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Genomic relationships across metafounders using partial EM algorithm and average relationshipsA. Legarra¹, M. Bermann², Q. Mei³ and O.F. Christensen⁴¹CDCB, 4201 Northview Drive, 20716 Bowie MD, USA, ²University of Georgia, Animal and Dairy Science, 425 River Rd, 30602 Athens GA, USA, ³Huazhong Agricultural University, No.1, Shizishan Street, Hongshan District, 430070 Wuhan, China, P.R., ⁴Aarhus University, Center for Quantitative Genetics and Genomics, C. F. Møllers Allé 3, bld. 1130, 8000 Aarhus C, Denmark; andres.legarra@uscpcb.com

Genomic relationships describe relationships among animals previously assumed as unrelated through pedigree, either within or across-breeds. Missing relationships can be modelled using the theory of metafounders, where relationships within and across base populations (metafounders) are encapsulated in a matrix Gamma. Values in Gamma are often hard to estimate, because, first, founder individuals are too far from genotyped individuals, second, the use of several metafounders within-breed to model missing pedigree, and third, many individuals are mixtures of several metafounders. Here we propose a hybrid method to estimate gamma within and across breeds. We use a partial EM maximum likelihood algorithm to estimate Gamma across breeds. We decompose the 'complete' likelihood of markers given Gamma and pedigree into a part that is a direct function of Gamma and a part that is a function of Mendelian sampling variance. We then approximate the first derivative by ignoring the Mendelian sampling variance. The following approximated EM algorithm consists in (1) postulate an initial value of Gamma (2) set up the H-inverse matrix as a function of G-inverse and A-inverse, with A-inverse including rows and columns for metafounders (3) invert the block of H-inverse corresponding to metafounders to obtain H(1:MF,1:MF) (4) set Gamma to the block H(1:MF,1:MF); iterate again. At convergence, we obtain an estimate of Gamma. The algorithm is completed by a check that the (total) log-likelihood is maximized at each iteration. Tests using simulated data show that the algorithm is accurate if the metafounders are not too distant from genotyped animals. For metafounders within breed along time, Gamma can be inferred using a structure that models the increase of relationships and relies on (1) the initial gamma parameter at foundation of the breed and (2) the increase of average relationships within breed along time, measured through pedigree analyses.

Impact of the correlation between SNP effects in different breeds on the accuracy of predictionsP. Croiseau¹, R. Saintilan^{1,2}, D. Boichard¹ and B. Cuyabano¹¹Université Paris-Saclay, INRAE, AgroParisTech, GABI, Domaine de Vilvert, 78350 Jouy-en-Josas, France, ²Eliance, 149 rue de Bercy, 75012, Paris, France; pascal.croiseau@inrae.fr

Rotational crossbreeding schemes in dairy cattle are an efficient way for breeders to obtain more adaptable and robust animals, as well as more sustainable breeding systems. It takes advantage of breed complementarities and of heterosis. Its practice is currently expanding among cattle breeding systems. Aiming to achieve a correct representation of crossbred animals in genomic evaluation, methods to account for the breed of origin of alleles (BOA) have been developed (BOA-GBLUP). Their results regarding the prediction accuracy of genomic estimated breeding values (GEBV), however, have not yet overcome those obtained with a standard GBLUP, which ignores the BOA, especially when true QTL-effects are similar across breeds. Using simulations, we studied the impact of the correlation between QTL-effects in different breeds, on the accuracy of the predicted GEBV using the standard GBLUP and the BOA-GBLUP. 50k SNPs in linkage disequilibrium were simulated for three different breeds; among these simulated SNPs a random subset of 200 were assigned as QTL for all breeds, and ten scenarios varying the levels of correlation, from high (0.9) to low (0), between the QTL effects on the different breeds were generated. Four traits were investigated with heritabilities ranging from 0.01 to 0.65, and each breed of purebred animals was selected for a different trait, while crossbred animals were selected for all four with a selection index weighting all traits equally. After evolving 10 generations under this scheme, A training population of 20,000 animals (6,000 purebred animals from 3 breeds and 2,000 crossbred animals) was used to predict the GEBV of 2,000 crossbreds in the final generation. Finally, the accuracy of the predicted GEBV and of the estimated SNP effects within breed allowed us to assess under which conditions of QTL-effects correlation, the use of BOA-GBLUP is beneficial for genetic evaluations in rotational crossbreeding schemes. This project has received funding from APIS GENE and from the European Union's Horizon 2020 research and innovation program – GenTORE – under grant agreement No. 727213.