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.39

TY1-*COPIA* RETROTRANSPOSON-BASED S-SAP MARKER DEVELOPMENT IN *CYNARA CARDUNCULUS* L.

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retrotransposons, S-SAP, globe artichoke, wild and cultivated cardoon

Long terminal repeat (LTR) retrotransposons are a class of mobile genetic elements that have been harnessed for the development of molecular markers in plants. One of the most popular and applied system to exploit the distribution of the LTR retrotransposon is the S-SAP technique. The only disadvantage of the S-SAP markers is the need to acquire a retrotransposon LTR sequence from a given species. As LTRs do not contain any conserved motifs, to isolate the sequence information it is necessary to perform an amplification between a conserved region in the RNAseH gene and a restriction site in the adjacent LTR sequence or flanking genomic DNA

Recently, we developed a transposons display assay based on a low copy number LTR-retrotransposon (CYRE-39) in *Cynara cardunculus* L; the species includes wild cardoon [var. *sylvestris* (Lamk) Fiori, cultivated cardoon [var. *altilis* (DC)] and globe artichoke (var. *scolymus* L.). The latter represents an important component of the European agricultural economy, crop production being in excess of one million tons and 100,000 ha in cultivation.

Here we report on the isolation and development of S-SAP assay for the analysis of distribution of high copy retro-elements in *C. cardunculus* . We applied a modified protocol derived from the one previously developed by Pearce and co-workers (1999; Plant Journal 19: 711-717). We successfully isolated three sequences containing LTR and RNAseH specific domains. They were named CYRE-5, CYRE-10 and CYRE-13; two primers CYRE-5for and CYRE-13for were derived and used for S-SAP analysis performed on 20 artichoke accessions, one cultivated and one wild cardoon. Six primer combination were applied and 124 polymorphic bands obtained with an average number of 20.6.

S-SAP data were compared with the ones obtained by applying 9 AFLP primer pairs, which originated 256 polymorphic bands (28.4 on average). Cluster analysis derived from the two marker systems showed congruent results. The S-SAP assay developed on CYRE-5 and CYRE-13 proved to be effective for the analysis of retrotransposon-based DNA polymorphisms in *C. cardunculus;* our ongoing research is addressed at positioning CYRE markers in a molecular genetic map of the species which is under construction.