PROGRESS IN THE REALIZATION OF PHYSICAL MAP FOR WHEAT CHROMOSOME 5A


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An integrated physical and genetic map represent a prerequisite for DNA sequence assembly of wheat chromosome 5A. 44,744 BAC clones for 5AS and 51,072 BAC clones for 5AL, were fingerprinted using Snaphot method and the useful fingerprints were assembled into contigs using both FPC and LTC softwares. Two minimal tiling paths (MTP), were defined: FPC-MTP consisting of 4,201 for 5AS and 6,560 for 5AL overlapping BAC clones and LTC-MTP made of 5,412 for 5AS and 8,709 for 5AL overlapping BACs. Both MTPs were organized in three dimensional (3D) pools, to increase the efficiency of further anchoring, that was performed using two different strategies.

The anchoring of FPC-MTP was done through screening of the 3D pools with molecular markers mapped on four segregating populations. The markers employed were ESTs (expressed sequence tags), COS (conserved ortholog set), TE junction (transposable elements) and SSRs (simple sequence repeat), these latter obtained either from literature or by in silico screening of 454-derived 2x coverage of 5AS flow sorted DNA. The physical position of these markers has been also assigned to 5A deletion bins.

To anchor the LTC-MTP an Agilent 15K specific array was produced using probes derived from the 5A Genome Zipper, all available ESTs mapped on 5A and all markers already genetically mapped on this chromosome. The information deriving from both anchoring will be merged, thanks to the partial overlapping between the two MTPs. So far we detected for 5AS 121 markers positive
for at least one BAC, and 309 contigs anchored by at least one marker, representing 32.6% of the assembly, while for 5AL we anchored 96 contigs (49 markers) representing 4.5 of the assembly.

A chromosome 5A radiation-hybrid panel has been produced and will be characterized using TE-based markers derived from the 5000 BAC-ends of BACs belonging to the MTP.