



P L A N T & A N I M A L G E N O M E X X I I I

The Largest Ag-Genomics Meeting in the World.

January 10-14, 2015
San Diego, CAwww.intlpag.org**P0916****Genetic Dissection of Complex Fruit Quantitative Traits in Peach Progenies**

Date: Monday, January 12, 2015

Room:

Igor Pacheco Cruz , UNIMI, Dipartimento di Scienze Agrarie e Ambientali (DiSAA), Milan, Italy
Angelo Ciacciulli , UNIMI, Dipartimento di Scienze Agrarie e Ambientali (DiSAA), Milan, Italy
Cassia Da Silva-Linge , UNIMI, Dipartimento di Scienze Agrarie e Ambientali (DiSAA), Milan, Italy
Stefano Gattolin , Parco Tecnologico Padano, Lodi, Italy
Cinzia Colombi , Parco Tecnologico Padano, Lodi, Italy
Stefano Foschi , CRPV soc. coop., Cesena, Italy
Martina Lama , ASTRA Innovazione e Sviluppo S.R.L., Faenza, Italy
Laura Rossini , University of Milan - DiSAA, Milano, Italy
Daniele Bassi , University of Milano, Milano, Italy

Major research efforts in peach are dedicated to the discovery of genomic variants causing phenotypic effects in complex fruit traits such as: maturity date (MD), fruit size (FW), sugar (SSC) and acid content (TA), flesh texture (slow softening, SSf) and resistance to brown rot by *Monilinia* spp. (BRr). Five segregating progenies showing phenotypic variation for at least one of these traits are available in our experimental fields. For SSC and TA, an already validated approach based on Near-Infrared spectroscopy (NIR), is being applied to phenotype some segregating progenies. For SSf and BRr instead, trait characterization has been performed, resulting in the identification of co-factor traits and definition of standardized phenotyping tools, which are currently applied in the characterization of segregating material (in the context of FruitBreedomics EU project). High-density linkage maps have been constructed with genotypic data obtained from IPSC Illumina 9K SNP chip (Italian Drupomics and FruitBreedomics frameworks) and Genotyping-by-Sequencing (GBS). Additionally, parents of these progenies have been re-sequenced (30-40x) and genetic variants present along their genomes have been identified. Multiple-QTL models (MQM) coupled with the use of co-factor traits is leading to the discovery of significant QTLs. Genomic variants are explored within QTL intervals on the genomes of progeny parents, in order to identify possible mutations causing phenotypic differences, and develop markers for marker-assisted selection approaches.

[Back to: Genome Mapping, Tagging & Characterization: Fruit Species - Even](#)

[<< Previous Poster](#) | [Next Poster >>](#)

[Home/Search](#)[Browse by Type](#)[Author Index](#)[Poster Categories](#)

Meeting Information

When:

January 10 - 14, 2015

Where:

San Diego, CA