

**W953**

Using PacBio Long Reads to Generate a High Quality Reference for the Allotetraploid *Coffea arabica* and its Maternal Diploid Ancestor *Coffea eugenioides*

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Time: 5:00 PM

Room: Pacific Salon 1

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Allopolyploids originate from hybridization between divergent genomes associated with chromosome set doubling. As a consequence, the genomes may undergo a wide range of structural, epigenetic, and functional changes. The world's most widely cultivated coffee species, representing 70% of the coffee market, is the allotetraploid, *Coffea arabica* ($2n=4x=44$; genome size 1.3 Gb). *C. arabica* evolved through the interspecific hybridization of the ancestors of two diploid *Coffea* species: *Coffea eugenioides* ($2n=22$, maternal donor, genome size 0.66 Gb) and *C. canephora* ($2n=22$, paternal donor, genome size 0.71 Gb). Sequencing and assembly of the *C. canephora* genome was published recently, Denoeud *et al.* 2014. Science 345: 1181-1184; genome assembly can be accessed at: <http://coffee-genome.org>. We report here progress to produce high quality reference assemblies for *C. eugenioides* and *C. arabica* using Pacific BioSciences (PACBio) long reads to enable coffee genetics and genomics of coffee and speed up adaptation of the crop to climate change. Climate change is probably the most severe threat currently facing the coffee industry on the global scale. In recent years, extreme weather events in Central America, Colombia, and Brazil have led to coffee production losses of more than US \$2 bn. Of major concern is the very narrow genetic base of cultivated coffee varieties, and therefore the urgent need to develop advanced genomic tools to speed up characterization of *Coffea* diversity in its Center of Origin, Ethiopia, which accounts for 98% of the genetic pool, to help broaden the genetic base of cultivated *C. arabica* and speed up adaptation of the crop to climate change.

This abstract will be presented by co-authors Marcela Yepes and Marco Cristancho.

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