

عنوان مقاله:

Assessment of the genomic prediction accuracy of discrete traits with imputation of missing genotypes using threshold Bayes A, GBLUP and random forest methods

محل انتشار:

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خلاصه مقاله:

Genomic selection as a promising tool for discovering genetic variants influencing complex traits and along with genotype imputation has an important role in increasing economic efficiency as well as genetic gain by accelerating the animal breeding programs and potentially improving the accuracy of breeding values. The objectives of present research were: (i) to quantify the accuracy of genotype imputation and to evaluate the factors affecting it and (ii) to assess the effects of genotype imputation and genomic architecture on the performance of the Random forest (RF), GBLUP and threshold Bayes A (TBA) methods for genomic predictions of binary traits. According to disease incidence and the genomic architecture (heritability (h^2) = 0.25 or 0.5, $QTL=81$ or 810 and linkage disequilibrium (LD) = low or high), reference and validation sets were organized in different simulated scenarios for 54K SNPs panel. To evaluate imputation accuracy, we randomly masked (90 and 50 percent of markers) and subsequently imputed certain genotypes using FImpute program. Negative effect of increase missing genotypes on accuracies of genomic prediction was observed when applying TBA and GBLUP more than RF

کلمات کلیدی:

complex trait / genomic selection / missing genotypes

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