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PREDICTOR TRAITS IMPROVE ACCURACY OF GENOMIC BREEDING VALUES FOR SCARCELY RECORDED TRAITS

Marcin Pszczola[1,2], Roel F. Veerkamp[1], Yvette de Haas[1], Tomasz Strabel[2], Mario P. L. Calus[1]
[1]Wageningen UR Livestock Research, Lelystad, The Netherlands, [2]Poznan University of Life Sciences, Poznan, Poland

For some traits reference populations may have limited size because of phenotyping costs (e.g. methane emission or dry matter intake (DMI) in dairy cattle). Using predictor traits, a trait of interest can be improved at reduced cost. Impact of using predictor traits in a genomic selection approach has not been studied yet on real data. This study aimed to empirically investigate the effect of using predictor traits on accuracy of direct genomic values (DGV) of DMI based on a small cow reference population. Accuracies were obtained in cross-validation by correlating DGV and phenotypes divided by the square root of heritability. Multivariate genomic BLUP was used to simultaneously evaluate DMI, fat protein corrected milk yield (FPCM) and live weight (LW). DMI was the predicted trait with a small number of observations (869). FPCM had 1,520 and LW 1,309 records and were used as predictors. Four cow reference populations were created by increasing the number of traits with phenotypic records for: 1) only DMI; 2) DMI and FPCM; 3) DMI and LW; or 4) DMI, FPCM, and LW. Evaluated animals (EVA) were cows with phenotypes on: 1) no traits, 2) FPCM, 3) LW, or 4) FPCM and LW. Lowest accuracies were obtained when no observations for EVA were available (from 0.32 to 0.33). With FPCM observations for EVA, accuracy increased to 0.50. Replacing FPCM by LW increased accuracy to 0.57. Highest accuracy was achieved for trivariate analyses (0.63), with information for EVA on both FPCM and LW. Estimates showed most bias were when no observations for EVA were available (slopes of regression of phenotype on DGV ranging from 0.68 to 0.73). Estimates were unbiased with multivariate approach (slopes from 0.99 to 1.12). Using predictor traits in multivariate genomic approach is an inexpensive way to considerably increase accuracy of scarcely recorded traits.