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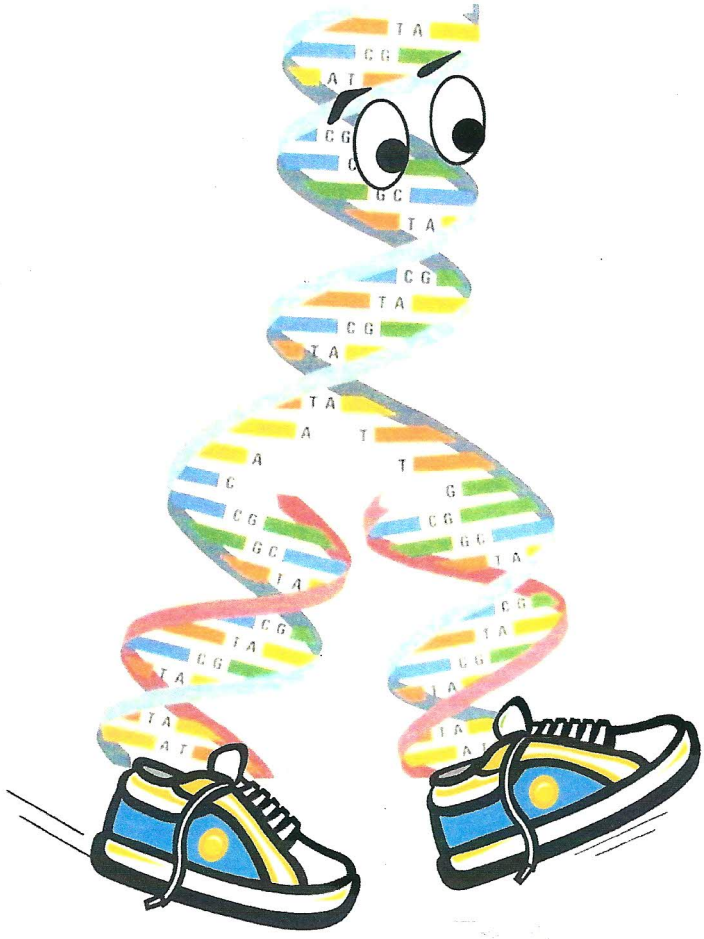

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RETROTRANSPOSONS AS SOURCES OF *QUERCUS SUBER* GENETIC VARIABILITIES

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Transposable elements (TEs) are present in multi-copy numbers that are integrated into genomes (including those of plants), ranging from just a few elements to thousands per genome and representing a major fraction of the DNA in some species of plants and animals. They are DNA segments with the ability to move within genomes, thereby providing new genetic variations as well as tremendous effects on genome structures and gene functions. However, TEs have been classified into two major classes: class I (or retroelements, RELs) and class II (or transposons, Tns).

Class I TEs, also termed retrotransposons (RTns), being actively propagated themselves via reverse transcription of a RNA intermediate, may contain or not long terminal repeats (LTRs), and thus they are sub-classified into LTR RTns and non-LTR RTns, respectively. On the orher hand, the LTR RTns may be of either the gypsy-type or the copia-type, this depending to the gene order of the enzymes reverse transcriptase (RTase) , ribonuclease H (RNAse H) and integrase (Intase). Nevertheless, numerous LTR RTns have been discovered in all plant species so far studied, and recent work indicated that LTR RTn-related DNA sequences play a significant role in the organization and evolution of the complex plant genomes.

In this context, to understand the genetic and molecular basis of the Quercus suber phenotypic variabilities, total DNA extracts obtained from cork oaks have been amplified by the polymerase chain reaction (PCR), using three sets of primers, in order to detect the presence of RTns belonging to R (R1, R2 and R4) family, since this type of RTns has been reported to specifically insert into the the rDNA 26S genes.

A comparison of the electrophoretic profiles of the resulting PCR products has allowed the detection of i) genetic polymorphisms among the studied cork trees and ii), after DNA sequencing of some of those PCR products, new RTn sequences that, although partials, have been already deposited in GenBank database (accessions numbers AY428554, AY099465, and AF512588).