



Executive Summary
USDA/NSF/IGROW Workshop on Wheat Genome
Sequencing
9–11 November 2003.

Workshop goals. To establish a plan, utilizing the expertise from other genome-sequencing projects, for a possible wheat genome-sequencing project. The workshop will pose broader questions such as: Do we need to sequence the wheat genome? What are the scientific needs for the sequence that cannot be met with existing cereal sequence resources? Is it time to sequence now? What genome should be sequenced (diploid or hexaploid)? What type of sequence should be generated (whole genome shotgun, selected BACs, etc)? What strategies could be used to yield the type of sequence needed? What timetable should be followed for the next steps? How will the broader community be engaged? A report will be published in hardcopy and posted on pertinent websites before the next Plant and Animal Genome meeting in January 2004.

Background.

- Wheat is the most widely grown crop, comprising 17% of all cultivated land, a staple of 40% of the world's population providing 20% of the calories consumed. Wheat also provides approximately 55% of the world's carbohydrates. To meet human demands in 2050, grain production needs to increase at an annual rate of 1.5+% on an area of land that will not increase much beyond present levels. This implies that significant advances in the understanding of the wheat plant and grain biology must occur in order to increase absolute yield as well as protect the crop from 25% loss due to biotic (pests) and abiotic stress (heat, drought, and salinity).
- Most of our food comes from plants, wheat included, that have evolved through the unique mechanism of polyploidy. The proposal to sequence the gene-rich regions of wheat is the first of its kind to study the genome sequence of a polyploid. This is only feasible in wheat because genetic resources are available to isolate segments of interest.
- Lack of genome/gene-sequence information and underinvestment in wheat genomics is adversely impacting crop genetics and polyploidy research.
- Although the wheat genome is large (16×10^9 base pairs, five times the size of the human genome sequenced at a cost of $\$4 \times 10^9$), recent research shows that the wheat genome consists of gene-poor and gene-rich components. Sequencing of the gene-rich regions of the wheat genome is feasible due to the abundance of cytogenetic, molecular, and human resources.
- In 2002, wheat scientists founded IGROW (International Genome Research on Wheat) to promote wheat genomics. An IGROW workshop was held at the 10th International Wheat Genetics Symposium, September 2003, in preparation for the USDA/NSF/IGROW workshop, to engage the international community and begin to develop a consensus on the strategy for sequencing of the wheat genome. Over 500 scientists from 45 countries participated in the meeting.

Outlook.

- Depending upon the strategy, a wheat-sequencing project may cost $\$60\text{--}250 \times 10^6$ over 5 years, and 10 countries have an interest in participating in the project.
- Scientists from 12 countries (Australia, Canada, China, Czech Republic, France, Germany, India, Italy, Japan, South Africa, Switzerland, and the United Kingdom) and groups in the USA have indicated their commitment to focusing on certain regions of the genome, with the aim of joining their sequencing efforts into a larger wheat genome-sequencing effort. This staged approach builds on the resources already established by large investments in the USA, as well as investments in other countries.
- It seems likely that a BAC-based approach will be combined with a genome fragment-based approach to determine the sequence of gene-rich regions of the wheat genome. A sequence-ready BAC contig map of bread wheat, integrated into the genetic and EST maps, would provide the basic framework for the sequencing of gene-rich regions.
- Continued comparative genomics utilizing the analysis of rice and *Brachypodium* would significantly enhance the functional analysis of genes in wheat.
- Key outputs from a major structure/function analysis of the wheat genome would include the identification of genes and chromosome regions controlling yield attributes, complex agronomic traits, disease resistance, quality traits, domestication, ploidy, and ploidy-regulated gene expression.

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