



Genomic evaluation combining different French dairy cattle breeds

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Genomic prediction within and between dairy cattle breeds with an imputed high density marker panel
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In the last years, genomic breeding value prediction in dairy cattle has become widely used especially for predicting breeding values of young bulls without progeny. Accuracy of prediction is clearly determined by the size of the reference set. Since building a purebred reference set of a useful size is challenging for small breeds, one strategy would be to build a multi-breed reference set by combining the reference animals of different breeds. The benefit of using a multi-breed reference set is expected to be even higher when denser marker sets are used since then phases between markers and QTL should be more stable over breeds. We used a data set of 2,257 Australian Holstein and 540 Australian Jersey bulls to study the accuracy of genomic prediction within and between breeds using 50K and imputed 777K (Illumina HighDensity (HD) SNP chip) SNP data. Phenotypes used were daughter yield deviations for three production traits. For predicting genomic breeding values of the youngest bulls, we used a new Bayesian method (BayesR). BayesR models the variances of the SNP effects as a series of four normal distributions. The proportion of SNPs in the distributions is not fixed, but modeled with a Dirichlet distribution. BayesR worked well in our data set and was comparable or in many scenarios even better than a genomic BLUP model. Using imputed HD data rather than 50K did not lead to a significant increase of accuracy for within breed prediction neither for Holstein nor for Jersey. Comparing pure-bred to multi-breed reference set, the minor breed, Jersey, could benefit from the augmented size of the reference only when using the imputed HD panel.

Genomic evaluation combining different French dairy cattle breeds

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We investigated the impact of increasing the number of genotyped candidates in the training set on the accuracies of genomic estimated breeding values (GEBV's) using a multi-breed French dairy cattle reference population, in contrast to single breed. Three traits (milk, fat content and female fertility) were analysed using a multi-breed and single breed reference populations. Three breeds of French dairy cattle were used in this study: Holstein (H), Montbéliarde (M) and Normande (N). Training populations included 2,976, 950 and 970 bulls; validation ones, 964, 222 and 248. All animals involved were genotyped with the Illumina Bovine SNP50 array. Two models were applied. The first, a random regression model, was used for estimation of genetic variances and genetic correlations between breeds for each trait and for estimation of GEBV's. The second, a multiple trait model between breeds for one trait was used only for estimation of GEBV's. Accuracy of GEBV's was evaluated under three scenarios for the genetic correlation between breeds (r_g): a) unknown r_g ; b) breeds highly related, $r_g=0.95$; c) uncorrelated, $r_g=0$. Accuracies of the GEBV's were assessed by the coefficient of determination (R^2) and the quality of prediction by the regression coefficient (δ) of daughter yield deviations on GEBVs of sires in the testing sets. Posterior means for r_g ranged from -0.01 for fertility between M and N to 0.79 for milk yield between M and H. Differences in R^2 for the three scenarios were manifest only in the case of fat content for Montbéliarde (from 0.27 in scenario c) to 0.33 in a) and b)). Accuracies for fertility were lower than for other traits and values of δ showed severe overestimation of GEBVs for this trait in M. The use of the multi-breed reference population only helped to increase accuracy of GEBVs for traits and populations that showed the largest correlation and in the breed with the smallest data set.

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