

**W353****A Draft Assembly of the Almond Genome**

Date: Saturday, January 9, 2016

Time: 10:51 AM

Room: Pacific Salon 3

Tyler S. Alioto, Centro Nacional de Análisis Genómico (CNAG-CRG), Centre for Genomic Regulation, Barcelona, Spain

Fernando Cruz, Centro Nacional de Análisis Genómico (CNAG-CRG), Centre for Genomic Regulation, Barcelona, Spain

Jèssica Gómez-Garrido, Centro Nacional de Análisis Genómico (CNAG-CRG), Centre for Genomic Regulation, Barcelona, Spain

Leonor Frias, Centro Nacional de Análisis Genómico (CNAG-CRG), Centre for Genomic Regulation, Barcelona, Spain

Paolo Ribeca, Centro Nacional de Análisis Genómico (CNAG-CRG), Centre for Genomic Regulation, Barcelona, Spain

Marta Gut, Centro Nacional de Análisis Genómico (CNAG-CRG), Centre for Genomic Regulation, Barcelona, Spain

Konstantinos Alexiou, IRTA, Center for Research in Agricultural Genomics CRAG (CSIC-IRTA-UAB-UB), Bellaterra, Spain

Werner Howad, IRTA, Center for Research in Agricultural Genomics CRAG (CSIC-IRTA-UAB-UB), Bellaterra, Spain

Jordi Morata, Center for Research in Agricultural Genomics CRAG (CSIC-IRTA-UAB-UB), Bellaterra, Spain

Josep Casacuberta, Center for Research in Agricultural Genomics CRAG (CSIC-IRTA-UAB-UB), Bellaterra, Spain

Maria J. Rubio-Cabetas, Hortofruticulture Department, Agrifood Research Center of Aragón (CITA), Zaragoza, Spain

Beatriz Galán, Environmental Biology Department, Centro de Investigaciones Biológicas, (CSIC), Madrid, Spain

José Luíís García, Environmental Biology Department, Centro de Investigaciones Biológicas, (CSIC), Madrid, Spain

Amit Dhingra, Department of Horticulture, Washington State University, Pullman, WA

Henri Duval, INRA, UR1052, Unité de Génétique et Amélioration des Fruits et Légumes (GAFL), Montfavet cedex, France

Angel Fernandez i Marti, Genome Center, University of California, Davis, CA

Michelle Wirthensohn, University of Adelaide, School of Agriculture, Food and Wine, Glen Osmond, SA, Australia

Ivo G. Gut, Centro Nacional de Análisis Genómico (CNAG-CRG), Centre for Genomic Regulation, Barcelona, Spain

Pere Arús, IRTA, Center for Research in Agricultural Genomics CRAG (CSIC-IRTA-UAB-UB), Bellaterra, Spain

Almond is one of the oldest cultivated nut crops with its origin in central and western Asia. The selection of the sweet type (*Prunus dulcis*) distinguishes the domesticated almond from its bitter wild relatives. It is economically important, especially in California with the highest worldwide production, followed by Australia and Spain. The almond belongs to the same subgenus as the peach, for which there already exists a reference genome. However, to fully understand the genetic underpinnings marking the key phenotypic differences between almond and peach, we have sequenced the genome of the 'Texas' almond, one of the traditional cultivars producing a sweet nut. Whole-genome shotgun sequencing of Illumina paired-end libraries gave an initial low-contiguity assembly of 512 Mbp, nearly double the estimated genome size. Counting of k-mers indicates a 275 Mbp genome with substantial

heterozygosity as well as repetitive sequence. In order to tackle both problems, we constructed a fosmid library and sequenced 68 pools of ~500 clones per pool. We then assembled the pools, merged them and finished the assembly by scaffolding with paired end and mate pair libraries, which resulted in a 240 Mbp assembly with a scaffold N50 of 500 kbp, a contig N50 of 33.5 kbp and CEGMA completeness of 99%. Two thirds of the assembly was anchored to the peach-almond genetic map, and using re-sequencing data of peach-almond hybrids and their parents we inferred the two haplotypes of the sequenced almond tree. We performed additional validation of the assembly using Oxford Nanopore MinION sequencing.

[Back to: Fruit/Nuts](#)

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

[Home/Search](#)

[Browse by Day](#)

[Browse by Type](#)

[Poster Categories](#)

Meeting Information

When:

January 08 - 13, 2016

Where:

San Diego, CA