



Using SNP arrays to leverage historic data sets for improved prediction accuracy and estimation of GxE of fruit maturity in sweet cherry

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Improved prediction accuracy of the genetic potential of advanced selections and cultivars for commercially relevant traits in commercially relevant conditions will lead to increased response to breeding. While a large number of loci might influence quantitative traits, QTLs with major trait effect have been identified, and can be used for selection if the effect of alleles on commercial performance can be accurately predicted. However, selection response will be compromised if the effect of major trait loci are confounded with polygenetic effects from the background genome - if not accounted for, and external factors such as management practices or environment conditions also influence the trait. Here, we propose a novel approach to improve prediction accuracy of genetic potential under commercial conditions by using SNP arrays to characterise variation at major effect QTLs and estimate realised additive and dominance relationships among individuals that have also been evaluated for traits of interest. This approach enables data from otherwise disconnected historical data sets to be combined into a single analysis, thereby increasing prediction accuracy, without the need for replication of individuals. In addition, the different locations from which the performance data have been collected represent samples of the variability of external factors. As such, this analysis can be also used to investigate the influence of these factors on the stability of both major-effect QTLs and polygenetic effects. As part of the RosBREED project, we demonstrate this approach and results using 800 sweet cherry individuals that have been genotyped using the 6K SNP sweet cherry array and evaluated in the USA (Prosser, Washington), Canada (Summerland British Columbia), France (Boudreaux), and Italy (Forli).