

QTL analysis of flowering time in sweet cherry

NOTE

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Abstract: Flowering time is a relevant trait in sweet cherry (*Prunus avium* L.) production. Flowering time depends on climatic conditions and varies for each genotype. Sweet cherry cultivars must be suited to climatic conditions in growing areas to prevent crop loss associated with floral freeze injury and irregular floral development. Cultivars with low chilling requirements often show early flowering and may be relevant for growing at low chilling regions. In this work, 411 individuals from six sweet cherry families (4 cross-pollinations and 2 self-pollinations) were used to investigate the genetics of flowering time. These families derive from the landraces 'Cristobalina' and 'Ambrunés' and breeding cultivars including 'Brooks', 'Lambert' and 'Vic', and show from extra-early to late flowering dates. The families were phenotyped during four years (2015 to 2018) and genotyped with RosBREED Cherry 6K Illumina Infinium SNP array. Quantitative trait loci (QTL) analysis was carried out in a combined way for the six populations using the Bayesian approach implemented in FlexQTL™ software. Various QTLs showing strong to decisive evidence were identified in various linkage groups. Major QTLs controlling this trait in this plant material as well as QTLs alleles putatively associated to extra-early flowering time in the low-chilling cultivar 'Cristobalina' will be discussed.

Key words: 'Cristobalina'; flowering date; early flowering; QTL; marker-assisted selection.

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Program and Abstracts

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Conference Program

14:40-14:50	Elucidating the Molecular Mechanisms Underpinning a Novel Acyanic Trait in Apple Khethani Mhelembe, Agricultural Research Council, South Africa	Sara Montanari
14:50-15:00	QTL Analysis of Flowering Time in Sweet Cherry Alejandro Calle, CITA-IA2, Spain	
15:00-15:10	Methylation Analysis of Dormancy Breaking in Almond Flower Buds [<i>Prunus dulcis</i> (Mill.) D.A. Webb] Pedro Martinez-Gomez, CEBAS-CSIC, Spain	
15:10-15:30	Tea and coffee break	
Session 12: Selected Presentation in All Areas		
15:30-15:40	Heritability of Epigenetic Marks and its Impact on Phenotypic Variability in Apple Perrin Adrien, IRHS-INRA, France	Anze Svava
15:40-15:50	Variation of Allergenic Lipid Transfer Protein in Diverse Chinese Peach Cultivars Zhongshan Gao, Zhejiang University, China	
15:50-16:00	Developing Genomic and Epigenomic Resources for Almond [<i>Prunus dulcis</i> (Mill.) D.A. Webb] Jonathan Fresnedo-Ramirez, The Ohio State University, USA	
16:00-16:10	Control of Bud Dormancy Process in Apple: A Genetic-Molecular Study Fernando Andrés, INRA, France	Valerio Pompili
16:10-16:20	Toward the Molecular Cloning of Two Genes Conferring Susceptibility to Apple Chlorotic Leaf Spot Virus Derived from Wild <i>Malus</i> Accessions Shigeki Moriya, Institute of Fruit Tree and Tea Science, NARO, Japan	
16:20-16:30	Allopolyploid Origin in <i>Rubus</i> (<i>Rosaceae</i>) Inferred from Nuclear Granule-bound Starch Synthase I (<i>GBSSI</i>) Sequences Yan Wang, Sichuan Agricultural University, China	
16:30-16:40	Genomic Selection - which Prospects in <i>Prunus armeniaca</i> ? Preliminary Results Issued from Fruit Quality Traits and Phenology Patrick Lambert, INRA, France	Daniel Edge-Garza
16:40-16:50	Polyploidy Influences Resistance to <i>Venturia inaequalis</i> in <i>Malus x domestica</i> Anze Svava, KU Leuven, Belgium	
16:50-17:00	Analyses of 127 Chloroplast Genomes Provide New Insights into the Phylogenetic Relationships among Cherry Species and Taxonomic Status of <i>Cerasus</i> (<i>Rosaceae</i>) Xiaorong Wang/Jing Zhang, Sichuan Agricultural University, China	
17:00-17:10	Introgressing Blue Mold Resistance into Elite Apple Cultivars with DNA Tests, a High-Density SNP Array, and Rapid Cycle Breeding Feixiong Luo, Washington State University, USA	Tingting Gu