

Increasing Effective Population Size by Strengthening Genetic Connectedness Between flocks: Case Study on Pag Sheep Breed

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ABSTRACT: The effective population size (N_e) is an indicator of genetic diversity, and genetic connectedness between flocks is a “proxy” for assessing bias in across-flock BLUP genetic evaluation. We hypothesized that there is a positive correlation between these two parameters in populations under selection and checked our assumptions on data collected in Pag sheep breed (pedigree and flock information of phenotyped ewes). Only animals with sufficiently informative pedigree (>3 full known generations) were used in the inferential statistical analysis (from 1457 to 1833 animals within 4-year spanning generation interval - “sliding window” approach). The N_e estimated from the mean rate of increase in coancestry in the last generation interval was 127 animals, and the overall connectedness estimated with prediction error variance of differences in estimated breeding values (EBVs) between animals belonging to different flocks ($\overline{PEVD_{i,j'}}$) was 0.81. By regressing partial (generational) N_e on partial $\overline{PEVD_{i,j'}}$, it was estimated that $\Delta\overline{PEVD_{i,j'}}$ of 0.01 increased the N_e for 5.5 animals in average. The results suggest that strengthening connectedness in populations under selection, in addition to unbiased ranking of animals’ EBVs, has positive implications to preservation of genetic diversity. However, some discrepancies in calculation of these two parameters posed limitations to relate them and make firm conclusions, therefore more research need to be conducted on this issue before generalization.

Keywords: Effective population size; connectedness; sheep; genetic diversity

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