

Poster 6. Survey of the wheat 5AS chromosome synteny in *Triticum* species with different ploidy levels.

D. Barabaschi ¹, V. Michelotti ¹, K. Lacrima ¹, F. Desiderio ¹, A. Gadaleta ², I. Centomani ², A. Giancaspro ², S. Giove ², A. Blanco ², E. Francia ³, V. Mazzamurro ³, N. Pecchioni ³, A. Fricano ⁴, P. Piffanelli ⁴, A.M. Mastrangelo ⁵, M. Valarik ⁶, A.M. Stanca ¹, L. Cattivelli ¹, and G. Valé ¹.

¹ CRA–Genomics Research Centre, Via San Protaso 302, I-29017 Fiorenzuola D'Arda, PC, Italy; ² Department of Environmental and Agro-Forestry Biology and Chemistry, University of Bari, Via Amendola 165-A, I-70126, Bari, Italy; ³ Department of Agricultural and Food Sciences, University of Modena and Reggio Emilia, Via Amendola 2, I-42100, Reggio Emilia, Italy; ⁴ Genomics Platform, Parco Tecnologico Padano, Via Einstein, I-26900, Località Cascina Codazza, Lo, Italy; ⁵ CRA–Cereal Research Centre, S.S. 16, km 675, I-71100, Foggia, Italy; and ⁶ Laboratory of Molecular Cytogenetics and Cytometry, Institute of Experimental Botany, Sokolovská 6, CZ-77200, Olomouc, Czech Republic.

In the frame of the project 'Physical mapping of wheat chromosome 5A', we have analyzed markers collinearity in the short arm of chromosome 5A (5AS) considering different species of the *Triticum* genus (*T. aestivum*, AABBDD, *T. turgidum* subsp. *durum* (AABB), and *T. monococcum* (AA) characterized by different ploidy levels and evolutionarily separated on a time scale in order to get insights into possible chromosomal rearrangements occurred during evolution. In detail, we relied on four mapping populations: (1) Chinese Spring (CS, *T. aestivum*) x Renan (*T. aestivum*), (2) CS x CS disomic substitution line for chromosome 5A (*T. turgidum* subsp. *dicoccoides*), (3) Latino (*T. turgidum* subsp. *durum*) x MG5323 (*T. turgidum* subsp. *dicoccum*), and (4) DV92 (*T. monococcum*) x G3116 (*T. monococcum*). Several categories of molecular markers, including SSRs (simple sequence repeat), SSR–EST (SSR-expressed sequence tags), TE junction (transposable elements), and COS (conserved ortholog set) were used to obtain high density genetic maps for the short arm of wheat chromosome 5A. The specificity of each marker for chromosome 5AS was assessed with nulli-tetrasomic lines derived from the reference cultivar Chinese Spring, and deletion lines were used to assign the physical position of the developed markers to deletion bins of 5AS. The evaluation of syntenic blocks and nonconserved regions among the homologous segments of different *Triticum* species is reported, while the mapping of EST-based markers allowed identification of syntenic regions in the rice genome. Identification of possible rearrangements in the different 5AS genetic maps of wheat is providing valuable information for the subsequent steps of BAC contigs anchoring, while the consensus map deriving from the integration of these four maps will provide a fundamental tool to link the genetic and physical maps.

Poster 7. Physical mapping resources for large plant genomes: Radiation hybrids for the D-genome of Chinese Spring and *Aegilops tauschii* accession AL8/78.

Ajay Kumar ¹, Vijay K. Tiwari ², Thomas Drader ³, Kristin Simons ¹, Muhammad J. Iqbal ¹, Monika M. de Jimenez ¹, Filippo M. Bassi ¹, Farhad Ghavami ¹, Omar Al-Azzam ⁴, Lingli Dong ³, Yi Wang ³, Ming-Cheng Luo ⁵, Yong Q. Gu ³, Anne Denton ⁴, Gerard Lazo ³, Jeffrey M. Leonard ², Oscar Riera-izarazu ², and Shahryar F. Kianian ¹.

¹ Department of Plant Sciences, North Dakota State University, Fargo, ND 58105, USA; ² Department of Crop and Soil Science, Oregon State University, Corvallis, OR 97331, USA; ³ USDA–ARS, Western Regional Research Center, Albany, CA 94710, USA; ⁴ Department of Computer Sciences, North Dakota State University, Fargo, ND 58105, USA; and ⁵ Department of Plant Sciences, University of California, Davis, CA 95616, USA.

Due to the lack of recombination in certain regions of the chromosomes, genetic mapping alone is not sufficient to develop a high quality marker scaffold for sequence ready physical maps. Radiation hybrid (RH) mapping, which uses radiation induced chromosomal breaks to identify physical marker linkages, has proven to be a valuable tool for generating physical maps for complete genome assembly in animal systems. In order to construct high-resolution, RH-based physical maps of the wheat D-genome chromosomes that integrate the BAC based contigs, we developed D-Genome Radiation Hybrid (DGRH1) panels for the wheat D-genome donor *Aegilops tauschii* accession AL8/78 (1,510 DGRH1) and the reference hexaploid wheat cultivar Chinese Spring (2,565 DGRH1). Characterization of these DGRH1s with a set of molecular markers evenly spanning the entire genome indicates a homogenous marker loss (2.1%) across the chromosomes. Four different marker systems used in this study, mostly detected unique deletions suggesting that a combination