Genotype imputation of Hereford and Bradford bovine breeds from Brazil

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The bovine breeding programs in Brazil are trying to adopt the use of genetic markers, a procedure called genomic selection (GS). GS consists in genotyping a given reference population with known phenotype and in the discovery of the associated genetic markers. The e ect of the markers are estimated and validated so it is possible to predict the genetic values of the candidates of selection based on their genotypes. High density genotyping is expensive so it is usual to genotype the reference population with higher density genotyping chips and to genotype the candidates of selection with lower densities genotyping chips. Genotype imputation is then applied to expand the genotyping data of the candidates, improving the selection intensity and reducing the costs. In this work three imputation softwares, Beagle v4.1, Minimac v3 and Fimpute v2.2, were used to impute genotypes from a lower to a higher density chip using genotyping data from 233 sires of Hereford and Bradford bovine breeds from the south region of Brazil. High-density genotyping data (777k markers) were available for all samples so lower density data (50k markers) could be obtained and the accuracies of the softwares could be measured. Results show that the softwares were able to impute above 94% of all imputable markers. The correctness of the imputation varied from 86% to 94%. The performance varied from 26.9 to 378.1 markers per second, using a sample of the data from chromosome 1. Overall, all three softwares showed good performance and appear to be good choices for the imputation of genotypes to use in GS.