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Poster Abstract - C.65

SSCP POLYMORPHISMS ANALYSES OF CATALASE GENE INTRONS FOR CLONAL IDENTIFICATION IN POPLAR

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Conventional clonal identification system, based on combination of morphological and phenological traits, represents a difficult, time consuming and subjective method. Considering the importance of varietal identification in poplar and the necessity to have certificated material to trade, the aim of this work is to develop new molecular markers simple and inexpensive for clonal identification for the breeding and genetic resource management programs.

Preliminary studies, performed in our laboratory, have allowed to develop SSCP (single-strand conformational polymorphism) markers for two poplar catalase genes of *P. deltoides* (*Cat1* and *Cat2*) by designing specific primers flanking introns. Four primer pairs have been selected: two primer pairs (Cat1-A and Cat1-B markers) have been designed based on *Cat1* gene coding sequence spanning intron II and introns V-VI-VII respectively. Two other primer pairs (Cat2-C and Cat2-D markers) have been designed based on *Cat2* gene coding sequence spanning introns II-III and IV-V respectively. In this study, the suitability of developed SSCP markers have been tested by differentiating 96 poplar commercially important clones belonging to *P. alba, P. deltoides, P. nigra, P. trichocarpa* species and largely to *P. x canadensis.*

The results emphasized that SSCP analysis was efficient to detect DNA polymorphism. It is a sensitive analytical tool for interspecific and intraspecific identification. Particularly it could be useful to analyze clones before their registration to RNCF (National Register of Forest Clones) to check material novelty. This type of analysis based on exclusion by similarity with registered clones could represent an economic and temporal saving because it avoids the long valuation procedure for the clones that have no novelty traits.