

# Building international partnerships for the collation of historical data to study the environmental stability of genomic predictions in sweet cherry

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## Abstract

Here we describe progress on the development of a RosBREED-led international collaboration to collate data on sweet cherry individuals (breeding progeny, selections, and cultivars) that have been phenotyped for traits of interest (maturity date, fruit size, firmness, acidity, and sweetness) and genotyped using the Illumina Infinium 6K cherry SNP array. Our hypotheses are that: (i) individuals evaluated at various sites can be utilised to

sample the phenotypic response of genome-wide alleles to varying environments, and (ii) SNP array data can be used to characterise variation in QTL alleles as well as minor-effect alleles (genetic background) such that data from these different environments can be combined into a multi-environment analysis. This approach is an extension of genomic selection methods and exploits replication among environments at the allelic level, such that clonal replication of individuals among environments is not required. Collaborators have provided access to SNP array data for 597 unique individuals and phenotypic data for these individuals from 18 locations (1 USA, 12 France, 1 Italy, 1 UK, 1 Switzerland, 1 Greece, 1 Australia). The data were used in genome-wide selection models to demonstrate that rankings of individuals for fruit maturity among 2 locations in France, 1 in Italy, and 1 in the USA are very stable, and thus performance of individuals tested in only a single location can be predicted across other locations (e.g. USA to Europe). We will genotype several hundred additional individuals in 2017, and welcome additional collaborators to help widen the extent of environmental variations sampled. The larger the phenotypic dataset from environments and individuals, the greater the opportunity to identify genotype-by-environment patterns of QTL and polygenetic effects, generate and test hypotheses of factors driving those patterns, and predict the performance of individuals in multiple environments. We invite additional collaborators to join this international effort.