Proceedings of the XLVIII Italian Society of Agricultural Genetics – SIFV-SIGA Joint Meeting
Lecce, Italy – 15/18 September, 2004
ISBN **88-900622-5-8**

Poster Abstract - F.68

DETECTION OF DNA POLYMORPHISM IN THE *POPULUS* GENUS BY INTRON ANALYSIS OF CATALASE GENES

S. CAPARRINI*, R. VELASCO**, M.L. RACCHI*, A. CAMUSSI*

*) Department of Agriculture Biotechnology - University of Florence, P.le delle Cascine 24, 50144 Firenze
**) Istituto Agrario San Michele All'Adige, Via Mach 1, 38010 S. Michele a/A (TN)

intron, clones identification, Populus, SSCP

The genus *Populus* contains many economically important species and hybrids. A fundamental problem confronting poplar breeders is the lack of knowledge of genetic constitution, relationships and identification of clones/cultivars. Conventional clonal identification system, based on combinations of morphological and phenological traits, represents a difficult, ambiguous, time consuming and subjective method. Recent progress in molecular biology has generated new analytical tools that are well suited for taxonomic and genetic investigations. A strategy to develop DNA markers is to design PCR primers targeting specific gene regions showing DNA variation. Because of less selection pressure, intron DNA sequences are potentially most polymorph than coding sequences and, therefore, it may be possible to exploit the information's of genomic-sequence designing PCR primers flanking intron regions with high specificity.

Polymorphism among introns within plant species for several genes have been detected, catalase genes in rice are an example In this study, we report the intron-exon structure of two poplar catalase genes and the potential of polymorph sequences of catalase introns as markers.

Using PCR approaches, two catalase genes (*Cat1* and *Cat2*) were identified and characterized in *P. deltoides*. Both genes contain seven introns in conserved positions. PCR-RFLP (restriction fragment length polymorphism) and SSCP (single-strand conformational polymorphism) markers were developed for *Cat1* and *Cat2* by designing specific primers flanking introns to investigate 12 species and 24 clones of 3 species. The evolutionary relationships among *Populus* species were investigated by sequencing of a *Cat2* gene fragment.

Four gene regions (two of *Cat1* and two of *Cat2*), among the analysed species and clones, revealed to be polymorph. SSCP markers show a greater ability than PCR-RFLP for detecting DNA polymorphism in intraspecific variants of the poplar *Cat1* and *Cat2* genes. The results indicate that catalase introns may be an excellent source of hypervariable markers in poplar.