MICROSATELLITE MARKERS COMPUTATIONAL ANALYSIS IN WHEAT FROM “TOTIPOTENT” cDNA LIBRARY

D’ONOFRIO O., CIFARELLI R. A., MANGO T., LAURIA G., CELLINI F.

Metapontum Agrobios S.S. Jonica 106, Km 448.2, 75010 Metaponto (Italy)

microsatellite, EST - SSRs, cDNA, durum wheat

Simple sequence repeats (SSRs) have become important molecular markers for many applications: genome mapping and characterization, phenotype mapping, marker assisted selection of crop plants and diversity studies.

The exponential growth of wheat published gene sequences along with the high cost of developing plant microsatellite libraries, is facilitating the “in silico” search of microsatellite motifs.

The discovery of SSR markers in ESTs (expressed sequence tags) provided the opportunity to develop microsatellites by the data mining of ESTs databases. This specific approach was first attempted in rice (Miyao et al., 1996) and has subsequently been applied to many other crops.

Nearly 630 SSRs were identified among 9,000 ESTs belonging to a “totipotent” cDNA library (patent n. WO2005003344) of durum wheat (Triticum Turgidum Desf. cv Ofanto).

Among all ESTs from the database, 6.76% contained the SSRs. This is equivalent to 1 SSR per 6.96 kb EST sequence. About 18% of the SSRs were mononucleotide, 26% were dinucleotides, 52% were trinucleotides, and the remaining approximately 4% consisted of tetra-, penta-, and hexanucleotides.

Among the identified SSRs, (CCG/CGG)n was the most frequent (19.87%) followed by (AG/CT)n at 15.58%, (A/T)n at 15.42%, and (AC/GT)n at 7.63%.

PCR primers are being designed and used to search for polymorphic variants on different wheat genotypes.