

Supplementary Materials

The European ground squirrel's genetic diversity in its ancestral land: landscape insights and conservation implications

Yordan Koshev, Štěpánka Říčanová, Maria Kachamakova, Oldřich Říčan

Table S1. Genetic diversity in ten populations of the European ground squirrel based on 12 microsatellite loci.

Locality	N	AR	NA	<i>He</i>	<i>Ho</i>	<i>F_{IS}</i>	Wilcoxon test
NP (Nikopol)	19	3.77	4.92	0.634	0.574	0.121	0.007
TS (Tsenovo)	18	3.62	5.50	0.555	0.557	0.027	0.365
BN (Belmeken)	20	3.34	4.92	0.564	0.484	0.167*	0.380
KZ (Knezha)	17	3.65	4.83	0.626	0.593	0.083	0.147
KAP (Kap. Petko Voivoda)	21	4.58	7.25	0.748	0.627	0.185*	0.622
TOP (Topolchane)	17	5.30	8.67	0.783	0.634	0.220*	0.301
RZ (Rozino)	22	3.69	5.83	0.588	0.505	0.166*	0.301
KRE (Kremikovtsi)	25	5.04	9.08	0.717	0.487	0.340*	0.176
CG (Chernogorovo)	8	4.81	5.83	0.669	0.594	0.177*	0.970
ISH (Proff. Ishirkovo)	6	4.15	4.42	0.602	0.667	-0.016	0.380

Sample size (N), allelic richness (AR), mean number of alleles per locus (NA), expected heterozygosity (*He*), observed heterozygosity (*Ho*), coefficient of inbreeding (*F_{IS}*) in the studied populations, *Wilcoxon test* - test detecting recent bottleneck in populations. Note: * value is significant at $p < 0.05$.

Table S2. F_{ST} values using ENA (from FreeNA. Chapuis & Estoup 2007) between EGS populations based on msats data.

	NP	TS	BN	KZ	KAP	TOP	RZ	KRE	CG	ISH
NP	-	0.094	0.199	0.119	0.198	0.173	0.240	0.148	0.175	0.121
TS	***	-	0.289	0.156	0.247	0.233	0.287	0.212	0.208	0.191
BN	***	***	-	0.212	0.245	0.209	0.286	0.167	0.251	0.232
KZ	***	***	***	-	0.214	0.161	0.222	0.134	0.139	0.160
KAP	***	***	***	***	-	0.113	0.187	0.149	0.161	0.194
TOP	***	***	***	***	***	-	0.193	0.135	0.131	0.177
RZ	***	***	***	***	***	***	-	0.205	0.170	0.244
KRE	***	***	***	***	***	***	***	-	0.124	0.162
CG	***	***	***	***	***	***	***	***	-	0.169
ISH	***	***	***	***	***	***	***	***	***	-

Pairwise values are above diagonal. Values of significance are below diagonal; *** value is significant at the level $P < 0.001$.

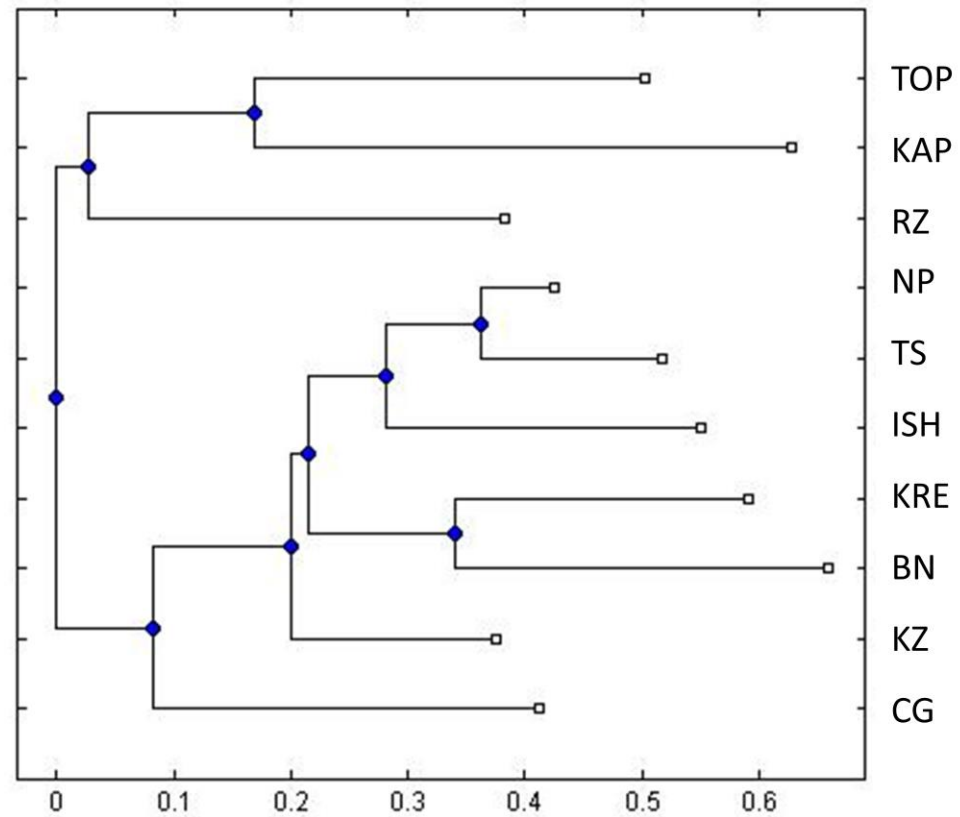


Figure S1. Neighbor- joining tree from BAPS based on Nei genetic distances divides studied populations into two clusters. i. e. Bulgarian northern and southern group of populations