**Oral Communication Abstract - 2.11** 

## WHEAT CHROMOSOMES FLOW SORTING: DIVIDING A COMPLEX GENOME INTO SUB-GENOMIC SPECIFIC BAC LIBRARIES

S. LUCRETTI\*, J. DOLEZEL\*\*

\*) Plant Genetics and Genomics Section, UTS BIOTEC, ENEA Casaccia Research Centre, Via Anguillarese 301, 00060 Roma, Italy – lucretti@casaccia.enea.it
\*\*) Laboratory of Molecular Cytogenetics and Cytometry, Institute of Experimental Botany, Sokolovská 6, CZ-77200 Olomouc, Czech Republic

## Triticum aestivum, Triticum durum, flow cytometry, genome sequencing

Wheat, together with rice and maize, provides more than 60% of the calories for the world diet. Bread wheat is an allohexaploid (2n=6X=42) consisting of three groups of homoeologous chromosomes belonging to the A, B, and D genomes. Sequencing the large wheat genome (17Gb, 5 times that of the human genome) represents a challenging endeavor. Even at reducing costs, the amount of founds required for a whole genome sequencing exceeds several hundreds of millions of Euros.

A large number of viable wheat aneuploid lines were developed for all chromosomes including a series of chromosome-arm aneuploids: monotelosomics, ditelosomics, tritelosomics and iso-chromosomics (Sears and Sears 1978). These genotypes are of most use for chromosome isolation and flow sorting, thus allowing chromosome discrimination and identification on the basis of a different DNA content. Dissecting the wheat genome into single chromosomes and chromosome arms may represent a promising approach that could greatly simplify its analysis, also knowing that most wheat genes are clustered in specific "gene reach islands" on chromosomes.

Recently, the possibility of preparing a high quality BAC library from flow-sorted wheat chromosomes was demonstrated and a chromosome 3B-specific BAC library was constructed (Safar et al, 2004). The work for cloning the short arm of chromosome 1B from hexaploid wheat has also been finished (Janda et al., in preparation) as well as the complete flow karyotyping for durum wheat (Kubaláková et al., 2005).

The flow sorting approach strongly suggest the possibility for an international initiative for physical mapping and sequencing of wheat genome. This endeavour could be facilitate by subdividing the whole genome into smaller and well defined subchromosomal entities (chromosome arms) which can be shared among partecipants, reducing costs while keeping the aim of the work.

Having the gene reach islands on chromosomes arms, and the complete genome sequence of bread wheat further, it will accelerate the improvement of this important crop, yielding the greatest rewards for economic development and global food security.

Part of this work was funded by the Italian Ministry for Agriculture Politics and Forestry, FRUMISIS project.