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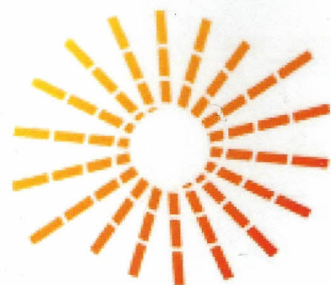
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Marker-assisted selection is traditionally used to improve traits in crops. However, it requests very long cycles selection and still unable to capture loci of minor effect. Genomic selection (GS), a new tool for selecting elite plants in a breeding program by predicting the performance of traits of interest in application of statistical model, is an exciting alternative approach. GS has the potential to catch the effect of all markers underlying the genetic architecture of the studied traits.

In this context, we aimed at evaluating the use of GS into tomato to evaluate the prediction accuracy for 25 traits related to the fruit quality for three different type of population (RIL, MAGIC and GWA panel). We conducted a cross validation approach while estimating the relative weight of parameters (training and testing populations sizes, genetic composition, predictive statistical models, markers density, heritability of the trait as well as the type of population) onto the prediction accuracy.

Our results demonstrated that GS seems very powerful at predicting phenotypes values with accuracies ranging from 0.12 to 0.84 in the panel. Precisely, we conclude that (1) optimizing the training set the better the predictions are (+13% on average) (2) the larger the heritability of the trait value is, the better the predictions are (3) the statistical prediction models perform very similarly and (4) the optimal markers density is depending of the population LD.

Thus, applying GS in tomato seems very promising and could be used tomato breeding programs and produce high-quality varieties.