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Mitochondrial DNA Variability among Some Saudi Arabian Goat Breeds

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Author's contribution

This work was carried out entirely by the author. Author SAMA conceptualized and designed the study, did the laboratory analysis and wrote the first draft and the revised form of the manuscript.

Short Communication

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ABSTRACT

Five hundred nucleotides of cytochrome b gene was sequenced for Pakistani, Tihami, Syrian, Masri and Aardi goat breeds inhabiting Saudi Arabia. Based on two computational maximum-parsimony and neighbor-joining methods, the constructed tree clustered the studied breeds into Masri and Tihami in one group and Pakistani and Aardi came basal to this group. Syrian breed came basal to all of the studied breeds. This division was based on a few mitochondrial DNA sites and few sampling size and it therefore needs to be supported in a further molecular study. The goat breeds studied herein did not show any non-synonymous genetic variability when the protein-coding gene of the mitochondrial genome was used as a molecular maker. However, the only mitogenome maker which can show base differences among these breeds was the non-coding displacement loop (d-loop). In conclusion, using the mitochondrial genes, rather than the d-loop, for studying genetic diversity among goat breeds is with no meaning and it is better to use other markers for this purpose.

Keywords: Arabian goats; cytochrome b gene; genetic variability; molecular markers.

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1. INTRODUCTION

Goats are distributed over all types of eco-niches, including tropical areas, dry zones and mountain regions. With wide distribution range and tolerance to varied environmental conditions one can expect high genetic variability within goat breeds [1].

Unfortunately there was no any solid evidence for how many goat breeds inhabiting Saudi Arabia. It is found that Aardi, Hibsi, Zumri [2] Pakistani, Tihami, Masri, Syrian and Beeshi (well-known traditionally) are the most common breeds inhabiting the Kingdom. In spite of this, one can find other breeds with local traditional names.

Genetic diversity is defined as the sum of genetic differences in multiple loci among individuals in a population, and is most readily reflected in the phenotypic variation seen in many populations. Genetic diversity is a valuable asset as the adaptability of a population, that is the population's ability to adapt to changes, depends on it [3].

In recent years, molecular genetics have experienced considerable advances and offer a convenient way for characterization of population structure. Nowadays, DNA molecular markers are extensively applied to the goat breed classification instead of blood protein and isoenzyme [4]. MtDNA (mitochondrial DNA) is an important maternal genetic marker in studying the genetic relationships of livestock species and breeds [5]. The mtDNA has proven to be especially valuable in the study of genetic variation because it shows the maternal inheritance and changes much more rapidly than single copy nuclear DNA in mammals [6]. Compared with analyses of allozymic variations, analyses of mtDNA polymorphism at the nucleotide level have shown to be very useful for detection of genetic variation.

The present study therefore aimed to sequence cytb gene in the mitochondrial DNA for addressing the available genetic variability within and among some Saudi Arabian goat breeds.

2. MATERIALS AND METHODS

2.1 Animals

Twenty four blood samples were freshly withdrawn from the jugular vein from five different goat breeds (approximately five males from each breed) from private owners in Taif city. These goat breeds were as follows: Pakistani, Tihami, Syrian, Masri and Aardi. The anti-coagulated blood samples were kept in the lab at -80ºC for further molecular study.

2.2 Molecular Techniques

The mitogenome of the collected blood samples was extracted with QIAGEN spin-column kits according to the manufactur's instruction. PCR experimets, purification of the resulted products and gene sequencing were conducted by the same conditions published by AL-Harbi et al. [7] using the same primers published for the cytb gene. The annealing temperature in the PCR experimets was 54ºC for one minute.

The sequnces of the cytb gene for *Capra hircus* (accessin number: AB044308) and *Capra ibex* (accession number: AF034735) were taken from the Genbank for rooting the constructed tree.

2.3 Statistical Analyses

The data from the aligned cytb gene were checked manually by MacClade v.4. The aligned data (500 bp) were used for tree construction. Maximum-Parsimony (MP) and Neighbor-Joining (NJ) methods in the package of PAUP 4.0b10 [8] were used for tree analyses. In both methods, heuristic searches with TBR branch swapping and 10 random taxon additions were conducted. Simple additions for 1000 bootstrap replications with simple additions were set.

3. RESULTS AND DISCUSSION

The cytochrome b gene did not show any variation among the studied breeds. The hydrophilic protein of cytb acquires higher mutations in abnormal cases of skeletal muscle weakness and exercise intolerance [9]. It is one of the cytochromes which showed variations when the respiratory capacity changes [10]. It is therefore possible to correlate the identity in the sequence of this gene to the similarity in the respiratory capacity of different goat breeds.

Single neighbor-joining tree (Fig. 1) was obtained from the data sets with some reasonable statistical supports for two computational methods (MP and NJ). The tree topology exhibited sister relationship between the breeds of Masri and Tihami (bootstrap percentages were 87 and 86 for both MP and NJ, respectively). Both breeds of Aardi and Pakistani grouped with the first cluster while Syrian goat was basal. It could be possible to attribute the unclear resolution of the constructerd tree to the sampling size or to the expected hybridization among the studied goats.

Herein, a small aligned fragment of the d-loop region was presented for some goat breeds from Pakistan (Fig. 2) and these data were taken from Genbank database. Few SNIPs (single nucleotide polymorphism) among these breeds were shown, most of which were transions (purines to purines or pyrimidine to pyrimidine) and were not transversions. Similar study was conducted by AL-Harbi and Amer [7] for Saudi Arabian sheep breeds in which the authors found that the d-loop region was the only mitochondrial DNA marker discrinminated clearly among sheep breeds. The authors have proved that none of the protein-coding genes (ND4, CO1, ATP6 and cytb genes) have aquired any base substitutions. It is therfore usefull to use the d-loop region for studying genetic diversity among the Saudi Arabian goat breeds and this could be conducted in future study.

The entire mitochondrial genomes available in GenBank database for this animal were roughly compared and there were no obvious variability obtained among the different breeds (data not shown) except for some SNIPs inside the displacement loop (Fig. 2). The use of highly variable molecular genetic markers, such as microsatellites, is one of the most powerful means for studying genetic diversity and pedigree reconstruction among goat breeds because of their high degree of polymorphism, random distribution across the genome and neutrality with respect to selection [11-13]. It is therefore invaluable to consider the application of mitochondrial genome sequence for studying genetic diversity among goat breeds and it is better to use the microsatellites markers for this purpose.

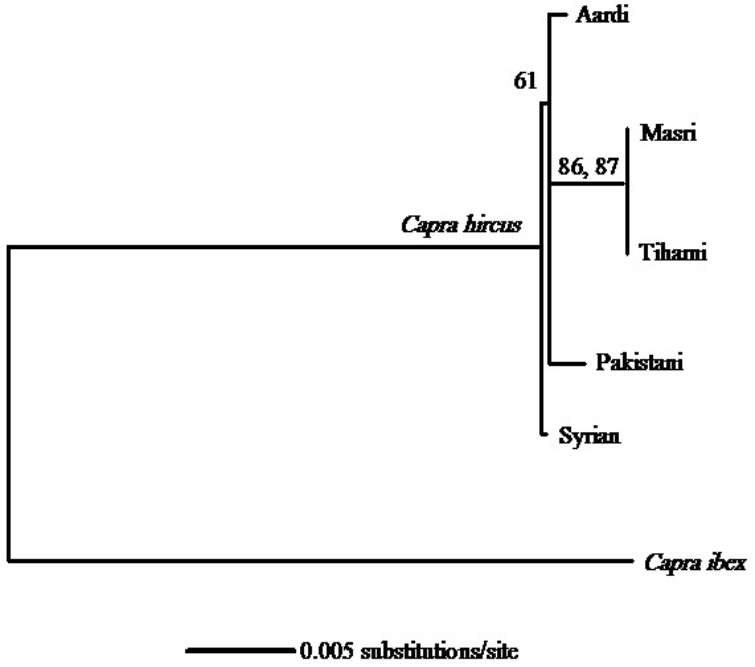

Fig. 1. A neighbor-joining tree constructed from approximately 500 bp cytochrome b gene sequenced for the different studied goat breeds. Bootstrap percentages were shown at nodes when they were above 50%

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                                                                      450
Barbari      ACAAGGACA TAGTATGTAT ATAGTACATT AAACGATTTT CCGCATGCAT
Kamori       ACAAGGACA TAGTATGTAT ACAGTACATT AAACGATTTT CCGCATGCAT
Damani       ACAAGGACA TAGTATGTAT ATAGTACATT AAACGATTTT CCACATGCAT
Khurasani    ACAGGGACA TAGTATGTAT ATAGTACATT AAACGATTTT CCACATGCAT
Lehri        ACAGGGACA TAATATGTAT ATAGTACATT AGACGATTTT CCACATGCAT
Nachi        ACAAGGACA TAGTATGTAT ATAGTACATT AAACGATTTT CCACATGCAT

                                                                      500
Barbari      TTAAGCACG TACATCAGTA TTAATGTAAT AAGGACATAG TATGTATATT
Kamori       TTAAGGACG TACATCAGTA TTAATGTAAT AAGGACATAG TATGTATATT
Damani       TTAAGCACG TAATATTAGTA TTAATGTAAT AAAGACATAA TATGTATATC
Khurasani    TTAAGCACG TACATCAGTA TTAATGTAAT AAGGACATAG TATGTATATT
Lehri        TTAAGGACG TACATCAGTA TTAATGTAAT AAGGACATAG TATGTATATT
Nachi        TTAAGCACG TACATCAGTA TTAATGTAAT AAGGACATAG TATGTATATT

                                                                      550
Barbari      TACATTAAA CGATCTTCCC CATGCATATA AGCGTGTATA ATGCTTCTAT
Kamori       TACATTAAA CGATCTTCCT CATGCATATA AGCATGTATA ATATTTCTAT
Damani       TACATTAAA CGATCTCCCC CATGCATATA AGCATGTACA ATATCTCTAT
Khurasani    TACATTAAA CGATCTTCCC CATGCATATA AGCATGTATA ATATTTCTAT
Lehri        TACATTAAA CGATCTTCCT CATGCATATA AGCATGTATA ATATTTCTAT
Nachi        TACATTAAA CGATCTTCCT CATGCATATA AGCATGTATA ATGCTTCTAT
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Fig. 2. An aligned fragment from d-loop region for some different Pakistani goat breeds. See the variability among the breeds as referred to by boxes.

4. CONCLUSION

The goat breeds studied herein did not show any non-synonymous genetic variability when the protein-coding gene of the mitochondrial genome was used as a molecular maker. However, the only mitogenome maker which can show base differences among these breeds was the non-coding displacement loop (d-loop). In conclusion, using the mitochondrial genes, rather than the d-loop, for studying genetic diversity among goat breeds is with no meaning and it is better to use the microsatellite markers for this purpose.

COMPETING INTERESTS

Author has declared that no competing interests exist.

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