Combination of genotype, pedigree, local and foreign information

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Simultaneous use of all data by Best Linear Unbiased Prediction is a condition to predict unbiased estimated breeding values (EBV). However, this condition is not always fully met. For example, small scale local populations lead to evaluations based only on local data while foreign bulls are used. Although these bulls were strongly selected, foreign data used to select them is unavailable leading to potential biases in local evaluations. Local EBV will be also less accurate because only incomplete data (i.e. foreign data not included) is available. Genomic selection could increase these problems. Initial implementations of genomic prediction used Multiple Across Country Evaluation (MACE) results which mitigated these issues for sires. Single step genomic evaluations (ssGBLUP) could reduce potential biases by the optimal combination of local genomic, pedigree and phenotype information. However, foreign information, like MACE EBV and associated reliabilities (REL), are usually not integrated into ssGBLUP. Therefore, the aim of this study was to assess the potential of a Bayesian approach, based on ssGBLUP, to simultaneously combine all available genotype, pedigree, local and foreign information in a local evaluation by considering a correct propagation of external information and no multiple considerations of contributions due to relationships and due to records. Local information refers here to local EBV and associated REL estimated from all available local data. The Bayesian approach has the advantage to directly combine EBV and REL without any deregression step. The approach was tested using a pedigree of 27,376 Holstein animals including 11,550 animals with a Walloon EBV and 1345 bulls with a MACE EBV. A total of 1351 cows and bulls were genotyped. For bulls with MACE EBV, correlations between MACE EBV and combined genomic EBV were 0.985 to 0.989 for yield traits. This approach has the potential to improve current genomic prediction strategies.