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Analysis of genomic prediction across populations in grapevine (*Vitis vinifera* L.)

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Abstract

Genomic prediction (GP) of breeding values has developed widely both in animal and plant breeding programs for its ability to accelerate genetic gains, saving cost and time while handling complex traits. However, its routine deployment in most of the major plant species is still not effective, mainly because of the many factors that are likely to influence prediction accuracies. In grapevine, very few studies have evaluated potential usefulness of GP in breeding contexts. Although the French grapevine breeding program for durable resistance to downy and powdery mildew (INRAE-ResDur) has now proved to be effective with about ten new varieties already officially registered, the duration of each breeding cycle remains long (about 15 years). GP can potentially help us to accelerate and diversify our breeding schemes by targeting complex traits involved in the determination of the optimal productivity and quality of the berries and wines. The main objective is to reduce as much as possible, the long intermediate selection phase of the breeding scheme where every genotype is evaluated in the yard during six years.

Here we evaluated GP across four different breeding populations for main phenological and agronomic traits to identify main factor affecting accuracies. This study brings additional information to the grapevine community regarding the implementation of GP to accelerate breeding programs.

Keywords: grapevine, genomic prediction, INRAE-ResDur, disease resistance, genetic architecture