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](http://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:
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Citation:

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