Genomic and phenomic predictions for accelerating grapevine breeding

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Abstract

The length of the breeding cycle in grapevine is a major obstacle to genetic progress. Several years are needed before phenotypic data are available. The required time between crossing and final variety registration is about 15 years in France. Genomic selection could accelerate breeding. It consists of using a training population, genotyped and phenotyped, in order to train a predictive model to be applied to a selection population, which is only genotyped. This way, phenotypes could be predicted at the seedling stage. Genomic selection is already used routinely in many species, but its application to grapevine remains rare in a breeding context. Recently, phenomic selection, based on near-infrared spectra, has also been proposed as a low-cost alternative to genomic selection, and so far, it has never been tested in grapevine. In this work, we implemented both genomic and phenomic selection within and between two contrasted grapevine populations: a diversity panel of 277 genotypes, chosen to represent the genetic diversity of *Vitis vinifera* L., and a half-diallel of 622 genotypes, which includes ten interconnected full-sibs families with five parents. These populations were genotyped by GBS (32 894 common SNPs) and phenotyped for 15 traits related to berry composition, yield, morphological, phenological and vigour traits, displaying various heritability and phenotypic structure. Genomic predictive ability was medium to high within populations and it tended to decrease in across populations. To study the determinants of genomic predictive ability, we decomposed it into between (cross mean) and within (Mendelian sampling) half-diallel crosses components. We found that distance between parents was the major determinant for cross mean, while heritability impacted Mendelian sampling component. For phenomic prediction, we used spectra collected on wood and leaf tissues, for two years. After having calculated the part of genetic variance in spectra, we used them for predicting phenotypes measured several years ago. Phenomic predictive ability was lower than genomic predictive ability but still encouraging for the application in breeding. Finally, we found that genomic and phenomic predictive abilities were correlated, underlining that phenomic prediction relies on genetics. These results showed that the delay for selecting new grapevine cultivars could be shortened by using genomic or phenomic prediction.

Keywords: genomic prediction, phenomic prediction, breeding, NIRS, BLUP