

Control of chilling requirement and flowering time in trees; linking genetics and genomics to understand these complex phenological traits in deciduous fruit and forest trees

Albert G. Abbott, Stéphanie Mariette, Lucia Andreini, Tatyana Zhebentyayeva, Zongrang Liu, Guillaume Roch, David Tricon, Patrick Lambert, Jean Marc Audergon, Macha Nicholski, et al.

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Control of Chilling Requirement and Flowering Time in Trees; Linking Genetics and Genomics to Understand These Complex Phenological Traits in Deciduous Fruit and Forest Trees

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Albert G. Abbott , *Clemson University, Clemson, SC*
Stéphanie Mariette , UMR BioGeCo, INRA, Villenave d'Ornon Cedex, France
Fabienne Wong Jun Tai , INRA-Bordeaux, Villenave D'Ornon, France
Lucia Andreini , INRA-Avignon, Montfavet, France
T. Zhebentyayeva , Clemson University, Clemson, SC
Zongrang Liu , USDA-ARS, AFRS, Kearneysville, WV
Guillaume Roch , UR1052 GAFL, INRA, Montfavet, France
David Tricon , UMR BFP1332 - INRA-Universite Bordeaux II, Villenave d'Ornon, France
Patrick Lambert , UR1052 GAFL, INRA, Montfavet, France
Jean-Marc Audergon , UR 1052 GAFL - INRA, Montfavet, France
Macha Nicholski , Centre de BioInformatique de Bordeaux CBIB, Bordeaux, France
Alexis Groppi , Centre de BioInformatique de Bordeaux CBIB, Bordeaux, France
Aurélien Barre , Centre de BioInformatique de Bordeaux CBIB, Bordeaux, France
Catherine Bodenes , INRA-Pierroton, Bordeaux, France
Gregoire Le Provost , INRA-Pierroton, CESTAS, France
Christophe Plomion , INRA Bordeaux, Bordeaux, France
Antoine Kremer , INRA Bordeaux, France
Christopher Dardick , AFRS-ARS, USDA, Kearneysville, WV
Ralph Scorza , USDA-ARS Appalachian Fruit Research Station, Kearneysville, WV
F. Hebard , The American Chestnut Foundation, Meadowview, VA
C. Dana Nelson , Southern Institute of Forest Genetics, US Forest Service, Saucier, MS
Scott Merkle , University of Georgia, Warnell Institute, Athens, GA
Campbell J. Nairn , University of Georgia, Warnell Institute, Athens, GA
Veronique Decroocq , UMR BFP1332 - INRA-Universite Bordeaux II, Villenave d'Ornon Cedex, France

As a consequence of broad adaptation by many perennial trees to different temperate zones, many important phenological traits (e.g. dormancy, chilling requirement, bud burst/bloom date,

seed vernalization requirement) exhibit complex inheritance patterns with multiple genes contributing to the final phenotype. Conceptually, these phenological traits can be viewed as cyclically entrained responses to environmental condition. Due to their importance to the success of the species, traits like chilling requirement (CR), bloom/bud burst date (BD), are traditionally selected through breeding to cover the range of predictable variation for the trait. In fruiting trees for example, genetically matching CR determinants to a particular geographic temperature zone, optimizes fruit production for each variety. These breeding materials also provide an excellent substrate to define and explore the links between phenological trait diversity and the foundational networks of gene activity influencing these phenological traits. This can be achieved by utilizing appropriate genetic materials to define chromosomal regions controlling the phenological trait then incorporating different levels of genomic analyses (e.g. transcriptomics, comparative and structural genomics, resequencing) to identify the candidate genes in these regions that are most likely affecting trait variation. Here, we present the integration of data from single family QTL mapping, germplasm association mapping, transcriptomics, resequencing, and transgenic analyses of key fruit (peach, apricot and plum) and forest tree (oak and chestnut) species as an initial comprehensive approach to defining candidate genes and gene networks contributing to the regulation of CR and BD.