



Collaborative project to identify direct and distant pedigree relationships in apple

Submitted by H el ene Muranty on Thu, 10/25/2018 - 16:20

Titre Collaborative project to identify direct and distant pedigree relationships in apple

Type de publication Communication

Type Communication sans actes dans un congr es

Ann ee 2018

Langue Anglais

Date du colloque 26-30/06/2018

Titre du colloque 9th International Rosaceae Genomics Conference

Auteur Howard, NP [1], Albach, DC [2], Luby, JL [3], Van de Weg, Eric [4], Troggio, Michela [5], Durel, Charles-Eric [6], Peace, C [7], Vanderzande, S [8], Volk, G [9]

Pays Chine

Ville Nanjing

R esum e en anglais Pedigree information is fundamentally important in breeding programs, enabling breeders to know the source of valuable attributes and underlying alleles and to enlarge genetic diversity in a directed way. Many apple cultivars are related to each other through both recent and distant common ancestors. As apple trees are clonally propagated, long-lived, and widely adapted, many of the ancestors of modern cultivars are still present in global germplasm collections. Use of apple SNP arrays enables identification of direct and distant pedigree relationships with precision. An example is the elucidation of the 'Honeycrisp' pedigree using the 8K SNP array, which enabled further findings regarding the inheritance of important alleles for traits including scab resistance and soft scald susceptibility.

To facilitate more discoveries across apple germplasm, a large-scale collaborative apple pedigree reconstruction project has been initiated. This project utilizes output from the Illumina Infinium 20K and Affymetrix Axiom 480K apple SNP arrays, a high quality genetic linkage map for the 20K array SNPs, and a data curation pipeline developed through the FruitBreedomics and RosBREED projects. Techniques using shared haplotype length statistics will be used alongside historical information to deduce distant pedigree relationships. The project involves various experts, germplasm collections, and academic institutions around the world and is open for further extension. It will provide findings useful for breeding programs, germplasm collections, geneticists, and historians.

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