SPEAKER AND POSTER ABSTRACTS – NATIONAL WHEAT GENOMICS CONFERENCE

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Note: Speaker abstracts are followed by the poster abstracts.

Accessing the barley genome.

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Assemblies of nearly 500,000 barley ESTs from a range of barley genotypes have been used to define more than 13,000 single nucleotide polymorphisms (SNPs). From these and several hundred SNPs from other sources, three pilot Illumina, GoldenGate assays were developed to test 4,596 SNPs for high-throughput genotyping. Two production-scale GoldenGate assays, BOPA1 and BOPA2, were developed from 3,072 of the tested SNPs and deployed within the USDA BarleyCAP (http://barleycap.cfans.umn.edu/) and UK AGOUEB (http://barleygenetics.net/lukesite/html/agoueb/guide_to_illumina_genotyping.htm) projects, and throughout the barley community. A barley consensus genetic linkage map composed of 2,943 SNPs was produced using data from four doubled-haploid mapping populations. An estimated two-thirds of all gene-bearing BACs in a Morex library were identified with ~12,500 overgo probes, increasing the compiled number of gene-positive BACs to 83,831 clones. High-information-content fingerprinting was applied to these BACs, yielding 1,700 Mb of gene-bearing BAC contigs, available at http://phymap.plantsciences.ucdavis.edu:8080/barley/. Combinatorial pools of part of the minimal tiling path (MTP) were applied to BOPA1 and BOPA2, anchoring 1,319 MTP BACs to 1,150 SNP loci representing 1,079 unique genes. Several groups have established TILLING populations, and a large portion of existing mutant and germ plasm collections are in the process of being analyzed using the barley GoldenGate assays. The SNP-based genetic map, with barley/rice synteny displays and information on gene-BAC relationships, is available through HarvEST:Barley for Windows (http://harvest.ucr.edu) or online (www.harvest-web.org). Work is underway in Europe to fully sequence thousands of gene-bearing BACs, create a physical map of the entire barley genome, and generate several 100,000 BAC-end sequences, which is intended to thoroughly relate the barley physical map to reference genomes. A whole-genome sequencing strategy is in a formative stage under the auspices of the International Barley Sequencing Consortium (http://barleygenome.org/) in coördination with the International Wheat Genome Sequencing Consortium (www.wheatgenome.org). As the density of information increases, it becomes ever easier to relate barley to wheat genomes, thus, the vision of barley as a genome model for wheat is becoming a reality.