



NRI Research Highlights

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High-Throughput Gene Expression Studies Provide Clues For How Cereal Crops Grow

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The information derived from barley studies will advance the development of new methods for disease resistance, increase crop yield and nutrition for all cereal crops, which are among the world's most important food sources.



Figure 1. Barley crop in Oregon.

Barley (*Hordeum vulgare* L.) was one of the first domesticated cereal grains, originating in the Fertile Crescent over 10,000 years ago. Barley ranks fourth among the cereals in worldwide production and is widely cultivated in all temperate regions from the Arctic Circle to the tropics. Barley's geographic adaptability may be in part due to its tolerance to cold, drought, alkali, and salinity. The barley genome – with five billion letters of genetic code – is one of the largest in cereal crops and twice the size of the human genome. The long-history of barley genetics research, however, lends it as an ideal model for cereal crop development.

International Cooperation Accelerates Barley Genomics

In recent years, access to complete genomic sequences, coupled with rapidly accumulating data related to RNA and protein expression patterns, has made it possible to examine how genes contribute to complex phenotypes. With support from CSREES's National Research Initiative (NRI), Initiative for Future Agricultural Systems (IFAFS), and the U.S. Barley Genome Project (USBGP), an International team of cereal scientists from the USDA-Agricultural Research Service, five U.S. Universities, and five international institutions on four continents partnered to develop the Barley1 GeneChip for high-throughput gene expression analysis.

A Pioneering Resource for Cereal Genomics

The Barley1 GeneChip contains probe sets corresponding to approximately 22,000 barley genes. The HarvEST (<http://harvest.ucr.edu/>) database was used to define the probe sets, which were derived from worldwide contribution of over 400,000 barley gene sequences. As the forerunner for new rice, corn, wheat, soybean, grape, cotton and poplar GeneChips, Barley1 has promoted cutting-edge genomic approaches to investigate disease defense, responses to abiotic stresses, development, quantitative trait identification, and biodiversity in cereal crops.

An Atlas of Gene Expression from Seed to Seed through Barley Development

The International team utilized the Barley1 GeneChip to evaluate the expression of 22,000 genes in fifteen tissues samples taken during different stages of barley development in plants grown under highly controlled conditions. The “Barley Gene Atlas” provides a unique opportunity to integrate detailed information on individual genes into a unified developmental framework that is available to the worldwide

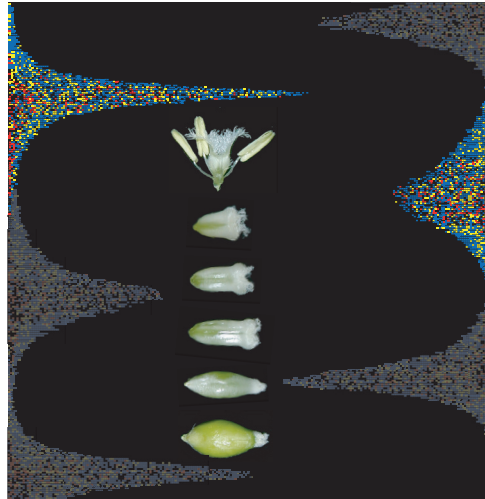


Figure 2. Six stages of barley grain development. Druka et. al., 2006, *Functional & Integrative Genomics* 6: 202-211

research community and a comparative data set for those investigating genes or regulatory networks in other plant species. Thus, this represents the first coordinated effort to characterize gene function from seed to seed in this important cereal crop.

Online Database for Gene Expression

To enhance the usability of the data, BarleyBase/PLEXdb (<http://barleybase.org/>; <http://plexdb.org/>), a new public functional genomics resource, features “click through” integration of expression profiling experiments from researchers worldwide. The integrated tool sets of PLEXdb make it possible for individual investigators to apply a comparative approach to

functional genomics through large-scale expression profiling data sets. Interconnecting links with the PlantGDB and Gramene comparative genomics databases allow BarleyBase/PLEXdb users to perform gene predictions using the 22,000 Barley1 gene sequences, or cross-species comparison at the genome level, respectively. In addition, Barley1 GeneChip sequences are aligned on the Gramene rice genome browser, enabling direct links to rice annotations, including gene function, pathway, and cellular location based upon associations to gene ontology (GO) terms. This linkage will facilitate future comparative and functional analyses of cereal genes.



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