



2008 National Wheat Genomics Conference

National Wheat Improvement Committee Subcommittee on Wheat Genomics
Indianapolis, IN – December 4 - 6, 2008

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

The National Wheat Improvement Committee (NWIC) Subcommittee on Wheat Genomics held their second 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 as well as a directed email solicitation, the **top five wheat genomics research priorities are:**

- 1) Increased support for mapping traits of economic importance for molecular breeding
- 2) More molecular markers
- 3) Physical map of hexaploid wheat genome
- 4) Improved ease of use and interoperability of wheat-related databases
- 5) Functional genomics studies to understand gene expression and gene networks

Recently funded projects that were listed in past surveys:

Complete, anchored physical map of *Aegilops tauschii* (highest priority in 2007)
Wheat radiation hybrid mapping to initiate genome sequencing

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 and also sent to U.S. wheat researchers by e-mail 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**)

- _____ Centralized catalog of genomics resources available to the community
- _____ Increased support for mapping traits of economic importance for molecular breeding
- _____ Improved doubled haploid technology
- _____ Enhanced quantitative genetics methods and tools
- _____ Improved ease of use and interoperability of wheat-related databases
- _____ 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
- _____ More molecular marker development including SNPs and SSRs
- _____ Improved wheat transformation methods
- _____ TILLING populations and services for different classes of wheat
- _____ A second BAC library for hexaploid wheat genome
- _____ Other _____

Response to Questionnaire:

41 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.

Rank Count Average Index Topic

Rank	Count	Average	Index	Topic
11	10	2.9	3.4	Centralized catalog of genomics resources available to the community
1	27	2.2	12.2	Increased support for mapping traits of economic importance for molecular breeding
8	13	3.4	3.8	Improved doubled haploid technology
13	10	3.4	2.9	Enhanced quantitative genetics methods and tools
4	18	2.8	6.5	Improved ease of use and interoperability of wheat-related databases
6	14	2.7	5.2	Complete genome sequence of <i>Aegilops tauschii</i>
3	17	2.1	8.0	Physical map of hexaploid wheat genome
9	13	3.4	3.8	Genome sequence of hexaploid wheat <u>gene space</u> , potentially linked to the genetic map
14	5	4.2	1.2	Draft BAC sequences for the <u>entire</u> hexaploid wheat genome
7	14	3.4	4.2	Full-length wheat cDNA collection (sequences and clone access)
5	18	3.2	5.7	Functional genomics studies to understand gene expression and gene networks
2	22	2.6	8.5	More molecular marker development including SNPs and SSRs
10	14	3.7	3.8	Improved wheat transformation methods
12	12	4.0	3.0	TILLING populations and services for different classes of wheat

Other Topics written on the surveys:

- 3 A second BAC library for hexaploid wheat genome
- 5 Need for a regional, perhaps USDA operated facilities for production of doubled haploids and transformation
- 1 wheat small RNA targeting libraries
- 1 improved markers for end-use quality traits
- 2 VIGS, transformation and RNAi related research
- 3 bioinformatics tools so breeders can properly integrate marker information in a molecular breeding strategy

Assessment of 2008 Survey Results:

The results of this survey differed substantially from the 2007 survey. The highest priority was for a new topic that was suggested in the “Other” category in last year’s survey. That topic was **“Increased support for mapping traits of economic importance for molecular breeding” which was likely influenced by the Wheat CAP project which is ending in 2009.** “More molecular marker development” moved up to number 2 and “Physical map of hexaploid wheat genome” dropped to #3. “Improved ease of use and interoperability of wheat-related databases” remained in 4th place. “Functional genomics studies to understand gene expression and gene networks” was ranked #5 while the topic that was 5th last year, “Full-length wheat cDNA collection”, dropped to #7.

Wheat researchers who responded to this year’s surveys placed a high priority on the use of molecular markers for mapping economic traits in wheat and new marker development is essential for that activity. Wheat genomics researchers also recognize the value of physical maps. A physical map for *Ae. tauschii* was the highest priority last year and it was funded by NSF. A physical map of hexaploid wheat was second last year and 3rd this year. Wheat-related databases have ranked high in all of our surveys as they are recognized as an essential tool for all wheat research. The lowest ranking topics were quite different from last year. Last year the three lowest priority topics were “si(micro)RNA collection”, “improved coordination of RFPs from NSF & USDA” and “improved wheat transformation methods” while this year they were “Draft BAC sequences for the hexaploid wheat genome”, “Enhanced quantitative genetics methods”, and “TILLING populations and services”. Five respondents wrote in “Facilities for production of doubled haploids and transformation”. Out of the 14 topics, sequencing priorities ranked 6, 7, and 9, almost identical to 2007. These results reflect a very strong and pressing need for marker resources, online databases and physical maps relating to positional cloning, mapping traits, and marker assisted selection as compared to genome sequencing, transformation, and TILLING population research. The success of the Wheat CAP project has clearly had an impact on the priority topics in this survey compared to 2007.