Genomic selection - which prospects in Prunus armeniaca? Preliminary results issued from fruit quality traits and phenology

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Abstract: Genomic selection (GS) refers to a selection method which intends to assess individuals according to their genomic values using genome-wide dense markers. Particularly efficient in animal improvement strategies, opening interesting perspective in crops, it is already engaged in perennial species such as apple where, genetic gain was maximized for fruit quality traits quantitatively inherited by comparison with conventional breeding strategy.

In the present work, GS was applied on a biparental apricot population (184 individuals) characterized over two consecutive years for phenology (blooming and maturity dates) and fruit quality traits (fruit weight, color, sugar and acidity content, ethylene production). A ridge regression (RR-BLUP) modelling has been used. The performance of GS was assessed by cross validation using the accuracy defined as the correlation between true phenotypes values and the estimated ones.

The effects of markers density and number, training set size and composition as well as the heritability of the investigated traits were evaluated on the accuracy of the model.

The main results issued from the two years multi-annual modelling approach are showing that (i) genomic predictions are accurate even with a little number of markers (>100 markers), (ii) the accuracy increases with the training population's size and with high heritability traits, (iii) and the optimization of the training set improves the performance of genomic selection model.

To conclude, a clear interest exists in continuing the evaluation of the genomic selection in biparental apricot populations even for traits that are difficult to measure. The robustness of the approach needs to be tested both on other progenies and on a large set of genetic resources.

Key words: Genomic selection, Apricot, RR-BLUP, Cross validation, Accuracy, Bi-parental population