

GENETIC VARIATION AND POPULATION STRUCTURE OF TWO TSIGAI SHEEP TYPES IN SERBIA

M.Cinkulov¹, I. Pihler¹, M. Tapio², M. Krajinovic¹ and J. Kantanen²,

¹Faculty of Agriculture, Trg D.Obradovica 8, 21000 Novi Sad, Serbia

²MTT Agrifood Research Finland, 31600 Jokioinen, Finland

INTRODUCTION

In Serbia, there are two types of Tsigai sheep, Old and New type. While the New type has become popular among farmers, the population size of the Old type is rapidly decreasing.

THE AIM

The objective of this work was to evaluate genetic variation, genetic differentiation and population structure of the Tsigai sheep types based on 23 microsatellites.

MATERIALS AND METHODS

Genetic variability parameters (mean number of alleles per locus, mean observed and expected heterozygosities) were calculated using POPGENE v1.21. Coefficients of inbreeding in populations (*f*) were calculated by FSTAT v2.9.1. Wilcoxon sing-rank test incorporated in BOTTLENEK were used to evaluate the presence of recent genetic bottlenecks.

RESULTS

Table 1. Mean observed (H_{obs}) and expected (H_{exp}) unbiased heterozygosities and mean number of alleles (*A*) per locus and inbreeding coefficients (*f*) with 95% confidence intervals (95% CI) in two types of Tsigai breed of sheep

Tsigai type	H_{obs}	H_{exp}	<i>A</i>	<i>f</i>	95% CI for <i>f</i>
Old	0.6397 (0.2055)	0.6924 (0.1674)	6.7	0.086*** (0.030)	0.033, 0.148
New	0.6596 (0.1579)	0.7026 (0.0913)	7.5	0.072 *** (0.037)	0.007, 0.150
Total	0.6489 (0.1555)	0.7452 (0.1054)	8.7		

Standard errors are presented in parentheses
*** P<0.001

Table 2. Number of loci showing heterozygosity excess or deficiency, obtained from Wilcoxon test assuming microsatellites evolve according to the Stepwise mutation model (SMM) and Two phased model of mutations (TPM)

	SMM		TPM	
Tsigai Type	p ¹ value	p ² value	p ¹ value	p ² Value
Old	0.1172	0.8887	0.6675	0.3434
New	0.0002	0.9998	0.0024	0.9978

p¹ - Probability of one tail for H deficiency
p² - Probability of one tail for H excess

CONCLUSION

We conclude that high level of variability was present in both Tsigai types. According to the bottleneck testing, the New type showed an excess of alleles suggesting the influence of gene flow from some other breed. The Old type appears to have remained pure but since the census size has decreased rapidly it is necessary to conserve it.

Acknowledgement

This work was funded by Norwegian Ministry of Foreign Affairs and by Norwegian Research Council. We are grateful for funding as it made this research possible.



Picture1. Old (up) and New (down) Tsigai types