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Below is the abstract for symposium nr 496, abstract nr 82:

Title:

Pistachio Genome Sequencing and Assembly

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Preferred presentation method:

Oral

Abstract body text:

Pistacia vera L. is the main cultivated species in the genus and belongs to Anacardiaceae family. The 'Siirt' and 'Kerman' are commercially important cultivars in Turkey and in USA, respectively. *P. vera* has a highly heterozygous genome that presented challenges during genome assembly. For the 'Siirt' cultivar, we used Illumina sequencing platform in our initial assembly of the genome of pistachio, which resulted in a fragmented assembly with N50=208.7 bp scaffold size. The addition of PacBio long read sequencing in combination with the Illumina assembly

resulted in an N50 of 1.51 Mb with 1787 scaffolds. In the third step, Hi-C scaffolding technology was used to generate a chromosome scale assembly for the 'Siirt' cultivar with N50=30.6 Mb and 1,193 scaffolds of which 16 scaffolds contained the majority of the genome. Assembly of the 'Kerman' cultivar is in progress. These assemblies of pistachio provide breeders with foundational information, new tools, and methodologies to accelerate cultivar and rootstock breeding programs.

Keywords:

pistachio, *P. vera*, genome, sequencing, assembly