

**Plant & Animal Genomes XVII Conference**

January 10-14, 2009  
 Town & Country Convention Center  
 San Diego, CA

**P427** : Fruit Trees

**Apple Genome Sequencing And Post-Genomic Program At IASMA Research Center**

**Riccardo Velasco<sup>1</sup>, Andrey Zharkikh<sup>2</sup>, Michela Troglio<sup>1</sup>, Silvio Salvi<sup>1</sup>, Massimo Pindo<sup>1</sup>, Alessandro Cestaro<sup>1</sup>, Paolo Fontana<sup>1</sup>, Paolo Baldi<sup>1</sup>, Fabrizio Costa<sup>1</sup>, Vadim Goremykin<sup>1</sup>, Mickael Malnoy<sup>1</sup>, Matteo Komjanc<sup>1</sup>, Diego Micheletti<sup>1</sup>, Pierluigi Magnago<sup>1</sup>, Giuseppina Coppola<sup>1</sup>, Marco Moretto<sup>1</sup>, Elena Zini<sup>1</sup>, Antonio Dal Ri<sup>1</sup>, Azeddine Si-Ammour<sup>1</sup>, Sara Castelletti<sup>1</sup>, Erika Stefani<sup>1</sup>, Charles-Eric Durel<sup>5</sup>, Pauline Lasserre<sup>5</sup>, Yves Lespinasse<sup>5</sup>, Amit Dhingra<sup>7</sup>, Sue Gardiner<sup>6</sup>, David Chagne<sup>6</sup>, Ami Mraz<sup>4</sup>, Keith Stormo<sup>4</sup>, Quanzhou Tao<sup>4</sup>, Robert Bogden<sup>4</sup>, Jason Affourtit<sup>3</sup>, Jerry Lanchbury<sup>2</sup>, Satish Bhatnagar<sup>2</sup>, Dmitry Pruss<sup>2</sup>, Alexander Gutin<sup>2</sup>, Michael Egholm<sup>3</sup>, Mark Skolnick<sup>2</sup>, Francesco Salamini<sup>1</sup>, Roberto Viola<sup>1</sup>**

<sup>1</sup> IASMA Research Center, Via E. Mach 1, San Michele all'Adige (TN), 38010, Italy

<sup>2</sup> Myriad Genetics Inc., 320 Wakara Way, Salt Lake City, 84108, USA

<sup>3</sup> 454 Life Science/Roche, 15 Commercial Street, Branford, CT, 06405, USA

<sup>4</sup> Amplicon Express, 2345 NE Hopkins Court, Pullman, WA, 99163, USA

<sup>5</sup> INRA, UMR 1259 GenHort, 42 Rue Georges Morel, BP 60057, 49071, Beaucouzé, France

<sup>6</sup> HortResearch, PB 11030, Manawatu Mail Centre, Palmerston North, 4442, NZ

<sup>7</sup> Washington State University, Johnson Hall 46, Pullman, WA, 99164-6414, USA

Apple is one of the most diffuse fruit crops over the temperate climates, and one of the most important representatives of the Rosaceae large family. In Trentino, Italy, apple represents the most important agricultural resource and is deeply rooted in our culture. Therefore our research has focussed on apple genomics, through genome sequencing and assembly, gene identification and annotation, and identification of nucleotide polymorphisms. The Golden Delicious variety is highly polymorphic with two clearly distinguishable haplotypes, expecting to reveal several million SNPs and small indels. A total coverage of 4 genome equivalents of libraries of ascending size sequenced by the Sanger method, coupled with 12 genome equivalents of 454 sequences, allowed us to create an effective genome sequence. Assembly has been based on adding sequences of a BAC and fosmid libraries, end-sequenced to assemble large meta-contigs. Contigs are being oriented and ordered on appropriate chromosomes by high throughput marker development and genotyping in an F1 cross of Golden Delicious x Scarlet and additional 4 other crosses and a Golden DH genotype supplied by INRA Angers, F and HortResearch, NZ. 1,600 SNPs of Golden Delicious have been developed and merged with 150 common SSRs in a dense genetic map. The sequencing information is helping to characterize apple genetic variation across the cultivated and wild accessions for the purposes of association mapping. Several candidate genes are being identified corresponding to major genes/QTLs for agronomic and quality traits. Sequencing and mapping data will be publicly available at IASMA, NCBI and GDR databases.

Return to the [Intl-PAG](http://intl-pag.org) home page.

For further assistance, e-mail [help17@intl-pag.org](mailto:help17@intl-pag.org)