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INCREASING ACCURACY OF GENOMIC PREDICTION COMBINING COW AND BULL REFERENCE POPULATIONS

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Genomic selection might enable selection for expensive or difficult to measure traits, like feed efficiency and methane emission in dairy cattle. However, only a few thousand phenotypic records are likely to be collected for these expensive traits. Therefore, we suggest that an optimal strategy may be to combine this genotypic and phenotypic information, with information of predictor traits that are available from national recording schemes. To combine this information optimally we investigated a Bayesian genomic prediction model that allows us to analyse two traits while animals only have a phenotype on either of the traits. The impact of adding the bull information was evaluated for accuracy of prediction, and for posterior QTL probabilities to assess effects on power for a genome-wide association study (GWAS). The model was tested on a data set with 1,609 cows and 296 bulls with phenotypes for fat and protein yield and with genotypes for 36,346 SNPs. All bulls had highly accurate daughter yield deviations (DYD) for fat and protein yield from the Irish national evaluations. Estimated genetic correlations between the cow and bull traits were either low (0.22-0.26) or moderate (0.55-0.56). Prediction accuracies were calculated via cross-validation, while the whole data set, including or excluding one of the bull traits, was analysed to investigate effects on GWAS. Results indicated that adding information of just a few hundred bulls did not significantly increase prediction accuracy, despite the high accuracy of their DYD. To achieve higher accuracy for the genomic predictions, apparently much larger national bull reference populations need to be added. Adding the bull information did however increase the power for GWAS. So, indicator traits used in a genomic prediction model improve power to identify genomic regions associated with traits of interest, even when the accuracy of genomic prediction with similar models remains unaffected.

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