



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.

► To cite this version:

Albert G. Abbott, Stéphanie Mariette, Lucia Andreini, Tatyana Zhebentyayeva, Zongrang Liu, et al.. 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. Plant and Animal Genome XXII Conference, Jan 2014, San Diego, United States. hal-02798021

HAL Id: hal-02798021

<https://hal.inrae.fr/hal-02798021>

Submitted on 5 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Plant and Animal Genome XXII Conference

January 10 - 15, 2014

W585

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

Date: Tuesday, January 14, 2014

Time: 4:00 PM

Room: Royal Palm Salon 4,5,6

Albert G. Abbott, Clemson University, Clemson, SC

Stéphanie Mariette, UMR BioGeCo, INRA, Villenave d'Ormon Cedex, France

Fabienne Wong Jun Tai, INRA-Bordeaux, Villenave D'Ormon, 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-Université Bordeaux II, Villenave d'Ormon, 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-Université Bordeaux II, Villenave d'Ormon 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.