

20 Nov 2006

TO: Anyone interested in the sorghum genome sequence (please circulate this as widely as possible).

As you may know, the US Department of Energy Joint Genome Institute, under its 'Community Sequencing Program' has made rapid progress toward its commitment to provide 8X sequence coverage of the genome of *Sorghum bicolor* L. genotype, BTx623. These data will be combined with publicly available sequences, assembled into 'contigs' (contiguous sequences without gaps) and 'scaffolds' (reconstructed stretches with any gaps spanned by at least two end-sequenced clones), and integrated with extensive physical and genetic maps to yield genetically-oriented pseudomolecules that are anticipated to substantially cover most sorghum chromosomes.

Sorghum sequence assemblies will be made available in advance of publication, under the principles of the 'Ft Lauderdale' agreement¹ to protect the interests of scientists who wish to share pre-publication data with the community, i.e. with a request that users defer publication of any whole-genome scale analyses until the sequencing group has published its primary analysis. Leading scientific journals are also being notified. A 4x assembly is now available at https://www.jgi.doe.gov/downloads/Sorghum_bicolor. Use *Sorghum_bicolor* and *^ico@hgr* as login and password, respectively. We anticipate that the genetically-oriented 8x assembly will be available in early 2007, barring unexpected delays.

A team has been assembled to conduct initial annotation and analysis of the sequence for publication in a leading refereed journal. Although many dimensions of the planned analysis are covered, inquiries about possible participation in this effort should be directed to Dr Paterson (paterson@uga.edu). Team members are responsible for providing their own funding to support their participation.

Since the primary publication of the sequence will only be able to succinctly describe a few key features, two leading journals have offered to consider companion papers that address specific features in detail, for coordinated publication shortly following the primary sequence, in a 'special section' or perhaps 'special issue'.

1. Genome Research (www.genome.org/) has agreed to consider large-scale genomic studies that present novel data of biological significance.
2. The Plant Genome (www.crops.org/genome/) has agreed to consider research that shows clear potential for translating genomic technology into agronomic advancement.

Both journals will review sorghum genome-related submissions according to their established mechanisms and standards. At an appropriate time, the respective journals will provide further details.

We hope that this information is useful in planning for engagement of these new genomic resources for sorghum in your work. We also hope that you share our excitement about these new resources, which promise to add new dimensions to our understanding of botanical and genomic diversity, as well as new opportunities for improvement of leading food, feed, forage & turf, and biofuels crops. We encourage you to consider how the sorghum sequence might fit into your research plans, to submit manuscripts to the coordinated reviews as appropriate, and to contact us with any questions.

Andrew H. Paterson
Lead Proposer, CSP Sorghum Sequencing Project
Chair, Sorghum Genomics Executive Committee

Daniel S. Rokhsar
Program Head for Computational Genomics
Joint Genome Institute

¹<http://72.14.209.104/search?q=cache:ag5ZX7CDIdkJ:www.wellcome.ac.uk/assets/wtd003207.pdf+Ft+Lauderdale+sequence&hl=en&gl=us&ct=clnk&cd=1>