

**W326**

The Peach v2.0 Release: An Improved Genome Sequence for Bridging the Gap Between Genomics and Breeding in *Prunus*

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Room: Pacific Salon 3

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Since its release the high quality peach genome sequence (Peach v1.0) has fostered studies on comparative genomics as well as on genetic diversity, domestication and crop improvement in *Prunus* and related species. To improve the chromosome-scale assembly and genome annotation we performed further analyses. Extensive mapping data allowed the improvement of Peach v2.0 assembly in terms of fraction of mapped (99.2%) and orientated (97.9%) sequences and correction of misassembly issues (about 12.2 Mb of

incorrectly positioned sequences). Assembled resequencing data (42x) improved base accuracy and contiguity: 859 SNPs and 1,347 Indels were corrected and 212 gaps were closed. As a result the contiguity of Peach v2.0 improved with a contig L50 of 255.4 kb (previously 214.2 kb) and a contig N50 of 250 (previously 294). Repeat annotation was enhanced including low copy repeats and the complete sequence and location of 1,157 non autonomous Helitrons. Gene prediction and annotation were improved using transcript assemblies obtained from 2.2 billion of RNA seq reads from different peach tissues and organs. In total, after masking with the improved repeat annotation, 26,873 protein-coding genes were predicted in Peach v2.1 annotation, 991 less than those predicted in Peach v1.0. Gene annotation was highly enhanced with the prediction of almost 20,000 new isoforms. The new peach release with improved assembly and annotation will be a pivotal resource for comparative genomics in the plant kingdom and will serve as a foundation for studies bridging the gap between genomics and breeding in *Prunus* and related species.

[Back to: Fruit/Nuts](#)

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

[Home/Search](#)

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[Author Index](#)

[Poster Categories](#)

Meeting Information

When:

January 10 - 14, 2015

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San Diego, CA