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GENOME-WIDE ASSOCIATION STUDY TO IDENTIFY LOCI CONTROLLING FRUIT QUALITY TRAITS IN SWEET CHERRY

Armel Donkpegan, Teresa Barreneche, Loick Le Dantec, Mathieu Fouche, José Quero-García, Elisabeth Dirlwanger

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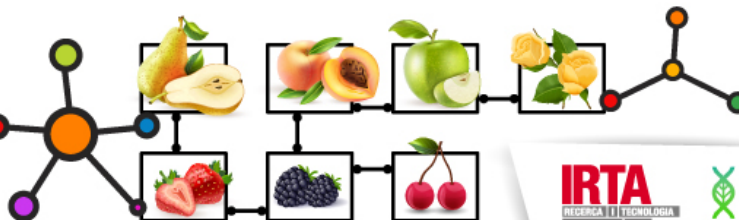
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C0077 GENOME-WIDE ASSOCIATION ANALYSES TO IDENTIFY LOCI CONTROLLING FRUIT QUALITY TRAITS IN SWEET CHERRY ()

Armel Donkpegan¹, Teresa Barreneche¹, Loick Le Dantec¹, Mathieu Fouche¹, José Quero-García¹,
Elisabeth Dirlewanger¹,

¹INRAE, Univ. Bordeaux, BFP, Villenave d Ornon, France

1 Abstract

In perennial fruit species, fruit quality traits are highly dependent on environmental conditions. In the context of climate change, the higher frequency of spring rainy periods has serious consequences for fruit quality, particularly on fruit cracking. There is a need to discover molecular markers associated with these traits in order to enhance the efficiency of breeding programs in sweet cherry. In this study we carried out a genome-wide association analysis for fruit quality description in a sweet cherry (*Prunus avium* L.) germplasm collection. An association mapping population consisting of 116 sweet cherry accessions was phenotyped for 25 fruit quality traits, and genotyped using the genotyping-by-sequencing (GBS) approach. The phenotypic and genotypic data collected were used to conduct a genome-wide association study (GWAS) that has identified important genomic regions underlying some of these traits. For example, we revealed that some traits such as fruit development period, fruit cracking on pistillar end and fruit cracking on stem end are controlled by genomic regions located on chromosomes 3, 4 and 6, respectively. For the first time, genome wide marker-trait associations were found on several chromosomes for traits related to sweet cherry fruit quality.