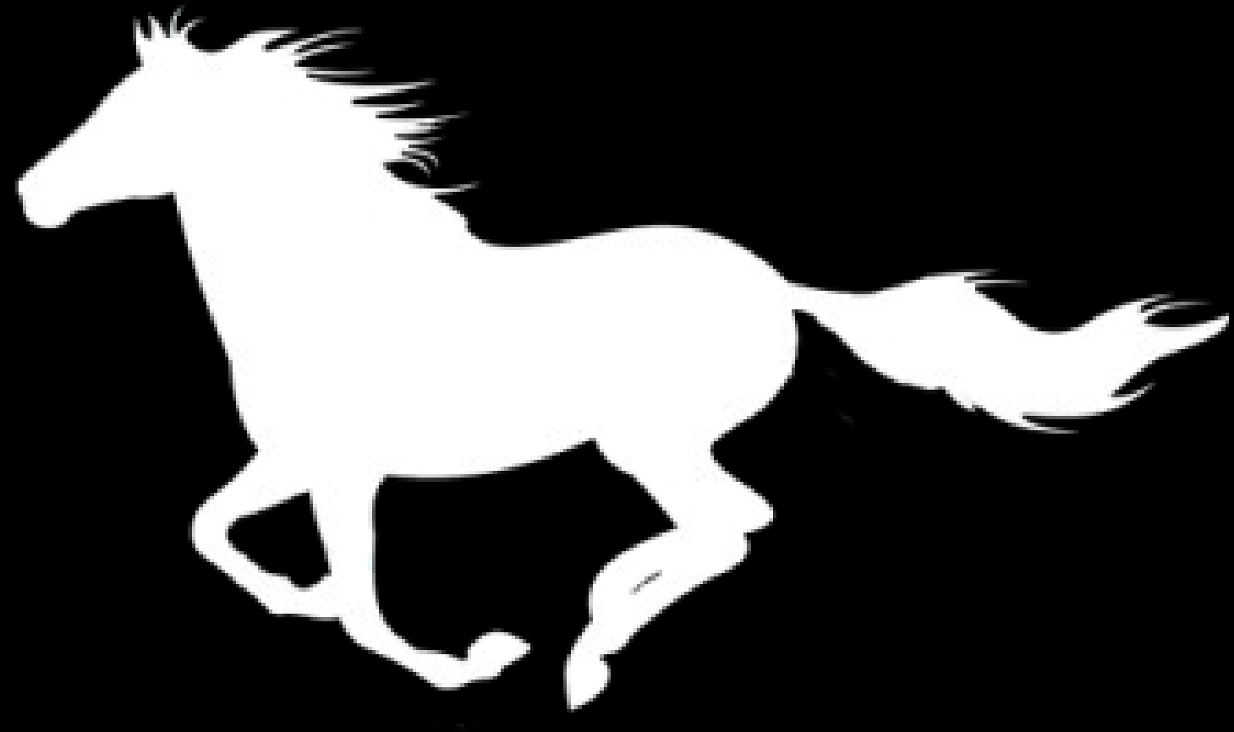
Estimation of genetic diversity level in local populations of Turano-Mongolian horse breeds using nuclear and mitochondrial DNA markers



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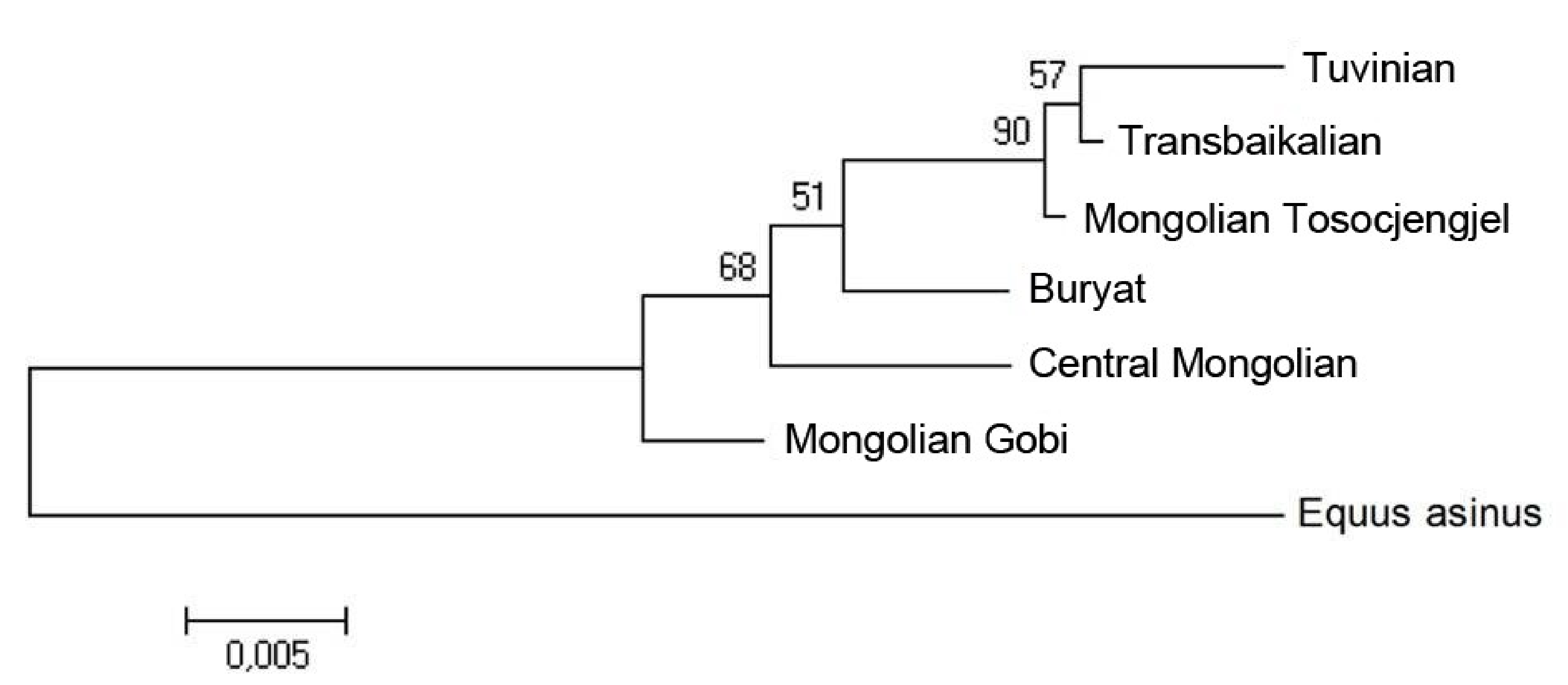
Turano-Mongolian horses are ancient horse breeds inhabiting Altaian, Tuvinian, Transbaikalian and Mongolian steppe that are the regions believed to be the origins of horse domestication. They've been herded in the northeast Eurasia prairies for centuries without noticeable changes in their lifestyle.

To determine the genetic diversity and phylogenetic relationships among 13 populations (n=531) of 5 indigenous horse breeds (Mongolian, Tuvinian, Altaian, Transbaikalian, Buryat) we employed two types of molecular markers: a 398bp D-loop mitochondrial DNA (mtDNA) fragment sequence and ISSR-analysis.

Sequences were made for 25 samples of 6 populations (Northern Mongolian, Gobi desert, Central Mongolian, Buryat and Transbaikalian). In the mtDNA-analysis the control region (D-loop) was sequenced between nucleotides 15341 and 15837, the 398bp long fragment (15399-15796) was taken after alignment for further analysis. We found 41 variable sites where 39 transitions and 2 transversions were observed. Phylogenetic tree was built using software MEGA 4.1 by a Neighbor-joining method. Three northern populations (Northern Mongolian, Transbaikalian and Tuvinian) with a high bootstrap value (90) were placed in one cluster.



Their natural habitats are closely located and migration between the populations may occur. Buryat, Central and Southern Mongolian populations are detached; Gobi desert population is the most distinct one.

For the ISSR-analysis 2 were chosen out of 6 primers for the final study. A total of 47 ISSR bands was obtained with 2 primers - $(ACC)_6G$ and $(GAG)_6C$ – among which 46 (97,9%) were polymorphic bands. High genetic diversity level (Nei, 1973) was shown for all the studied populations in comparison with stud horses. Two Altai populations had the highest genetic diversity level what can indicate a gene flow or crossbreeding. Genetic distances were calculated and analyzed with a method of principal components. Population distribution was in accordance with their geographical affiliations.