

Potential of genomic selection in perennial crops: illustration in the context of *Eucalyptus* and oil palm breeding.

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Introduction

The methodology of selection in plant breeding has markedly evolved with the advent of high throughput molecular technology, the increasingly reasonable cost of genotyping, and the implementation of genomic selection (GS). For perennial crops, the potential of GS is high and gives the opportunity to shorten the breeding cycle by selecting at the juvenile stage using marker information. Here we present preliminary results of GS experiments for two perennials crop, *Eucalyptus* and oil palm, that play an important economical role in tropical regions.

Genomic selection in *Eucalyptus*

Simulation studies : In the case of *Eucalyptus*, a simulation study was developed to test the efficiency of genomic selection (GS) in the frame of a recurrent selection scheme for clone production over four breeding cycles. Scenarios crossing broad sense heritabilities ($H^2=0.6$ and 0.1), dominance to additive variance ratios ($R=0.1$; 0.5 and 1) and training population structure were compared using Bayesian LASSO method. 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, progenies and clones.

Performance of GS over breeding cycles

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 $R=0.1$), illustration with Figures 1a and 1b.

Performance of GS by updating the training population

The accuracy of GS was tested with different numbers of generations included in the training population. GS accuracy increased as the number of cycles constituting the training data set increased. This trend was observed whatever the heritability and the variance ratio. This increase in accuracy was more pronounced for higher numbers of cycles constituting the training data set (Figs 2a and 2b).

Genetic gain per unit time

The distinction between GS and PS was significant for the genetic gain per unit time (Figs. 3a and 3b), GS presenting a gain per unit time two to three times higher than that of PS, demonstrating the advantage of reducing the cycle length in tree breeding.

Genomic selection in oil palm

Experimental procedure

For oil palm, we implemented a cross-validation approach with 111 individuals of the last generation of a key breeding population, evaluated through progeny tests including 40,000 individuals and genotyped with 140 microsatellites. Marker effects were estimated using RR-BLUP. Two traits were studied: the percentage of pulp to fruits and the percentage of fruits to bunch.

Results

The accuracy of GS increased when increasing the training population size and reached 0.6-0.7, according to the trait, with a 3:1 ratio for training and validation populations respectively. The small effective population size of in this breeding population explains the good GS performance even with a limited panel of markers (Fig. 4).

Perspectives

It is of great importance to know whether genomic selection is valuable versus phenotyping in terms of genetic progress in plant breeding schemes. However, only a few studies on perennial plants have addressed the utility of GS in genetic improvement. These two studies demonstrate the great interest of GS in perennial crop breeding.

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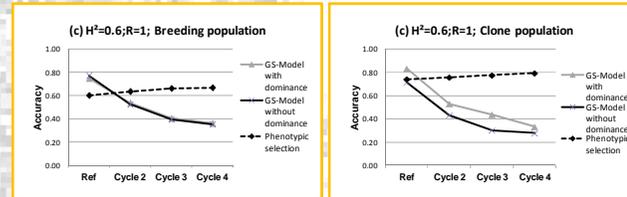


Fig.1 : Change in selection accuracy over cycles for (a) breeding population and (b) clone population without updating the training set: illustration with $H^2=0.6$ and $R=1.00$. For GS, the training population is constituted of the individuals of the cycle 1 progeny tests to predict the candidate populations of subsequent cycles.

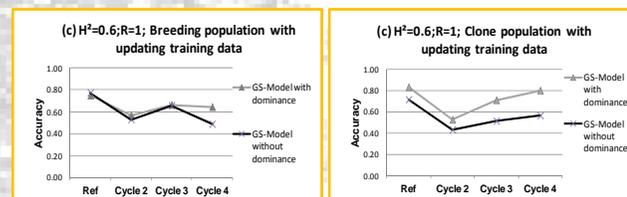


Fig. 2: Change in selection accuracy over cycles for (a) breeding and (b) clone population with updating of the training set: illustration with heritability $H^2=0.6$ and $R=1$. GS without updating: training population in cycle 1 to predict subsequent cycles. GS-updating the training population: training population made of cycles C1+C2 to predict candidate population in C3 and training population made of cycles C1+C2+C3 to predict candidate population in C4.

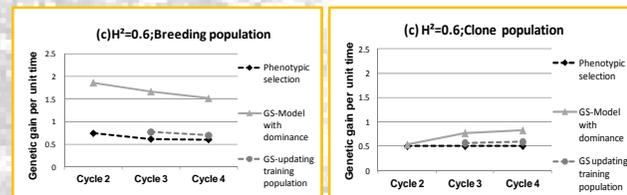


Fig. 3 Change in genetic gain per unit time over generations averaged over the three additive to dominance ratios for the breeding and clonal population comparing PS and GS methods : illustration with heritability $H^2=0.6$.

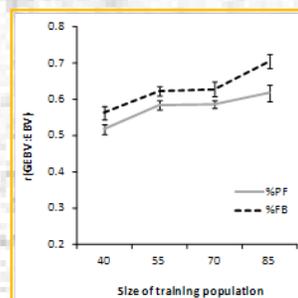


Fig. 4 Change in accuracy of genomic selection for two traits of oil palm yield (%PF: percentage of pulp to fruits, %FR: percentage of fruits to bunch) when increasing the size of the training population. Values are averages over 30 replicates SEM.

Bibliography

Denis Marie and Jean-Marc Bouvet (2012) Efficiency of genomic selection with models including dominance effect in the context of *Eucalyptus* breeding. Tree Genetics and Genome. In press.

