

Efficiency of genomic selection with models including dominance effect in the context of perennial crop breeding

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Abstract : In perennial plants, varieties can be produced by clones or elite full-sib families, where both additive and non-additive effects are taken into account in the selection process. Although this point is crucial in perennial crops, very few studies have analysed the value of including non-additive effects in the Genomic Selection (GS) model (Meuwissen et al. 2001) and there is a growing interest in testing new models (Lorenzana and Bernardo 2009).

We developed a simulation study to test the efficiency of GS in the case of perennials crop breeding with the example *Eucalyptus* one of the most used forest tree genus in plantation. We simulated a recurrent selection scheme for clone production over four breeding cycles. Scenarios crossing broad sense heritabilities ($H^2=0.6$ and 0.1) and dominance to additive variance ratios ($R=0.1$; 0.5 and 1) were compared. GS was performed with 1000 SNPs and 22 QTLs per morgan and tested against phenotypic selection (PS) based on best linear unbiased prediction of parents and clones. Our analyses are based on data simulated with R software version 2.13.0 (R Development Core Team 2009) and the HaploSim package, developed by Coster and Bastiaansen (2009).

When the training population was made up of the first cycle progeny tests and the candidate populations were the progeny tests of three successive cycles, GS accuracy decreased with breeding cycles (e.g. from 0.9 to 0.4 with $H^2=0.6$ and $R=0.1$), whereas PS presented constant performances (accuracy of 0.8 with $H^2=0.6$ and $R=0.1$). When the training population set was updated by associating data of previous cycles, GS accuracy was improved from 25 to 418%, especially with $H^2=0.1$. The GS model including dominance effects performed better in clone selection (genotypic value) when dominance effects were preponderant ($R=1$), heritability was high ($H^2=0.6$ and with an updated training set), but no improvement was detected for parent selection (breeding value). The genetic gains over cycles were lower with the GS method without updating the data set but, with an updated training set, were similar to PS. However, the genetic gain per unit time with GS was 1.5 to 3 times higher than with PS for breeding and clone populations.

Our results demonstrate how GS efficiency is augmented by increasing the relationship between the training and candidate populations, the training population size and heritability. Moreover, our study brings new insight by analysing the value of modelling the dominance effect in GS when both additive and non-additive effects are taken into account to select genotypes. These results highlight the value of GS in perennial crop and especially in *Eucalyptus* breeding.

References

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