

III. NATIONAL WHEAT GENOMICS CONFERENCE SPEAKER AND POSTER ABSTRACTS

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Note: Speaker abstracts are followed by the poster abstracts.

IWGSC: A physical map and sample sequencing of the homoeologous group-3 chromosomes of wheat.

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Hexaploid wheat (*Triticum aestivum*) presents a challenge in constructing physical maps, which are prerequisite for genome sequencing and annotation, mainly due to its large genome size (~17 Gb), polyploid nature, and repetitive sequence content (>90%). The complexity of the analysis can be reduced by establishing physical maps and sequences of isolated chromosome BAC libraries using flow cytometry and wheat aneuploids developed in Chinese Spring wheat (CS) by the late E.R. Sears. Under the auspices of the IWGSC, a pilot project on chromosome 3B was initiated in France, and a new project on the physical map of chromosome 3D has been funded by the EU. The USDA–CSREES funded a pilot project on chromosome arm 3AS in the U.S. with the specific objectives to (1) develop an anchored physical map for the short arm of chromosome 3A, fingerprint BAC libraries constructed from a 3AS telosomic chromosome isolated by flow cytometry, assemble the fingerprints using the FPC program, and anchor the FPC contigs to the cytogenetic and genetic maps using a combination of EST, RFLP, and SSR markers and markers derived from BAC-end sequences (BES); (2) generate 18.4 Mb of sequence from the chromosome 3AS BAC libraries, sequence 48 targeted BAC clones (5.8 Mb) to 8X sequence coverage and BAC end sequence 10,000 random clones (12.6 Mb), annotate these sequences for repeats and genes using a combination of automated and manual annotation, and identify chromosome-specific markers from the BES for physical and genetic mapping; (3) perform comparative sequence analysis in wheat, compare the 3AS BAC sequences (objective 2) with sequences already (and to be) generated from homoeologous chromosome arm 3BS for new insight into structural and functional specificities of the genomes in a polyploid context, and perform comparative analyses with rice, a related cereal for which finished sequence is available; (4) further wheat genome annotation and bioinformatics and construct an expanded wheat genome annotation resource; and (5) train and educate the wheat community in genomics and hold two workshops. From a BAC library for CS 3AS from flow-sorted chromosomes with 12× chromosome equivalent, 55,584 BAC clones were fingerprinted and assembled into 1,677 contigs (10-fold 3AS coverage) and 11,939 singletons. Ten thousand random BACs were end sequenced and 16,795 high-quality BESs with an average read-length of 500 bp and a total of 8.3 Mb of genomic sequences. Microsatellite primers were successfully developed from 598 SSRs found in the BES and, on average, 20 and 11 % of markers were polymorphic in *T. monococcum* and *T. turgidum* species, respectively. Another 504 genic sequences were identified from the BES and screened in the 3AS BAC fingerprint database. Primers were developed from 279 genic sequences that were present in contigs and will be used for anchoring BAC contigs to genetic map. EST–STS markers are being developed from 3AS EST bin-mapped markers. In addition to already bin mapped ESTs, another 250 ESTs were designed on the basis of similarity with rice chromosome 1 and are being used to physically anchor the BAC contigs using 190 six-dimensional pools. Progress is being made on the construction of 20 Mb BAC-contig for comparative sequencing of *Fhb1/Rph7* region.