



## Genetic Diversity in Farm and Wild Animals: A Review

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**Abstract** | The diversity among domestic and wild animals are known to contribute about half of the genetic variation found among animals within species, while the other half is attributed to genetic variation within breeds. Domestication of livestock species and a long history of migrations, selection and adaptation have created an enormous variety of breeds. Mitochondrial based genetic studies allow a comparison of genetic diversity. This has been summarized for cattle, buffalo, sheep, goats, horse, camel, dog, elephant, deer, bear, donkey and monkey.

**Keywords** | Domestic animal, Wild animal, Mitochondrial genome, Diversity, Phylogeny.

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## INTRODUCTION

The mitochondrial DNA of most animals is about 16 kb of circular, supercoiled DNA. Mitochondria is a power house of a cell it produce energy for cell, it has double standard circular DNA, which has 37 genes, thirteen protein-coding, two ribosomal RNA and twenty two transfer RNA genes (Gray, 1989). MtDNA is easier to extract than nuclear DNA, nDNA will degrade more quickly than the multicopy mtDNA (Loftus et al., 1994). MtDNA accumulates mutations faster than nuclear DNA which provides more genetic variation for evolutionary studies. Two features of mtDNA make it precious for phylogenetic studies. First evolution of mtDNA happen particularly as single base pair substitutions with only rarely major sequence rearrangements (Wolstenholme, 1992). Second the rate of mtDNA evolution develops as much as 10 times rapid than that of nuclear DNA (Brown et al., 1979). MtDNA is extra-nuclear genome and has multiple copies and has a high mutation rate and mtDNA evolution rate is about 5 to 10 times faster than nuclear DNA (Xingbo et al., 2000). It lacks recombination and is highly diverse within a species because of high mutation rate and lack of repair mechanisms as a result mtDNA is an fundamental material for phylogenetic studies and for analyzing

genetic diversity (Wang et al., 2007). These characteristics make use of mtDNA as a tool for control relationships among individuals within species and between closely related species with current times of divergence (Avise et al., 1979; Brown et al., 1979)

## CATTLE

Cattle have had a central role in the evolution of human cultures and are the most economically important of domesticated animal species (Cunningham, 1992). Cattle have a close and malleable alliance with human civilization, it has a religious roles (Isaac, 1962). Large number of animal genetic variety has been found in Pakistan due to its wide range of geographical and environmental diversity strengthening its agricultural economy. In Pakistan 42.8 million cattle with 15 distinguishable cattle breeds located across the country raised mainly for milk, meat and draft purposes (Ministry of National Food Security and Research). Cattle species of the genus *Bos* can be subdivided into wild and domestic types. Wild cattle contain *Bos gaurus* (gaur) and *Bos javanicus* (banteng), while domestic cattle contain *Bos indicus* (zebu cattle) and *Bos Taurus* (taurine cattle) (Shabthar et al., 2013). Hybridization of *Bos Premigenius* with domestic cattle originate with domestic cattle originate from Southwestern Asia is an obvi-

ous possibility (Troy et al., 2001). In Malaysia, four species of cattles are found throughout the Malay Peninsula and Borneo. Wild Malayan gaurs (*Bos gaurus hubbacki*) can only be found in Peninsular, Malaysia and wild banteng (*Bos javanicus lowi*) can only be found in Sabah a part of Borneo (Medway, 1983; Wilson and Reeder, 2005). Both domestic cattle species can be found in the Malay Peninsula and Borneo. The selembu is a hybrid cattle bred in Malaysia by crossbreeding wild Malayan gaur with domestic cattle (zebu and/or taurine) (Hamidi et al., 2009).

Domestic cattle illustrate a major source of milk, meat, hides, and draft energy (Lenstra and Bradley, 1997). Domestic cattle has 800 different breeds which is found around the world and these are classified in two major morphological groups the hump less taurine and the humped zebu types. Hump less cattle (*Bos taurus*) are the most common in regions with a mild region. Conversely humped cattle (*Bos indicus*) are better adapted to dry and warm climates. The cattle species, hump less taurine (*Bos taurus*) and zebu (*Bos indicus*) are believed to be emerge from the aurochs *Bos primigenius* through domestication event that occurred 8,000–10,000 years before present (Epstein and Mason, 1984; MacHugh et al., 1997). All the indigenous Pakistani cattle belong to zebu humped type cattle (*Bos indicus*).

The classification of the native cattle breeds have traditionally been based on differences in phenotypic features (Ciampolini et al., 1995; Garcia–Moreno et al., 1996; MacHugh et al., 1998; Edwards et al., 2000; Canon et al., 2001; Tapio et al., 2006; Ginja et al., 2009; Li and Kantanen, 2009). Zebu was probably imported into Africa after the Arabian occupation in the 7th century. Interestingly, the discovery that African zebu carry taurine mitochondrial DNA indicate that African zebu was the result of crossing zebu bulls with taurine cows (Bradley et al., 1998). Some original cattle breeds saved as a genetic resource in Turkey. Four Turkish native breeds evaluate in this study are as follows. East Anatolian Red is a native breed adapted to the rasping climate. Anatolian Black cattle are raised all over Turkey, Turkish Grey originated from the Balkan region of Europe, so the other name of the Turkish Grey cattle breed is Pleven. They are raised in Trakya (European part of Turkey) Turkish Grey cattle breed is used for three purpose like for milk and meat as well as being used as a work animal. South Anatolian Red Cattle are raised in the southern Anatolia region of Turkey. SouthAnatolian Red is known for giving greater milk yield than other Turkish native cattle breeds (Soyasal et al., 2004).

Brazil holds the immense commercial cattle populations worldwide with over 190 million animals raised both for dairy products and meat (IBGE, 2003). Bovine breeds

presently raised in Brazil can be classified into two groups according to their origin as exotic or Creole. The group of exotic breeds include both zebrine and taurine (Georges, 1996). In Bolivia 4 different Creole cattle breeds can be recognized Yacumeno Creole a breed adapted to the seasonal flood plain of the northern region and raised primarily for beef. Chaqueno Creole a beef breed found on the dry forest environment at the southeastern parts of the country Saavedreno Creole a breed mainly found on a tropical plain at the east of Bolivian territory which is bred for dairy. Chusco Creole a beef breed adapted to the highland plain of western Bolivia. In Argentina, a single Creole cattle breed can be recognized with a broad geographical distribution, from subtropical region in the north to the Patagonian region in the south, adapted to a wide range of environments (MacHugh et al., 1994, 1997; Moazami-Goudarzi et al., 1997; Loftus et al., 1999; Kantanen et al., 2000; Cannon et al., 2001; Hanotte et al., 2002; Beja-Pereira et al., 2003) since the differentiation between wild and domesticated forms of a species is not always clear from the archeological record. These artifacts generally do not supply satisfactory information on the types or breeds of early domesticated cattle. To address some of these issues we have examined mitochondrial DNA from representative breeds of European, African, and Indian cattle. Sequences of 900 base pair consisting the whole displacement loop (D loop) the most variable mitochondrial DNA regions were determined for two animals from each breed (Anderson et al., 1982). A previous survey of mitochondrial DNA variation (Loftus et al., 1994) combined with the explication of early neolithic faunal remains in Baluchistan (Meadow, 1993) argue strongly for a separate origin for the cattle populations of the Indian subcontinent. The modern (as well as the earliest) domestic cattle of this region are of the humped subspecies *B. indicus* whereas those of Europe are hump less or of *B. taurus* type.

A number of techniques have been used to study genetic diversity and molecular phylogeny of domestic animals. Microsatellite markers due to their co-dominant and multi-allelic attributes have been proven to be useful markers for a variety of purposes such as genetic variation, parentage, breeds genetic diversity and determining population substructure (Ciampolini et al., 1995; Garcia–Moreno et al., 1996; MacHugh et al., 1998; Edwards et al., 2000; Canon et al., 2001; Tapio et al., 2006; Ginja et al., 2009; Li and Kantanen, 2009).

## BUFFALO

In general water buffalo (*Bubalus bubalis*) is of two types riverine buffalo found in the Indian sub-continent Middle East and Eastern Europe while swamp buffalo in north-eastern part of India, Bangladesh, China and South East Asian countries in particular (Thomas et al., 1989).

The domestic water buffalo *Bubalus bubalis* is thought to have been domesticated in Indus valley 5000 year ago (Cockrill, 1981) and in China as early as 7000 years ago (Chen and Li, 1989). The ancestral wild water buffalo *Bubalus arnee* was common across in Indian subcontinent but the number have been decrease due to unfavorable conditions. The wild form is now listed as endangered and is thought to survive only in a few areas of India, Nepal, Bhutan and Thailand (Scherf, 2000). There are about 170 million head of buffalo in the world (Food and Agriculture Organization of the United Nations, 2004) and out of 170 million 97% found in Asia and 29.9 million buffalo found in Pakistan (Van Den Busscher et al., 1993).

Major native breeds are Nile, Ravi, Nili-Ravi, Kundi and Aza-kheli. There are at least nine well-defined breeds in India depicting approximately 30% of the total buffalo population of 90 million the remaining animals are non-descript (George et al., 1988). 23 million buffalo found in china. It is the third largest population of buffalo in the world showing 17.37% of the total bovine populations in China (FAO, 2003). The Asiatic water buffalo is dissect into two types the riverine buffalo (2n = 50) and the swamp buffalo (2n = 48) according to ecotypes and geographical distribution (Macgregor, 1941) as well as diploid status. The riverine buffalo have been primarily developed for milk and secondarily for meat and draught whereas the swamp buffalo have been developed primarily for draught while meat and milk production are secondary (Indramangala, 2001). Ministry of National Food Security and Research).

The time and place of domestication of this species has not yet been resolved. There is a controversy about the origin of buffalo some believe that it is domesticated in Indus valley 5000 year ago (Cockrill, 1981). It is domesticated in china 7000 year ago (Chen and Li, 1989). Two opposing suggestions have been proposed that these two types were domesticated separately and that these are a product of a single domestication event (Tanaka et al., 1996; Lau et al., 1998; Kierstein et al., 2004). Previous study of mitochondrial DNA variation using restriction fragment length polymorphism show genetic difference between two types and have consider their origin divergence and domestication (Amano et al., 1994; Tanak et al., 1995). But now a days mitochondrial DNA control region & cytochrome b is used. The D loop is most variable portion of the mammalian mitochondrial genome & is commonly variable at the intraspecific level making it useful for phylogenetic study while cytochrome b usually has moderate level of intra specific variation (Barker et al., 1997a). After the analyzing the mitochondrial D region (Kierstein et al., 2004) suggest that these buffalo show single domestication, but (Kikkawa et al., 1997) using the cytochrome b suggest that river and swamp buffalo originate separately.

## SHEEP

Sheep (*Ovis aries*) were domesticated in Southwestern Asia about 12 000 years old and present one of the first livestock animals (Zeder et al., 2006). There are two main haplotypes found in Asia but one of this dominates in Europe (Meadows et al., 2005). The third haplotype is less but found in Portugal, Turkey, Caucasus and China (Tapio et al., 2006b). The fourth haplotype found in Rumanian Karachi and Caucasian animals is related to the first haplotype. Fifth haplotype is intermediate between the first and third is rare and found in two Turkish animals only. Furthermore in comparision to the taurine cattle haplotypes the sheep haplogroups rarely associate with geographical origin. Different lineages reflect multiple regions of origin while another possibility is a coexistence of different maternal lineages in the predomestic population. Small variation has been observed in the paternal lineage. One SNP in the Y-chromosomal SRY mutation with high frequency in European breeds and in European origin. (Meadows et al., 2004). The microsatellite SRYM18 defines other haplotypes but excluding of the major haplotypes, with low frequency and scattered over different continents (Meadows et al., 2006).

A current study of retrovirus incorporation has provided further detail on the introduction of sheep into Europe. A high frequency of one incorporation or the lack of other incorporation reveals an early arrival of the primitive sheep populations (European mouflons, North-Atlantic Island breeds). Another retrovirus copy was found in most other European breeds reported the arrival of wool-producing sheep. This study also narrate an interesting genetic link of English Jacob sheep with Asian or African population of sheep. several groups have studied the diversity of sheep as described by microsatellites this has provided relatively brief insight into the relationship between breeds (Chessa et al., 2009). In a study of 20 European breeds Analysis of Molecular Variance analysis describes that only 1% of the variation is between regions and less than 3% is between seven types of breed (Lawson Handley et al., 2007]. In Baltic breeds lack of divergence at the breed level found (Tapio et al., 2005a).

On the other sight with eight microsatellites observed grouping of three English breeds relative to Merino-type breeds and to Awassi most data on phylogeographical relationships of breeds arise from the EU Econogene project which analyzed 57 breeds with 31 microsatellites unrelated positions were observed for three clusters of breeds Southwest-Asian, Southeast-European and Central- and Western-European in the last group there was a weak differentiation of Merino and Alpine breeds (Buchanan et al., 1994). There was obvious reduction of the heterozygosity and allelic abundance from Southwestern Asia and Southeastern Europe to the west and the north-west repeated

impact during the moderate introduction of domestic sheep into Europe (Peter et al., 2007).

Another study of independent analysis suggested a separate position of Northern-European short tailed sheep which could be divided into a north-western northeastern and a heterogeneous Swedish-Norwegian group (Tapio et al., 2005b). The relationships of Portuguese sheep which were different from the imported Assaf breed (Santos-Silva et al., 2008). Genetic differentiation of the PramenkawithBalkans, a native mountain sheep breed (Cinkulov et al., 2008). A fragmented differentiation of three breed clusters that had been successively introduced to Ethiopia thin tailed, short- and long-fat-tailed and thick-rumped breeds (Gizaw et al., 2007). The differentiation of European and Asian sheep and the weak geographical structure of European sheep were justify by analysis of a 1536-SNP dataset (Kijas et al., 2009).

The difference between Asian and African populations and an unrelated position of the North Atlantic Soay sheep. The diversity pattern of European sheep breeds which is clearly more panmictic than observed for cattle and goats probably reflects a history of cross-breeding promoted by commercial interests (Lenstra, 2005). From the 17th century onwards Merino sheep from Spain were exported to several European countries (Wood and Orel, 2001).

## GOAT

Goats (*Capra hircus*) were domesticated about 10, 000 years ago in Southwestern Asia in the same time and in the same zone as sheep. However the species are of same size goats found their particular use due to their alternation to significant conditions. Goats most likely descend from the wild bezoar *Capra aegagrus* (Naderi et al., 2007, 2008). More than 90% of goats worldwide contain the first haplogroup. Second haplogroup has so far been found mostly in Asia and South Africa, third in Southern Europe, fourth in Asia, fifth only in the Sicilian Girgentata breed and sixth in Southwestern Asia and Northern Africa. Subgroup of second clade is confined to China and Mongolia. Another subgroup of second subgroup is documented to fixed to the Canary Islands which is possibly due to their genetic insulation since their apparence 3000 years ago data on African goats are relatively deficient (Amills et al., 2004).

First haplogroups present in the bezoar goat (Naderi et al., 2008). The assignment of the haplogroups recommended that eastern Anatolia and possibly Northern and Central Zagros were the most fundamental domestication centres. The diversity of the third haplogroup demenstrate a second domestication on the Central Iranian plateau and in the Southern Zagros but this domestication center likely did not provide markedly to the recent domestic goat gene pool. Mitochondrial DNA haplotypes propound a genetic

link between Southwest-Asia, Iberiangoaatsand between Southern/Central American goats and Canarian goats both via marine deport (Amills et al., 2009). The frequent hypothesis that the geographical structure of goats is weaker than for cattle and sheep rests mainly on the worldwide frequent of first haplogroup (Luikart et al., 2001).

Although the scattering of first haplotypes seems to be indigenous and Y-chromosomal data show appreciable geographical partitioning. Three Y-chromosomal haplotypes belong to two haplogroups Y1 and Y2 (Lenstra 2005; Pereira et al., in press). Y2 has not been found in Switzerland and Germany and is shorten in Italy, although it is predominant. Microsatellites also declare a high degree of geographical structuring however conflicting of datasets again limits the range of most studies to the regional scale. Found a clear link of tree topology and genetic distance for Southeast Asian goats (Barker et al., 2001).

The enormous dataset reported so far include 45 breeds from Europe and the Middle East Four distinct clusters were found: Middle East, central Mediterranean, western Mediterranean and central/northern Europe. Again there was a diminish in allelic richness from south-east to north-west, probably the result of founder that also define the dispersion of Y-chromosomal alleles (Canon et al., 2006). Geographical structuring of microsatellite genotypes was also reported for goat populations from Burkina-Faso, India and northern Vietnam (Traore et al., 2009; Bertholy et al., 2009; Rout et al., 2008). Preservation value of Swiss goat breeds on the basis of microsatellite diversity was examine (Glowatzki-Mullis et al., 2008). The clear phylogeographical structure of European goats apparently reflects the style of preservation.

In distinction to the condition of sheep and cattle and with the exclusion of the epidemic use of Swiss dairy animals goats are of more confined economic value and breeding has remained largely a local issues. In the Econogene dataset Western Europe was only comparatively represented. Correlation with Asian and African breeds will likely define additional groups of breeds. We terminate that further molecular studies of autosomal and Y-chromosomal diversity of goats offer excellent approaches to reclame the history of their domestication and migrations.

## CAMEL

There are 24.1 million camels have been found all around the world Wirtschafts- und Sozialwissenschaftliches Institute (German: Institute for Economic and Social Science; Germany) called their family Camiladae, camiladae has *Camalus* and *Lama* genera. Both genera share long necks, high water efficiency and two toes with padded feet. This pseudo ruminant has some unique features as horns/antlers are missing, hump (energy reservoir in the form of

fats) is present, it walks on pads and what makes it very unique is its ability to conserve body water (Al-Swailem et al., 2007). Humankind has been using camel for leather, fiber, hair, milk, meat, transportation, as a war, entertainment and votive animal since 3000 Before Christ (Vijh et al., 2007). Common habitats of camels around the globe are arid, semi-arid and desert areas. That is why Australian outback, Iran, India, Pakistan, Somalia, Sudan, Ethiopia and Saudi-Arabian Peninsula are the major habitat of camel population (Al-Swailem et al., 2007). Pakistan have one million camels being considered the second largest population in the world (Ministry of national food security and research).

The Camiladae family consist four domesticated species belonging to three genera (Skidmore et al., 1999; Potts, 2004; Mengoni & Yacobaccio, 2006). Two of which are wild species the guanaco & the vicuna & two of which are domestic for whose evolutionary origins are debated (Wheeler, 1995). The llama (*Lama glama*) and alpaca (*Vicugna pacos*) are found in the Andean mountains in South America (Jianli). All species of the family have the same conventionally karyotype ( $2n = 74$ ) and can produce fertile hybrids between species both within and even between genera (Skidmore et al., 1999; Potts, 2004; Mengoni and Yacobaccio, 2006; Wheeler et al., 2006). The Bactrian camel also known as the two-humped camel is uniquely adapted to hot and arid environments (Schwartz, 1992). Bactrian camels provide a range of products and services, including milk, meat, wool, and blood, to the people who inhabit cold-arid and semi-arid desert regions so it is used for domestication (Groeneveld et al., 2010).

In addition scholars believe that the Bactrian camel made a great contribution to transportation on the Silk Road and could be portrayed as a bridge between the Eastern and Western cultures (Potts, 2004). Bactrian camel is used for economic development of human societies. Bactrian camels include the domestic Bactrian camel (*Camelus bactrianus*) and the wild Bactrian camel (*Camelus ferus*) (Ji et al., 2009a). The domestic Bactrian camel is found mainly in central Asian countries including Mongolia, China, Kazakhstan, Turkmenistan, North Eastern Afghanistan, Russia and Uzbekistan (Mirzaei, 2012; Vyas et al., 2015). It is found in north Pakistan Iran, Turkey and India (Isani and Baloch, 2000; Vyas et al., 2015; Moqaddam and Namaz-Zadeh, 1998). The wild Bactrian camel are mainly found in the regions of the Gobi and Taklamakan Deserts of Mongolia and Xinjiang (Ji et al., 2009a). It is also found in cold places. There are three breeds identify the Hos Zogdort, Galbiin Gobiin Ulaan and Haniin Hetsiin Huren (Saipolda, 2004). The bactrian camel can be divided into six subspecies *Camelus bactrianus xinjiang*, *Camelus bactrianus sunite*, *Camelus bactrianus alashan*, *Camelus bactrianus red*, *Camelus bactrianus brown* and *Camelus*

*bactrianus normal*, according to the morphological characters. (He, 2002; Indra et al., 2003). The extant wild bactrian camel the only representative of the wild tribe *Camelina* as a result of the elimination of the wild dromedary, survives in north-western (Hare, 1997). Solifugae (Arachnida) is the sixth most diverse order of arachnids and constitutes an important component of desert fauna worldwide (Roewer, 1934; Punzo, 1998; Harvey, 2002). The order Solifugae comprise more than 1110 species which are known as camel spiders, sun spiders or wind scorpions (Harvey, 2003).

Twelve families of Solifugae are distributed worldwide except in Australia, (Roewer, 1934; Harvey, 2003). The study of camel spider fauna of Iran has been ignored for decades and according to the literature it includes 65 species belonging to five families namely, Daesiidae, Galeodidae, Gylippidae, Karschiidae and Rhagodidae (Birula, 1890, Birula, 1905, 1906, 1937, 1938; Kraepelin, 1899, 1901; Pocock, 1900; Roewer, 1932, 1933, 1934, 1941, 1952, 1960; Kraus, 1959; Harvey, 2003; Khazanehdari et al., 2016). First mitochondrial DNA phylogenetic analysis of camel spiders of Iran based on COI sequences. As a molecular marker these characteristics of mitochondria DNA sequences have been very important for studies of molecular evolution over past decades (Quan et al., 2000; He et al., 2009; Chuluunbat et al., 2014). The cytochrome b gene (Cytochrome b) in the mitochondria DNA genome is an important protein-encoding gene for studies of phylogenetic evolution and species classification (Johns and Avise, 1998; Li et al., 2005; Zhong et al., 2014).

Mitochondrial Cytochrome-b gene and D-loop region are most powerful markers for the characterization of different genetic resources (Goldstein and Pollock, 1997). Thus the aim of this study was to discover the variation in the said regions of camel breeds of Pakistan. Mutations in mitochondrial genome are very rapid and distinctive among species but when it comes to within species i.e. Breeds these are very rare. Their rarity helps us to define breeds clearly. Side advantage of using Cytochrome-b gene and D-loop region is intimation in defining milk production marker along with development of forensic analysis in case of parentage conflicts.

## HORSE

Feral and domestic equine cells carry a large number of maternally inherited mitochondria (from 100 to 1000) (Xu et al., 1994). Phylogenetic studies of 37 variable mtDNA control region sequences from domestic horses submitted in GeneBank 616 base pairs in length relish at least six divergent sequence clades the first whole mtDNA sequence for this species has been accessible (Pereira et al, 1994). Horses diverged from the lineage leading to extant stenoid equids (zebras and asses) at least 2 million years ago as

the fossil data defines (A. Forsten et al., 1992), or about 3.9 million year ago according to molecular data (M. George et al., 1986). It was determined an average rate of equid mtDNA sequence divergence 4.1% or 8.1% per million years to extend their presentation of current and ancient breeds, 355 base pair are sequenced of the left domain of the mtDNA control region in 191 horses from 10 definite breeds containing some are very old such as the (Icelandic pony, Swedish Gotland Russ, and British Exmoor pony).

Hence current horse lineages coalesce at about 0.32 or 0.63 million year ago long before the first domestic horses emerge in the archaeological data (J. Clutton-Brock, 1992). A total in which 100 definite equine mtDNA haplotypes are narrate in multiple analysis describing the domestication of horses or the origin of particular breeds (Bowling et al., 2000; Vila et al., 2001; Jansen et al., 2002; Kavar et al., 2002; reviewed in Kavar & Dovc, 2008). In a dataset extinct horse breeds as well as wild horses from 12,000 to 28,000 years ago an abrupt high genetic divergence between clades was found (Vila et al., 2001). Studies of DNA from horses of Chinese tombs from the 3rd century BC (Keyser-Tracqui et al., 2005) and from the Bronze Age showed that the high mtDNA diversity is of ancient origin (Lei et al., 2009).

The divergence of horse mtDNA must have foredated domestication which on the basis of archaeological evidence has been dated at around 6000 YBP in a wide region of the Eurasian Steppe. This is often with the suspicion that hold and exploitation of wild mares took place unconventional in multiple locations over a wide time span (Lister, 2001; Vila et al., 2001; Kavar and Dovc 2008). Supposedly the know-how required for domestication instead of domestic animals themselves scatter from one region to the next inspiring the ideas that the domestication process was crumped to a restricted area.

Although the horse domestication scenario has currently been convoluted by the study of matrilineal from Lusitano and Soraia populations which proposes a role of the Iberian Peninsula as a glacial refugium and a possible second center of horse domestication (Lopes et al., 2005). Study of fossil remains showed that domestication of horses from 5000 YBP onward was followed by the spread of mutations resulting in a large variety in coat colours (Ludwig et al., 2009). Analysis of Molecular Variance study of 72 populations from Europe, Southwestern Asia, Eastern Asia and Africa revealed a non-random division of diversity among populations and a clear although weak geographical partitioning of mtDNA variation (McGahern et al., 2006). In a few occurrences mtDNA has provided evidence for the origins of definite horse breeds. Iberian haplotypes in new world breeds with a high frequency which is in line with historic evidence for the origin of American horses (Luis

et al., 2006). Mongolian haplotypes in the Korean Cheju breed (Yang et al., 2002).

Analysis of Y-chromosomal data assist a strong sexbias in the domestication process (Lindgren et al., 2004). 14.3 kb of non-coding Y chromosome sequence in 52 male horses of 15 different breeds and did not recognize a single segregating site their observations cannot prohibit the possibility that Y-chromosomal variation was low before domestication took place their results strongly propose that only a some stallions have provide genetically to the domestic horse. Several studies have compared horse breeds or determined the genetic structure of single breeds on the basis of microsatellites. Most of the local breeds and used their own marker panel meaning that data from different studies cannot be contrast directly.

Data of many breeds on genetic diversity are available but perception of breed relationships are still segmentary. The unrealized potential of a standardized microsatellite panel for the annotation of breed relationships is emphasized by three well-supported arrays of two riding breeds (Arabian, Hanoverian) two primitive breeds (Exmoor and Sorraia) and six German cold-blooded breeds (Aberle et al., 2004). Similarly found 12 marker grouping of the Thoroughbred and Anglo-Arabian breeds and of Haflinger, Italian heavy draught and Bodaglino (Bigi et al., 2007). Based on 17 protein and 12 microsatellite markers eight breed groups among 33 breeds of which four groups were well assisted (Andalusian with Lusitano; Friesian with two pony breeds; Morgan, Standardbred, Rocky Mountain and American Saddlebred; Irish Draught, Quarter Horse, Hanoverian, Holsteiner and Thoroughbred) (Luis et al., 2007).

Microsatellites have also been used to approach possible origins of specific horse breeds. Documentation for a relationship of Mongolian and Norwegian breeds on the basis of 26 microsatellites was only insufficient but it is often with the morphological appearance of the Nordic breeds (Bjornstad et al., 2003).

## DONKEY

Domestic donkeys vary in appearance and several breeds are typically found (Epstein and Mason, 1971; Kugler et al., 2008). The Asian onager (*Equus hemionus*) was once considered a possible ancestor of the domestic donkey (Epstein and Mason, 1971). Now it is accepted that the African wild ass (*Equus africanus*) is the ancestor of the donkey (Beja-Pereira et al., 2004). Wild onagers were later bred with domestic donkeys in some regions of Western Asia (Champlot et al., 2010). Darwin admits the theory of the origins of the donkey, from a single and common African trunk (Salvans and Torrens, 1959). Nevertheless other authors (Adametz, 1943; Epstein, 1984; Clutton-Brock, 1987; Camac, 1989) indicate that today's domestic asses,

including the Spanish breeds, seem to be derived from two ancestral sources: the Nubian ass (*Equus asinus africanus*), a native of the Nile Basin which gave rise to the North African breeds, as well as to the Andaluza (from South of the Iberian Peninsula) and Majorera (from the Canary Islands) breeds, both of grey-brown coat (Aparicio, 1960; Garcia Dory et al., 1990; Yanes 1999; Jordana and Avellanet, 2002), and the Somalian ass (*E.a. somaliensis*) which subsequently gave rise to the donkeys of Southwest Asia and probably also to the majority of European breeds including the Catalana, Mallorquina, Encartaciones and Zamorano-Leonesa breeds the four of black coat (from North of the Iberian Peninsula). Notwithstanding, some other authors support the theory of two different ancestral sources: one for the (*E. africanus*) originating in Northeast Africa, and the other for the (*E. europaeus*) originating in the Mediterranean Basin and especially the Balearic Isles giving rise to the majority of the European donkey breeds including the four black-coated Spanish breeds (Dechambre and Sanson, cited by Aparicio 1960; Sotillo and Serrano 1985; Lorenzo 1997). According to mtDNA analysis the difference between the donkey and the horse suggests that the evolutionary separation of the two species occurred 9 million years ago (Xu et al., 1996). This is distinctly earlier than the paleontological data of 3–5 million year ago (Lindsay et al., 1980).

*Equus asinus* was domesticated approximately 6000 years ago probably in either Egypt or Mesopotamia (Littauer and Crowell, 1979). Genetic studies suggest that donkeys were most likely domesticated in northeastern Africa (Beja-Pereira et al., 2004). However mitochondrial genetic variation divide donkeys into two clades (Beja-Pereira et al., 2004; Chen et al., 2006; Zhang et al., 2010). Analysis of 440 bases of the mitochondrial control region showed that both clades are separated by 10 mutations and they diverged at least 100,000 years ago (Kimura et al., 2011). Both clades are found worldwide in approximately equal proportions. A higher proportion of one clade found in West Africa compared to other regions of Africa. In a study of Italian donkey breeds, five out of one contained second clade mtDNA (Pellecchia et al., 2007).

Phylogenetic analysis of domesticated donkeys in Europe is complicated due to the decline in donkey populations up to 80 % in the twentieth century cause loss of first clade animals (Aranguren-Mendez et al., 2001). The nucleotide diversity of first clade was 0.0177 in Northeast Africa and 0.0101 in entire Africa, with the highest diversity outside Africa being 0.0076 in the Near East. Second clade showed greater levels of nucleotide diversity as 0.0976 in Northeast Africa as well as 0.0118 in Africa as entire and 0.0140 in the Near East (Vila et al., 2006). First clade was closely associated to the Nubian wild ass and second clade may acquire from the Somali wild ass. The first domestica-

tion study focus on wild ass than domestic donkeys from over 30 extant Somali wild asses and ancient DNA from 9 historic Nubian wild ass. The Nubian wild ass was the ancestor of first clade but the Somali wild ass could not be the ancestor of second clade because 12 mutations separate Somali wild ass from second clade (Kimura et al., 2011). Possible ancestors of second clade contain the Atlas wild ass, wild ass in Yemen, or another now-extinct African wild ass. Archaeological, historic, and ethnographic sources narrates that at least three definite groups of wild asses existed in Africa 2,000 years ago, only two of which sustain in modern times (Groves, 1986; Marshall, 2000). The Somali wild ass is differentiated by its striped legs and large size. It is crucially endangered but can still be found in Somalia, Ethiopia, and Eritrea (Moehlman et al., 2011). The Nubian wild ass has a prominent shoulder cross and was found in northern Sudan and Eritrea in the nineteenth century few of the animals have been seen in current years and these populations have been dread extinct (Kimura et al., 2011; Moehlman et al., 2002). The Atlas wild ass was known from rock engravings and mosaics to have both a shoulder cross and striped legs, became extinct in Roman times (Lothe, 1984; Muzzolini, 2000).

Paleontological and archaeological describes that the ancient administration of the African wild ass spanned the northeastern part of Africa from at least ~20,000 years ago this administration also have expended into Yemen and the Levant (Groves, 1986; Marshall, 2007; Kimura et al., 2011; Uerpmann, 1991). Due to the lack of confirmation of African wild ass in the Upper Paleolithic of the Levant and the possibility of emulsion of early domestic donkey and wild ass skeletons, there is now confusion whether (*E. africanus*) ranged into Western Asia (Marshall et al., 2010; Marshall and Weissbrod, 2011).

## DOG

The dog *Canis familiaris*, is the only member of the family canidae and is the oldest animal that can be fully domesticated in the world since the historical evidence showing its strong connection with humans can be traced back to the far preagricultural age (Turnbell and Reed, 1974). The domestic dog is unique because it was the only domestic animal accompanying humans to every continent in ancient times. The dog has been present as the sole domestic animal in ancient Australia in the form of feral dingoes since at least 3500 years BP (Milham, 1976; Gollam, 1984). Dog is the most ancient and domesticated mammal on the earth (Turnbell and Reed, 1974). Modern breeds of dog were domesticated from wolves (Vila et al., 1997). Almost 300 hundred breeds of dog exist on the earth today. Dog has close relationship with human (Parker et al., 2004). In Pakistan German shepherd and Labrador retriever (LR) are major pet dog breeds. Many microsatellite markers have been reported can be used for DNA fingerprinting in dogs

A panel of 15 microsatellite markers consisting of fourteen di repeat and one tetra repeat markers was selected for analyzing genetic diversity and population structure of GS and LR for the first time in Pakistan. The earliest finds believed to be from domestic dogs are a single jaw from 14,000 years before the present in Germany and an assemblage of small canids from 12,000 year B.P. in Israel (Davis Valla, 1978; N.Beneck, 1987; G Nobis Umschau 1979). This indicates an origin from Southwest Asia or Europe (Clutton. Brock, 1999). Domestic dogs (*Canis familiaris*) are the oldest domesticated species and were domesticated in Eurasia from wolves at least 15,000 years ago (Clutton-Brock, 1995). Despite the long coexistence of wolves and dogs in Europe, there is no evidence for significant introgression of dog DNA into natural wolf populations (Vila and Wayne, 1999; Randi et al., 2000). However in Africa the critically endangered Ethiopian wolf has been shown to hybridize with local domestic dogs and as much as 17% of individuals in one population may have hybrid ancestor (Gottelli et al., 1994). During the 9000 years that domestic dogs have been present in North America they have shared the continent with the grey wolf, red wolf and coyote (Schwartz, 1997). In *The Origin of Species*, Darwin, 1859 suggested that several wild species of Canidae have been tamed and that their blood in some cases mingled together flows in the veins of our domestic [dog] breeds. We now know that dogs (*Canis familiaris*) are entirely derived from the domestication of wolves (*Canis lupus*) (Vila et al., 1997).

However, the origin of the huge morphological diversity that led Darwin to his speculation remains largely unknown (Sutter and Ostrander, 2004). The domestic dog is the most phenotypically diverse mammal on earth. The large differences in size, conformation, behavior, and physiology between dog breeds exceed the differences among species in the dog family Canidae (Coppinger and Coppinger, 2001; Wayne, 2001). Recent studies show that the origin of most dog breeds may derive from very recent selective breeding practices and are probably <200 Year old (Parker et al., 2004). However, selection acts upon existing variability. However using molecular genetical analysis report domesticated dog is closely related to grey wolf differing from it by 0.2% of the DNA sequence (Wayne et al., 1991, 1997).

### MUSK DEER

Musk deer (*Moschus* spp.) are domestic to Asia and are dispersed from Siberia and Mongolia in the north to Afghanistan, Nepal, Pakistan and India in the south to Vietnam and China in the east (Cobert and Hill 1992; Groves et al., 1995; Guha et al., 2007). Musk deer (genus

*moschus*) are commonly distributed in china and related areas (especially the Qinghai-Tibetan Plateau and Himalayan areas) (Groves et al., 1995). *Moschus berezovskii* (Class: Mammalia; Order: Artiodactyla; Family: Moschidae; (Sheng, 1992; Wang et al., 2006) commonly called forest musk deer, musk deer, river deer, donkeys, or roe, are famous for secretions called musk that the males of the species secrete from their musk glands. Musk has been an ingredient in many traditional Chinese medicines. Data indicate that over 70% musk and musk-related products in the world come from China (Sheng, 1996; Zou et al., 2005).

The genetic diversity of forest musk deer a significant investigated for conservation of the forest musk deer resources. The major group of large mammals ruminantia is commonly divided into the infra-orders Tragulina and Pecora (Flower 1883; Scott and Janis 1993; Agnarsson and May-Collado 2008). The interrelationships of pecoran families including the position of the Moschidae, have been important issues among phylogeneticists. Most morphologists have concluded that Moschidae are more closely associated to Cervidae than to Bovidae (Simpson 1945; Janis and Scott, 1988; Vislobokova, 1990) has suggested that Moschidae are closer to Bovidae. Investigations of the phylogenetic relationships between Moschidae and other pecoran families have used both mitochondrial and nuclear sequences (Cronin et al., 1996; Gatesy et al., 1996; Gatesy, 1997; Li et al., 1999; Su et al., 1999, 2001; Matthee et al., 2001; Hassanin and Douzery, 2003; Guha et al., 2007). In current era of molecular genetics, Cytochrome-b, c and d-loop region of mitochondria are important markers that can be used for characterization of different genetic resources (Goldstein and Pollock, 1997). While, the phylogenetic relationships among and within the genera of this subfamily (*Axis*, *Cervus*, *Dama*, and *Elaphurus*) still unresolved and challenging particularly within the genus *Cervus* (Groves and Grubb, 1987). Cytogenetically studied the mitotic and synaptonemal karyotypes of the forest musk deer (*M.berezovskii*) (Shi and MA, 1986). The diploid number was found to be 58, which concurred with the report on *M.moschiferus* by (Sokolov et al., 1980).

### BEAR

There has been considerable interest in polar bears (*Ursus maritimus* Phipps) and brown bears (also called grizzly bears; *Ursus arctos*) from an evolutionary standpoint because these sister species have a paraphyletic mitochondrial DNA (mtDNA) phylogeny and largely species specific nuclear DNA lineages. Paraphyletic mtDNA involves brown bears from the Admiralty, Baranof, and Chichikof islands in southeast Alaska that have mtDNA sequences more similar to those of polar bears than to those of other brown bears. The ABC brown bears and polar bears also share up to 10% of the nuclear genome (Hailer et al., 2012; Miller



et al., 2012; Cahill et al., 2013). Study of mtDNA can produce measures of genetic variability and phylogeny that are of considerable practical relevance for conservation. Since mtDNA is inherited from the maternal line, it can only tell the matrilineal history of populations. Thus, studies of mtDNA are of special value in conjunction with nuclear variation, which is biparentally inherited (Moritz, 1994). Phylogenetic relationships of mitochondrial control region sequences of brown bears (*Ursus arctos*) in Europe (Taberlet and Bouvet 1994; Kohn et al., 1995). European brown bears are divided into two major lineages, eastern and western based on mtDNA control region sequences (Taberlet and Bouvet, 1994). MtDNA analyses show the polar bear (*Ursus maritimus*) embedded within the brown bear clade and to be most closely related to the ABC islands brown bear (Shields et al. 2000; Lindqvist et al., 2010; Miller et al., 2012; Cronin et al., 1991; Shields and Kocher 1991; Talbot and Shields 1996) Population genetic assessment of extant populations of both species with microsatellites and DNA sequences reveals extant polar bears and brown bears, including contiguous populations, have separate gene pools with little or no hybridization (Cronin and McNeil 2012; Hailer et al., 2012).

Analysis of modern samples also provides little information about the timing of evolutionary events (e.g., divergence between taxa), which are important for linking phylogeographic patterns with particular historical processes. Indeed, inferences made on the basis of modern samples alone have been characterized as 'time trapped' (Paabo, 2000).

## MONKEY

The Papionini contain a cluster of six genera of Old World monkeys that are geographically predominant and ecologically sundry. They possibly subdivided into two clusters, the entirely African papionins, as well as geladas (*Theropithecus*), baboons (*Papio*), mandrills and drills (*Mandrillus*), and the mangabeys (*Cercocebus* and *Lophocebus*), as divergent to the widely Asian administration macaque genus (*Macaca*) (Strasser and Delson 1987; Disotell, 1992; 1994; Disotell et al., 1992; Morales and Melnick 1998). The coalescence period of homologous gene orders examined from two sister species will precede the divergence time of the species. While the coalescence of homologous gene sequences happen in the most contemporary common ancestral population of two species, the topographic anatomy of the gene tree will be the identical as the species tree.

However, two homologous DNA sequences fail to combine in the ancestral population of these two species alternatively consolidating in the common ancestral population that these species share with a third species then the gene tree may not revert the authentic sequence of divergences between the species. Because the DNA lineages found in

the ancestral population have unsystematically divided into the three successor species lineages. The conflict among gene trees and the species tree will happen with a possibility that can be measured by population genetics theory and may be appreciable under definite conditions for example when species divergences have happened comparatively close in period (Nei, 1987; Pamilo and Nei 1988).

The Old World monkeys family Cercopithecidae have been cleaved into two subfamilies Cercopithecinae with the type Miopithecus, Cercopithecus, Erythrocebus, Allenopithecus, Cercocebus, Macaca, Papio, Mandrillus and Theropithecus and Colobinae, with Presbytis, Semnopithecus, Trachypithecus, Pygathrix, Rhinopithecus, Nasalis, Simias, Colobus, Ptilocolobus, and Procolobus (Hershkovitz, 1977; Nowak, 1991). In the subfamily Cercopithecinae in Africa drill and mandrill are occurred, and in Asia the rhesus monkeys are found. In the subfamily Colobinae the colobus monkeys are originate in Africa, while several are originate in Asia. Quickly develop mitochondrial DNA is a precious molecule for analyzing evolutionary relationships and genetic differences within and among primate species (Wilson et al., 1985; Zhang & Sin, 1992, 1993a, b, c). DNA sequences can provide bountiful evolutionary data (Nei, 1987; Zhang, 1996a). Diminution fragment length polymorphism (RFLP) of two species of leaf monkey (*Trachypithecus phayrei* and *T. francoisi*) has been described (Zhang and Shi, 1993d). Although mitochondrial DNA sequences from colobines have not still been unloaded in GenBank to our command. Analyzed mitochondrial cytochrome b gene fragment from the snub-nosed langurs (Zhang and Ryder, in press). Members of the genus *Aeromonas* are worldwide in environmental habitats, such as soil, fresh and saline water, effluent and sewer water (Brandt et al., 1996; Holmes et al., 1996). They are incriminated as pathogens of cold-blooded animals and different mammals as well as humans where they cause serious gastroenteritis, soft-tissue contaminations and bacteraemia (the presence of bacteria in blood) (Janda and Abbott, 1998). *Aeromonas* insulates have been reclaim from faeces in serious cases of gastroenteritis additionally in asymptomatic cases (Hanninen and Siitonen, 1995). Throughout a routine regard to govern the presence of probable pathogens in the intestinal tract of monkeys (*Macaca fascicularis*) from Mauritius that had been put in isolation in the Centre for Primatology. Two phenotypically associated pedigree which were recognized experimentally as *Aeromonas* sp. were isolated. These pedigrees could not be recognized as members of any earlier described *Aeromonas* species. In the recent investigation phylogenetic study of 16S rRNA gene sequences DNA-DNA hybridization and inclusive phenotypic tests were attempt to demonstrate the taxonomic posture of the two monkey quarantine. Established on the described data a novel species of the genus *Aeromonas* for which the name

*Aeromonas simiae* sp. novel is determined.

## ELEPHANT

The Asiatic elephant is an extensively scattered species covering most of South Asia in the west to Indochina in the east and a larger part of Southeast Asia excluding Peninsular Malaysia Sumatra and Borneo. Few populations are differentiate through morphological characters such as the skin colour, pigmentation and sometimes by the characteristics veins in the ears (Kurt & Kumarasinghe, 1998). However, different populations prefer to live in definite habitats. These differences considered for the identification of different subspecies. Three are rapidly identified i.e *Elephas maximus indicus* (Indian elephant), *E. m. maximus* (Sri Lankan elephant) and *E. m. sumatrensis* (Sumatran elephant) (Sukumar, 1989; Sukumar et al., 1991; Fleischer et al., 2001). While a number of morphometric studies on Asian elephant were finished and published (Wemmer and Krishnamurthy, 1992; Daniel, 1998; Othman, 1990; Othman, 2003) there was no morphometric study taken out to distinguish the sub-species. The Bornean elephant the recently clustered sub-species, is believed to be the little in size and observed to have immense ears, longer tails, straighter and long tusks and a more rounded body. The subspecies was clustered based on genetic analysis by the known historical accounts of its origin (Fernando et al., 2003; De Silva, 1968; Ibbotson, 2003; Shim, 2003). A morphological study to observed a definite group of organism which provoked this study (Hawksworth, 1995).

Although the woolly mammoth (*Mammuthus primigenius*) is one of the most intensively studied extinct species at the DNA level mitochondrial DNA (mtDNA) markers have failed to unambiguously resolve its phylogenetic integration within Elephantidae. Most mtDNA-based elephantid phylogenies associate mammoths with African elephants (*Loxodonta africana* and *Loxodonta cyclotis*) to the exclusion of the Asian elephant (*Elephas maximus*) (Debruyne et al., 2003; Noro et al., 1998). However other mt DNA studies (Ozawa et al., 1997) including recent sequencing reports that yielded the complete mitochondrial genomes of two woolly mammoths (Krause et al., 2006; Rogaev et al., 2006) suggested that the Asian elephant is the closest living affine of mammoths. However relationships inferred from mtDNA may be misleading due to the absence of a closely related outgroup species or to the radiation of the three elephantidae genera in rapid succession which can produce discordance between a species tree and a gene (mtDNA) tree due to lineage sorting processes. Nuclear DNA sequences from mammoths and other well-preserved extinct megafauna have been reported (Greenwood et al., 1999; Greenwood et al., 2001; Poinar et al., 2003; Poinar et al., 2006) and in principle it should be possible to characterize mammoth nuclear DNA sequences for the purpose of phylogenetic analysis.

Besides nuclear markers present a stronger structure than do the mitochondrial sequences. The elephants are known to have a strong social structure governed by a matrilineal operation of herds. Juvenile males are eliminate from the herds after teen age and live lonely (Moss, 2000; Nyakaana et al., 2001). Patterns of migration are biased male because the herds show a philopatric behavior (Nyakaana and Arctander, 1999). These characteristics lead low rate of intra-populational genetic variation and a strong level of inter-populational differentiation especially for mtDNA. While that the counterstatement between the two types of molecular markers is possibly an artefact due to inadequate molecular sampling by previous researchers (Nyakaana and Arctander, 1999; Eggert et al., 2002; Nyakaana et al., 2002). To shed more light on this affair longer particles of the mitochondrial genomes sequenced cross all published sequences one protein coding gene (cytochrome b), one ribosomal gene (12S rRNA), three transfer RNA genes (tRNA-Thr, tRNA-Pro, and tRNA-Phe), and the mitochondrial control section were sequenced. Two groups are analyzed 1961 bp for 48 African elephants and 3700 bp for 18 African elephants assign to here as short and long pieces suitably. During the last decades methods for amplification and sequencing of DNA pieces were applied to fossil remains and provided a means for comparative genetic studies on extinct and related living forms.

DNA of an extinct animal (a quagga) was first studied (in 1984 cited from Paabo et al., 1992). DNA was cloned from a 4400 year old Egyptian mummy (Paabo, 1985) 7000 year old human brain (Paabo et al., 1988) and a number of fossil animals and birds. As regards the Elephantidae successful PCR amplification and sequencing was performed for the following mitochondrial genes of mammoths aged by radiocarbon method >50,000 to 9,700 BP 93 base pair fragment of the 16S ribosomal RNA gene (Hoss et al., 1994), 961 bp complete sequence of the 12S rRNA gene (Noro et al., 1998), and fragments of the cytochrome b gene of 242 bp, 277 bp (Hagelberg et al., 1994), 228 bp (Yang et al., 1996), 1005 bp (Ozawa et al., 1997), and a complete sequence of 1137 bp (Noro et al., 1998). These data were compared with the sequences for living Asian and African elephants.

## CONCLUSION

Genetic Variation is the trait of interest is the basis for future breeding variation is display by genetic difference between individual, families and population within a given species.

Our understanding of breed diversity has been deepened significantly by technological progress in molecular genetics. MtDNA data have allowed the elucidation of the relationship with wild ancestor species and-for most spe-

cies it is also informative at the intercontinental level. In combination with archeological data, it has been shown that most important areas for domestication event of the main livestock species are found in Asia, Europe and South America.

There is evidence of multiple domestication event for most species. Often involves subspecies and repeated introgression event of closely related ancestor species using mtDNA indicate that the cattle and river buffalo originate from Indus valley while swamps from Yangtze valley and horses were domesticated in broad area across the Eurasian steppe and in this species the husbandry style has left considerable signature. Elephant originates from South Asia and Indochina. This result is extracted by using mitochondrial DNA and Genes of mitochondria.

## CONFLICT OF INTEREST

There is no conflict of interest.

## AUTHOR'S CONTRIBUTION

SR, SB and SA have contributed equally.

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