Abstract

Grapevine (*Vitis vinifera* L.) varieties are composed by clones originated from a unique plant propagated by vegetative multiplication. This process theoretically ensure the transmission of genetic information from mother to daughter's plants, but spontaneous mutations sometimes arise and can lead to the creation of new genotypes. Due to their ability to transpose, transposable elements are a source of mutation that causes genetic variability. To understand global mechanisms that participate to plant genome evolution during vegetative multiplication cycles, the main goal of this thesis is studying the structure and dynamics of grapevine retrotransposons.

When this work started, only three grapevine retrotransposons were described. Therefore, the first part of this work is based on the characterization of ten new families, which are different from the elements previously described in grapevine or in other plant genomes. This ten new families represent near 1,700 copies, from full-length to degenerated, representing altogether about 1.2% of the genome. Some of these copies were integrated in the grapevine genome during the last two million years. In a second part, the transcription level of grapevine retrotransposons is evaluated by complementary approaches. The results show that their transcription level is regulated in different organs under normal growing conditions, each family showing a specific transcription profile. Moreover, the expression of many retrotransposons in leaves is induced by wounding and pathogen infection.

The role of retrotransposons in grapevine genome evolution and in the genesis of intra-varietal diversity has not been established, but induction of expression of several families under stress conditions allow us to suppose that this elements might have participated to genome adaptation in response to environmental challenges and grapevine culture by man. Moreover, the characterization of new transposable families contributes to the development of molecular tools allowing the identification and distinction of grapevine clones.

Key words: *Vitis vinifera* L., genetic diversity, retrotransposon, mobile elements, stress, transcription, RT-PCR