

W180**Dihaploid *Coffea arabica* Genome Sequencing and Assembly**

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Time: 5:20 PM

Room: Esquire - Meeting House

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Coffea arabica which accounts for 70% of world coffee production is an allotetraploid with a genome size of approximately 1.3 Gb and is derived from the hybridization of *C. canephora* (710 Mb) and *C. eugenioides* (670 Mb). To elucidate the evolutionary history of *C. arabica*, and generate critical information for breeding programs, a sequencing project is underway to finalize a reference genome using a dihaploid line and a set of

30 *C. arabica* accessions. For the reference genome, we have generated two assemblies, one from Illumina data (>150x coverage) and a second from PacBio sequences (>50x coverage). The present assemblies cover 1,031 and 1,042 Mb, respectively. After further refinement, using Illumina mate pairs and optical mapping, the genome assemblies will be annotated using RNA-Seq. Resequencing of *C. eugenioides* and *C. canephora* has been completed and is being used to better assess homeologs within the sub-genomes. Furthermore, 30 *C. arabica* accessions, representing wild and cultivated genotypes, are being resequenced (20x coverage) using Illumina. A *C. arabica* genetic map, currently including over 600 SSR markers, that differentiate between the two sub-genomes, is used to anchor the assemblies. Newly identified SNP markers are being added to the map.

The final goals of the project are to produce a high quality reference genome, assess an eventual neo-diversification occurring in the cultivated varieties, have a better understanding of the species formation and evolution, and develop tools that will make the finished genome accessible and useful to breeders and researchers.

[Back to: Coffee Genomics](#)

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

Meeting Information

When:

January 10 - 14, 2015

Where:

San Diego, CA