

Identification of key contributors to increase phasing accuracy in complex population structures

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Knowledge of the genetic contribution of individuals is essential to select informative individuals for genotype imputation. Based on the Eigen Value Decomposition (EVD) of a relationship matrix we describe a novel approach to determine the genetic contribution of individuals within populations. The approach was applied and validated in four disparate datasets including simulated population, a highly structured experimental sheep population and two large complex pedigreed populations namely horse and cattle. In the simulated and sheep datasets, we identified all known key contributors within the populations, whilst in the horse and cattle dataset we applied the method to select small reference populations that increased phasing accuracy. Compared to commonly applied strategies to select informative individuals for genotype imputation including the identification of marginal gene contributions (PEDIG) and the optimization of genetic relatedness (REL) the selection of key contributors provided the highest phasing accuracies within the selected reference populations. Therefore, this method provides a valuable complement to common applied tools to select individuals for re-sequencing.

Multi-varietal genomic selection in French pig populations

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Reference population size is a limiting factor to succeed in genomic selection. Multi-breed genomic evaluations were proposed as a solution to increase reference population size but did not always lead to genomic breeding value (GEBV) accuracy improvement. The aim of this study is to investigate multi-varietal genomic evaluation using varieties of Piétrain pigs. The data consisted in a main reference population (V1) of 96 genotyped boars, their 752 genotyped and phenotyped offspring and two additional populations of 13 (V2) and 17 (V3) genotyped boars with their 118 and 177 genotyped and phenotyped offspring, respectively. We study the interest of adding the largest reference population to each of the two small populations on GEBV accuracies. Sixty traits were studied including production traits, skin lesions, hormonal and blood parameters. Single-step genomic evaluations were carried out either separately for each variety or by grouping the varieties (V1 and V2 or V1 and V3). Theoretical accuracies obtained in the single variety genomic evaluations were compared to the ones obtained in multi-varietal evaluations for the sires and the offspring. The breeding value predictability in single variety and multi-varietal genomic evaluations were also compared using a 4-fold cross-validation. Average genomic kinship coefficient between the main reference population and the other two populations was of 8% (V1 and V2) and 12% (V1 and V3). GEBV theoretical accuracies and predictive ability of animals from the smallest reference populations (V2 and V3) improved when considering multi-varietal evaluation. These improvements were higher for V2 which was most related to the main reference population. Slightly higher theoretical accuracies were obtained for the offspring than for the boars. This preliminary study suggests that increasing the reference population size with animals from another variety enhances the GEBV accuracy and the predictive ability of animals from small size populations. This enhancement is proportional to the degree of relatedness between varieties.