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Genetic Characterization of Nubian and Nilotic Goats in Sudan by using Microsatellites Techniques

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Abstract: **Eighteen microsatellite loci were analyzed in 80 random individuals to characterize the genetic variability of two domestic goat breeds found in Sudan: Nubian goat, Nilotic goat. Heterozygosity, Allele diversity, polymorphism information, F-statistics, unintended estimates of gene flow (Nm) and Nei's standard distances were measured. Based on the estimated mean heterozygosity, the lowest genetic diversity was confirmed in Nubian goat (HE=0.381), and the highest in Nilotic goat (HE=0.669). After corrections for multiple significance tests, deviations from Hardy-Weinberg equilibrium were statistically significant overall populations and loci, reflecting the deficiencies of heterozygotes (global FIS=0.053). Based on pairwise FST and Nm between different breeds, there was no genetic differentiation between a Nubian goat and Nilotic goat, indicating that these breeds have been genetically subdivided. Likewise, individual clustering based on the proportion of shared alleles showed that Nubian goat individuals formed a single cluster separated from the other Nilotic goat breeds.**

Keywords: **Microsatellites, Genetic Diversity, Nubian Goat, Nilotic Goat Gene Flow.**

1. MATERIALS AND METHODS

Sample collection and DNA extraction:

Blood samples were collected from a total of 80 individuals belonging to three different goat breeds: Nubian goat (n=40), Nilotic goat (n=24). Fresh blood was taken from individuals from distinct geographical areas who were chosen at random without consideration of the relationship between animals.

2. MICROSATELLITE, PCR CONDITION AND FRAGMENT ANALYSIS

Eighteen microsatellites were used: 10 ovine, OarFCB20 (GenBank accession no. L20004), OarFCB193 (L01533), OarFCB304 (L01535), OarFCB48 (M82875), OarAE129 (L11051), OarJMP58 (U35058), BM8125 (G18475), MAF65 (M67437), MAF214 (M88160) and OarHH47 (L12557); three bovine, ILSTS005 (L23481), ILSTS011 (L23485) and ILSTS028 (L37211); and five caprine, SR-CRSP-1 (L22192), SR-CRSP-3 (L22195), SR-CRSP-7 (L22199), SR-CRSP-8 (L22200), SR-CRSP-9 (L22201). PCR amplification was carried out in a PTC-100TM. With a total volume of 10 ll reaction containing ten ng DNA, one ll 10 · PCR standard reaction buffer, four pmol dNTPs, 30 mmol MgCl2, four pmol each forward and reverse primer, 1 U Taq DNA polymerase and 4.2 ll distilled water. Following an initial denaturation at 95C for 5 min, 35 cycles were performed with 94C for 30 s, annealing temperature for 1 min, and 72C for 2 min. The final cycle was followed by an extension at 72C for 10 min.

3. STATISTICAL ANALYSIS

The observed and expected heterozygosity (Ho and He; Nei 1973) for each population were estimated with Popgene (Version 1.32; http://www.ualberta.ca/fyeh/ download.htm). For each locus, FSTAT software (Version 2.9.3; http://www.unil.ch/ izea/software/fstat.html) was used to calculate Fit, Fst, and Fis according to Weir and Cocker ham (1984), and gene diversity for each locus in each population. SPSS10.0 software was used to test the significance of

differences in gene diversity among populations using the data of each locus. The polymorphic information content (PIC) for each locus and the standard genetic distance. DISPAN software was used to construct the phylogenetic tree using the unweighted pair group method with arithmetic mean (upgma) from a standard genetic distance (Nei 1972).

4. RESULTS

Genetic diversity of each locus and population, the observed number of alleles and their size for each locus, varies from 4 to 13 and from 79 to 335 base pairs, respectively. PIC values and gene diversity among loci are significantly different ($p < 0.01$). The Ho, He, gene diversity and Fis of each population. There is no significant difference of gene diversity, and Fis among populations ($p > 0.05$), and none of the Fis estimates is significant.

5. DISCUSSION

Genetic diversity among loci and populations Genetic diversity differed significantly among loci ($p < 0.01$). Eight loci (MAF65, OarFCB48, OarFCB20, ILSTS011, ILSTS005, SR-CRSP-3, SR-CRSP-7 and SR-CRSP8) were also used by Luikart et al. (1999). PIC values were similar, although slightly higher in the latter study. Estimates of Fis for OarFCB48, OarFCB193 and ILSTS005 are 0.259, 0.186 and 0.100, respectively, but were 0.161, 0.184 and 0.278, respectively, in Barker et al. (2001). The value of Fst (0.054) is much smaller than the estimated 0.17 for Nubian goat breeds (Ibrahium.2008) and 0.143 for Nilotic goat breeds (Ibrahium. 2008), indicating lower between breed diversity of Sudan indigenous goat breeds. Differences among studies probably are inherent to the different breeds from very different countries. The average Fis of Nubian indigenous goat breeds is 0.171, ranging from 0.069 to 0.258. For Nilotic goat breeds, the mean Fis was 0.192, ranging from 0.090 to 0.333 (Ibrahium. 2008). It appears that Sudanese indigenous goat breeds might have similar inbreeding to other African goats, although the average Fis of Sudanese indigenous goat breeds is not significantly different from zero. Nubian goat has the lowest Ho (0.511), He (0.608), and gene diversity (0.574), but it has the highest Fis (0.258), although the highest Fis is not significantly different from zero, in agreement with the results for RAPD markers (Ibrahium. 2008). Further study should be carried out in future with more samples to obtain more accurate results. The average PIC value (0.575) of Sudanese indigenous goat breeds is slightly higher than 0.48 Egyptian goat breeds (Ganai and Yadav 2001). The Ho (0.569) of Sudanese indigenous goat breeds is similar to 0.54 of Egyptian goat breeds (Ganai and Yadav 2001). Ethiopian goat (0.617) and Kenya (0.654), Luikart et al. 1999) also have similarly observed heterozygosity. Consequently, it could be inferred that African goat breeds have similar genetic diversity.

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