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## Domestic and Interbull information in the single step genomic evaluation of Holstein milk production

J. Příbyl, J. Bauer, P. Pešek, J. Příbylová, L. Vostrý, L. Zavadilová

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Estimated breeding values and genomic enhanced breeding values for milk production of young genotyped Holstein bulls were predicted using a conventional animal model, ridge regression genomic prediction procedure, genomic best linear unbiased prediction, single-step genomic best linear unbiased prediction, and one-step blending procedures. For prediction, the nation-wide database of domestic Czech production records was combined with deregressed proofs from Interbull files through 2008, which had been transformed by multiple across country evaluation to reflect domestic production conditions. 1259 genotyped bulls had already been proven in 2008. Analyses were run that used Interbull values only for these genotyped bulls and used Interbull values for all available sires. Predictions were validated by comparing correlations of breeding value predictions with estimated breeding values and daughter-yield-deviations after progeny test in 2012 of 140 young genotyped bulls and their associated reliabilities. Combining domestic data with Interbull estimated breeding values improved prediction of both estimated breeding values and genomic enhanced breeding values. Prediction by animal model (traditional estimated breeding values) using only the domestic database had 0.29 validated reliability of prediction; whereas combining the nation-wide domestic database with all available deregressed proofs for genotyped and non-genotyped sires from Interbull resulted in reliability of 0.34, compared to 0.36 when using Interbull data only. The highest reliabilities were for predictions from the single-step genomic best linear unbiased prediction procedure using combined data, or with all available deregressed proofs from Interbull only (one-step blending approach), which reached validated reliabilities for genomic enhanced breeding values predictions 0.53 and 0.54, respectively.

### Keywords:

genomic breeding value; single-step prediction; animal model; validated reliability

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