Current status of physical mapping on wheat chromosome 6B.

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For the purpose of better understanding the genome structure in wheat and accelerating the development of DNA markers for gene isolations and future breeding, the Japanese research consortium, as a member of IWGSC, is now conducting a project for the physical mapping and genomic sequencing of Chinese Spring chromosome 6B (914Mb). With a sequence-based finger printing method (Whole Genome Profiling; Amplicon Express, KeyGene Inc.), physical maps for the short and long arms of chromosome 6B have been successfully established using the 6BS- and 6BL-specific BAC libraries, respectively, which consist of 2,667 and 1,842 BAC contigs. And the estimated chromosomal coverage is more than 80% of both arms. Overlap analysis between the neighboring clones within the BAC contigs resulted in a total number of 5,079 and 4,889 MTP (Minimal Tiling Path) BACs on 6BS and 6BL, respectively. For the confirmation and the chromosomal assignment of the BAC contigs onto their corresponding genomic regions, we currently develop a large number of 6B-specific DNA markers using the public marker resources, available EST databases, and the 6B survey sequence. To date, among 3,743 markers tested for their availability, 2,480 markers were found to be useful for the PCR screening of BACs, and 451 BAC contigs has been anchored by 627 markers to the specific genomic regions on chromosome 6B presumed on the basis of genetic maps, deletion maps and/or Genome Zipper. In parallel, a high-resolution radiation hybrid map and a genetic map using recombinant inbred lines are under development for further improvement of physical maps. This work was supported by grants from the Ministry of Agriculture, Forestry and Fisheries of Japan (Genomics Agricultural Innovation; KGS-1001 and KGS-1003) and funding from Nisshin Flour Milling Inc.

SESSION II: HISTORICAL PERSPECTIVES

ITMI: The early years and impacts on Triticeae research.

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The International Triticeae Mapping Initiative was launched at a meeting in Davis, California, in 1989. Motivation for a collaborative effort was twofold: find research funds and foster progress through collaboration. The informal nature of ITMI was meant to encourage independent research among the primary participating laboratories and at the same time encourage collaboration so that good maps would be obtained rapidly and materials and resources could be shared. The bigger challenge was funds for research. Several companies provided some support funds, but really only to conduct workshops and coordination meetings. CIMMYT provided support for producing the first public RFLP map in wheat and both CIMMYT and ICARDA provided funds in support of ITMI management. Barley workers in the U.S. were able to secure Cooperative Agreement funds from the USDA. A DOE/NSF/USDA Joint Program provided a grant that greatly assisted in conducting workshops and short courses and preparing research grant proposals. Several national ITMI groups were formed and a roster of more than 130 Affiliate Scientists was amassed. The ITMI was coordinated in the office of the California Genetic Resources Conservation Program at UC Davis for 12 years, 1989-2000; thereafter the coordination has been rotated to other countries. Coordinators of chromosome groups or species were appointed to collect data and monitor progress. The first successful grant for the U.S. ITMI scientists was obtained from the USDA for detailed RFLP mapping of four chromosomes of wheat. Oddly, when this project was successfully completed, the grant application for mapping the three remaining chromosomes was not funded. Later, NSF supported a large grant for producing and mapping ESTs. This was a very successful activity with about 100,000 ESTs produced and about 8,000 mapped, producing about 18,000 loci mapped to deletion bins in hexaploid wheat. Next efforts have emphasized sequencing and ITMI has retained its momentum in coordinating workshops almost every year till now with this 22nd workshop. Maps were produced, genetic stocks developed, and dozens of scientific papers have been produced by ITMI collaborating scientists. ITMI still remains a legacy of Ernie Sears, whose nulli-tetra and other aneuploid stocks facilitated much of the mapping research.