

The initial release of the *Oryza glaberrima* genome from the Arizona Genomics Institute and the Rounsley Lab

News

Posted by : webmaster

Posted on : 2014/6/6 23:50:00

Oryza glaberrima genome sequence release announcement

We are pleased to announce the initial release of the *Oryza glaberrima* genome from the Arizona Genomics Institute and the Rounsley Lab. *O. glaberrima* is a west African species of cultivated rice that was domesticated independently of Asian rice (*O. sativa* ssp. *japonica* and *indica*) about 3,500 years ago. *O. glaberrima* contains many important adaptive traits for cultivation in African soils and climates. The specific strain sequenced (IRGC accession # 96717 [variety name CG14]) is the parent used for the development of the new rice for African (NERICA) lines that revolutionized rice cultivation in Africa.

Sequencing:

The *O. glaberrima* genome was sequenced using a hybrid BAC pooling/ whole genome shotgun approach with Roche GSFLX/454 Titanium sequencing technology. Sequences were assembled and combined with a subset of previously sequenced BAC clones to produce a whole genome assembly.

Three sources of DNA were used for the *O. glaberrima* sequencing project:

1. Individual BAC clones: 155 bacterial artificial chromosome (BAC) clones were shotgun Sanger sequenced and manually finished, including the entire short arm of chromosome 3 (Chr3S);
2. BAC pools: We selected a minimum tiling path of 3,321 BAC clones from the OG_BBa BAC library (Details here) across the *O. glaberrima* genome (except Chr3S). DNA from each BAC was purified, quantified and pooled (~28 BAC DNA preps/pool) to produce a total of 115 3Mb pools. 3Mb or chromosome arm pools were Roche GSFLX/454 sequenced using either Titanium shotgun or Titanium paired-end libraries, respectively;
3. Genomic DNA from *O. glaberrima* seedlings (accession # 96717 [variety name CG14]) was purified from nuclei and GSFLX/454 sequenced using a Titanium shotgun library.

Assembly:

The assembly is available from www.omap.org for downloading and Genbank (GenomeProject ID #47325). The assembly consists of 5,309 scaffolds with a Scaffold N50 of 230.6kb resulting in a total length of 316.1Mb for the genome with 4% gaps. 85% of the genome is in scaffolds larger than 50kb. 90% of the genome (Scaffold N50: 255kb) can be unambiguously ordered and oriented based on the *O. sativa* ssp. *japonica* genome sequence. The sequences from these regions are numbered sequentially from the top to bottom of each chromosome. While the remaining 10% of the genome (Scaffold N50: 50.5kb) cannot be ordered and oriented with precision, the BAC-pooling strategy allows placement in a single 3Mb region on the physical

map map. These general locations are described in the comment for each unplaced sequence.

Annotation:

A preliminary annotation is now underway at MIPS led by Klaus Mayer and will be available for browsing and BLAST analysis shortly.

Funding:

The *O. glaberrima* genome sequencing project was funded by the National Science Foundation Plant Genome Research Program (#082224) to R. Wing, S. Rounsley and Y. Yu.

Citation:

Muhua Wang, Yeisoo Yu, Georg Haberer, Pradeep Reddy Marri, Chuanzhu Fan, Jose Luis Goicoechea, Andrea Zuccolo, Xiang Song, Dave Kudrna, Jetty S S Ammiraju, Rosa Maria Cossu, Carlos Maldonado, Jinfeng Chen, Seunghee Lee, Nick Sisneros, Kristi de Baynast, Wolfgang Golser, Marina Wissotski, Woojin Kim, Paul Sanchez, Marie-Noelle Ndjiondjop, Kayode Sanni, Manyuan Long, Judith Carney, Olivier Panaud, Thomas Wicker, Carlos A Machado, Mingsheng Chen, Klaus F X Mayer, Steve Rounsley & Rod A Wing. [The genome sequence of African rice \(*Oryza glaberrima*\) and evidence for independent domestication](#). 2014. Nature Genetics - doi:10.1038/ng.3044

Download the complete *Oryza glaberrima* genome [here](#).