

Sweet cherry: new genomic tools for the creation of varieties adapted to future conditions

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Abstract: Sweet cherry (*Prunus avium* L.) is one of the most popular temperate fruit crops despite of its relatively high price. As sweet cherry ripens first among stone fruits, followed by apricot, peach and plum, the demand for this fruit is very high in fresh market during late spring and early summer. The annual global sweet cherry production is about 2.2 million t and shows a slightly increasing tendency. However, this species is seriously threatened by the impact of climate change. Warmer winters and higher risks of frosts in the early spring, lead to a wide range of problems related to flower and fruit set, pollen fertility, desynchronization of pollinators or novel host-pest interactions. Additionally, a higher frequency of rainfall events in spring is responsible of important damages due to fruit cracking, which is one the main agronomic problems for cherry growers. Hence, breeding programs should integrate new traits to create better adapted varieties in terms of bloom date, and its components chilling and heat requirements, in addition to classical traits related to fruit quality such as fruit weight, firmness and cracking tolerance. Given that sweet cherry has a long juvenility period and required large areas to evaluate thousands of new hybrids, Marker Assisted Breeding (MAB) will allow breeders to rationalize their programs and plant only hybrids with favorable allelic combinations for the most critical agronomic traits. With the advent of new-generation sequencing technologies, a great number of genomic data are now available in sweet cherry. High saturated linkage maps have been built using SNPs identified using the RosBreed SNP arrays (6K array and more recently the 15K array) or Genotyping By Sequencing technology, allowing the detection of numerous and accurate Quantitative Trait Loci. Using the new 'Regina' genome sequence obtained with a combination of sequencing strategies (PacBio RSII sequencing and BioNano optical mapping), we are able to identify numerous molecular markers in the QTL areas allowing a more precise MAB. Moreover, the genomic selection methodology to select hybrids for traits difficult to phenotype on many hybrids and in a short period of time is in progress. All these genomics tools will considerably increase the efficiency of sweet cherry breeding programs.

Key words: *Prunus avium* L., phenology, fruit quality, climate change, adaptation, marker assisted breeding