

MICROSATELLITE MARKERS REVEAL DIFFERENTIATION OF SOUTHEASTERN AND WESTERN EUROPEAN SHEEP BREEDS

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Summary

Fifty-seven European, particularly Mediterranean, and Middle Eastern sheep breeds from 15 countries were typed with 31 microsatellite markers. Principle component and Bayesian model-based clustering analysis based on allele frequencies revealed a clear distinction between Western European breeds on the one hand and Southeastern European and Middle Eastern breeds on the other hand.

Keywords

Sheep, microsatellites, genetic variability, principle component analysis, Bayesian model-based clustering analysis

Abstract

Thirty-one microsatellite markers covering 22 chromosomes, including ten markers recommended by the FAO [1], were used to analyse the genetic variability of 57 European, particularly Mediterranean, and Middle Eastern sheep breeds from 15 countries. A total of 1748 animals were typed. After calculation of allele frequencies with the GENEPOP programme [2] a principle component analysis (PCA) and a Bayesian model-based clustering analysis assuming $K = 2$ clusters were performed using SPSS and the STRUCTURE programme [3].

The first component of the PCA, explaining 9.39 % of the variability, reveals a clear distinction between Western European breeds on the one hand and Southeastern European and Middle Eastern breeds on the other hand. Studies on mtDNA by Hiendleder et al. [4] suggest contribution of two different maternal ancestors as origin of modern domestic sheep, leading to a European and an Asian mtDNA-lineage that might explain such a pattern. Additionally migration during the Neolithic demic population expansion and subsequent adaptation to the environment could have caused this structure.

Furthermore the second component of the PCA, explaining 7.17 % of the variability, shows a clear separation of the Graue gehörnte Heidschnucke (GGH) from all other breeds. This German breed has kept a lot of its nativeness, as crossbreeding with other breeds in former times failed due to strong adaptation to heathland environmental conditions. In addition in this study the GGH is the only breed belonging to the Northern heath sheep group. Inclusion of other Northern heath sheep breeds might possibly result in an also separated grouping of the GGH with these breeds.

Moreover all analysed fat-tailed sheep (Cypriot fat-tailed sheep, Saudi-Arabian Najdi, Naemi and Heri, Turkish Mor- and Akkaraman, Egyptian Ossimi and Romanian Karakul (KKL))

form a separate cluster within the Southeastern European and Middle Eastern set. This indicates the clear separation of this type of sheep from all other breeds, presumably also as a result of strong adaptation to environmental conditions and consequential natural and artificial selection.

Bayesian model-based clustering analysis assuming $K = 2$ clusters supports the results of the PCA leading also to a clear differentiation of the two groups (Figure 1), though two is not the most probable number of subpopulations considering the log-likelihood of K .

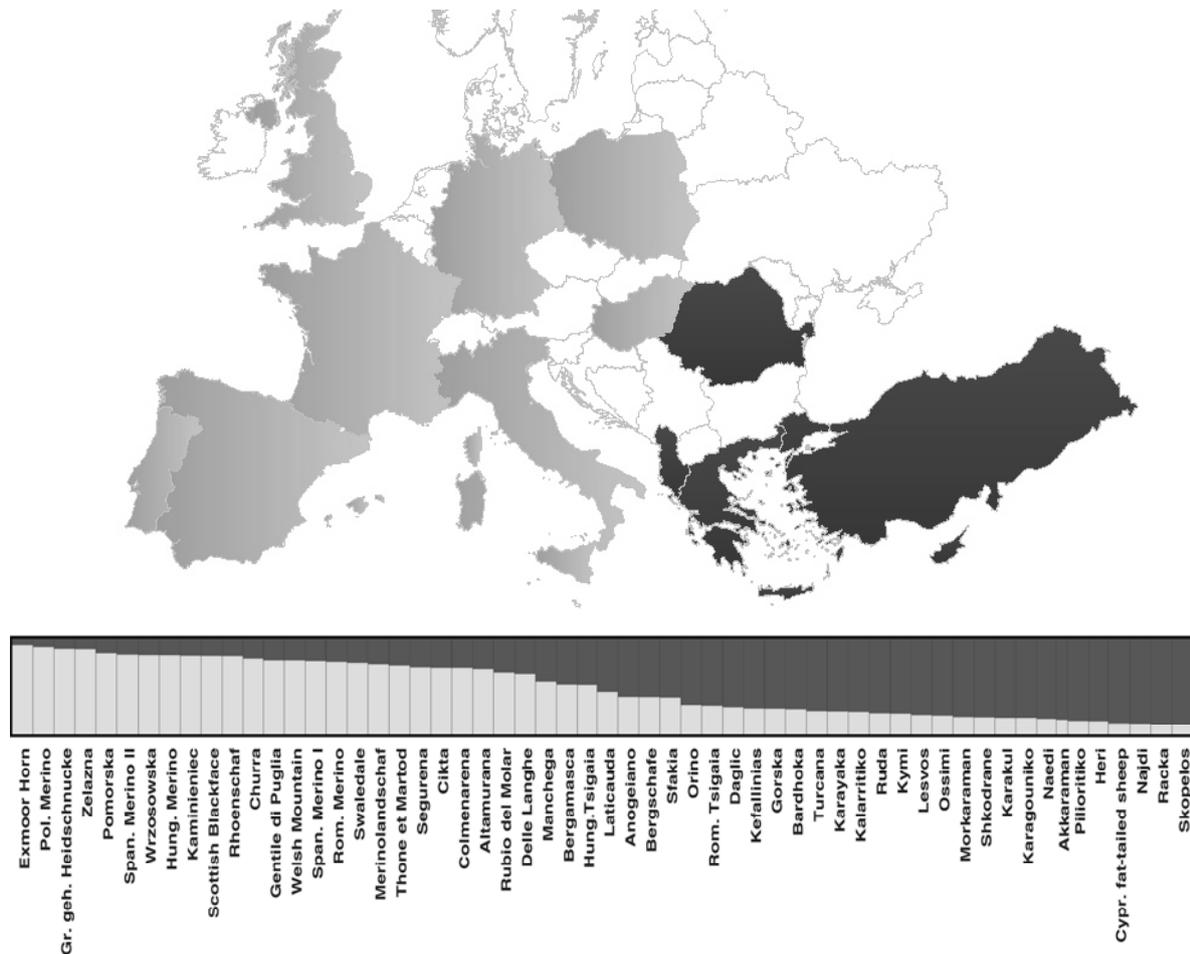


Figure 1: Bayesian model-based clustering analysis of 57 sheep breeds assuming $K = 2$ clusters indicates clear distinction between Western European breeds on the one hand and Southeastern European and Middle Eastern breeds on the other hand

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