Expanded version of Phytozome.net released

May 29 2009

An enhanced version of Phytozome.net, a web portal for comparative plant genomics geared to advance biofuel, food, feed, and fiber research, has been released by the U.S. Department of Energy (DOE) Joint Genome Institute (JGI).

Phytozome provides a central "hub" for web access to a rapidly growing number of plant genomes, and includes tools for visualization of plant genomes and associated annotations, sequence analysis, and bulk, as well as targeted, plant data retrieval. The gene families available in Phytozome, defined at several evolutionarily significant epochs, provide a framework for the transfer of functional information to important biofuel and agricultural crops from model plant systems, as well as allowing users to explore land plant evolution.

The 4.0 release of Phytozome now spans fourteen plant genomes, including eight that have been sequenced at the DOE JGI:

- *Populus trichocarpa*, the black cottonwood tree, the first tree sequenced and being explored as a feedstock for a new generation of cellulosic biofuels.
- Sorghum bicolor, a drought-tolerant grass and the second most prevalent biofuels crop in the U.S.
- Soybean (Glycine max), the number two U.S. crop in both harvested acreage and sales and the principal source of biodiesel,

a renewable, alternative fuel with the highest energy content of any current alternative fuel.

- *Chlamydomonas reinhardtii*, a single-celled green alga, a powerful model system for the study of photosynthesis and source of hundreds of genes associated with carbon dioxide capture and generation of biomass.

- *Brachypodium distachyon*, a temperate wild grass and model plant for temperate grasses and herbaceous energy crops.

- *Arabidopsis lyrata*, a close relative of the model plant *Arabidopis thaliana* and a reference genome shedding light on the genetics, physiology, development, and structure of plants in general and how they respond to disease and environmental stress.

- *Physcomitrella patens*, a moss widely recognized as an experimental organism of choice not only for basic molecular, cytological, and developmental questions in plant biology, but also as a key link in understanding plant genome evolution.

- *Selaginella moellendorffii*, a spikemoss with a compact genome that is helping to define an ancient core of genes common to all vascular plants.

Phytozome also includes the completed sequences of rice, papaya, grape, *Medicago* (the genus which includes alfalfa as a member), *Arabidopsis thaliana*, as well as maize bacterial artificial chromosome (BAC) sequences from the Maize Genome Sequencing Project (http://www.maizesequence.org).

Phytozome, accessible to the public at www.phytozome.net, is a collaboration between scientists at the DOE JGI, Lawrence Berkeley

National Laboratory, and the University of California, Berkeley Center for Integrative Genomics. It was developed with funding from the Department of Energy, the National Science Foundation, the National Institutes of Health, and the Gordon and Betty Moore Foundation.

Source: DOE/Joint Genome Institute (news : web)