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In Genetic and Animal Breeding

The joint effect of genomic selection and promotion of alleles by genome editing on improvement of quantitative traits in animal breeding programs

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heritability was increased and the trait specific heritability decreased. The accuracy of estimation breeding values in model 1 was the lowest and in models 3 to 6 was the same. Model 5 with the lowest false positive QTN and the highest true positive proportion was the appropriate model for genetic evaluation of the studied traits. By including polygenic and non-additive effects in the model, the number of false positive errors was reduced. The effect of promotion alleles by genome editing was effective on genomic variance and increased additive variance. When 1 QTNe was promoted and inherited by one generation to offspring, the increase in variance relative to genome selection increased by 0.139, and with the promotion of more alleles (20, 25, and 50 QTNe) over 20 generations, the variance increased. The response to cumulative selection in GS + PAGE mode increased by 0.07 when promoted in 5 bulls and 1 QTN in each one. When 20 and 50 QTNs were promoted, the cumulative response to genomic editing increased by 0.17 and 0.31, respectively. It seems that the response to cumulative selection is increased by increasing the frequency of alleles desirable for the desired trait that can be transmitted to the next generation. With increasing the number of QTNe, the inbreeding coefficient also increased slightly, but there was no significant difference between the inbreeding coefficient in the case of 20 QTNe and 25 QTNe when 5 males were edited and 10 males were edited at the same time. The effect of promotion alleles by genome editing was effective on genomic variance and increased additive variance. When 1 QTNe was promoted and inherited by one generation to offspring, the increase in variance relative to genome selection increased by 0.139, and with the promotion of more alleles (20, 25, and 50 QTNe) over 20 generations, the variance increased. The response to cumulative selection in GS + PAGE mode increased by 0.07 when promoted in 5 bulls and 1 QTN in each one. When 20 and 50 QTNs were promoted, the cumulative response to genomic editing increased by 0.17 and 0.31, respectively. It seems that the response to cumulative selection is increased by increasing the frequency of alleles desirable for the desired trait that can be transmitted to the next generation.

Abstract

The availability of thousands of polymorphic single nucleotides (SNPs) spread across the genomes made it possible to use genome-wide marker information to predict total breeding value in the implementation of genomic selection. The interaction between several gene loci contributes to the phenotypic changes associated with the expression of complex polygenic traits. The present study aimed to compare the performance of different models with additive and non-additive genetic effects, especially epistasis effects in predicting variance components and genomic breeding values as well as QTN in a dairy cow population based on Bayes Lasso model. Then, the effect of promotion of alleles by genome editing was investigated on genomic variance, response to genomic selection and inbreeding. For this study, a population of dairy cattle was simulated based on a choice of four pathways to maximize the rate of genetic progress over ten generations with an effective size of 100 individuals in the base population. The genomic structure was assumed consisting of 3 chromosomes with a length of 100 cM and On each chromosome were located 1000 markers 2 allelic markers with a frequency of 0.5. 50 QTL double alleles with equal frequency were randomly assigned to each chromosome. For QTL allelic effects, a gamma distribution with a parameter slope of 0.4 was used in QMSim software and sampling was performed. Phenotypic and genotypic data of the last 10 generations were used for analysis. Marker effects, variance components, and genetic parameters were estimated using Bayes Lasso method. To control the type I error in estimating marker effects, Bonferroni test was used at 1% probability level. Initially, promotion of alleles was performed on 5 bulls. In the first stage 1 QTN, then 20, 25 and 50 QTN was promoted by genome editing. Programming in R software was used to promote allele. Secondly, promotion of alleles was performed on 10 bulls. And these enhanced alleles were inherited on to the next generation. The BGLR package in R software was used to estimate the additive effects. In the next step, the mean inbreeding coefficient for GS + PAGE was calculated and compared with the GS inbreeding coefficient only. PLINK software was used to evaluate the rate of inbreeding.

The results of this study showed that the additive model or the polygen model alone could not show the missing or hidden variance, in such a way that adding non-additive genetic effects including dominance and epistatic effects reduced the residual variance effects. Also in the complete model including additive and non-additive effects, the total genetic variance increased. With the addition of non-additive effects in the statistical model the general