

## FLUORESCENT BAC-FINGERPRINTING TECHNOLOGY TO CONSTRUCT CHROMOSOME-SPECIFIC PHYSICAL MAPS OF WHEAT

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### *Triticum aestivum*, fluorescent fingerprinting, physical map

*Triticeae* are the main cereal crops in Europe. For many years the size and complexity of the wheat, barley and rye genomes have hampered the development of genomics and its application to produce *Triticeae* crops with improved composition and characteristics. Recently, however, new and more efficient scientific capabilities and resources have been developed that allows robust genomic programs to be established for the *Triticeae*.

The EU-FP7 project *TriticeaeGenome* is designed to achieve significant progresses in *Triticeae* genomics and support efficient breeding of improved varieties for the European agriculture.

In the framework of this project, the Institute of Applied Genomics (IGA), is committed to build physical maps of three chromosomes of *Triticum aestivum* (1A, 1B, 3D), starting from chromosome-arm specific BAC libraries built from Dr Dolezel group in Olomouc (Czech Republic) and using a modified version of the High Informative Content Fingerprinting Technology developed by Luo *et al.* (Genomics 2003). In particular six chromosome-arm specific BAC libraries will be fingerprinted for a total number of 400,000 clones correspondent to a 15x coverage per chromosome.

BAC DNAs will be isolated, simultaneously digested with 5 restriction endonucleases, and electrophoresed on a capillary automated sequencer after 4 fluorescent dye labeling. In order to reduce costs and increase throughput, all the phases have been modified with respect to the protocol already utilized at IGA to construct other physical maps (i.e. grapevine).

Here these modifications to the fluorescent BAC-fingerprinting procedure will be presented.