Accuracy of genomic prediction for protein yield using different models in Slovenian Brown bulls

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Use of genomic (SNP) information enables more accurate inference of breeding values (BV), especially for young animals. The objective of this study was to compare the correlation between progeny based and genomically based evaluation for protein yield of Slovenian Brown bulls based on different sources of information and scenarios. Emphasis was to integrate genomic information into national evaluation. Four data sets were constructed as follows: 1) DS1 - phenotypic data (PD) from national genetic evaluation (1.342.134 test-day records of 57.670 cows recorded between years 1997 and 2011); 2) DS2 - DS1 + 50K Illumina SNP genotypes for 183 bulls; 3) DS3 - DS1 + direct genomic value (DGV) for 183 Slovenian bulls evaluated at InterBull (InterGenomics) treated as correlated trait; 4) DS4 - DS1 + DGV for 399 bulls in the national pedigree. Two scenarios were evaluated. In the first scenario, all PD was used in analysis, while in the second PD was removed for years 2008 to 2011 to exclude daughter information of 35 genotyped bulls. Animal model was used for the analysis of DS1, while the joint pedigree and genomic relationship model was used for the analysis of DS2. For the analysis of DS3 and DS4, bivariate animal model was used. Both theoretical and validation based accuracies were evaluated. Application of joint pedigree and genomic relationship model did not increase validation accuracies due to the limited number of genotyped animals. Theoretical accuracies were 0.58 (DS1), 0.61 (DS2), 0.84 (DS3), and 0.74 (DS4), while validation accuracies were 0.56 (DS1), 0.54 (DS2) 0.86 (DS3), and 0.72 (DS4). For comparison, theoretical accuracy of genomically enhanced breeding value at InterGenomics for validation bulls is 0.90. Results show that integration of genomic information into national evaluation was successful.