

Cocoa genomic selection

Genomic selection for improving cocoa resistance and yields

ABSTRACT

Genomic selection (GS) is a statistical approach that utilizes all available genome-wide markers simultaneously and phenotypic traits of a “training population” to estimate breeding values or total genetic values.

The use of the appropriate statistical model remains one of the critical issues of the GS. The relative performance of models is expected to depend on the genetic background of the phenotyped traits. Two agronomic traits of cacao were tested 1) bean weight which heritability is generally high (over 0.5) and 2) resistance to *Phytophthora* which heritability is generally lower (under 0.5).

The reliability of different models of genomic selection to predict traits was estimated using a breeding population from a farm plot in Cameroon. 291 trees were characterized for production traits (weight of a bean) and resistance traits to *Phytophthora megakarya* (number of rotten pods) during 3 years, and genotyped with more than 8000 SNP markers using GBS (genotyping by sequencing).

Two models were used: Best linear unbiased prediction model based on markers and Bayesian lasso model. Cross-validation was used to test their predictive ability. It is an assumption-free method using an estimation set for model training and an independent test set for prediction. Predictive ability of models was good for both traits but was slightly higher for average weight of a bean ($R^2 = 0.59$) than for resistance to *Phytophthora* ($R^2 = 0.40$).

Keywords : Developing the plant of the future, Microscopic (Gene/cell), Plant disease, Breeding, QTL, Resistance, Cacao

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PERSPECTIVES

It was the first time GS was used for cocoa. The high predictive ability values found indicate that GS is a promising method to improve both cocoa traits. For breeding programs, GS will be a promising alternative to the traditional marker-assisted selection for manipulating complex polygenic traits often controlled by many small effect genes. It could also allow to make predictions of trait values, from a training population, on trees only genotyped by molecular markers.