Genomic analysis of dominance and inbreeding effects on milk production traits in Pag sheep

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Local breeds are reservoirs of genetic diversity and have phenotypic characteristics that could be an important resource for meeting future challenges to livestock systems. For example, Pag sheep are a local Croatian breed adapted to a Mediterranean island with a marginal grazing system, raised for milk (mainly used for cheese) and lamb production. Sustainable selection programmes for small local breeds like Pag sheep, may need to consider the effects of dominance and inbreeding. Our aim was to estimate additive and dominance genetic variances and genomic inbreeding for milk traits (milk, fat and protein yields and somatic cell score). We had genotype data (50K SNPs) for 2134 animals, while 1744 ewes had milk records. We detected runs of homozygosity (ROH) with plink 1.9 to estimate genomic inbreeding (FROH). The four single-trait models with additive and dominance effects, including FROH as a covariate to account for directional dominance, were fitted both via the Bayesian method and REML as implemented in BLUPF90 software. Our results revealed stable additive variance across different models. In contrast, dominance variance varied across models, and was significantly impacted by whether or not the FROH covariate was in the model. Dominance variance accounted from 10-30% of genetic variance across models and traits. In conclusion, SNPs allow us to estimate dominance variance and inbreeding in small populations, which can contribute to the knowledge needed to develop sustainable genomic selection programmes in such populations.