

Validation of genomic and genetic evaluations: Nordic Red Dairy cattle 305 d

production traits

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As genomic selection has been used already for several years it has become evident that the validation of genomic evaluations relying on traditional animal models is becoming unsuitable. The GEBV validation test recommended by INTERBULL is cross-validation based on the forward prediction. It was designed at the time when the multi-step genomic evaluation was the standard method. The GEBV validation test is generally poorly suited for testing genomic animal models (single-step GBLUP). The aim of this study was to take a closer look on accuracy and stability of (G)EBVs. The validations for GEBVs were done using yield deviations (YD) or daughter yield deviations (DYD) calculated with single-step GBLUP instead of EBV model. Moreover, we studied the stability of (G)EBV estimations in consecutive evaluations. We used Nordic RDC 305d production data containing ca. 4 million cows with 8.8 million observations. The pedigree included 5.4 million animals. Genotypes were for 33321 animals which had either records or offspring in the full 305 days data. The test setup consisted of four data sets: the newest data, called data0, included calvings up to March 2016. Three reduced data sets were data-1, data-2, and data-3, from which one year of calvings was deleted at a time. Thus, e.g. data-3 included calvings up to March 2013. The data structure allowed studying the accuracy of predictions by production years, and also the stability of (G)EBV estimates across lactations. The bull validation was regression of DYD_{data0} on PA_{data-3} or, for GEBV, regression of $ssDYD_{data0}$ on $GEBV_{data-3}$. The results indicated that after use of genomic selection the DYD from EBV model become biased and that GEBVs can be validated using DYDs from the ssGBLUP model. The validation reliability for protein GEBV (r^2) was 0.28 using DYD from EBV model and 0.36 using DYD from ssGBLUP. Similarly, when making cow validations, it would be better to use YDs calculated from ssGBLUP for validation of GEBVs. The r^2 in GEBV validations using YD from ssGBLUP were on average 14% units higher compared to validations using YDs from the EBV model.