VARIABILITY OF GENETIC RESPONSE TO SELECTION UNDER GBLUP EVALUATION

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Novel breeding methods including genomic selection are based on genome-wide predicted breeding values (GEBV). Recent development coincides well with the new single nucleotide polymorphism (SNP) technology that is high throughput, accurate and relatively inexpensive. Genomic best linear unbiased prediction (GBLUP) is a statistical method that has been used to estimate GEBVs of various complex traits in both agriculture and forestry, GBLUP and its variations have become commonly used for selection in crop breeding. GBLUP is not dramatically different from traditional BLUP approach (Henderson 1975), as standard software available for linear mixed models can be used to solve mixed model equations, which is a major advantage of such methodology for breeders. Genetic relationships derived from pedigrees (basis of BLUP) ignore the random sampling of the two possible alleles from each parent at each locus during meiosis - variation defined as the Mendelian sampling term. GBLUP is based on a so- called genomic relationship matrix or more often realized relationship matrix as it describes identity- by-descent (IBD) at SNPs. Exploiting this variance could be the major added benefit of GBLUP.

While previous studies described GBLUP theoretical efficiency in agriculture, forestry diametrically differs in terms of production system, where the emphasis is on the use of seed orchards. This study represents a potential role of genomics in launching the new breeding program. The main objective of this work was to assess, through simulations, the impact of selection strategy in conjunction with BLUP vs. GBLUP on the predicted selection accuracies of mentioned statistical methods in a real-world forest tree breeding context. We evaluated the impact of genetic architecture of the target trait on the predicted accuracy of both strategies and primarily on the response to selection in production population.

We discuss: (1) BLUP/GBLUP relative efficiency and show that GBLUP is not always superior to traditional phenotypic evaluation, (2) large sensitivity of GBLUP's efficiency to trait's genetic architecture, and (3) excessive variance of the predicted genetic response in seed orchards.

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