Proceedings of the 52nd Italian Society of Agricultural Genetics Annual Congress
Padova, Italy – 14/17 September, 2008
ISBN **978-88-900622-8-5**

Poster Abstract – D.01

CHARACTERIZATION OF EST-DERIVED SSR OBTAINED FROM A cDNA TOTIPOTENT LIBRARY OF DURUM WHEAT

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EST-SSR, wheat, microsatellites, molecular markers

Molecular markers are widely used in crop genetics and breeding. Genetic linkage, detection of quantitative trait loci (QTLs), positional cloning, and marker-assisted selection (MAS) are among the main applications. Genomic microsatellites have attracted relatively more attention because of their abundance in plants genome, reproducibility, high level of polymorphism, and codominant inheritance. Recently, due to the availability of enormous data for expressed sequence tags (ESTs), more emphasis has been given to EST-derived SSRs. They belong to the transcribed regions of DNA and have a higher rate of transferability across species than genomic SSR markers.

A collection of 10,000 ESTs deriving from a "totipotent" cDNA library constructed in durum wheat variety Ofanto (Patent n. WO2005003344) were screened for the presence of microsatellites.

One hundred forty out of these EST-SSRs were characterized in eleven durum wheat cultivars (Ciccio, Svevo, Latino, Primadur, Messapia, Creso, Pedroso, Ofanto, Cappelli, Orlù, Cosmodur) and in the *Triticum turgidum* var. *dicoccum* accession MG4343, parents of several mapping populations. Markers were opportunely chosen among di- and tri-nucleotide microsatellites in order to study relationships between number of repeat unit, type of motifs and level of markers polymorphisms. Of the 140 primer set tested, 85% amplified PCR products successfully and the other 15% failed to amplify any product. Multiple discrete PCR products were observed among both di- and trinucleotide EST-SSR markers including bands of expected and unexpected size. Differences between the expected and the observed size of the amplification products were observed. The data reported in the present work indicated the presence of a significant relationship between motif sequence types and polymorphism. The mean value of polymorphism was 35%. Polymorphism was calculated as number of primers that gave at least two alleles among the 12 genotypes analysed on the total number of primers amplifying PCR products. A set of Chinese Spring nullisomic and ditelosomic lines was also used in order to map markers on chromosomes.