

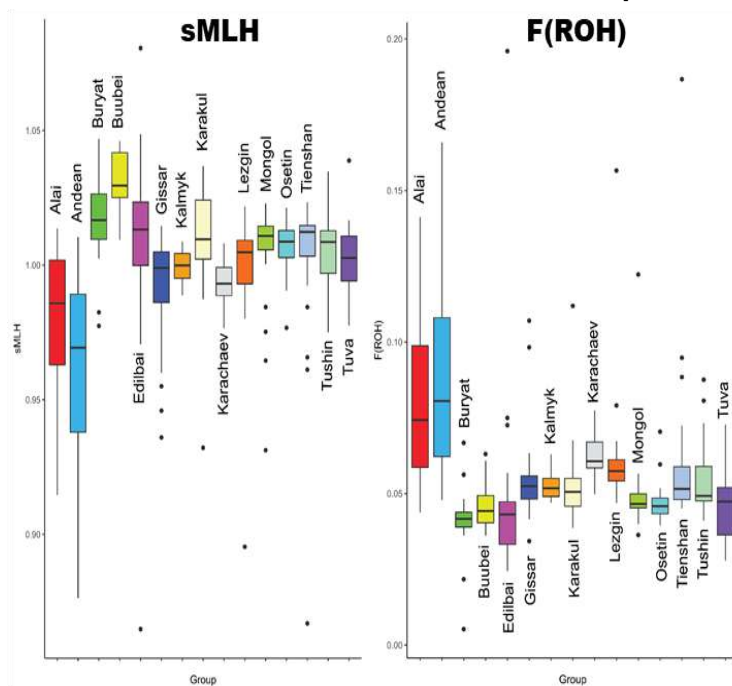
Estimation of inbreeding in local sheep breeds of West Asian and Central Asian origin based on high-density SNP-genotypes

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Introduction. Maintaining high levels of genetic diversity is a key factor of successful breeding of resilient, resistant to diseases and productive sheep. Prevention of inbreeding is of special importance in the mountainous hard-to-get habitats where gene flow is limited or absent. An assessment of inbreeding coefficients based only on pedigree information is not always correct.

Aim. We aimed to assess inbreeding in 15 local sheep breeds inhabiting severe environments of Russia and neighboring Asian countries based on estimations of standardized multilocus heterozygosity (sMLH) and runs of homozygosity (FROH).

sMLH and FROH values in 15 local sheep breeds



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Materials and Methods. SNP genotypes of twelve Russian (n=316) and three Kyrgyz local sheep breeds (n=68) were generated using Ovine Infinium® HD SNP BeadChip (Illumina, USA). The sMLH values were calculated in R package inbreedR and visualized in R package ggplot2. The FROH values were calculated using the R package detectRUNS by applying the consecutive runs method.

Results. Mean sMLH values varied from 0.962 in the Andean breed to 1.031 in the Buryat breed and averaged to 1.001. The lowest FROH value was detected in the Mongolian breed (0.0043) while the greatest ones were observed in the Alai and Andean breeds and were 0.0364 and 0.0357. The strong negative correlations between sMLH and FROH were detected for all studied breeds ($r^2 = -0.8496$, $CI = -0.8752 \dots -0.8192$).

Conclusions. Data is relevant for control of inbreeding level in the populations and for future sustainable management of native fat-tailed sheep breeds.

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