

Abstract of the doctoral dissertation of Dawid Słomian, M.Sc., entitled.:

Assessment of the breeding value of cattle using the single-step model

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The single-step model will soon become the standard procedure of most national genetic evaluations of dairy cattle. The use of all available information about the animal, i.e., phenotype, genotype, and pedigree information, characterizes these models. The benefit of using a single-step model is the joint estimation of breeding values for both ungenotyped and genotyped animals. However, the complexity of the model due to the large number of correlated effects leads to computational challenges. The most commonly used models are the single-step genomic best linear unbiased prediction (**G-BLUP**) model and the single-step best linear unbiased prediction based on single nucleotide polymorphism (**SNP-BLUP**).

The purpose of this dissertation was to apply and test the quality of breeding value prediction using single-step models based on the *Holstein-Friesian* cattle population from routine evaluation in Poland. In particular, it focused on methodological aspects such as the effect of pedigree depth on model convergence, comparison of different single-step approaches, comparison between the two programs MiXBUP and BLUPF90, and comparison of different approaches for coding missing information in the pedigree depending on the amount of missing data.

In summary, the depth of the pedigree has a significant impact on the rate of convergence; the higher the number of generations, the more time the model takes to converge. Different single-step model approaches give similar results, and no significant differences were observed; however, the number of core animals in the **APY** (Algorithm of Proven and Young) approaches has an impact because too few animals as core animals can result in underestimated results. Another aspect is computational efficiency, which is important when we are analyzing large amounts of data. The **SNP-BLUP** single-step model took the least amount of time to

converge and used the least amount of memory. Comparisons of breeding values results between MiXBUP and BLUPF90 software showed similar results. Coding missing pedigree information affects the quality of breeding value estimates. Approaches using genetic groups and metafounders show better results than using a raw pedigree. However, approaches using metafounders can lead to underestimates of breeding values when pedigrees are highly incomplete.

The obtained results expand the knowledge of single-step models and their application in the assessment of the breeding value of cattle. Genomic data complements the information used in conventional breeding value evaluation, improves convergence, and makes the model resistant to missing data. The choice of model, software, and coding approach for missing parents depends on the completeness, quality, and type of data.