Genomic predictions improve the performance of clonal cultivars in oil palm

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Abstract

Prediction of clonal genetic value is among the difficulties of the genetic improvement of oil palm (Elaeis guineensis Jacq.) yield. Presently, clonal selection requires two stages of phenotypic selection (PS): preselection on the phenotypic values of one or two yield components having high heritability, and final selection on performances in clonal trials. The current study evaluated the efficiency of genomic selection (GS) for clonal selection on eight traits. The GS models were trained on 295 and 279 Delil × La Mé crosses for bunch production and quality components, respectively, and were validated on 42 Delil × La Mé of known clonal value. Genotyping by sequencing led to a dense genome coverage with 15,054 single nucleotide polymorphisms (SNP). We assessed the effects of SNP dataset (SNP density and quality) and of two GS modelling approaches on prediction accuracy. The results showed prediction accuracies that ranged between 0.70 and 0.03 according to trait, SNP dataset and model. Modeling disregarding the parental origin of alleles was preferable given the simplicity of implementation. For parental origin effects could slightly increase prediction accuracies for the traits used to define the two oil palm genotypic groups (bunch number and average bunch weight). The greatest GS prediction accuracies were beyond those of PS for most of the traits. Prediction accuracies from 0.70 to 0.45 for all traits can be achieved combining GS and PS. The best GS prediction accuracies are achieved with at least 7,000 SNPs. This will enable preselecting clonal candidates at all trials before clonal trials, thus increasing the selection intensity and the genetic progress.

Introduction

• Oil palm is the major oil crop worldwide with a production of 45 Mt (2018). The expected demand of palm oil in 2050 is 120–150 Mt
• Clones (ramets) of top-ranking commercial hybrid individuals (orrets) can considerably increase the yield, hence the need of an efficient method to measure their total genetic value.
• Most yield components have a low heritability, therefore only one or two traits are considered for phenotypic preselection of clone candidates. Consequently, the estimation of the yield genetic values is of low reliability. For that reason, breeders set clonal trials. This gives an accurate genetic value estimation of yield but increases the selection process of 10 years and reduces the selection intensity.

• Objectives: evaluation of the efficiency of GS for clonal selection, using orrets of known clonal value to validate genomic predictions.

Materials and methods

Genotyping: genotyping by sequencing (GBS) on the parents of the training crosses, 15,054 SNPs

Results and Discussion

Effect of GS prediction model and SNP dataset on prediction accuracy

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References