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Use of phenotypes from multi-trait national evaluations in genomic evaluation

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Multi-trait national evaluations using correlated traits as predictors were developed to increase the reliability of estimated breeding values (EBV) for functional traits. In genomic selection (GS), only single-trait evaluations are used so far. This study focuses on the use in GS and MA-BLUP evaluations of 'combined' phenotypes obtained from multi-trait national evaluations. Different approaches were tested in the Holstein and Montbéliarde breeds. Data consisted in 16,632 Holstein and 2,111 Montbéliard bulls genotyped on the Illumina commercial chip BovineSNP50@. Phenotypes used were daughter yield deviations (DYD) for somatic cell count and cow fertility and deregressed proof (DP) for longevity. QTL detections based on a combination of Linkage Disequilibrium and Linkage analysis and Elastic Net were performed for both direct and combined phenotypes. Then, a MA-BLUP model was tested using either direct or combined traits as phenotypes. Efficiency was measured through a validation study where the youngest bulls formed the validation population. Mean correlation between DYD or DP and EBV increased from 0.51 to 0.56 and from 0.41 to 0.50 respectively, for the Holstein and Montbéliarde breeds when phenotypes used for QTL detection were coming from the multi-trait evaluation instead of the single-trait one. Use of combined phenotypes in MA-BLUP and QTL detection allowed a gain in correlation of 0.08 in Montbéliarde but a loss of 0.06 in Holstein compared with a situation where phenotypes came from single-trait evaluation. Using more accurate phenotypes coming from multi-trait evaluations appears to increase the efficiency of GS, particularly for breeds with smaller reference population. This strategy using phenotypes from multi-trait evaluations for QTL detection is now implemented in national French genomic evaluations