Partitioning of genetic trends by flock in Istrian sheep breed

M. Spehar[1], J. Ramljak[2] and A. Kasap[2]
[1]Croatian Agency for Agriculture and Food, Svetošimunska 25, 10000 Zagreb, Croatia, [2]University of Zagreb Faculty of Agriculture, Department of Animal Science and Technology, Svetošimunska 25, 10000 Zagreb, Croatia; marija.spehar@hapih.hr

Genetic trends play an important role in monitoring success of selection and partition of breeding values is an effective tool for detecting main providers of selection gain. Istrian sheep have been traditionally selected for milk yield, while little or no attention, has been paid to fat (FC) and protein (PC) content until recently. The objectives of this study were to: (1) estimate genetic trends for FC and PC from 2000 to 2019; and (2) partition genetic trends (BV's) by flock. A single-trait repeatability fixed regression test-day model was used to estimate BV's. Parity, litter size, season of lambing, flock, stage of lactation, and age at lambing were fitted as fixed effects, while additive genetic, permanent environment, and flock-test-day as random effects. Decomposition of the overall genetic trend was conducted by quantifying the sources of genetic gain related to a particular flock. This task was conducted using R package 'AlphaPart' especially designed for this purpose. There was no consistent genetic trend for PC and FC neither for the population as a whole nor for any of the flocks under study. The obtained results implicate absence of systematic selection for PC and FC, regardless of regular provision of breeders with BV's for these traits. We hope that upgrading the existing pedigree based BLUP to a single step genomic BLUP in the near future should be sufficiently simulative for breeders to pay more attention in making selection decisions.