

Analysis of genealogical information and estimation of population parameters in population of Istrian sheep

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Summary

Regardless of living in the era of genomics, pedigrees still play an important role in quantitative and conservation genetics. Transition to genomic selection is upcoming in many livestock populations, including Istrian sheep, but that won't happen instantly, and for sure won't make the pedigrees redundant. The study aimed to determine some important pedigree information and population parameters of Istrian sheep under selection. The pedigree with 6480 individuals was constructed by tracing back all the known ancestors for the 5701 phenotyped ewes. The average (and max) *number of full generation*, *number of equivalent complete generations (equiGen)*, and *index of pedigree completeness (PCI)* were 1.34 (5), 2.16 (6.56), and 0.46 (1), respectively. The average *PCI* from 1st to 5th recent generation was 0.92, 0.79, 0.63, 0.43, and 0.26, respectively. The maximum *mid-parent age* was 11 years, and the average *generation interval* was 3.8 years. The *coefficient of inbreeding (F)* and *effective population size (Ne)* estimated as increase in pairwise coancestry were obtained on individuals with *equiGen*>3 that were born within the last generation interval (year 2015 to 2018, $N_{ref}=650$). The average F_{ref} was 0.089. The females ($F_{ref}=0.091$) were more inbred than males ($F_{ref}=0.056$). The slope of regression of annually obtained F on birth year (BY) was ≈ 0 ($P>0.1$). The estimated N_{eref} was 117 animals, and the regression of annually estimated N_{eref}/N_{ref} on BY was also insignificant ($P>0.1$) and ≈ 0 . Despite the stagnation of the F in the last couple of years, its' magnitude is still high and poses risk to this population. Carefully designed matting plan based on all the available information is required to keep it under control while trying to achieve desired selection progress.

Key words: pedigree, completeness, inbreeding, effective population size