

Solutions for the fixed effects, yield deviations and daughter yield deviations from a data subject to genomic selection

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Proper genetic ranking of animals of different age requires an unbiased estimate of genetic trend. In the breeding value evaluation model the trend estimate comes from multiple sources: records from animals of different age in the same contemporary groups, overlapping generations, and distinguishable selection differential among parent candidates. When the population is subject to genomic selection, the traditional non-genomic animal model (AMBLUP) is considered biased because the main information for the genetic trend is not in the data. Estimated breeding values (EBVs) from such evaluations cannot be further used as reference phenotypes in genomic evaluations or as input data for international evaluations. The goal of this study was to pinpoint basis of the differences in traditional AMBLUP and the single-step genomic (ssGBLUP) evaluations (GEBVs), and to extract corrected phenotypes from the evaluations to be used as meta-data for international evaluations. The data were 305d protein yields of 5 million Nordic Holstein cows. Records were from calving years 1990 to 2016. Almost all bulls (6600) and 29800 of the cows had genotypes available. The data were analyzed with AMBLUP and ssGBLUP. The genetic trends based on birth year means of the (G)EBVs of bulls with more than 50 daughters were consistent until the effective use of genomic sire selection in 2009. After that, the GEBVs continued to improve with the consistent trend until 2012, while the EBVs remained in the level of 2009. In the birth year of 2012, the difference was 6.7 kilograms, which resembles roughly 0.3 sire EBV standard deviations. Unexpectedly only one-third of the difference was attributed to the difference in the estimate of environmental trend which was described by the calving-year-month and calving-herd-year solutions. The main source of the difference in the yearly bull EBV and GEBV means was attributed to (G)EBV averages of daughters of the different age bulls in the most recent contemporary groups. To cover all differences caused by the fixed effects, phenotypes corrected with respect to the fixed effects were obtained. For the cows we calculated yield deviations (YD) and for the sires daughter yield deviations (DYD, the sire wise means of YD corrected with respect to dams of the daughters). Generally the YD and DYD from both evaluation models (AMBLUP vs. ssGBLUP) were in the same level.