MICROSATELLITE ANALYSIS OF MONGOLIAN GOAT POPULATIONS : HIGH GENETIC VARIATION WITHIN AND LOW GENETIC DIFFERENTIATION BETWEEN POPULATIONS

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INTRODUCTION

At present, 1,100,000 heads of goat are distributed throughout Mongolia and they have become valuable livestock for the national economy, producing one of its major export products, cashmere. An introgression of Russian goat breeds has been occurred in some region in the 1960`s. A number of geographically and morphologically distinct native goat populations have been recognized and they have been given existing local names to distinguish them from the general goat population, however, genetic information on each population is limited. The objectives of the study are to examine genetic differentiation and genetic relationships among Mongolian goat populations by microsatellite DNA variation.

MATERIAL AND METHODS

Goat populations and microsatellite markers examined. 384 unrelated animals were sampled in eight different geographical locations (figure 1) from the morphologically distinct goat populations in the following: seven as representative of native goat: Zavkhan Buural (ZB,50), Zalaajinst White (ZW,51), Erchim Black (EB,49), Ulgii Red (UR,41), Bayandelger (BD,73), Dorgon (DO,30), Sumber (SU,60) and newly established breed created by crossing Gobi local goats with Russian Don breed: Gobi Gurvan Saikhan (GGS,30). Ten markers (*HUJ625, ILSTS0005, INRA127, INRABERN192, MAF50, MAF65, OarVH34, SRCRSP08, SRCRSP26* and *TGLA53*) were selected and used to analyze Mongolian goat populations.

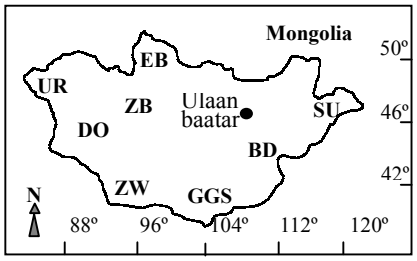

Figure 1. Geographical distribution of goat populations used in the study

PCR amplification and genotyping. PCR was performed using Platinum GENOTYPE^{TM} Tsp DNA Polymerase (Gibco BRL, Life Technologies, France). PCR products were run with the internal size standard GENOTYPE^{TM} ROX 60-500 DNA ladder (Gibco BRL) on an ABI 310 DNA sequencer (PE Applied Biosystems). Sizing of microsatellite alleles was performed on a ABI Prism 310 Genetic analyzer.

Statistical analyses. Allelic frequencies and observed heterozygosity (H_o) were calculated directly from observed genotypes. The expected heterozygosity (H_e) in each population was calculated using a GENETIX Version 4.01 (Belkhir *et al*. 2000) software package. *Fis,* that

shows deficiencies of heterozygotes relative to Hardy-Weinberg expectations within sample, and *Fst* that shows genetic differentiation among populations, were calculated in each population using a FSTAT Version 2.9.3 (Goudet 2001) package. From the pairwise *Fst* matrices unrooted NJ tree was constructed using PHYLIP 3.6 software (Joseph Felsenstein, 2001).

RESULTS AND DISCUSSION

All ten microsatellite loci examined were polymorphic in all populations. A total of 126 alleles

Table 1. H_o and H_e in each population, *Fis* value and HWE test for deviation

	Ho	He	*Fis*	HWE
ZB	0.697+0.117	0.721±0.125	0.044	Ns
ZW	0.687±0.087	0.728±0.115	0.066	Ns
EB	0.730±0.131	0.746±0.110	0.032	Ns
UR	0.669±0.124	0.720±0.116	0.083	Ns
BD	0.686±0.141	0.727±0.099	0.064	Ns
DO	0.714±0.164	0.726±0.109	0.034	Ns
SU	0.694±0.113	0.729±0.093	0.045	Ns
GGS	0.693±0.151	0.725±0.136	0.064	Ns

were observed in the populations (2 to 21 allele per locus) Observed and expected heterozygosities *Fis* values and test of HWE are given in table 1. Heterozygosities in Mongolian goats were average as compared to the other data (Saitbekova *et al*.,1999; Luikart *et al*., 1999; Yang *et al*., 1999).

Table 2. Pairwise *Fst* comparison between populations

	ZW	EB	UR	BD	DO	SU	GGS
ZB	0.018	0.010	0.012	0.013	0.010	0.016	0.021
ZW		0.016	0.004	0.011	0.019	0.022	0.020
EB			0.015	0.017	0.015	0.021	0.016
UR				0.013	0.018	0.022	0.022
BD					0.025	0.017	0.027
DO						0.027	0.011
SU							0.026

Table 2 shows the pairwise *Fst* values and P values between the eight populations. The *Fst* value in each population pair were significantly different only at $0.01<P<0.05$ level except ZW-UR pair ($P>0.05$). The *Fst* values ranging from 0.004 to 0.027 with a mean value of 0.017 among Mongolian goat populations suggest that there is high gene flow among the population.

The *Fst* values among Mongolian goat populations are lower than other domestic animal breeds, e.g., horse (Canon *et al*. 2000), European cattle (MacHugh *et al*. 1998), European pig (Laval *et al*. 2000). These data suggest that Mongolian goat populations still have semi-wild genetic structures and have not reached at the level of breeds yet. These data might reflect long history of nomadism and short-range history of goat breeding in Mongolia. Although the relationships among the populations are very close in terms of *Fst* values, our study demonstrates that the Mongolian goat populations can be distinguished using microsatellite polymorphisms. Unrooted NJ tree constructed from pairwise *Fst* matrix (figure 2) suggests that there may be occured substantial genetic interaction between ZB and other native goat populations. Hence ZB is considered as a large gene pool among Mongolian native goats because ZB is in the middle position of the populations and has largest population size (figure 1 and figure 2). SU and GGS reveal relatively high *Fst* values, which is consistent with the geographically isolated location of SU and breeding history of GGS.

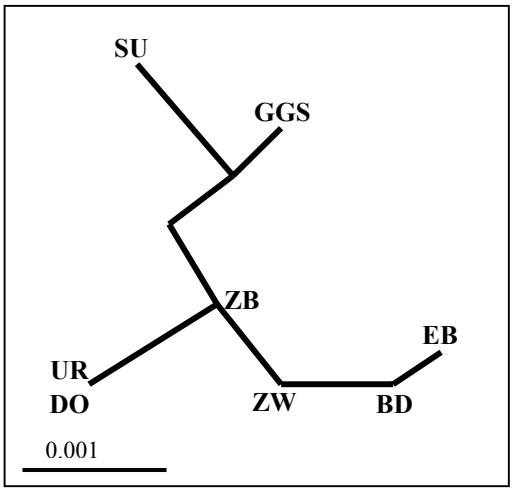

Figure 2. Unrooted NJ tree drawn from pairwise *Fst* matrix between goat populations

CONCLUSION

In conclusion, Mongolian native goat populations have not been differentiated to the level of breeds, even though one type analyzed here has been designated as a breed (GGS).This data set proves that microsatellites will be useful for the identification of the closely related goat populations. Since microsatellite markers are highly polymorphic in Mongolian goats, they can also used for QTL analysis especially focusing on cashmere fiber quality.

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