ISSR ANALYSIS OF GENETIC POLYMORPHISM AMONG CULTIVATED AND WILD NICOTIANA SPECIES

L. DEL PIANO, L. BARBATO, M. ABET, C. SORRENTINO, E. COZZOLINO, A. CUCINIELLO, M. SICIGNANO

Istituto Sperimentale per il Tabacco, Via P. Vitiello n.108, 84018 Scafati (SA), Italy
istgenetica@uniserv.uniplan.it

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The Inter Simple Sequence Repeat (ISSR) is a PCR based technique in which DNA fragments located between adjacent, oppositely oriented microsatellites (Simple Sequence Repeats, SSR), are amplified by Polymerase Chain Reaction (PCR) using primers that are anchored at 5’ or 3’ end of a repeat region and extend into the flanking region.

The aim of this paper was to value the potential of ISSR technique to determine the degree of intra- and inter-specific genetic variation in the genus Nicotiana.

Genomic DNA of twenty-four tobacco lines (Nicotiana tabacum L.) and thirty-six Nicotiana species, belonging to almost all the sections of the genus, was extracted and amplified utilizing 10 different primers (14-22 bp). PCR products were resolved on agarose gel, stained with ethidium bromide and visualized by UV transilluminator. The electrophoretic banding patterns were recorded and analyzed by utilizing an image analysis system. The number of markers generated per primer ranged from 15 to 30, and the dimensions from 200 and 2500 bp.

The amount of genetic polymorphism present among N. tabacum lines was limited as evidenced by the high degree of similarity in the ISSR profiles of different tobacco examined. A greater amount of polymorphism was revealed among wild Nicotiana species, as generally different band patterns were observed.

These results are consistent with our previous findings on genetic variability in Nicotiana tabacum and Nicotiana species by RAPD analysis confirming the high genetic similarity among cultivated tobacco varieties.