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Poster Abstract – A.54

MAPPING OF NEW EST-DERIVED SSR ON 6A AND 6B CHROMOSOMES OF WHEAT

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The level of molecular polymorphism in cultivated hexaploid and tetraploid wheats was found to be low as compared to many other species. Use of molecular markers in genome analysis, the systematic mapping of agricultural important traits, and marker-assisted selection have been greatly advanced by the development of reliable PCR-based markers, such as amplified fragment length polymorphism (AFLP) and microsatellite o simple sequence repeat (SSR). Over the past decade microsatellites have attracted considerable attention of researchers. The overall frequency of microsatellites among species was found inversely related to genome size and to the proportion of repetitive DNA but remained constant in the transcribed portion of the genomes. Bioinformatic analysis indicated that the frequency of microsatellites was significantly higher in ESTs than in genomic DNA across all species. At present over three million sequences from approximately 200 plant species have been deposited in the publicly available plant expressed sequence tag databases. Many of the ESTs have been sequenced as an alternative to complete genome sequencing and this creates a formidable resource for microsatellite marker development. The objectives of this study were to construct a high density EST chromosome map of wheat chromosome group 6 to determine the distribution of ESTs, examine patterns of duplication and investigate the putative function. A total of 23 new EST-derived SSRs were genetically mapped on chromosome 6A and 6B in a RIL mapping population developed by crossing two durum wheat cultivars (Ciccio and Svevo). Two gene rich islands flanked by relatively gene-poor regions on both the short arms of chromosome 6A and 6B were discovered. Three times more loci were mapped on the short arms than on the long arms. A higher number of EST-SSRs, detecting multiple loci mapped on the same chromosome was found on chromosome 6B. The co-localization of separate PCR fragments detected by one couple of primer to the same chromosome region could be due to duplication of genetic material. Good colinearity was observed among the two homoeologous chromosomes.