

Bayesian estimation of genetic parameters highly associated with health traits in cattle

Radovan Kasarda, Michal Vlček & Nina Moravčíková

Slovak University of Agriculture in Nitra, Slovakia: radovan.kasarda@uniag.sk

The aim of this study was to estimate the heritability and genetic correlations for traits associated with dairy cattle health, including claw parameters, claw disorders and metabolic status. It is very well accepted that those traits are important especially in dairy cattle both, from economical and animals' welfare point of view. The dataset consisted of 299 Holstein cows kept in two farms in west part of Slovakia, with a total of 382 functional trimming records. The records were collected after functional trimming in period from 2015 to 2017. Claw parameters as claw angle, claw length, heel depth, claw height, claw diagonal and width including total claw area and functional claw area were measured by use of computer digital images analysis with software NIS Elements 3.0. Average milk production was 10050 kg (3.85%fat and 3.12% protein). In the dataset, 38.91% of evaluated cows showed presence of interdigital dermatitis and heel erosion (IDHE) or digital dermatitis (DD), presence of the sole ulcers (SU) were registered as well. With use of animal model, based on observed claw measures, was estimated heritability of claw angle by 0.1, claw length by 0.2, claw height by 0.03 and claw diagonal by 0.02, confirming genetic background of analysed traits. Further analysis using advances of Bayesian methods were used to estimate the inheritance of claw disorder presence. Estimated heritability of IDHE was 0.012, DD 0.041 and SU 0.033. To better understand joint influence of conformation traits as well as claw disorder traits, multi trait model was established to estimate genetic correlations within them. To connect prevalence of claw disorders with metabolic status of cows F/P ration was further considered. The study confirmed previous assumption that F/P ratio is inherited as well as original traits used in calculation (fat and protein content). Heritability of F/P ratio estimated using Bayesian single trait approach was 0.59 making it highly considerable for the further use in selection of metabolically resistant animals. Based on obtained results, construction of new selection indices, better responding to today's welfare requests and use of new generation indicators made possible.

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