8	N/A	Distantly related to # 23 (could be cousins)	0.321
# 53	Ghanzi	M	> 96 < 144	Lone 9	N/A	Distantly related to # 46	0.472
						Distantly related to # 27	0.470
# 54[b]	Ghanzi	M	> 30 < 48	Lone 10	N/A	None	N/A
# C6[d]	Moremi GR	M	> 30 < 48	Lone 11	Yes	None	N/A
# C15[b]	Moremi GR	F	> 48 < 96	Lone 12	Yes	None	N/A
# C21[b]	Moremi GR	F	> 30 < 48	Lone 13	Yes	None	N/A
# C33[b]	Moremi GR	M	> 48 < 96	Lone 14	Yes	None	N/A
WD1[b]	Sekoma	M	> 48 < 96	Lone 15	Yes	None	N/A
# 63[b]	Tshabong	M	> 48 < 96	Lone 16	Yes	None	N/A
TULI[b]	Tuli	F	> 30 < 48	Lone 17	Yes	None	N/A
# 2[b]	Jwaneng	F	> 48 < 96	Female Coalition 1	Yes	Sibling of # 3	0.853
						Related to # 4 (possibly mother)	1.000
# 3	Jwaneng	F	> 48 < 96	Female Coalition 1	Yes	Sibling of # 2	0.853
						Related to # 4 (possibly aunt)	0.853
# 4	Jwaneng	F	> 30 < 48	Female Coalition 1	Yes	Related to # 2 (possibly daughter)	1.000
						Related to # 3 (possibly niece)	0.853
# 14[b]	Jwaneng	M	> 48 < 96	Male coalition 1	No	None	N/A
# 15	Jwaneng	M	> 48 < 96	Male coalition 1	Yes	Sibling of # 16	1.000
# 16[b]	Jwaneng	M	> 48 < 96	Male coalition 1	Yes	Sibling of # 15	1.000
# 10[b]	Ghanzi	M	> 18 < 30	Male coalition 2	No	None	N/A
# 11	Ghanzi	M	> 18 < 30	Male coalition 2	Yes	Sibling of # 24 and 25	1.000
# 24[b]	Ghanzi	M	> 30 < 48	Male coalition 2	Yes	Sibling of # 11 and 25	1.000
# 25	Ghanzi	M	> 30 < 48	Male coalition 2	Yes	Sibling of # 11 and 24	1.000
# 45[b]	Ghanzi	M	> 30 < 48	Male coalition 3	No	None	N/A
# 46[b]	Ghanzi	M	> 30 < 48	Male coalition 3	No	Distantly related to # 53	0.472
						Distantly related to # 27	0.547
# 47	Ghanzi	M	> 48 < 96	Male coalition 4	Yes	Sibling of # 48	1.000
						Related to # 32 (father or uncle)	1.000
# 48	Ghanzi	M	> 48 < 96	Male coalition 4	Yes	Sibling of # 47	1.000
						Related to # 32 (father or uncle)	1.000

# 12[b]	Sekoma	M	> 18 < 30	Male coalition 5	No	None	N/A
# 13[b]	Sekoma	M	> 18 < 30	Male coalition 5	No	None	N/A
# 31[b]	Ghanzi	F	> 6 < 12	Orphaned siblings 1	No	None	N/A
# 32[b]	Ghanzi	F	> 6 < 12	Orphaned siblings 1	No	Related to # 47 (daughter or niece)	1.000
						Related to # 48 (daughter or niece)	1.000
# 61[b]	Sekhutlane	M	> 6 < 12	Orphaned siblings 2	Yes	Sibling of # 62	1.000
# 62	Sekhutlane	M	> 6 < 12	Orphaned siblings 2	Yes	Sibling of # 61	1.000

[a] As determined by grouping and behaviour at time of capture; [b] Individuals used in population genetic analysis; [c] Genetic probability as determined by COLONY. M: Male; F: Female; [d] Individual #C6 was not included in the analysis as its profile was only 56% completed

Lab #	μsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
AEg001	x	x	JX946208	SAP	United Arab Emirates	Omani	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEg002	x	x	JX946240	SAP	United Arab Emirates	Omani	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEg003		x	JX946231	SAP	United Arab Emirates	Omani	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEg004		x	JX946241	SAP	United Arab Emirates	Omani	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEg005		x	JX946232	SAP	United Arab Emirates	Omani	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEs006		x	JX946208	SAP	United Arab Emirates	Khalfan	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEs007	x	x	JX946208	SAP	United Arab Emirates	Khalfan	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEs008	x	x	JX946208	SAP	United Arab Emirates	Khalfan	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEs009	x	x	JX946211	SAP	United Arab Emirates	Khalfan	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEs010	x	x	JX946242	SAP	United Arab Emirates	Khalfan	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEr011		x	JX946208	SAP	United Arab Emirates	na	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEr012		x	JX946211	SAP	United Arab Emirates	na	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEr013		x	JX946208	SAP	United Arab Emirates	na	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEr014		x	JX946208	SAP	United Arab Emirates	na	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEr015		x	JX946225	SAP	United Arab Emirates	na	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEr016		x	JX946206	SAP	United Arab Emirates	na	Murdoch University, Dubai, UAE	DNA	Vetmeduni
AEr017	x			SAP	United Arab Emirates	Sougahn	Dubai, UAE	Blood (FTA card)	Nottingham
AEr018	x			SAP	United Arab Emirates	Sougahn	Dubai, UAE	Blood (FTA card)	Nottingham
AEr019	x			SAP	United Arab Emirates	Sougahn	Dubai, UAE	Blood (FTA card)	Nottingham
AEr020	x			SAP	United Arab Emirates	Sougahn	Dubai, UAE	Blood (FTA card)	Nottingham
AEr021	x			SAP	United Arab Emirates	Sougahn	Dubai, UAE	Blood (FTA card)	Nottingham
AEr022	x			SAP	United Arab Emirates	Sougahn	Dubai, UAE	Blood (FTA card)	Nottingham
AEr023	x			SAP	United Arab Emirates	Sougahn	Dubai, UAE	Blood (FTA card)	Nottingham
AEr024	x			SAP	United Arab Emirates	Sougahn	Dubai, UAE	Blood (FTA card)	Nottingham
AEr025	x			SAP	United Arab Emirates	Sougahn	Dubai, UAE	Blood (FTA card)	Nottingham
AEr026	x			SAP	United Arab Emirates	Sougahn	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr027	x			SAP	United Arab Emirates	Sougahn	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr028	x			SAP	United Arab Emirates	Shaheen	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr029	x			SAP	United Arab Emirates	Shaheen	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr030	x			SAP	United Arab Emirates	Shaheen	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr031	x			SAP	United Arab Emirates	Shaheen	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr032	x			SAP	United Arab Emirates	Shaheen	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr033	x			SAP	United Arab Emirates	Shaheen	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr034	x			SAP	United Arab Emirates	Shaheen	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr035	x			SAP	United Arab Emirates	Shaheen	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr036	x			SAP	United Arab Emirates	Shaheen	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr037	x			SAP	United Arab Emirates	Shaheen	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr038	x			SAP	United Arab Emirates	Misihan	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr039	x			SAP	United Arab Emirates	Misihan	Al Ain, UAE	Blood (FTA card)	Nottingham
AEr040	x			SAP	United Arab Emirates	Misihan	Al Ain, UAE	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
AEr041	x			SAP	United Arab Emirates	Misihan	Al Ain, UAE	Blood (FTA card)	Nottingham
AUx001	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx002	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx003	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx004	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx005	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx006	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx007	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx008	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx009	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx010	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx011	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx012	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx013	x	x	JX946209	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx014	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx015	x	x	JX946209	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx016	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx017	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx018	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx019	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx020	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx021	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx022	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx023	x	x	JX946206	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx024	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx025	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx026	x	x	JX946210	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx027	x	x	JX946211	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx028	x	x	JX946207	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx029	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx030	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx031	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx032	x			SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Nottingham
AUx033	x	x	JX946226	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx034	x	x	JX946211	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx035	x	x	JX946209	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx036	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx037	x	x	JX946211	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx038	x	x	JX946211	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx039	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
AUx040	x	x	JX946227	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx041	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx042	x	x	JX946228	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx043	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx044	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx045	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx046	x	x	JX946206	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx047	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx048	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx049	x	x	JX946229	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx050	x	x	JX946207	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx051	x	x	JX946207	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx052	x	x	JX946209	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx053	x	x	JX946226	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx054	x	x	JX946226	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx055	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx056	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx057		x	JX946207	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx058	x	x	JX946209	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx059	x	x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx060		x	JX946208	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
AUx061	x	x	JX946214	SAS	Australia	na	Murdoch University, Perth, Australia	DNA	Vetmeduni
BDx001	x	x	JX946208	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx002	x	x	JX946208	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx003	x	x	JX946211	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx004	x	x	JX946208	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx005	x	x	JX946206	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx006	x	x	JX946206	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx007	x	x	JX946208	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx008	x	x	JX946206	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx009	x	x	JX946208	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx010	x	x	JX946206	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx011	x	x	JX946211	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx012	x	x	JX946206	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx013	x	x	JX946208	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx014	x	x	JX946208	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx015	x	x	JX946211	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx016	x	x	JX946208	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx017	x	x	JX946208	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
BDx018	x	x	JX946208	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
BDx019	x	x	JX946206	SAS	Rajasthan, India	na	Dhaka, Bangladesh	Hair	Vetmeduni
DZw001	x	x	JX946208	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw002	x	x	JX946208	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw003	x	x	JX946208	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw004	x	x	JX946208	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw005	x	x	JX946243	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw006	x	x	JX946233	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw007	x	x	JX946208	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw008	x	x	JX946208	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw009	x	x	JX946206	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw010	x	x	JX946214	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw011	x	x	JX946208	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw012	x	x	JX946208	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw013	x	x	JX946208	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw014	x	x	JX946208	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw015	x	x	JX946208	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw016		x	JX946227	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZw017	x	x	JX946208	SHR	Algeria	Sahraoui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz018	x			SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz019		x	JX946208	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz020	x	x	JX946211	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz021	x	x	JX946208	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz022		x	JX946208	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz023	x	x	JX946208	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz024	x	x	JX946206	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz025	x	x	JX946208	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz026	x	x	JX946208	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz027	x	x	JX946208	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz028	x	x	JX946208	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz029	x	x	JX946208	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz030	x	x	JX946206	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz031		x	JX946208	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz032	x	x	JX946211	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz033	x	x	JX946208	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
DZz034	x	x	JX946208	SHR	Algeria	Targui	Sahara, Algeria	Blood (FTA card)	Vetmeduni
EG_001	x	x	JX946230	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_002	x	x	JX946209	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_003	x	x	JX946211	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_004	x	x	JX946206	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_005	x	x	JX946208	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
EG_006	x	x	JX946206	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_007	x	x	JX946208	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_008	x	x	JX946222	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_009	x	x	JX946208	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_010	x	x	JX946209	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_011	x	x	JX946214	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_012	x	x	JX946208	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_013	x			NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_014	x	x	JX946256	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_015	x	x	JX946208	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_016	x	x	JX946214	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_017	x	x	JX946206	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_018	x	x	JX946208	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_019	x	x	JX946214	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_020	x	x	JX946249	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_021	x	x	JX946209	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_022	x	x	JX946208	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_023	x	x	JX946209	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_024	x	x	JX946250	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_025	x	x	JX946257	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_026	x	x	JX946214	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_027	x	x	JX946206	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_028	x	x	JX946208	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_029	x	x	JX946209	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
EG_030	x	x	JX946214	NAP	Egypt	Jabali	Sinai, Egypt	Blood (FTA card)	Vetmeduni
ET_001		x	JX946214	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_002	x	x	JX946261	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_003	x	x	JX946218	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_004		x	JX946262	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_005	x	x	JX946214	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_006	x	x	JX946208	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_007	x	x	JX946208	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_008	x	x	JX946218	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_009	x	x	JX946211	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_010	x	x	JX946218	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_011	x	x	JX946208	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_012	x	x	JX946218	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_013	x	x	JX946258	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_014	x	x	JX946208	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_015	x	x	JX946259	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
ET_016	x	x	JX946208	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_017	x	x	JX946218	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_018	x	x	JX946206	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_019	x	x	JX946218	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_020	x	x	JX946260	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_021	x	x	JX946208	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_022	x	x	JX946208	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_023	x	x	JX946218	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_024	x	x	JX946258	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_025	x	x	JX946208	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_026	x	x	JX946214	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
ET_027	x	x	JX946214	HAF	Ethiopia	Borena	South Ethiopia	Blood (FTA card)	Vetmeduni
IRx001	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx002		x	JX946220	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx003	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx004	x	x	JX946221	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx005	x	x	JX946238	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx006	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx007	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx008	x	x	JX946250	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx009	x	x	JX946230	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx010	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx011	x	x	JX946238	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx012	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx013	x	x	JX946211	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx014	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx016	x	x	JX946210	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx017	x	x	JX946251	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx018	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx019	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx020	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx021	x	x	JX946252	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx022	x	x	JX946206	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx023	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx024	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx025		x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx026	x	x	JX946236	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx027	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx028	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx029	x	x	JX946208	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
IRx030	x	x	JX946206	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
IRx031	x	x	JX946236	SAS	Iran	na	Ahwaz, Iran	Blood (FTA card)	Vetmeduni
JOp001	x	x	JX946208	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp002	x	x	JX946208	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp003	x	x	JX946209	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp004	x	x	JX946209	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp005	x	x	JX946209	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp006	x	x	JX946208	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp007	x	x	JX946218	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp008	x	x	JX946214	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp009	x	x	JX946225	NAP	Jordan	na	Irbid, Jordan	Blood (FTA card)	Vetmeduni
JOp010	x	x	JX946208	NAP	Jordan	na	Irbid, Jordan	Blood (FTA card)	Vetmeduni
JOp011	x	x	JX946208	NAP	Jordan	na	Irbid, Jordan	Blood (FTA card)	Vetmeduni
JOp012	x	x	JX946208	NAP	Jordan	na	Irbid, Jordan	Blood (FTA card)	Vetmeduni
JOp013	x	x	JX946233	NAP	Jordan	na	Irbid, Jordan	Blood (FTA card)	Vetmeduni
JOp014	x	x	JX946208	NAP	Jordan	na	Irbid, Jordan	Blood (FTA card)	Vetmeduni
JOp015	x	x	JX946211	NAP	Jordan	na	Irbid, Jordan	Blood (FTA card)	Vetmeduni
JOp016	x	x	JX946208	NAP	Jordan	na	Irbid, Jordan	Blood (FTA card)	Vetmeduni
JOp017	x	x	JX946208	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp018	x	x	JX946208	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp019	x	x	JX946209	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp020	x	x	JX946208	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp021	x	x	JX946208	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp022	x	x	JX946211	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp023	x	x	JX946232	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp024	x	x	JX946206	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp025	x	x	JX946209	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
JOp026	x	x	JX946233	NAP	Jordan	na	Mafraq, Jordan	Blood (FTA card)	Vetmeduni
KEk001	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk002	x	x	JX946208	HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk003	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk004	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk005	x	x	JX946208	HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk006	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk007	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk008	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk009	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk010	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk011	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk012	x	x	JX946208	HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
KEk013	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk014	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk015	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk016	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk017	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk018	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk019	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk020	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk021	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk022	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk023	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk024	x	x	JX946218	HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk025	x	x	JX946208	HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk026	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk027	x			HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk028	x	x	JX946214	HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk029	x	x	JX946214	HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk030	x	x	JX946270	HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEk031	x	x	JX946208	HAF	Kenya	Rendille	North Kenya	Blood (FTA card)	Nottingham
KEl032	x	x	JX946206	HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl033	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl034	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl035	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl036	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl037	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl038	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl039	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl040	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl041	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl042	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl043	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl044	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl045	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl046	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl047	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl048	x	x	JX946214	HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl049	x	x	JX946208	HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl050	x	x	JX946208	HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl051	x	x	JX946214	HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl052	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
KEl053	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl054	x	x	JX946214	HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl055	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl056	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl057	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl058	x	x	JX946206	HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl059	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl060	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl061	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl062	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEl063	x			HAF	Kenya	Turkana	North Kenya	Blood (FTA card)	Nottingham
KEm064	x	x	JX946263	HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm065	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm066	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm067	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm068	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm069	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm070	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm071	x	x	JX946214	HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm072	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm073	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm074	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm075	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm076	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm077	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm078	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm079	x	x	JX946214	HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm080	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm081	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm082	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm083	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm084	x	x	JX946208	HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm085	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm086	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm087	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm088	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEm089	x			HAF	Kenya	Gabbra	North Kenya	Blood (FTA card)	Nottingham
KEx090	x			HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx091	x			HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx092	x			HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
KEx093	x			HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx094	x			HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx095	x	x	JX946206	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx096	x			HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx097	x	x	JX946218	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx098	x	x	JX946219	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx099	x	x	JX946208	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx100	x	x	JX946208	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx101	x			HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx102	x	x	JX946208	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx104		x	JX946214	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx105		x	JX946214	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx107		x	JX946214	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx108		x	JX946214	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx109		x	JX946214	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx112		x	JX946208	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
KEx113		x	JX946218	HAF	Kenya	na	Eastern Kenya	Hair	Vetmeduni
LYx001	x	x	JX946208	SHR	Libyia	na	Tripoli, Lybia	Hair	Vetmeduni
LYx002	x	x	JX946208	SHR	Libyia	na	Tripoli, Lybia	Hair	Vetmeduni
LYx003	x	x	JX946208	SHR	Libyia	na	Tripoli, Lybia	Hair	Vetmeduni
LYx004	x	x	JX946208	SHR	Libyia	na	Tripoli, Lybia	Hair	Vetmeduni
LYx005	x	x	JX946208	SHR	Libyia	na	Tripoli, Lybia	Hair	Vetmeduni
LYx006	x	x	JX946208	SHR	Libyia	na	Tripoli, Lybia	Hair	Vetmeduni
LYx007	x	x	JX946208	SHR	Libyia	na	Tripoli, Lybia	Hair	Vetmeduni
LYx008	x	x	JX946207	SHR	Libyia	na	Tripoli, Lybia	Hair	Vetmeduni
LYx009	x	x	JX946227	SHR	Libyia	na	Tripoli, Lybia	Hair	Vetmeduni
NEx001	x	x	JX946208	SHR	Niger	na	Northeastern Nigeria	Hair	Vetmeduni
NEx002	x	x	JX946206	SHR	Niger	na	Northeastern Nigeria	Hair	Vetmeduni
NEx003	x	x	JX946207	SHR	Niger	na	Northeastern Nigeria	Hair	Vetmeduni
NEx004	x	x	JX946208	SHR	Niger	na	Northeastern Nigeria	Hair	Vetmeduni
NEx005	x	x	JX946208	SHR	Niger	na	Northeastern Nigeria	Hair	Vetmeduni
NEx006		x	JX946208	SHR	Niger	na	Northeastern Nigeria	Hair	Vetmeduni
NEx007	x	x	JX946206	SHR	Niger	na	Northeastern Nigeria	Hair	Vetmeduni
NEx008	x	x	JX946208	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx009	x	x	JX946221	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx010	x	x	JX946247	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx011	x	x	JX946208	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx012	x	x	JX946208	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx013		x	JX946208	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx014		x	JX946208	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
NEx015	x	x	JX946208	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx016	x	x	JX946208	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx017	x	x	JX946209	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx018	x	x	JX946218	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx019	x	x	JX946208	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx020	x	x	JX946208	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx021	x	x	JX946208	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx022	x	x	JX946208	SHR	Niger	Ja	Northeastern Nigeria	Hair	Vetmeduni
NEx023		x	JX946214	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx024	x	x	JX946211	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx025	x	x	JX946208	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx026	x	x	JX946211	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx027	x	x	JX946208	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx028	x	x	JX946211	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx029		x	JX946208	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx030		x	JX946208	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx031		x	JX946249	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx032		x	JX946208	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx033	x			SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx034		x	JX946209	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx035	x	x	JX946206	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx036	x	x	JX946207	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx037	x	x	JX946211	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx038		x	JX946211	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx039	x	x	JX946206	SHR	Niger	Kala	Northeastern Nigeria	Hair	Vetmeduni
NEx040	x	x	JX946206	SHR	Niger	Kubule	Northeastern Nigeria	Hair	Vetmeduni
NEx041		x	JX946208	SHR	Niger	Kubule	Northeastern Nigeria	Hair	Vetmeduni
NEx042	x	x	JX946209	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni
NEx043	x	x	JX946211	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni
NEx044	x	x	JX946248	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni
NEx045		x	JX946249	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni
NEx046	x	x	JX946208	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni
NEx047	x	x	JX946209	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni
NEx048	x	x	JX946208	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni
NEx049	x	x	JX946206	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni
NEx050	x	x	JX946227	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni
NEx051		x	JX946207	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni
NEx052	x	x	JX946208	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni
NEx053		x	JX946206	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni
NEx054	x	x	JX946208	SHR	Niger	Kurri	Northeastern Nigeria	Hair	Vetmeduni

Lab #	μsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
OMp005		x	JX946268	SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp007		x	JX946269	SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp015		x	JX946207	SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp017		x	JX946249	SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp018		x	JX946207	SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp019		x	JX946207	SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp020		x	JX946211	SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp021		x	JX946208	SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp022		x	JX946227	SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp023		x	JX946227	SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMr024		x	JX946211	SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr025		x	JX946267	SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr026	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr027	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr028	x	x	JX946208	SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr029	x	x	JX946208	SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr030	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr031	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr032	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr033	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr034	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr035	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr036	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr037	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr038	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr039	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr040	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr041	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr042	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr043	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr044	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr045	x	x	JX946208	SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr046	x	x	JX946208	SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr047	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr048	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr049	x			SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMr050	x	x	JX946206	SAP	Oman	Batinah	North Oman	Blood (FTA card)	Nottingham
OMp051	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp052	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp053	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
OMp054	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp055	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp056	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp057	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp058	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp059	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp060	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp061	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp062	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp063	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp064	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp065	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp066	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp067	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp068	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp069	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp070	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
OMp071	x			SAP	Oman	Dhofar	South Oman	Blood (FTA card)	Nottingham
PKt001	x	x	JX946253	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt002	x	x	JX946209	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt003	x	x	JX946209	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt004	x	x	JX946254	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt005	x	x	JX946208	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt006	x	x	JX946208	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt007	x	x	JX946208	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt008	x	x	JX946209	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt009	x	x	JX946208	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt010	x	x	JX946208	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt011	x	x	JX946208	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt012	x	x	JX946208	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt013	x	x	JX946249	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt014	x	x	JX946208	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt015	x	x	JX946206	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt016	x	x	JX946208	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt017	x	x	JX946208	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt018	x	x	JX946206	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt019	x	x	JX946249	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt020	x	x	JX946208	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKt021	x	x	JX946249	SAS	Pakistan	Kohi	Suleiman Mountainous region, Pakistan	Hair	Vetmeduni
PKu022	x			SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
PKu023	x	x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu024	x	x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu025	x	x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu026	x	x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu027	x	x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu028	x	x	JX946249	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu029	x	x	JX946207	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu030	x	x	JX946209	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu031	x	x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu032	x	x	JX946207	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu033	x	x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu034	x	x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu035	x			SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu036		x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu037	x	x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu038	x	x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu039	x	x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
PKu040	x	x	JX946208	SAS	Pakistan	Raidi	Kachi, Pakistan	Hair	Vetmeduni
SAa001		x	JX946208	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa002		x	JX946214	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa003		x	JX946217	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa004	x	x	JX946214	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa005	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa006	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa007	x	x	JX946209	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa008	x	x	JX946214	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa009	x	x	JX946208	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa010	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa011	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa012	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa013	x	x	JX946216	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa014	x	x	JX946209	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa015	x	x	JX946214	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa016	x	x	JX946208	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa017	x	x	JX946215	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa018	x	x	JX946208	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa019	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa020	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa021	x	x	JX946208	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa022	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
SAa023	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa024	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa025	x	x	JX946206	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa026	x	x	JX946208	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa027	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa028	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa029	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa030	x	x	JX946208	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa031	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa032	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa033	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa034	x	x	JX946214	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa035	x	x	JX946207	SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAa036	x			SAP	Saudi Arabia	Awarik	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb037		x	JX946208	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb038	x	x	JX946211	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb039	x	x	JX946208	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb040	x	x	JX946212	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb041	x	x	JX946211	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb042	x	x	JX946206	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb043	x	x	JX946208	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb044	x	x	JX946208	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb045	x	x	JX946208	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb046	x	x	JX946213	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb047	x	x	JX946208	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb048	x	x	JX946208	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb049	x			SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb050	x	x	JX946208	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb051	x			SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb052	x			SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb053	x	x	JX946209	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb054	x			SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb055	x	x	JX946208	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb056	x			SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb057	x			SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb058	x			SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb059	x			SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb060	x	x	JX946208	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb061	x			SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAb062	x			SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
SAb063	x	x	JX946208	SAP	Saudi Arabia	Awadi	South Saudi Arabia	Blood (FTA card)	Nottingham
SAc064	x	x	JX946237	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc065	x	x	JX946208	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc066	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc067	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc068	x	x	JX946209	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc069	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc070	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc071	x	x	JX946208	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc072	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc073	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc074	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc075	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc076	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc077	x	x	JX946208	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc078	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc079	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc080	x	x	JX946206	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc081	x	x	JX946206	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc082	x	x	JX946209	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc083	x	x	JX946208	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc084	x	x	JX946208	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc085	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc086	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc087	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc088	x	x	JX946208	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc089	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc090	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc091	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc092	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc093	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc094	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc095	x	x	JX946208	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc096	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc097	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc098	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc099	x	x	JX946208	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc100	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc101	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc102	x	x	JX946208	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
SAc103	x	x	JX946214	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc104	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc105	x			NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc106	x	x	JX946208	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc107	x	x	JX946208	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc108	x	x	JX946211	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc109	x	x	JX946206	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc110	x	x	JX946211	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc111	x	x	JX946255	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc112	x	x	JX946256	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAc113	x	x	JX946208	NAP	Saudi Arabia	Hadana	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd114	x	x	JX946208	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd115	x	x	JX946208	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd116	x	x	JX946208	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd117	x	x	JX946232	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd118	x			NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd119	x			NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd120	x			NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd121	x			NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd122	x			NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd123	x	x	JX946208	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd125	x	x	JX946209	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd126	x			NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd127	x			NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd128	x			NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd129	x			NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd130	x			NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd131	x	x	JX946209	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd132	x	x	JX946208	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd133		x	JX946206	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd134	x	x	JX946206	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd135	x			NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd136	x	x	JX946209	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd137	x	x	JX946208	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd138	x	x	JX946208	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd139	x	x	JX946213	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd140	x			NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd141	x	x	JX946211	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd142	x	x	JX946208	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham
SAd143		x	JX946218	NAP	Saudi Arabia	Sahlia	West Saudi Arabia	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
SAe144	x	x	JX946206	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe145	x	x	JX946218	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe146	x	x	JX946208	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe147	x	x	JX946208	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe148	x	x	JX946208	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe149	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe150	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe151		x	JX946208	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe152	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe153		x	JX946208	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe154	x	x	JX946208	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe155	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe156	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe157	x	x	JX946264	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe158	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe159	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe160	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe161	x	x	JX946208	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe162	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe163	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe164	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe165	x	x	JX946208	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe166	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe167	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe168	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe169	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe170	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe171	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe172	x	x	JX946214	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe173	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe174	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe175	x	x	JX946211	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe176	x	x	JX946208	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe177	x	x	JX946211	NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAe178	x			NAP	Saudi Arabia	Hurra	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf179	x			NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf180	x			NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf181	x			NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf182	x			NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf183	x			NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham

Lab #	μsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
SAf184	x			NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf185	x			NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf186	x	x	JX946211	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf187	x	x	JX946208	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf188	x	x	JX946206	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf189	x	x	JX946208	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf190	x	x	JX946206	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf191	x	x	JX946266	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf192	x	x	JX946209	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf193	x	x	JX946232	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf194	x	x	JX946211	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf195	x	x	JX946208	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf196	x			NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf197	x	x	JX946208	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf198	x			NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf199	x			NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf200	x			NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf201	x	x	JX946208	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf202	x	x	JX946208	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf203	x	x	JX946209	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf204	x			NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf205		x	JX946208	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAf206		x	JX946208	NAP	Saudi Arabia	Mugatter	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh207	x	x	JX946208	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh208	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh209	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh210	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh211	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh212	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh213	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh214	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh215	x	x	JX946273	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh216	x	x	JX946208	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh217	x	x	JX946208	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh218	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh219	x	x	JX946208	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh220	x	x	JX946208	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh221	x	x	JX946232	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh222	x	x	JX946207	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh223	x	x	JX946208	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
SAh224	x	x	JX946208	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh225	x	x	JX946208	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh226	x	x	JX946206	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh227	x	x	JX946208	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh228	x	x	JX946245	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh229	x	x	JX946208	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh230	x	x	JX946218	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh231	x	x	JX946208	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh232	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh233	x	x	JX946208	NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh234	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh235	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh236	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAh238	x			NAP	Saudi Arabia	Sufur	North Saudi Arabia	Blood (FTA card)	Nottingham
SAi239	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi240	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi241	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi242	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi243	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi244	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi245	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi246	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi247	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi248	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi249	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi250	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi251	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi252	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi253	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi254	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi255	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi256	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi257	x	x	JX946265	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi258	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi259	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi260	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi261	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi262	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi263	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi264	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
SAi265	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi266	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi267	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi268	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi269	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi270	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi271	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi272	x	x	JX946208	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi273	x	x	JX946244	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi274	x	x	JX946209	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi275	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi276	x	x	JX946208	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi277	x	x	JX946208	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi278		x	JX946206	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi279		x	JX946211	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi280		x	JX946218	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi281	x	x	JX946206	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi282		x	JX946209	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi283	x	x	JX946206	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi284	x	x	JX946227	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi285	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi286	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi287	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi288	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi289	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi290	x			NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAi292		x	JX946208	NAP	Saudi Arabia	Magaheem	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj294	x	x	JX946206	NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj295	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj296	x	x	JX946218	NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj297	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj298	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj299		x	JX946208	NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj300	x	x	JX946211	NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj301	x	x	JX946208	NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj302	x	x	JX946206	NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj303	x	x	JX946206	NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj304	x	x	JX946208	NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj305	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj306	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
SAj307	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj308	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj309	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj310	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj311	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj312	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj313	x	x	JX946208	NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj314	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj315	x	x	JX946208	NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj316	x	x	JX946271	NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj317	x	x	JX946208	NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj318	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj319	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj320	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj321	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj322	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj323	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj324	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj325	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj326	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj327	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj328	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SAj329	x			NAP	Saudi Arabia	Shual	East Saudi Arabia	Blood (FTA card)	Nottingham
SDo001	x	x	JX946209	SHR	Sudan	Hawari	Sudan	Hair	Vetmeduni
SDo002	x	x	JX946209	SHR	Sudan	Hawari	Sudan	Hair	Vetmeduni
SDo003	x	x	JX946207	SHR	Sudan	Hawari	Sudan	Hair	Vetmeduni
SDo004	x	x	JX946227	SHR	Sudan	Hawari	Sudan	Hair	Vetmeduni
SDx005	x			SHR	Sudan	Hawari	Sudan	Hair	Vetmeduni
SDn006	x	x	JX946219	SHR	Sudan	Hasani	Sudan	Hair	Vetmeduni
SDo007	x	x	JX946208	SHR	Sudan	Hawari	Sudan	Hair	Vetmeduni
SDo008	x	x	JX946227	SHR	Sudan	Hawari	Sudan	Hair	Vetmeduni
SDn009	x	x	JX946208	SHR	Sudan	Hasani	Sudan	Hair	Vetmeduni
SDn010	x	x	JX946214	SHR	Sudan	Hasani	Sudan	Hair	Vetmeduni
SDq011	x	x	JX946208	SHR	Sudan	Kababish	Sudan	Hair	Vetmeduni
SDq012	x	x	JX946206	SHR	Sudan	Kababish	Sudan	Hair	Vetmeduni
SDq013	x	x	JX946208	SHR	Sudan	Kababish	Sudan	Hair	Vetmeduni
SDq014	x	x	JX946227	SHR	Sudan	Kababish	Sudan	Hair	Vetmeduni
SDq015	x	x	JX946248	SHR	Sudan	Kababish	Sudan	Hair	Vetmeduni
SDq016		x	JX946208	SHR	Sudan	Kababish	Sudan	Hair	Vetmeduni
SDx024	x	x	JX946208	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
SDx025	x	x	JX946208	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx026	x	x	JX946206	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx027	x	x	JX946272	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx028	x	x	JX946208	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx029	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx030	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx031	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx032	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx033	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx034	x	x	JX946208	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx035	x	x	JX946208	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx036	x	x	JX946209	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx037	x	x	JX946208	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx038	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx039	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx040	x	x	JX946208	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx041	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx042	x	x	JX946249	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx043	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx044	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx045	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx046	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx047	x	x	JX946208	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx048	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx049	x	x	JX946272	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx050	x	x	JX946209	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx051	x	x	JX946206	SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx052	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx053	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx054	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx055	x			SHR	Sudan	Baladia	Southern Darfu state, Sudan	Blood (FTA card)	Nottingham
SDx056	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx057	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx058	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx059	x	x	JX946214	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx060	x	x	JX946222	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx061	x	x	JX946223	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx062	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx063	x	x	JX946209	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx064	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
SDx065	x	x	JX946209	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx066	x	x	JX946209	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx067	x	x	JX946224	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx068	x	x	JX946206	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx069	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx070	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx071	x	x	JX946209	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx072	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx073	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx074	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx075	x	x	JX946207	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx076	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx077	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx078	x	x	JX946208	SHR	Sudan	na	South Sudan	Hair	Vetmeduni
SDx079	x	x	JX946218	SHR	Sudan	na	El Obeid, Sudan	Hair	Vetmeduni
SDx080	x	x	JX946206	SHR	Sudan	na	El Obeid, Sudan	Hair	Vetmeduni
SDx081	x			SHR	Sudan	na	El Obeid, Sudan	Hair	Vetmeduni
SDx082	x	x	JX946209	SHR	Sudan	na	El Obeid, Sudan	Hair	Vetmeduni
SDx083	x			SHR	Sudan	na	El Obeid, Sudan	Hair	Vetmeduni
SDx084	x	x	JX946208	SHR	Sudan	na	El Obeid, Sudan	Hair	Vetmeduni
SDx085	x			SHR	Sudan	na	El Obeid, Sudan	Hair	Vetmeduni
SDx086	x	x	JX946208	SHR	Sudan	na	Kartoum, Sudan	Hair	Vetmeduni
SDx087	x	x	JX946208	SHR	Sudan	na	Kartoum, Sudan	Hair	Vetmeduni
SDx088	x			SHR	Sudan	na	Kartoum, Sudan	Hair	Vetmeduni
SDx089	x	x	JX946246	SHR	Sudan	na	Kartoum, Sudan	Hair	Vetmeduni
SDx090	x	x	JX946208	SHR	Sudan	na	Kartoum, Sudan	Hair	Vetmeduni
SDx091	x	x	JX946208	SHR	Sudan	na	Kartoum, Sudan	Hair	Vetmeduni
SDx092	x	x	JX946208	SHR	Sudan	na	Kartoum, Sudan	Hair	Vetmeduni
SDx093	x	x	JX946208	SHR	Sudan	na	Kartoum, Sudan	Hair	Vetmeduni
SOx001		x	JX946208	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx002	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx003	x	x	JX946214	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx004	x	x	JX946214	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx005	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx006	x	x	JX946233	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx007	x	x	JX946233	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx008	x	x	JX946218	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx009	x	x	JX946214	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx010	x	x	JX946214	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx011	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
SOx012	x	x	JX946214	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx013	x	x	JX946236	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx014	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx015	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx016	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx017	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx018	x	x	JX946208	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx019	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx020	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx021	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx022	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx023	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx024	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx025	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx026	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx027	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx028	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx029	x	x	JX946214	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx030	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx031	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx032	x			HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx033	x	x	JX946214	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SOx034	x	x	JX946218	HAF	Somalia	na	South Somalia	Blood (FTA card)	Nottingham
SYv039		x	JX946206	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
SYv040		x	JX946208	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
SYv041	x	x	JX946208	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
SYv042	x	x	JX946208	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
SYv043	x	x	JX946230	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
SYv044	x	x	JX946208	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
SYv045	x	x	JX946214	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
SYv046	x	x	JX946208	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
SYv047	x	x	JX946214	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
SYv048	x	x	JX946208	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
SYv049	x	x	JX946231	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
SYv050	x	x	JX946206	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
SYv051	x	x	JX946223	NAP	Syria	Raka	Palmyra, Syria	Blood (FTA card)	Vetmeduni
TD_001	x	x	JX946208	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni
TD_002	x	x	JX946208	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni
TD_003	x	x	JX946209	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni
TD_004	x	x	JX946211	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
TD_005	x	x	JX946208	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni
TD_006	x	x	JX946239	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni
TD_007	x	x	JX946208	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni
TD_008	x	x	JX946209	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni
TD_009	x	x	JX946208	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni
TD_010	x	x	JX946227	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni
TDx011	x	x	JX946209	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni
TDx012	x	x	JX946208	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni
TDx013		x	JX946227	SHR	Chad	Arabi	Abeché, Chad	Blood (FTA card)	Vetmeduni
TNx001	x	x	JX946233	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx002	x	x	JX946211	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx003	x	x	JX946234	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx004	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx005	x	x	JX946227	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx006	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx007	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx008	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx009	x	x	JX946233	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx010	x	x	JX946211	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx011	x	x	JX946227	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx012	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx013	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx014	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx015	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx016	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx017	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx018	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx019	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx020	x	x	JX946218	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx021	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx022	x	x	JX946211	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx023	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx024	x	x	JX946235	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx025	x	x	JX946234	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx026	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx027	x	x	JX946208	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx028	x	x	JX946227	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx029	x	x	JX946211	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx030	x	x	JX946211	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni
TNx031	x	x	JX946218	SHR	Tunisia	na	Bouchifa, Tunisia	Blood (FTA card)	Vetmeduni

Lab #	µsat	mtDNA	Accession #	Region	Country of origin	Breed	Place of collection	Type of sample	Institution[1]
YEx001	x	x	JX946208	SAP	Yemen	na	Al Gowf, Yemen	Blood (FTA card)	Vetmeduni
YEx002	x	x	JX946208	SAP	Yemen	na	Al Gowf, Yemen	Blood (FTA card)	Vetmeduni
YEx003	x	x	JX946208	SAP	Yemen	na	Al Gowf, Yemen	Blood (FTA card)	Vetmeduni
YEx004	x	x	JX946208	SAP	Yemen	na	Al Gowf, Yemen	Blood (FTA card)	Vetmeduni
YEx005		x	JX946208	SAP	Yemen	na	Al Gowf, Yemen	Blood (FTA card)	Vetmeduni
YEx006		x	JX946208	SAP	Yemen	na	Al Gowf, Yemen	Blood (FTA card)	Vetmeduni
YEx007	x	x	JX946211	SAP	Yemen	na	Al Gowf, Yemen	Blood (FTA card)	Vetmeduni
YEx008		x	JX946208	SAP	Yemen	na	Al Gowf, Yemen	Blood (FTA card)	Vetmeduni
Total	970	662							

overlapping 566

Table S3: Dromedary sample list

x: complete profile available for the 17 microsatellite markers (µsat) / the 867-bp mitochondrial segment (mtDNA)

Accession #: GenBank – ncbi, accession numbers of the 68 mtDNA profiles

Region: HAF: Horn of Africa; SAS: Southern Asia; SHR: Sahara; NAP: North Arabian Peninsula; SAP: South Arabian Peninsula.

na: not applicable

[1]: Vetmeduni Vienna - Veterinärplatz 1 - AT 1220

University of Nottingham - University Park - UK NG92RD