

SSCP POLYMORPHISMS OF GENE INTRONS AND MORPHOLOGICAL TRAITS: NOVEL PROCEDURES FOR CLONAL IDENTIFICATION IN POPLAR

A. TURCHI*, S. CAPARRINI*, A. GIORCELLI**, F. PICCO**, M.L. RACCHI*, A. CAMUSSI*

*) Department of Agricultural Biotechnology, Genetics Unit, University of Florence,
Via Maragliano 77 50144 Florence, Italy – alessandro.camussi@unifi.it

***) Istituto di sperimentazione per la Pioppicoltura- CRA, Casale Monferrato, Italy

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The definition of genetic relationships and identity is important for germplasm resources management, variety identification and registration to protect breeders, growers and industry.

Molecular markers may play a major role to achieve these objectives.

Most of the commercially relevant cultivars in Poplar are clones and many identification procedures based on molecular markers are in progress. The use of AFLP and SSR markers is recently applied by Fossati et al. (2005) to classify a collection of 66 clones. In our laboratory SSCP (single-stand conformational polymorphism) markers were developed by designing specific primers flanking introns of two specific genes of the Catalase family. These SSCP marker have been tested on a sample of more than 100 poplar clones representative of the germplasm collection including some experimental clones of known genetic relationships.

The results show that SSCP intron markers have a very high efficiency, allowing to differentiate most of the clones defined as identical in previous reports.

Though molecular marker are considered a powerful tool for clonal identification, the UPOV convention still requires a detailed description of 64 morphological and phenological traits to allow to a novel clone to access to the DUS (Distinction-Uniformity-Stability) tests and, consequently, the inscription to National and International Registers of forest clones. In fact, neutral molecular markers cannot predict from the level of genetic identity the effective amount of diversity when many complex morphological traits are considered.

We developed a novel approach for the joint analysis of molecular diversity and morphological variability by means of Modified Location Models (MLM). Without inferring any causal relationship between SSCP polymorphism and the morphological characteristics of the clones, the procedure allows to evidence the degree of morphological differentiation existing within clusters of clones with a reduced level of marker based diversity.

The results are discussed in the view of possible integrate strategies to simplify registration procedures in poplar breeding.

Fossati et.al. (2005) Tree Genetics & Genomes 1: 11-19

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