L.K. Ernst Federal Science Center for Animal Husbandry &
The Mountain Hunters Club,
Russia

AN ASSESSMENT OF APPLICABILITY OF ILLUMINA GOATSNP50 BEADCHIP FOR GENETIC STUDIES OF CAUCASIAN TUR (*CAPRA CAUCASICA*)

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The area of habitat of Caucasian tur

Map with sampling sites of Caucasian tur used in this study and the area of the species habitat. W_TUR = West-Caucasian tur, E_TUR = East-Caucasian tur, M_TUR = Mid-Caucasian tur

West-Caucasian tur *

East-Caucasian tur *

Caucasian tur (*Capra caucasica*) habitat is limited to Greater Caucasus Mountain Chain from Azerbaijan and Georgia in the East to Krasnodar region of Russia in the West. Its range is one of the smallest habitats of all ungulates—around 770 km in length and 80 km in width.

Taxonomically, the species is divided into two subspecies: West-Caucasian tur (*C. c. severtzovi*) and East-Caucasian tur (*C. c. cylindricornis*). Sometimes these populations are even considered as different species. The areas of these subspecies are united and in the territory between them a hybrid form, which is referred to as a Mid-Caucasian tur, is distinguished.

The aim of the study

The aim of our study was to assess the applicability of Illumina GoatSNP50 BeadChip, created for domestic goats, for genetic studies of Caucasian tur (*Capra caucasica*).

A total of 15 specimens of *Capra caucasica*, including East Caucasian tur from Dagestan (E_TUR, n = 5), West Caucasian tur from Karachay-Cherkessia (W_TUR, n = 5) and Mid-Caucasian tur from Kabardino-Balkaria (M_TUR, n = 5) were selected for this study.

SNP quality filtering was performed in PLINK 1.9. SNPs that were genotyped in less than 90% of individuals (−geno 0.1) with a minor allele frequency (MAF) < 5% (–maf 0.05) and in linkage disequilibrium (–indep-pairwise 50 5 0.5) were pruned.

The software used in this study:

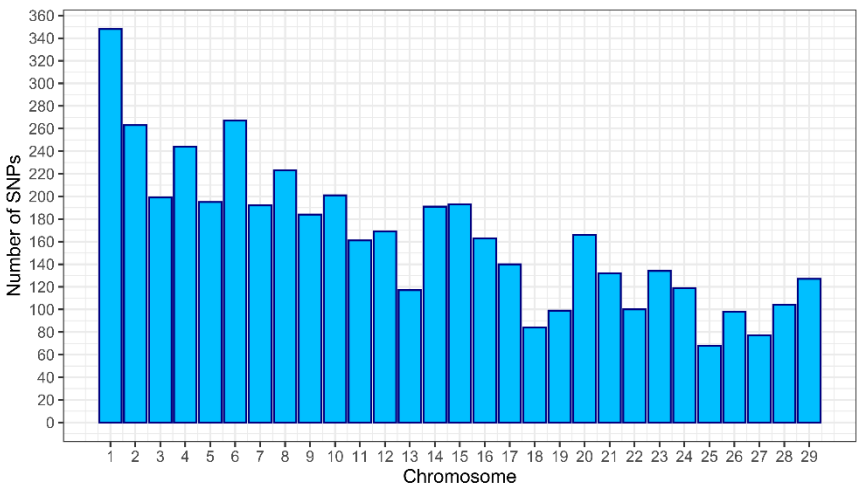
PLINK 1.9

SplitsTree 4.14.6

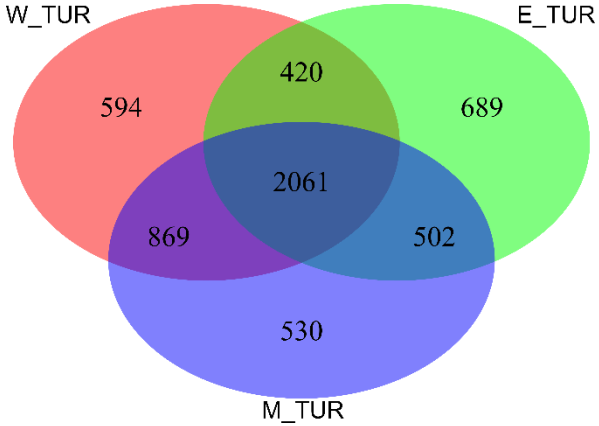
R packages:

diveRsity, StAMPP, inbreedR, VennDiagram, maps, ggplot2

Results



Number of polymorhic SNPs per chromosome in Caucasisan tur (Capra caucasica).

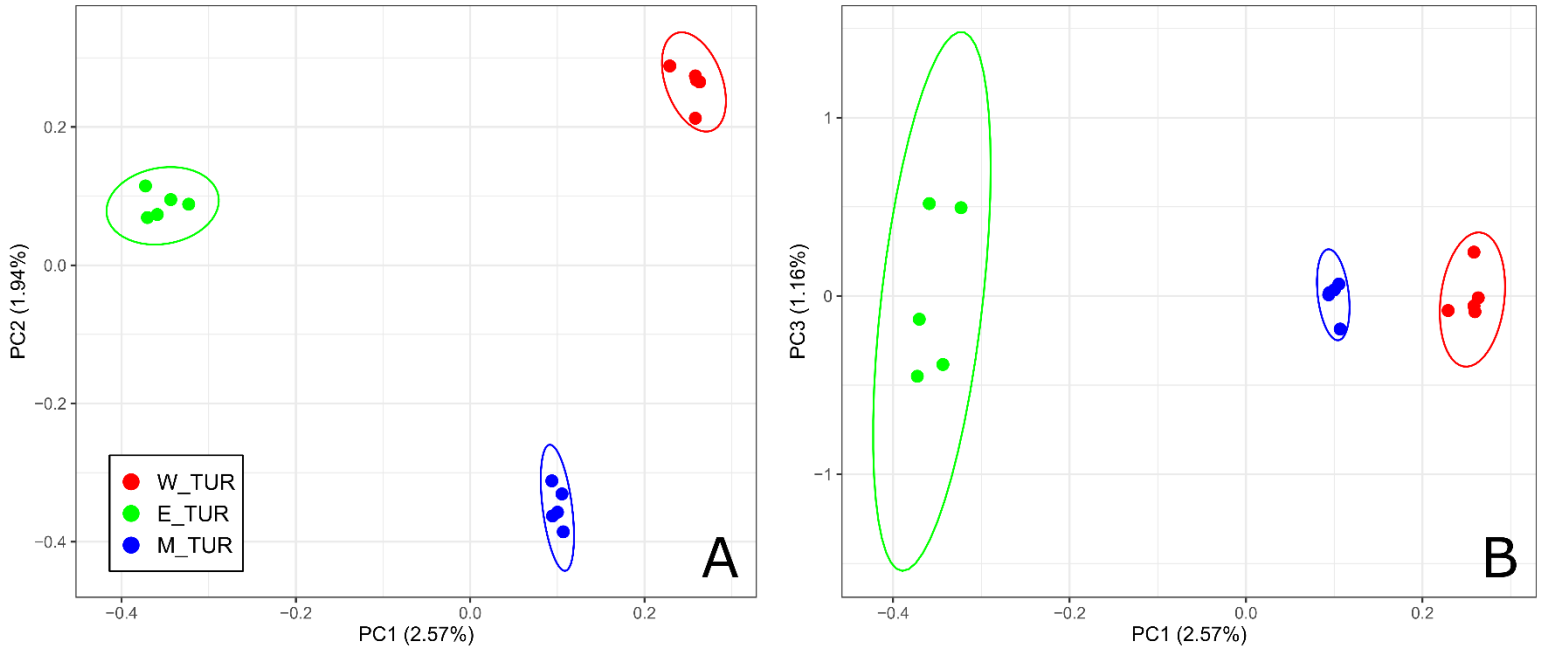


Venn diagram representing the number of unique and shared polymorphic SNPs in the three groups of Caucasian tur (Capra caucasica). W_TUR = West-Caucasian tur, E_TUR = East-Caucasian tur, M_TUR = Mid-Caucasian tur.

From the initial set of 53,347 SNPs available in the Illumina GoatSNP50 BeadChip, after quality control, 4758 polymorphic loci (8.92%), distributed all over 29 autosomes, were selected. The lowest number of SNPs was found on the 25th chromosome—68, and the highest on the 1st chromosome—348

While 2061 polymorphic SNPs were common for all the Caucasian tur groups, the number of unique SNPs for W_TUR, E_TUR and M_TUR was 594, 689 and 530, respectively. The most shared SNPs among two groups was found in W_TUR—M_TUR pair—869, and the least number of shared loci were observed for W_TUR—E_TUR pair—420

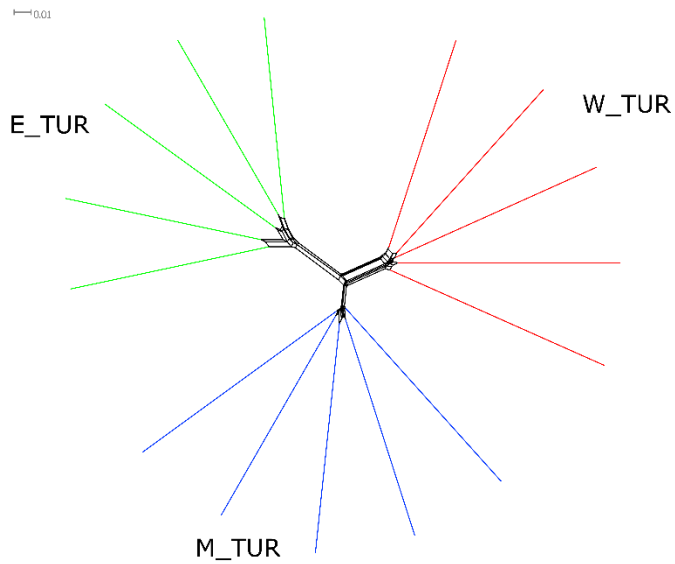
Results



Principal component analysis (PCA) of the groups of Caucasian tur (*Capra caucasica*): (A) the first two components (PC1 and PC2), (B) the first and third components (PC1 and PC3). W_TUR = West-Caucasian tur, E_TUR = East-Caucasian tur, M_TUR = Mid-Caucasian tur

The results of principal component analysis (PCA) revealed that all the studied groups of Caucasian tur clustered separately. The first component (PC1), which explained 2.57% of genetic variability, divided Caucasian tur into two groups. The first group consisted of E_TUR (PC1 < 0) and the second one included W_TUR and M_TUR (PC1 > 0).

Results



Neighbor-Net dendrogram of fifteen Caucasian tur (Capra caucasica) individuals, based on IBS distances

The level of genetic differentiation was estimated with pairwise F_{ST} distances. We observed a high F_{ST} value among W_TUR and E_TUR—0.161. M_TUR was genetically more close to W_TUR than to E_TUR, but in both cases the differentiation was moderate—0.100 and 0.134, respectively.

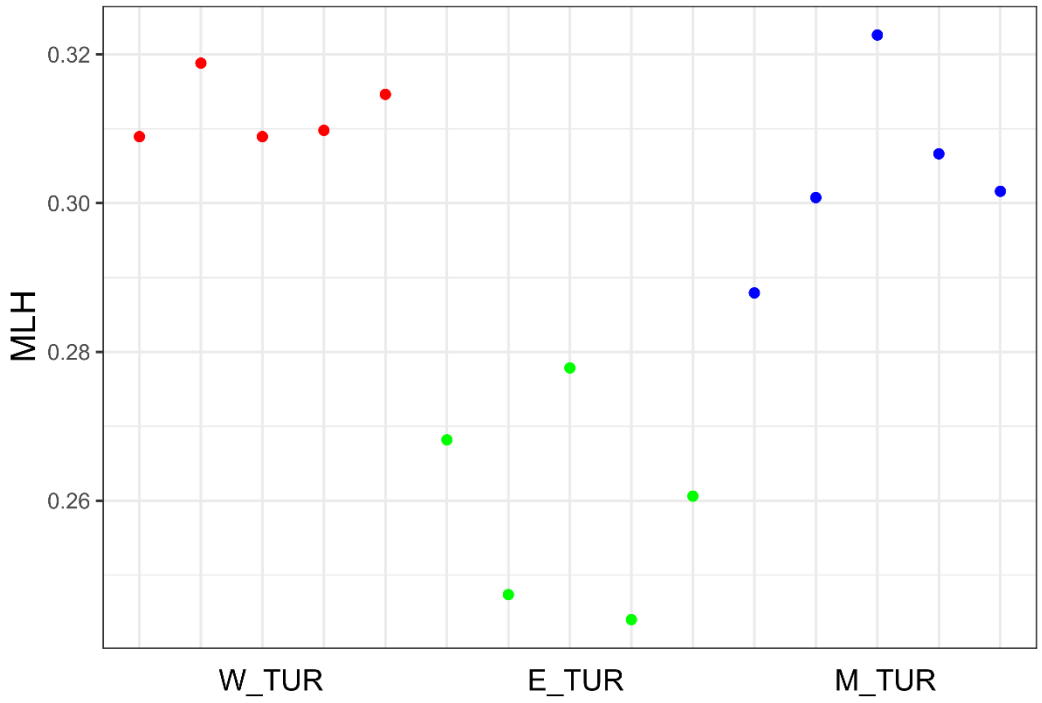
The above-mentioned results were also supported with Neighbor-Net dendrogram. All the studied individuals were placed in clades according to their geographical origin. This analysis also revealed that there were no close relatives among the 15 genotyped animals.

Pairwise F_{ST} genetic distances between the groups of Caucasian tur (*Capra caucasica*)

	W_TUR	E_TUR	M_TUR
W_TUR	0.000		
E_TUR	0.161	0.000	
M_TUR	0.100	0.134	0.000

Notes: W_TUR = West-Caucasian tur, E_TUR = East-Caucasian tur, M_TUR = Mid-Caucasian tur

Results



Individual multilocus heterozygosity (MLH) in the groups of Caucsian tur (*Capra caucasica*). W_TUR = West-Caucasian tur, E_TUR = East-Caucasian tur, M_TUR = Mid-Caucasian tur.

Individual heterozygosity values, which were represented by multilocus heterozygosity (MLH) showed that all the E_TUR individuals had lower heterozygosity than both W_TUR and M_TUR. Although mean values of observed heterozygosity were almost equal in W_TUR and in M_TUR, the range of values was wider in M_TUR than in E_TUR.

Results

Genetic diversity in the groups of Caucasian tur (*Capra caucasica*)

Pop	n	Ho	He	Fis	Ar
W_TUR	5	0.334±0.004	0.339±0.003	0.016 [0.003;0.029]	1.825±0.006
E_TUR	5	0.279±0.004	0.308±0.003	0.08 [0.066;0.094]	1.772±0.007
M_TUR	5	0.333±0.004	0.345±0.003	0.03 [0.017;0.043]	1.844±0.006

Notes: *n*—number of samples, Ho—observed heterozygosity, He—expected heterozygosity, Fis—inbreeding coefficient, Ar—allelic richness, SE—standard error, CI—confidence interval, W_TUR = West-Caucasian tur, E_TUR = East-Caucasian tur, M_TUR = Mid-Caucasian tur

Expected heterozygosity (He) and allelic richness (Ar) in W_TUR were significantly higher than in E_TUR. But the highest genetic diversity parameters were observed in M_TUR. The within population inbreeding coefficient (Fis) was close to zero in W_TUR and M_TUR which showed that these groups were in a fairly stable state, and slightly higher than zero in E_TUR, which indicated weak heterozygote deficit.

Conclusions

In our study we demonstrated that the Illumina GoatSNP50 BeadChip designed for domestic goats can be used as useful tool for genetic studies of Caucasian tur. It was shown that West-Caucasian tur, East-Caucasian tur and Mid-Caucasian tur clustered separately from each other. Genetic diversity parameters in East-Caucasian tur were lower than in the other groups. To obtain more accurate information about population structure and genetic diversity of Caucasian tur, more studies based on Illumina GoatSNP50 BeadChip with larger number of samples are needed.

Research Team

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**the photos of Caucasian tur were taken from the web site:*
https://gorets-media.ru/page/kavkazskij-tur
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THANK YOU FOR YOUR ATTENTION