



# 2007 National Wheat Genomics Conference

National Wheat Improvement Committee Subcommittee on Wheat Genomics  
Kansas City, MO – November 30 – December 2, 2007

## Executive Summary: *The Future of Wheat Genomics Research in the United States*

The National Wheat Improvement Committee (NWIC) Subcommittee on Wheat Genomics organized their first annual meeting – The National Wheat Genomics Conference (NWGC). The purposes of the meeting were to provide a venue for U.S. wheat workers to learn of current endeavors in U.S. wheat genomics and related research, and to provide a forum to foster interaction, discussion, and collaboration among wheat scientists. The meeting also provided the opportunity to formulate and communicate the future research needs of the U.S. wheat genomics community. Although the main theme of the conference was wheat genomics, the session topics and presentations encompassed other aspects of wheat research related to genomics. To guide strategic planning, key speakers relating to critical research topics important for the future of wheat improvement were invited to give presentations. These research topics were considered relative to the overarching goal of understanding the genetic basis of traits in wheat. The research topics listed below and the prioritized research necessary to achieve the goal of advancing wheat genomics serve as the foundation for basic research and provide the tools for improving food, fuel, and crop yields in a changing environment. Based on surveys distributed at the conference, the **top five wheat genomics research priorities are:**

- 1) Complete, anchored physical map of *Aegilops tauschii*
- 2) Physical map of hexaploid wheat genome
- 3) More molecular markers
- 4) Improved ease of use and interoperability of wheat-related databases
- 5) Full length wheat cDNA collection

### Key research topics that define our research goals and priorities:

- Wheat is the ideal model species for studying polyploidy genome evolution and trait variation because of the unmatched complement of aneuploid genetics stocks, natural diversity, and wide adaptation.
- Public wheat breeding and research is critical to U.S. agriculture because three quarters of all wheat varieties were developed by public wheat breeders.
- The open exchange and publication of wheat research contributes to the rapid advancement of new scientific knowledge for improvement of wheat and other crops.
- Study of polyploidy genetics and gene expression will provide key information about how genes and alleles interact in a polyploid genome.
- Wheat research has led to novel discoveries in the genetics and biology of vernalization, genetic control of chromosome behavior, and end-product quality.
- Wheat is well situated to continue as a leading model for comparative genomics and genome evolution.
- Wheat cytogenetics has made major contributions and continues to provide novel genetics stocks and other tools for understanding mechanisms of chromosome pairing and for chromosome manipulation.

### Community resources will help achieve our research goals:

To advance these research areas, community resources must be created or strengthened. The questionnaire below was distributed to attendees of the Wheat Genomics Conference to develop a consensus of priorities among wheat researchers in the U.S.

### Prioritize General Community Needs (1=highest rank; rank up to 5 topics)

- \_\_\_\_\_ Improved coordination of RFPs from NSF & USDA to minimize overlap or omit important research topics
- \_\_\_\_\_ Improved ease of use and interoperability of wheat-related databases
- \_\_\_\_\_ Complete, anchored physical map of *Aegilops tauschii*
- \_\_\_\_\_ Complete genome sequence of *Aegilops tauschii*
- \_\_\_\_\_ Physical map of hexaploid wheat genome
- \_\_\_\_\_ Genome sequence of hexaploid wheat gene space, potentially linked to the genetic map
- \_\_\_\_\_ Draft BAC sequences for the entire hexaploid wheat genome
- \_\_\_\_\_ Full-length wheat cDNA collection (sequences and clone access)
- \_\_\_\_\_ Functional genomics studies to understand gene expression and gene networks

- \_\_\_\_\_ High Density Wheat SNP HapMap
- \_\_\_\_\_ More molecular markers (including SNPs and SSRs)
- \_\_\_\_\_ Improved wheat transformation methods
- \_\_\_\_\_ si(micro)RNA collection
- \_\_\_\_\_ TILLING populations and services for different classes of wheat
- \_\_\_\_\_ Other \_\_\_\_\_

### **Response to Questionnaire:**

30 responses were received

The rank is based on the number of scores a topic received (count) as well as the average score. The index was calculated as count /average score. Thus, the index reflects both average score and the number of times the topic was selected as a priority. Topics are shown in the original order that they appeared on the survey.

<u>Rank</u>	<u>Average</u>	<u>Count</u>	<u>Index</u>	<u>Topic</u>
13	3.0	2	0.67	Improved coordination of RFPs from NSF & USDA to minimize overlap or omit important research topics
4	3.8	16	4.27	Improved ease of use and interoperability of wheat-related databases
<b>1</b>	<b>2.0</b>	<b>21</b>	<b>10.76</b>	<b>Complete, anchored physical map of <i>Aegilops tauschii</i></b>
7	3.2	11	3.46	Complete genome sequence of <i>Aegilops tauschii</i>
2	2.2	17	7.61	Physical map of hexaploid wheat genome
6	2.7	10	3.70	Genome sequence of hexaploid wheat <u>gene space</u> , potentially linked to the genetic map
10	3.4	8	2.37	Draft BAC sequences for the <u>entire</u> hexaploid wheat genome
5	3.3	14	4.26	Full length wheat cDNA collection (sequences and clone access)
9	3.5	10	2.86	Functional genomics studies to understand gene expression and gene networks
8	3.4	11	3.27	High Density Wheat SNP HapMap
3	2.5	12	4.80	More molecular markers (including SNPs and SSRs)
14	4.5	2	0.44	Improved wheat transformation methods
12	2.0	2	1.0	si(micro)RNA collection
11	4.2	5	1.19	TILLING populations and services for different classes of wheat
Other _____				

Other Topics written on the surveys:

- VIGS community library
- Make existing genomics resources cataloged and available to the community
- Accelerate mapping traits of economic importance for MAS
- SNP development from ESTs
- Doubled haploid technology and support genetics stocks
- Support for maintenance and distribution of genetics stocks
- Mutants and characterization
- Pilot study on de novo high throughput sequencing to decide on sequencing strategy
- Wheat radiation hybrid mapping to initiate genome sequencing
- Mutant populations and radiation mapping
- Quantitative genetics methods

### **Assessment of Survey Results:**

The results of this survey were similar to the May 2007 survey for those questions in common except for “Improved coordination of RFPs from NSF & USDA” and “Genome sequence of the wheat gene space” which moved down in rank, while “Full length wheat cDNAs” moved up in rank.

Wheat researchers clearly recognize the value of physical maps and made those topics a high priority. They strongly support the completion of the physical map for *Ae. tauschii* and ranked a physical map of hexaploid wheat second. More molecular markers ranked third followed by improved ease and interoperability of wheat-related databases. Support for the wheat related databases has ranked high in each of the previous surveys as well. The three lowest priority topics were “si(micro)RNA collection”, “improved coordination of RFPs from NSF & USDA” and “improved wheat transformation methods”. Two respondents each wrote in support for genetics stocks, radiation hybrids and mutant populations. Out of the 14 topics, sequencing priorities ranked 6, 7, and 10. These results reflect a very strong and pressing need for physical maps and marker resources relating to positional cloning, mapping, and marker assisted selection as compared to genome sequencing, transformation, and microRNA research. Support for information availability through databases such as GrainGenes continues to be a high priority.