Proceedings of the XLIX Italian Society of Agricultural Genetics Annual Congress
Potenza, Italy – 12/15 September, 2005
ISBN **88-900622-6-6**

Poster Abstract – C.09

CHARACTERIZATION OF DI- AND TRINUCLEOTIDE SSR MOTIFS IN WHEAT

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molecular markers, EST-SSR, polimorphic information content(PIC), wheat

Over the past decade microsatellites have attracted considerable attention of researchers. Microsatellite represent a valid alternative marker system, because of their abundance in plants genome, high level of polymorphism, and could be easily detected as PCR-based molecular markers on polyacrylamide or high resolution agarose gel. The advantages of SSRs include high information content, co-dominant inheritance, reproducibility and locus specificity. Recently a new source of SSR was represented by EST (expressed sequences tags). mRNA transcripts contain repeat motifs and actually the abundance of microsatellites in the expressed sequences tags of many species makes this markers very interesting because of a possible role in gene expression or function.

The aim of the present paper were to analyze EST-SSR variability in wheat and to investigate the relationships between type and number of repeat units and level of microsatellite polymorphism. 242 new EST-SSR available in public database (http//wheat.pw.usda.gov) were characterized in eight durum wheat cultivars (Svevo, Ciccio, Primadur, Duilio, Meridiano, Claudio, Latino, Messapia) three accession of *Triticum turgidum* var. *dicoccoides* (MG5323, MG4343, MG29896) and in the bread wheat cultivar Chinese Spring. 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 242 primer set tested, 80% produced one or two discrete PCR products. Markers based on di-nucleotide microsatellites were highly polymorphic in the 12 wheat genotype tested, approximately 53% of tri-nucleotide SSR were polymorphic compared to 73% of di-nucleotide SSR, with a average of 3.1 alleles for di-nucleotide SSR end 2.0 alleles for tri-nucleotide SSR. In conclusion 242 new EST-SSR were well-characterized and molecular analysis indicated dinucleotide SSR more powerful in the searching of polymorphisms.