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Poster Abstract – D.07

EST-SSR MARKERS DEVELOPMENT FOR MAPPING AND PHYLOGENY STUDIES IN EGGPLANT

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Eggplant (*Solanum melongena* L.) is a member of the *Solanaceae* family, but unlike most of the solanaceous crop species, it is endemic to the Old, not the New World. In spite of its widespread cultivation, and its nutritional and economic importance, its genome has not as yet been extensively investigated. Few analyses have been carried out to determine the genetic diversity of eggplant at the DNA level, and linkage relationships have not yet been well characterised. As for the other *Solanaceae* crop species (potato, tomato and pepper), the level of intra-specific polymorphism appears to be rather limited, thus it is important that an effort is made to develop more informative DNA markers to make progress in understanding the genetics of eggplant and to advance its breeding. The aim of the present work was to develop and characterize a set of functional microsatellite (SSR) markers via an *in silico* analysis of publicly available DNA sequences, and to evaluate their transferability among other solanaceous species.

A computer search of 3,357 sequences from the *Solanaceae* Genomics Network database (SGN; http://www.sgn.cornell.edu) and EMBL Nucleotide Sequence Database (http://www.ebi.ac.uk/embl), was performed using the Sequence Retrieval System (SRS6, http://srs.ebi.ac.uk/). In order to obtain non-redundant sequences containing SSRs, a cluster analysis was performed; the contigs obtained were carefully evaluated and redundancies were removed. The non-redundant sequence pool contained 1,864 sequences corresponding to approximately 740 Kb. Within these, 64 sequences contained one or more SSRs (including 20 mono-, 11 di-, 36 tri-, one tetra- and two hexanucleotide motifs). Primer pairs could be designed for 50 SSR-containing sequences, the remaining contained either too little DNA sequence flanking the microsatellite or the sequences were inappropriate for primer modelling. Thirty-nine EST-SSR were functional, and were then applied to a panel of 44 accessions, made up from 38 cultivated eggplant varieties, breeding lines and rootstocks, and six related wild *Solanum* species: *S. viarum*, *S. sodomaeum*, *S. sisymbrifolium*, *S. torvum*, *S. aethiopicum* and *S. integrifolium*

The usefulness of the SSR assays for diversity analysis and taxonomic discrimination was demonstrated by constructing a phylogeny based on SSR polymorphisms, which was in good agreement with prior taxonomic classification based on both genomic and plastidial markers. Most EST-SSRs were also functional when tested with templates from tomato, pepper and potato. As a results of BLASTN analyses, several eggplant SSRs were found to have homologous counterparts in the phylogenetically related species, which carry microsatellite motifs in the same position.

Since EST-SSRs lie within expressed sequences, they have the potential to serve as perfect markers for genes determining variation in phenotype. Their high level of transferability to other *Solanaceae* species can be used to provide anchoring points for the integration of genetic maps across species.