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Mitochondrial diversity and phylogenetic structure of Mahabadi goat population

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Abstract

The genetic diversity and phylogenetic structure was analyzed in Mahabadi goat population by mitochondrial DNA sequences. Phylogenetic analysis was carried out using hyper variable region 1 (896 bp) obtained from 30 animals. Mahabadi goat proved to be extremely diverse (average haplotype diversity of 0.999) and the nucleotide diversity values 0.022. A total of 30 Mahabadi goats were grouped into six haplotypes and the large majority of haplotypes were present in 15 animals. All Mahabadi haplotypes were classified into a haplogroup and revealed remarkably high genetic distances within the population when compared with other Asian goat populations, indicating high genetic variation in the Mahabadi goat. These results indicate high-divergence status of the Mahabadi goat and will influence breeding and conservation strategies adopted for this breed.

Keywords: genetic diversity, marghoz goat, mtDNA, phylogenetic

Introduction

The mitochondrial DNA (mtDNA) polymorphism, especially the displacement loop (D-loop) region, has been largely applied to understand phylogenetic relationships in many animal species, including cattle (Ilie *et al.* 2015) [15], pig (Li *et al.* 2015), sheep (Agaviezor *et al.* 2012) [1], chicken (Hoque *et al.* 2013) [14], horse (Zernekova *et al.* 2013) [33] and goat (Hoda *et al.* 2014 [1]; Pakpahan *et al.* 2015 [24]; Çinar Kul and Ertugrul, 2011) [8]. Previous studies on domestic goats identified at least four major mtDNA lineages (Joshi *et al.* 2004; Luikart *et al.* 2001; Sultana *et al.* 2003) [16, 20, 28]. Lineage A is the most diverse and widely distributed across all continents. Lineage B is confined to eastern and southern Asia, including Mongolia, Laos, Malaysia, Pakistan and India. Lineage C is present in low frequencies in Mongolia, Switzerland, Slovenia, Pakistan, India and Iran.

Finally, lineage D is rare and only observed in Pakistani and Indian local goats (Naderi *et al.* 2007) [23]. The time since divergence among these four lineages (more than 200,000 years ago) far pre-dated the time of domestication around 10,000 years ago (Joshi *et al.* 2004; Luikart *et al.* 2001; Sultana *et al.* 2003) [16, 20, 28]. The control region (D-loop) is the most variable and non-coding portion of the mitochondrial genome (Wilson *et al.* 1985) [31]. This region controls the mitochondrial DNA (mtDNA) replication by regulating the activities of various enzymes and proteins that are coded by the nuclear genes (Ghivizzani *et al.* 1993; Nass, 1995) [11]. The sequences of the control region vary greatly in different mammalian species, however, preservation of several conserved regions indicate fundamental harmony in its function (Saccone *et al.* 1991) [26]. It contains the origin of heavy strand and the promoters for the light and heavy strand replication (Anderson *et al.* 1982) [5]. Because of their rapid evolution (Brown *et al.* 1979) [6], the control region sequences are valuable for investigating the genetic diversity and evolutionary relationships among species (Wilson *et al.* 1985) [31]. The extent and pattern of genetic variability in livestock species will contribute to the conservation of livestock genetic resources. On the basis of the previously mentioned archaeological studies and bio-geography, it is likely that the molecular studies of diversity in Iranian goats will yield new understanding of the origin and process of goat domestication, and will contribute to the resolution of goat phylogeny.

More than 20 breed of goats have been recognized in Iran but only breeds namely Marghoz and Raeni produces attractive and expensive Mo-hair and Kashmir fiber. These small breeds of goat are dis-tributed over the western and north-west of Iran near to the Turkey and Iraqi borders. Marghaz goats are fertile animals with twin kidding over 30% (Moradi *et al.* 2014) [22]. It is believed the Angora goats are originated from this breed (Moradi *et al.* 2014) [22].

Angora goats appear in one color which is white to silver, but Mahabadi goats produce mohair in different natural colors which are a unique character of this breed. Keeping above in view in present study, the current phylogenetic status and genetic diversities of Mahabadi goat has been investigated in order to understand the genetic basis of this breed.

Phylogenetic Reconstruction

The sequences obtained were compared by alignment to the international Gene Bank data-base in 1 Chinese (KM 360063), 1 Switzerland (KR059147), 1 Italy (KR059205), 1 Jordan (KR059160), 1 Iran (KR059191), 1 Spain (KR059156), 1 Austria (KR059180), 1 Egypt (KR059159), 1 Turkey (KR059200), 1 Cyprus (KR059163), 1 Saudi Arabia (KR059154), 1 Romania (K059198), 1 Albania (KR059146),

1 Kyrgyzstn (059122) and 1, Malaysia (KR059220) using the Bio Edit software program version 7.2 (Hall, 1999) [12]. To investigate genetic relationship between mitochondrial sequences, an unrooted neighbor-joining phylogeny (Saitou and Nei, 1987) [27] was constructed using the Tamura-Nei distance method (Tamura and Nei, 1993) [30]. The distance computation and phylogenetic tree construction are incorporated in the MEGA Package version. 5.1 (Kumar *et al.* 2004) [17]. Haplotype diversity (h), nucleotide diversity (p) and daverage number of nucleotide were calcu-lated using Dna SP software version 4.2 (Rozas *et al.* 2003) [25].

Results and Discussion

(mtDNA variation in Marghoz goat) In the present study, we analyzed the mtDNA control region sequences of 30 Mahabadi goats to further elucidate its diversity. There were no insertions/deletions in 30 sequences of HVRI of the control regions. The HVRI sequences were highly polymorphic. Our 30 sequences gave 7 different haplotypes with 44 variable sites defined. The two largest haplotype group consisted of 6 individuals, two haplotype groups included 3 individuals, and three haplotypes included 4 individuals (table2).

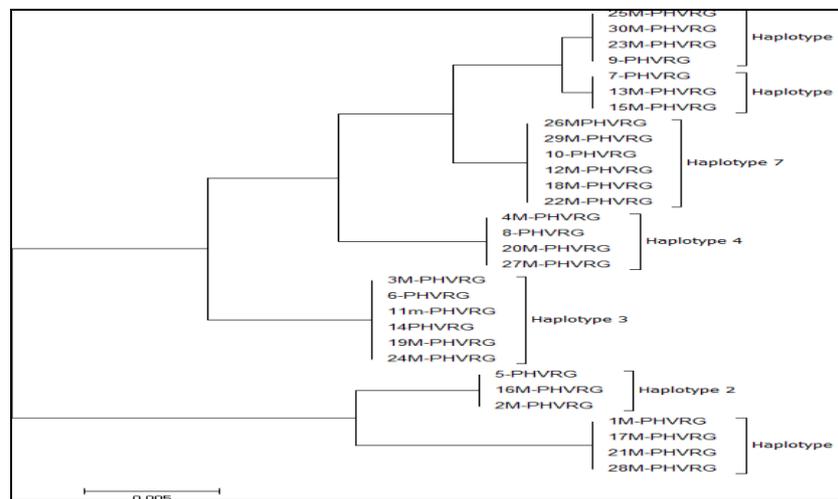


Table 1: Haplotype diversity phylogeny tree bead on HVR1 sequence within Mahabadi goat population

The average base composition of the control region sequences was as follows; A: 30.38%, C: 23.77%, G: 15.70% and T: 30.16% and the molecular weight of single this sequence was 271807.00 Daltons and the molecular weight of pairs was 540684.00 Daltons. (Figure 1). This indicates that the caprine mtDNA control region has high A/T contents as well as in all artiodactyls (cattle, sheep, goat and pig) and other mammalian

species such as mouse (Ameur *et al.* 2011) [4], donkey (Xu *et al.* 1996) [32] and whale (Arnason *et al.* 1991) [3]. However, in the case of primates (Foran *et al.* 1988) [10], seal (Arnason *et al.* 1993) [2] and rabbit (Mignotte *et al.* 1990) [21], the control region is rich in A/C contents. This is attributed to the species-specific variations that exist in the control regions among different mammalian species.



Fig 1: Average base composition of the HVR1 region sequences in Mahabadi goat

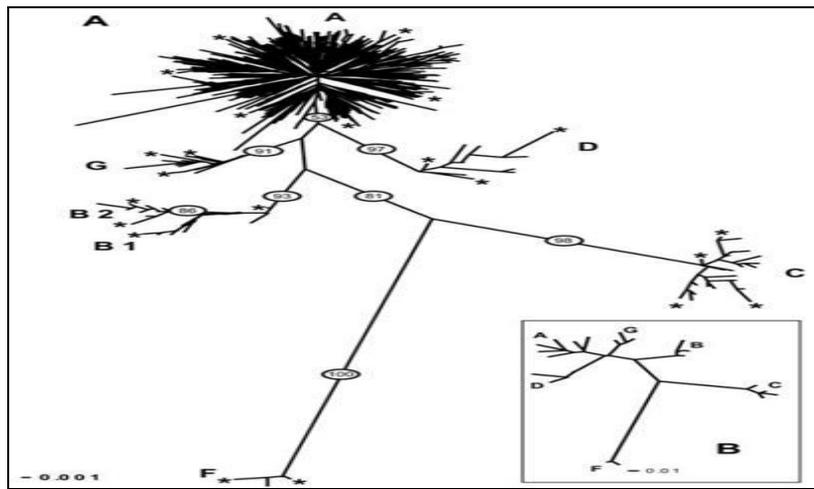
Naderi *et al.* (2007) [23] investigated 2430 goats from different countries and shows six very different groups according to mitochondrial haplogroup are referred to as A, B, C, D, F and G. The re-sults of the research show that the haplogroup A is at most at 53%. A haplogroup spread almost all over the world and is the first haplogroup. Haplogroup B is found throughout most of Asia and a small portion coming from Sub-Saharan Africa and goat Europe from Greece. Goats of haplogroup C is present in central Asian, Middle East, Iran and hap-logroup D is present throughout Asia and northern Europe. Group F goat came from Sicily and the group G is present in the Middle East and North Africa. The results were in general agreement with the pattern described in previous study (Naderi *et al.* 2007) [23]. However more detailed molecu-lar studies are required in near future. It is urgent to

take measures that promote a sustainable management of these genetic resources (Taberlet *et al.* 2008) [29]. We also estimated haplotype diversity for the six haplogroups. In a study carried out on samples obtained from different countries we found that A, B, C have identified. We found that A had the highest distribution in the samples. We found that A had the highest distribution in the samples.

We found that in countries like China and Pakistan, Laos, India and Malaysia were observed only in the countries of Switzerland and Slovenia We found that C is also observed in small populations (rare *et al.* 2009).

We found that A belongs to group analysis every 5 samples. Goat Farm has six haplotype groups A, B, C, D, F, G, has been detected (Nader *et al.* 2007) [23] haplotypes between haplotype other Group A is most frequent. (Table 3)

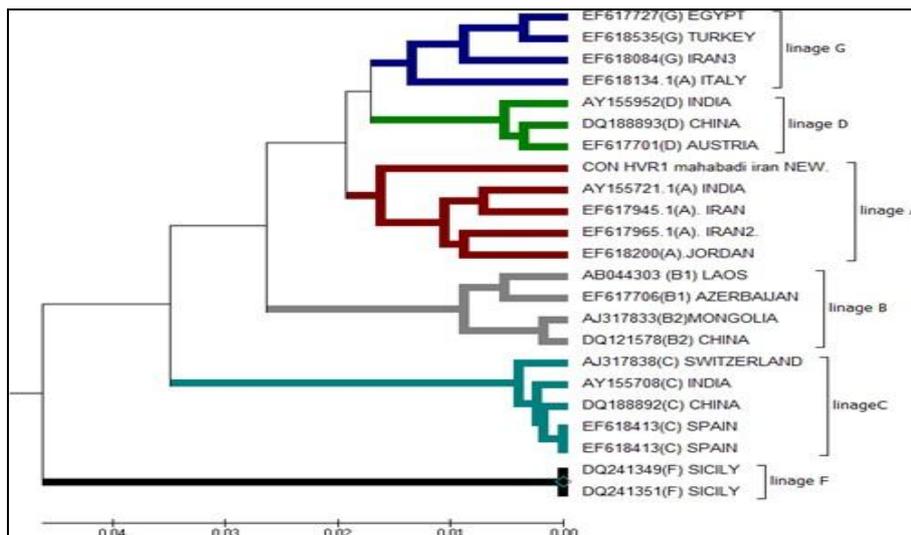
Table 2: The frequency of haplotype groups goat species around the world



By comparing the sequence obtained from district HVR1-of-breed goats Mahabadi sequences of these six groups of haplotypes as a sequence of reference in the study by Nader *et*

al. in 2009 took the form of a table in the study that Mahabadi goats belonging to haplotype group A is based on the analysis. (Table 3).

Table 3: Haplotype phylogeny tree of the six group based on compare HVR1 of Mahabadi goat by other.

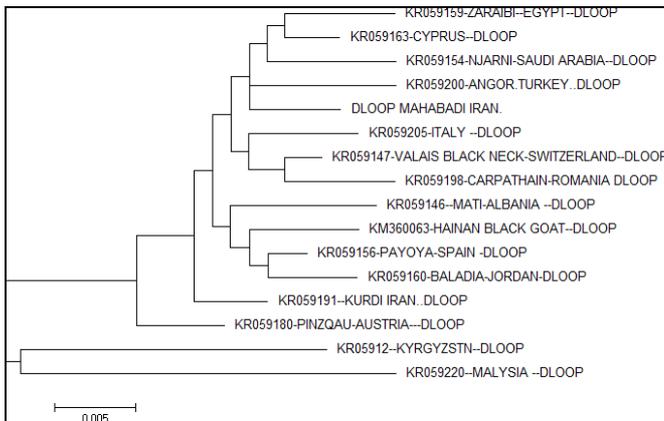


Mahabadi goat the haplotype diversity was 0.8759. This haplotype diversity is in accordance with the previously described values in Albanian and Turkish goat breeds (Hoda *et al.* 2014; Çinar Kul and Ertugrul, 2011) [13, 8]. The level of haplotype diversity of 18 goat breeds (0.7121-0.9804) by Chen *et al.* (2005) [7] is closed to Mahabadi goat (0.8759) in our study. Haplotype diversity of mtDNA is important indices

for assessing population polymorphism and genetic differentiation. High values of haplotype indicate high polymorphism of the population (Liu *et al.* 2006) [19]. Mahabadi goats are compared of 21 species goats from different countries by drawing phylogenetic that is showed in below (Table 4).

Table 4: Phylogenetic relationship among 12 Gen Bank accession number of HVR1 region from goat breeds

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1. DLOOP MAHABADI IRAN.																
2. KM360063-HAINAN BLACK GOAT--DLOOP	0.0078															
3. KR05912--KYRGYZSTN--DLOOP	0.0661	0.0291														
4. KR059146--MATI-ALBANIA --DLOOP	0.0482	0.0414	0.0728													
5. KR059147-VALAIS BLACK NECK-SWITZERLAND--DLOOP	0.0258	0.0090	0.0202	0.0190												
6. KR059154-NJARNI-SAUDI ARABIA--DLOOP	0.0370	0.0291	0.0582	0.0011	0.0112											
7. KR059156-PAYOYA-SPAIN -DLOOP	0.0146	0.0280	0.0997	0.0224	0.0325	0.0190										
8. KR059159-ZARAIBI-EGYPT--DLOOP	0.0190	0.0056	0.0213	0.0235	0.0011	0.0146	0.0302									
9. KR059160-BALADIA-JORDAN-DLOOP	0.0213	0.0112	0.0358	0.0101	0.0022	0.0045	0.0190	0.0034								
10. KR059163-CYPRUS--DLOOP	0.0056	0.0056	0.0504	0.0224	0.0101	0.0146	0.0090	0.0078	0.0056							
11. KR059180-PINZQAU-AUSTRIA---DLOOP	0.0549	0.0280	0.0190	0.0202	0.0056	0.0146	0.0560	0.0101	0.0101	0.0291						
12. KR059191--KURDI IRAN..DLOOP	0.0101	0.0280	0.1086	0.0381	0.0414	0.0325	0.0022	0.0370	0.0280	0.0112	0.0717					
13. KR059198-CARPATHAIN-ROMANIA DLOOP	0.0347	0.0112	0.0090	0.0325	0.0022	0.0224	0.0504	0.0034	0.0090	0.0190	0.0056	0.0594				
14. KR059200-ANGOR.TURKEY..DLOOP	0.0034	0.0179	0.0918	0.0683	0.0448	0.0560	0.0190	0.0370	0.0381	0.0146	0.0817	0.0101	0.0560			
15. KR059205-ITALY --DLOOP	0.0034	0.0090	0.0649	0.0280	0.0179	0.0202	0.0056	0.0146	0.0112	0.0011	0.0414	0.0056	0.0291	0.0090		
16. KR059220--MALYSIA --DLOOP	0.0661	0.0291	0.0000	0.0728	0.0202	0.0582	0.0997	0.0213	0.0358	0.0504	0.0190	0.1086	0.0090	0.0918	0.0649	



Distribution of the samples between the groups was made in accordance with the cluster obtained. Apparently, the longest distance separated the KR059220 (Malysia) from the others and Mahabadi goat has shortest genetic distance with Angora Turkey goat (KR059200), and also has longest genetic distances with Malysia (KR059220), Kyrgystn (kr059122)). This is possible because of geographical distance and distributed.

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References

1. Agaviezor BO, Adefenwa MA, Peters SO, Yakubu A, Ade-bambo OA, Ozoje MO *et al.* Genetic diversity analysis of the mitochondrial D-loop of Nigerian indigenous sheep. *Anim. Gen. Resour.* 2012; 50:13-20.
2. Arnason U, Gullberg A, Johnsson E, Ledje C. The nucleotide sequence of the mitochondrial DNA molecule of the grey seal, *Halichoerus grypus* and a comparison with the mitochondrial sequences of other true seals. *J Mol. Evol.* 1993; 37:323-330.
3. Arnason U, Gullberg A, Widegren B. The complete nucleotide sequence of the mitochondrial DNA of the çn whale *Balaenoptera physalus*. *J Mol. Evol.* 1991; 33:556-568.
4. Ameur A, Stewart JB, Freyer C, Hagstro E, Ingman M, Ran N *et al.* Ultra-deep sequencing of mouse

mitochondrial DNA: mutational patterns and their origins. *PLoS Gent.* 2011; 7:1-15.

5. Anderson S, De Bruijn MHL, Colson AR, Eperon IC, Sanger F, Young IG. Complete sequence of bovine mitochondrial DNA conserved features of the mammalian mitochondrial genome. *J Mol. Biol.* 1982; 156:683-692.
6. Brown WM, George MJ, Wilson AC. Rapid evolution of animal mitochondrial DNA. *Proc. Nat. Acad. Sci. USA.* 1979; 76:1967-1971.
7. Chen SY, Su YH, Wu SF, Sha T, Zhang YP. Mitochondrial diversity and phylogeographic structure of Chinese domestic goats. *Mol. Phylogenet. Evol.* 2005; 73:804-814.
8. Çinar Kul B, Ertugrul O. mtDNA diversity and phylogeography of some Turkish native goat breeds. *Ankara Üniv. Vet. Fak. Derg.* 2011; 58:129-134.
9. Cozzi MC, Strillacci MG, Valianti P, Bighignoli B, Cancedda M, Zanotti M. Mitochondrial D-loop sequence variation among Italian horse breeds. *Genet. Sel. Evol.* 2004; 36:663-672.
10. Foren DR, Hixson JE, Brown WM. Comparisons of ape and human sequences that regulate mitochondrial DNA transcription and D-loop DNA synthesis. *Nucleic Acids. Res.* 1988; 16:5841-5861.
11. Ghivizzani SC, Madsen CS, Hauswirth WM. In organello footprinting: analysis of protein binding at regulatory regions in bovine mitochondrial DNA. *J Biol. Chem.* 1993; 268:8675-8682.
12. Hall TA. Bio edit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids. Symp. Ser.* 1999; 41:95-98.
13. Hoda A, Bicoku Y, Dobi P. Genetic diversity of Albanian goat breeds revealed by mtDNA sequence variation. *Biotechnol. Biotec. Equip.* 2014; 28:77-81.
14. Hoque MR, Choi NR, Sultana H, Kang BS, Heo KN, Hong SK *et al.* Phylogenetic analysis of a privately-owned Korean Native chicken population using mtDNA D-loop variations. *Asian-Australas J Anim. Sci.* 2013; 26:157-162.
15. Ilie DE, Cean A, Czisster LT, Gavojdian D, Ivan A, Kusza S. Microsatellite and mitochondrial DNA study of native eastern European cattle populations: the case of the Romanian Grey. *PLoS One.* 2015; 10:1-18.
16. Joshi MB, Rout PK, Mandal AK, Tyler-Smith C, Singh L, Thangaraj K. Phylogeography and origin of Indian domestic goats. *Mol. Biol. Evol.* 2004; 21:454-462.

17. Kumar S, Tamura K, Jakobsen IB, Nei M. MEGA3.1: Molecular Evolutionary Genetics Analysis Soft-ware. Arizona State University Press, Tempe, USA, 2004.
18. Li KY, Li KT, Cheng CC, Chen CH, Hung CY, Ju YT. A genetic analysis of Taoyuan pig and its phylogenetic relationship to Eurasian pig breeds. *Asian-Australas J. Anim. Sci.* 2014; 28:457-466.
19. Liu ZG, Lei CZ, Luo J, Ding C, Chen GH, Chang H *et al.* Genetic variability of mtDNA sequences in Chinese native chicken breeds. *Asian-Australas J. Anim. Sci.* 2006; 17:903-909.
20. Luikart G, Gielly L, Excoffier L, Vigne JD, Bouvet J, Taberlet P. Multiple maternal origins and weak phylogeographic structure in domestic goats. *Proc. Nat. Acad. Sci. USA.* 2001; 98:5927-5932.
21. Mignotte F, Gueride M, Champagne AM, Mounolou JC. Direct repeats in the non-coding region of mitochondrial DNA. Involvement in the generation of intra and inter-individual heterogeneity. *European J Biochem.* 1990; 194:561-571.
22. Moradi MH, Rostamzadeh J, Rashidi A, Vahabi K, Farah-mand H. Analysis of genetic diversity in Iranian mo-hair goat and its color types using Inter Simple Sequence Re-peat (ISSR) markers. *Agric. Commod.* 2014; 2:55-62.
23. Naderi S, Rezaei HR, Taberlet P, Zundel S, Rafat SA, Na-ghash HR *et al.* Large-scale mitochondrial DNA analysis of the do-mestic goat reveals six haplogroups with high diversity. *PloS One.* 2007; 2:1-10.
24. Pakpahan S, Tunas Artama W, Widayanti R, Suparta G. Genetic variations and the origin of native Indonesian goat breeds based on mtDNA D-Loop sequences. *Asia J Anim. Sci.* 2015; 9:341-350.
25. Rozas J, Sached-Delbarrio JC, Messeguer X, Rozas R. DnaSP, DNA polymorphism analyses by the coales-cent and other methods. *Bioinformatics.* 2003; 19:2496-2497.
26. Saccone C, Pesole G, Sbisa E. The main regulatory region of mammalian mitochondrial DNA: structure function model and evolutionary pattern. *J Mol. Evol.* 1991; 33:83-91.
27. Saitou N, Nei M. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol. Biol. Evol.* 1987; 4:406-425.
28. Sultana S, Mannen H, Tsuji S. Mitochondrial DNA diversity of Pakistani goats. *Anim. Genet.* 2003; 34:417-421.
29. Taberlet P, Valentini A, Rezaei HR, Naderi S, Pompanon F, Negrini R *et al.* Are cattle, sheep, and goats endangered species. *Mol. Ecol.* 2008; 17:275-284.
30. Tamura K, Nei M. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Mol. Biol. Evol.* 1993; 10:512-526.
31. Wilson AC, Cann RL, Carr SM, George M, Gyllensten UB, Helm-Bychowski KM *et al.* Mitochon-drial DNA and two perspectives on evolutionary genetics. *Biol. J Linn. Soc.* 1985; 26:375-400.
32. Xu X, Gullberg A, Arnason U. The complete mitochondrial DNA (mtDNA) of the donkey and mtDNA compari- sons among four closely related mammalian species pairs. *J Mol. Evol.* 1996; 43:438-446.
33. Zernekova C, Kott T, Majzlik I. Mitochondrial D-loop sequence variation among Hucul horse. *Czech J Anim. Sci.* 2013; 58:437-442.
34. Naderi S, Rezaei HR, Taberlet P, Zundel S, Rafat SA, Naghash HR *et al.* Largescale mitochondrial DNA analysis of the domestic goat reveals six haplogroups with high diversity. *PLoS ONE.* 2007; 2:e1012.
35. Parma P, Feligini M, Greppi G, Enne G. Thecomplete nucleotide sequence of goat (*Capra hircus*) mitochondrial genome. *DNA Seq.* 2003; 14:199-203.
36. Luikart G, Gielly L, Excoffier L, Vigne JD, Bouvet J, Taberlet P. Multiple maternal origins and weak phylogeographic structure in domesticgoats. *Proceedings of the National Academy of Sciences USA,* 2001; 98:5927-32.
37. Saitou N, Nei M. The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution.* 1987; 4:406-425.
38. Amer SAM. Mitochondrial DNA Variability among Some. Saudi Arabian Goat Breeds. *British Biotechnology Journal,* 2014, 4(8):877-882.
39. Amills M, Ramirez O, Tomas A, Badaoui B, Marmi J, Acosta J *et al.* Mitochondrial DNA diversity and origins of South and Central American goats. *Anim. Genet.* 2009; 40:315-322.
40. Avise JC. Molecular markers, natural history and evolution. Chapman & Hall, New York, 1994.
41. NY Boyazoglu J, Hatziminaoglou I, Morand-Fehr P. The role of the goat in society: past, present and per spectives for the future. *SmallRumin. Res.* 2005; 60:13-23.
42. Esposti MD, Crimi M, Ghelli A, Patarnello T, cytochrome b: evolution and structure of theprotein. In: *Biochim. Biophys. Acta.* 2005; 1143(3):243-271.
43. Howell N. Evolutionary conservation of protein regions in the protonmotive cytochrome b and their possible roles in redox catalysis. In: *J Mol. Evol.* 1989; 29(2): 157- 169.
44. Librado P, Rozas J. DnaSP v5: A software for comprehensive analysis ofDNA polymorphism data. *Bioinformatics.* 2009; 25:1451-1452.