Poster 6. Discovery and mapping of single-feature polymorphisms in wheat using Affymetrix arrays.

A.N. Bernardo [1], P.J. Bradbury [2], H-X. Ma [3], S-W. Hu [4], R.L. Bowden [5], E.S. Buckler [2], and G-H. Bai[5].

[1] Department of Plant Pathology, Kansas State University, Manhattan, KS 66506, USA; [2] USDA–ARS Maize Genetic Diversity Laboratory, Ithaca, NY 14853, USA; [3] Institute of Plant Genetics and Biotechnology, Jiangsu Academy of Agricultural Sciences, Nanjing, China; [4] Department of Agronomy, Kansas State University, Manhattan, KS 66506, USA; and [5] USDA–ARS Plant Science and Entomology Unit, Manhattan, KS 66506, USA.

Affymetrix arrays have been used to discover single feature polymorphisms (SFPs) in several crop species. To demonstrate the utility of the Affymetrix GeneChip® Wheat Genome Arrays in SFP discovery and mapping in wheat (*Triticum aestivum* L.), complimentary RNAs synthesized from mRNA isolated from seedlings of 71 F_{8-12} recombinant inbred lines (RILs) from the cross 'Ning 7840/Clark' were hybridized to the Affymetrix array. SFP prediction on the array data followed the method of Kirst et al. A total of 955 SFPs were selected and combined with simple-sequence repeat (SSR) data for mapping. A high-density, genetic map consisting of 923 SFPs and 269 SSR markers and covering a genetic distance of 1,944 cM was constructed with 877 SFPs assigned to 21 chromosomes. The SFPs were distributed randomly within a chromosome and effectively filled gaps between SSRs but were unevenly distributed among the different genomes. The B genome had the most SFPs and the D genome the least. Map positions of a selected set of SFPs were validated by SNaPshot analysis and comparison with previous EST physical mapping data. Results indicate that the Affymetrix array is a cost-effective platform for SFP discovery and mapping using RILs. The new map will be an important source of markers for detecting quantitative trait loci and high-resolution mapping.

Poster 7. New wheat data in GrainGenes.

David E. Matthews [1], Victoria L. Carollo [2], Gerard R. Lazo [3], and Olin D. Anderson [3].

[1] USDA–ARS, Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY 14853, USA; [2] Department of Plant Sciences and Plant Pathology, Montana State University, Bozeman, MT 59717, USA; and [3] USDA–ARS Western Regional Research Center, 800 Buchanan Street, Albany, CA 94710, USA.

Several wheat maps have been added to GrainGenes this year. A durum map, 'Kofa/UC1113', containing SSR and SNP markers, was submitted from the Wheat CAP project. A dozen more maps from this project are expected in the next year. Another tetraploid map, 'Langdon/*T. turgidum* subsp. *dicoccoides* G18-16', containing SSR and DArT markers, was obtained from Peleg et al. (Tzion Fahima). A bread wheat map, 'Nanda 2419/Wangshuibai', was obtained from Zhengqiang Ma; in addition to the MAG markers (expressed STSs and SSRs) that were placed on this map, data on a total of 2,500 MAG markers was added to the database.

The NSF-sponsored, D-genome, physical mapping project has anchored many BACs to genetically mapped markers. Now, several GrainGenes maps display the positions of these BACs relative to loci on chromosomes 1–7D, which is the beginning of an integrated physical/genetic map for wheat.