



21 July 2014

Ed Kaleikau, PhD
USDA Plant Breeding Inter-Agency Working Group
National Program Leader
USDA National Institute of Food & Agriculture
Washington, DC 20250

Dear Ed:

On behalf of the IWGSC, I appreciate greatly the opportunity to comment on the USDA Roadmap for Plant Breeding. We applaud the USDA for establishing a plant breeding roadmap that aligns with the USDA Strategic Goals and Objectives 2014-18 as well as the needs of public and private breeders who utilize molecular as well as conventional methods.

The challenges facing breeders and producers of the world's most widely consumed crop have been well documented recently by scientists, policy makers, and journalists. To meet the burgeoning demands of the growing population, we must increase wheat production by 70 percent by 2050, a task difficult under any circumstance. This objective must be achieved, however, sustainably and without an increase in available land at the same time growers and breeders face a changing climate, the globalization of disease threats, as well as limited fertilizer, nutrient, and water resources. To complete this task under these daunting circumstances, a paradigm shift in wheat breeding will be necessary.

It was the recognition that new approaches would be required to meet the challenges we are facing now and to reverse declining US production that led Kansas wheat growers, through the Kansas Wheat Commission, to join with wheat scientists to establish the International Wheat Genome Sequencing Consortium in 2005. The goal of the consortium is to obtain a reference sequence of the wheat genome comparable in quality to that of rice and to develop the tools and resources needed to empower the broadest possible application of genomic selection, molecular breeding, and genome-wide association studies in wheat.

While significant progress has been made in establishing high quality genomic resources that relate directly to the large (17Gb), hexaploid, highly repetitive bread wheat genome, we do not agree that "genomics research has come of age" for wheat. It is true that glimpses of what may be possible are emerging as new genomic information that has become available in the past two years is accelerating the development of new genotyping approaches for screening markers and gene variants associated with specific traits, most significantly as a result of our efforts to produce chromosome-based physical maps, draft sequences, and reference sequences. Highlighted in the special issue of *Science* published



last week (18 July 2014) with a focus on wheat genomics(1), is the first draft survey sequence for all 21 bread wheat chromosomes(2) and the first high quality reference for a chromosome (3B) (3). With the exception of the 3B reference sequence, however, the data are partial and do not provide crucial information about the structure and organization of the genome sufficient to enable the utilization of genomic tools for accurate predictions of phenotypic outcomes.

For wheat genomics to truly come of age, breeders and plant scientists must have access to a high quality, reference genome sequence for all of the bread wheat chromosomes. In addition, the sequence must integrate genetic and phenotypic information and be available via a database that provides access and sharing of complex data sets, bioinformatics tools, and analyses. These resources will provide a template for genome-wide varietal comparisons enabling the systematic molecular characterization of germplasm collections and the development of effective breeding tools. They will also support research aimed at enhancing our fundamental understanding of mechanisms that underlie complex traits and adaptation responses, thereby providing essential information for future molecular and conventional breeding programs.

To date, rice is the only crop genome that has a high quality reference sequence. We strongly encourage the USDA to include in its plant breeding roadmap a concerted effort to ensure that bread wheat and other key food, feed, and fiber crops have genome sequences comparable in quality to rice that will efficiently underpin the high throughput genomics and phenotyping so important for future plant breeding programs.

With regard to the specific requirements remaining for wheat, the IWGSC developed a strategic roadmap in 2006 that has been updated regularly to take account of progress and new technological developments. The IWGSC roadmaps have been endorsed and designed with the support of public and private sector breeders through their involvement in the consortium's coordinating committee. Specific contributions toward the roadmap that USDA has made to date include:

- 1) Production of a BAC-based physical map of chromosome 3A, and
- 2) Partial funding for the survey sequencing of chromosome 3A.

In addition, the US NSF funded the physical mapping of chromosomes 1D, 4D and 6D and radiation hybrid mapping of the D-genome as part of a wider physical mapping program on *Aegilops tauschii* and, most recently, the BAC-based sequencing of *Ae. tauschii*.

When the IWGSC roadmap was updated this past year at the request of the Wheat Initiative, the strategy was updated to take into account the (1) efficiencies that grew out of the successful 3B reference sequencing project, (2) latest high throughput sequencing technologies, including the emergence of long read technologies, and (3) centralization of tasks where feasible. Under the IWGSC plan, the full reference sequence of bread wheat based on chromosome-specific physical maps could be delivered within three years if sufficient funding (i.e., \$16.2 million) were obtained.



Since the launch of the internationally coordinated initiative to sequence the wheat genome occurred in the US, we hope that the US, and in particular the USDA, will play a significant role in the effort to complete the wheat genome sequence. To this end, we strongly encourage the USDA to build on previous US contributions by:

- 1) Funding BAC-based sequencing of one or more bread wheat chromosomes;
- 2) Funding a centralized radiation hybrid mapping project for all 21 wheat chromosomes that will facilitate construction of pseudomolecules from sequence contigs by providing relative mapping information; and
- 3) Establishing a database for the distribution of IWGSC resources in the US that mirrors the IWGSC repository currently hosted by the URGI at INRA, France.

USDA support will reinforce the US commitment to all plant breeders and will provide an underpinning resource that will enhance the value of genome-based programs for the future and enhance the cost-effectiveness and speed at which molecular and other genome-sequence enabled tools can impact improvements in wheat breeding.

Thank you again for this opportunity to provide comments on the USDA Roadmap for Plant Breeding.

With best regards,



Kellye A. Eversole
Executive Director, IWGSC

1. K. Eversole, C. Feuillet, K. F. X. Mayer, J. Rogers, Slicing the wheat genome. *Science* **345**, 285-287 (2014); published online EpubJuly 18, 2014 (10.1126/science.1257983).
2. The International Wheat Genome Sequencing Consortium, A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome. *Science* **345**, (2014); published online EpubJuly 18, 2014 (10.1126/science.1251788).
3. F. Choulet, A. Alberti, S. Theil, N. Glover, V. Barbe, J. Daron, L. Pingault, P. Sourdille, A. Couloux, E. Paux, P. Leroy, S. Mangenot, N. Guilhot, J. Le Gouis, F. Balfourier, M. Alaux, V. Jamilloux, J. Poulain, C. Durand, A. Bellec, C. Gaspin, J. Safar, J. Dolezel, J. Rogers, K. Vandepoele, J.-M. Aury, K. Mayer, H. Berges, H. Quesneville, P. Wincker, C. Feuillet, Structural and functional partitioning of bread wheat chromosome 3B. *Science* **345**, (2014); published online EpubJuly 18, 2014 (10.1126/science.1249721).

