Poster 55. Construction of low-coverage, non-gridded BAC libraries for isolation of a genomic region involved in resistance to the stem rust in Sinvalocho wheat variety.

William Marande [1], Sonia Vautrin [1], Arnaud Bellec [1], Gensèric Beydon [1], Elisa Prat [1], Maria-Fernanda Pergolesi [2], Maria-José Dieguez [2], and Hélène Bergès [1].

[1] INRA/CNRGV, Chemin de Borde Rouge, Castanet-Tolosan, France, and [2] INTA, Instituto de Genética Ewald A. Favret, Buenos Aires, Argentina.

Plant genomes are complexes regarding many aspects, their large size that often reach gigabases, their polyploidy due to their multiple hybrid origins and the high percentage of repetitive elements that may represent the majority of the genome size. Next-generation DNA sequencing (NGS) technologies have revolutionized the genomic research in several domains, as it offers the capacity to obtain large amount of sequences in a short time. However, this approach is not sufficient to decipher the high complexity of plant genomes because of their size (the wheat genome is 40 times the rice genome, 17Gb), their level of polyploidy (the wheat genome is hexaploïd) and their high percentage in transposable elements (80 % in the wheat genome). Bacterial Artificial Chromosome (BAC) libraries are still invaluable tools for plant genome analysis. They allow physical mapping, map-based cloning, and sequencing projects. They facilitate gene cloning and contribute to rapidly identify homologous genes in polyploid species. During the last decade, BAC libraries from many plant species have been constructed world wide.

The French Plant Genomic Resource Center (Centre National de Ressources Génomiques Végétales–CNRGV) is in charge of more than 9 million unique BAC samples belonging to more than 100 model and crop plant genomic libraries (http://cnrgv.toulouse.inra.fr/en/Library) and is a leader in the development of approaches involving BAC libraries to study plant genomes. In order to focus directly on a genomic region of interest in specific genotypes and rapidly isolate BAC clones spanning a genomic region, we have developed a non-gridded BAC library approach. This method avoids time and cost expensive steps of BAC clones re-arraying and screening, and may give an efficient access to sequence diversity among plant cultivars in specific genomic region. This strategy has proven to be an efficient way to identify and sequence region of interest and will be illustrated with the characterization of the region of wheat variety Sinvalocho responsible for the resistance to the stem rust disease.

Poster 56. Simultaneous transfer, genomic localization and introgression of genes for resistance to stem rust race Ug99 from the wheat D-genome progenitor species, Aegilops tauschii, to cultivated wheat, Triticum aestivum.

Eric Olson [1], Jesse Poland [2], Robert L. Bowden [2], Bernd Friebe [1], and Bikram S. Gill [1]. [1] Department of Plant Pathology, Wheat Genetics and Genomics Resource Center and the [2] USDA–ARS Hard Winter Wheat Genetics Research Unit, Kansas State University, Manhattan, KS 66506-5502, USA.

The diploid, D-genome species, *Aegilops tauschii*, has provided numerous genes for resistance to fungal pathogens and insect pests of hexaploid wheat, *Triticum aestivum*. Wheat production is currently threatened by widely virulent races of the wheat stem rust fungus, *Puccinia graminis* f.sp. *tritici*, that are part of the Ug99 lineage. Screening of a large set of *Ae. tauschii* germplasm for resistance to TTKSK (Ug99) identified potentially novel sources of resistance.

To expedite TTKSK resistance from *Ae. tauschii*, we established a direct-hybridization protocol that integrates gene transfer, mapping and introgression into one process. Direct crossing of *Ae. tauschii* accessions with an elite wheat breeding line combines the steps of gene transfer and introgression while development of mapping populations during gene transfer enables the identification of closely linked markers. Direct crosses were made using TTKSK-resistant *Ae. tauschii* (2n=2x=14,DD) accessions as a male and a stem rust susceptible *T. aestivum* (2n=6x=42, AABBDD) breeding line as a female. Embryo rescue enabled recovery of F_1 (2n=28, ABDD) plants that were backcrossed as females to the hexaploid recurrent parent. Stem rust-resistant BC_1F_1 plants from each *Ae. tauschii* donor source were used as males to generate BC_2F_1 mapping populations. A bulked-segregant analysis of BC_2F_1 genotypes at 70 SSR loci across the D genome identified the chromosome locations of stem rust resistance genes and facilitated genetic mapping. Using this approach, three genes for resistance to TTKSK, located on chromosomes 1DS, 6DS, and 7DS, have been transferred from *Ae. tauschii* to *T. aestivum* and are present in genetic backgrounds suitable for stem rust resistance breeding.