Small Ruminant Research 130 (2015) 90–94

Contents lists available at ScienceDirect

Small Ruminant Research

journal homepage: www.elsevier.com/locate/smallrumres

Short communication

Microsatellite based genetic diversity and population structure of three Saudi goat breeds

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ARTICLE INFO

Article history:
Received 6 April 2015
Received in revised form 27 July 2015
Accepted 29 July 2015
Available online 3 August 2015

Keywords:
Genetic differentiation
Goat
Admixture
SSR markers

ABSTRACT

The genetic diversity of goat breeds in the Kingdom of Saudi Arabia has declined by 20% in the last five years. Three local breeds, Bishi, Jabali, Tohami and the exotic Somali goats were genotyped using 17 microsatelliate markers to assess their genetic diversity. The overall mean number of alleles was 5.74, the highest being observed in Jabali (6.88) and the lowest in Tohami (5.00). The highest overall values of observed (H_o) and expected (H_e) heterozygosity were 0.673 (Tohami) and 0.730 0.656 in (Somali), respectively. Coefficient of population differentiation value was highest for Somali–Bishi (0.068) and lowest for Jabali–Tohami (0.022). Similarly, The genetic distance Bishi and Somali were the least genetically related reflected by longest genetic distance (0.420) while Jabali and Bishi were the most closely genetically related as a result of shortest genetic distance (0.109). Consequently, UPGMA phenogram tree revealed grouping of Jabli, Bishi, and Tohami in one clade indicating close genetic relationship. Finally, the structure and admixture analyses figure out three inferred population are the best number of the studied goat populations. This study concludes that the three studied Saudi goat populations were classified into distinct breeds with a good level of genetic diversity. Summing up, there were a clear division observed between the Jabali and Bishi, while, Tohami individuals had some genetic shard proportion with exotic Somali individuals.

1. Introduction

Goats in Kingdom of Saudi Arabia (KSA) play an important role in sustaining the livelihoods of the Bedouins and peri-urban people. The goats are raised under harsh desert conditions in low input production systems. As a consequence, goats have been preferred because of this comparative advantage over other local livestock species. However, the population of goats has declined in the last five years by about 20% (Saudi Ministry of Agriculture, 2013). Therefore, efforts were made to stem the declining trend in population size. Goats in KSA represent few breeds in which four major breeds namely Ardi, Bishi, Jabaly, and Tohami. The Ardi is the most common goat breed in KSA and its genetic diversity using microsatelliate DNA markers was earlier investigated (Aljumaah et al., 2012) and its phylogeny with goats of nearby countries was constructed (Al-Atiyat and Aljumaah, 2014). The other three breeds, Jabali, Bishi, and Tohami need to be genetically characterized, considering that they are mainly found in the southern region of KSA. Furthermore, there are many exotic breeds in the KSA that are used for different production and rearing purposes. For example, the Somali goat has been imported for meat production.

The most commonly used characterization tool in the developing countries is still microsatellite markers (Groeneveld et al., 2010; Ajmone-Marsan et al., 2014). In general, the microsatellite markers are still useful for parentage testing and assessing genetic diversity and relatedness (FAO, 2007; Amills, 2014). In this study, the genetic diversity and differentiation of Jabali, Bishi, and Tohami Saudi goat population as well as Somali goat as a reference population were investigated based on seventeen microsatellite markers.

2. Materials and methods

2.1. DNA Sampling, extraction and genotyping

Blood samples were collected from Jabali (34), Bishi (44) and Tohami (17) goat population reared at Jazan province of the south-

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http://dx.doi.org/10.1016/j.smallrumres.2015.07.027
0921-4488/

Table 1
The seventeen Microsatelliate loci, chromosome number, mean number of alleles (*MNA*), observed (H_o) and expected heterozygosity (H_e) and deviation from Hardy–Weinberg Equilibrium (*HWE*) on each locus for four Saudi goat breeds.

Locus		Jabali			Bishi			Tohami			Somali		
	Chr	*MNA*	H_o	H_e	*MNA*	H_o	H_e	*MNA*	H_o	H_e	*MNA*	H_o	H_e
OarAE54	18	9	0.622	0.784	6	0.500	0.733	6	0.875	0.85	4	0.444	0.739
SPS113	3	5	0.526	0.746	5	0.600	0.788	3	0.800	0.653	3	0.667	0.706
ILSTSO11	17	7	0.641	0.777	4	0.677	0.675	6	0.667	0.699	5	0.6	0.667
MAF70		9	0.385	0.841*	8	0.36	0.794	5	0.626	0.818	7	0.667	0.909
McM527	10	8	0.789	0.82	6	0.774	0.783	4	0.636	0.723	5	0.625	0.75
BM6444	17	8	0.391	0.453	7	0.474	0.452	7	0.444	0.612	7	0.5	0.864
INRA63	4	5	0.525	0.745	5	0.516	0.654	4	0.667	0.732	3	0.75	0.649
SRCRSP3	25	7	0.61	0.654	4	0.407	0.533	6	0.444	0.562	4	0.625	0.767
INRABERN172	5	5	0.675	0.553	3	0.733	0.495	3	0.667	0.503	8	1	0.83
OarFCB48	14	7	0.811	0.772	6	0.857	0.793	7	0.700	0.874	6	1	0.762
MAF209	5	2	0.4	0.487	3	0.429	0.455	2	0.364	0.312	3	0.273	0.687
CSRD247	15	8	0.677	0.698	6	0.429	0.574	5	0.750	0.850	7	0.889	0.325
ETH10	10	3	0.405	0.672**	4	0.576	0.685	4	0.929	0.643	3	0.833	0.856
MAF65	26	8	0.9	0.832	10	1	0.839	6	1	0.732	5	0.75	0.857
DRBP1	23	9	0.576	0.794	8	0.636	0.761	5	0.333	0.752	5	0.25	0.65
OarFCB20	14	7	0.976	0.639***	5	0.848	0.637*	4	0.830	0.739	4	0.375	0.517
ILSTS029	2	10	0.78	0.798	12	0.788	0.872	8	0.714	0.73	7	0.625	0.875
Mean		6.88	0.628	0.710	6.00	0.624	0.678	5.00	0.673	0.693	5.06	0.64	0.730

* Significant deviations from *HWE* ($p < 0.05$).
** Significant deviations from *HWE* ($p < 0.01$).
*** Significant deviations from *HWE* ($p < 0.001$).

west region of KSA. Furthermore, twelve individuals of Somali exotic goat breed were also sampled as a reference population. They were selected randomly from different flocks of importing commercial company located at livestock sale yard in Riyadh city. The blood sampling and animal handling protocol was approved by the Animal Ethics Committee at King Saud University. A total of 107 samples from mature unrelated male goats were subjected to DNA extraction using DNA extraction kit from blood produced by Amersham Bioscences Company®. The DNA was successfully genotyped with seventeen microsatellites recommended by International Society for Animal Genetics (ISAG) (FAO, 2007) (Table 1). The PCR amplification was performed using a GeneAmp® PCR system 9700. The PCR mixture of 10 μl was made according to recommended protocols by Sambrook et al. (1989) and detailed by Aljumaah et al. (2015). The resulted PCR products were then visualized in 1% Agroase gel Electrophoresis and performed on ABI Prism LIZ 500 molecular weight standards labeled with the fluorescent dye. The resulted allele sizes were scored for further analysis.

2.2. Genetic data analysis

All genetic variation and differentiation parameters, mean number of alleles (*MNA*), observed heterozygosity (H_o) and expected heterozygosity (H_e), *F*-statistics (F_{st} and F_{is}) genetic distances of Nei, (1972), were computed using ARLEQUIN software (Excoffier et al., 2005). The phylogenetic trees were constructed using the UPGMA and Neighbor-Joining algorithms using MEGA software (Tamura et al., 2011). The population structure was analyzed using STRUCTURE software (Pritchard et al., 2000) considering an admixture model and correlated allele frequencies between the studied breeds. The length of the burn-in and subsequent Monte Carlo Markov chain (MCMC) simulations were 50,000 and 100,000, respectively. One hundred runs were performed for each *K* ranging between two and six. For each *K* value, logarithmic probability of data (ln Pr(X|K)) for each cluster was also estimated. The results were then exported into STRUCTURE HARVESTER (Earl and vonHoldt, 2012) to determine Delta-K values for the most likely number of population.

3. Results

3.1. Genetic variation

The *MNA* per population ranged from 5.00 in the Tohami to 6.88 in the Jabali breed (Table 1). The highest *MNA* per locus (12) was found at the locus *ILSTS029* in the Bishi breed, whereas, the lowest number (5) was found at locus *MAF209* in the Tohami and Jabali breeds. In general, the locus *ILSTS029* exhibited the highest *MNA* in all breeds except the Somali breed (8 alleles at *INRABERN17*). In particular, the Somali goat showed a total of 86 alleles across all the loci studied, with four loci (*SPS113, INRA63, MAF209,* and *ETH10*) exhibiting only 3 alleles.

The highest average overall H_o (0.673) was found in the Tohami breed and in which the H_e was higher and averaged 0.693. The highest H_e value (0.73) was observed in the Somali breed in which H_o was 0.640. The average H_o and H_e in the other two breeds, Jabali and Bishi goats, were 0.62 and 0.710 and 0.624 and 0.678, respectively. The highest H_e per locus (0.909) was observed in the Somali breed at *MAF70*, while it was lowest (0.452) in the Bishi goat at locus *BM6444*. Overall, all values of H_e were greater than those of H_o per locus in all the studied breeds. Significant deviations from Hardy Weinberg equilibrium (*HWE*) at the studied loci were only observed in the Jabali and Bishi breeds (Table 1). Three (*MAF70*, *ETH10* and *OarFCB20*) out of the seventeen microsatellites tested in the four breeds deviated significantly from *HWE*.

3.2. Genetic differentiation

F-statistics were estimated to statistically differentiate the goat breeds (Table 2). The lowest F_{st} value (0.022) was observed between Jabali and Tohami, whereas, it was highest (0.068) between the Somali and Bishi breed and 0.066 between Somali and the Jabali goat. Finally, the F_{st} value between Jabali with Bishi and Tohami were, respectively, 0.026 and 0.0219, while between Bishi with Tohami was 0.378. The F_{is} value was negative in all the breeds, indicating an excess of heterozygotes. They were −0.059, −0.056, −0.400 and −0.333 in Jabali, Bishi, Tohami and Somali, respectively.