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W319 **WholeGenome Comparisons of Fragaria, Prunus and Malus Reveal Different Modes of Evolution Between Rosaceous Subfamilies**

Date: Saturday, January 14, 2012

Time: 11:25 AM

Room: Pacific Salon 3

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Whole genome sequence of three economically important crop species, peach, apple and strawberry, which belong to different genera of the Rosaceae family, have been analyzed to study the evolutionary history. The analysis identified 1399 orthologous regions in three genomes with the mean length of the regions around 100 kb. Each peach chromosome showed major orthology mostly to one strawberry chromosome, but to more than two apple chromosomes, suggesting apple genome went through more chromosomal fission event in addition to the whole genome duplication (WGD) in apple after the divergence of the three genera. On the other hand, the distribution of contiguous ancestral regions suggested that *Fragaria* genome went through a greater number of small scale rearrangements compared to other genomes. Using the contiguous ancestral regions, we reconstructed hypothetical ancestral genome for Rosaceae with nine chromosomes and the evolutionary steps from the ancestral genome to *Fragaria*, *Prunus* and *Malus* lineage. Our analysis shows that different mode of evolution may have played major roles in different subfamilies of Rosaceae.

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