

CHARACTERIZATION OF *S* ALLELES AND ESTABLISHMENT OF INCOMPATIBILITY GROUPS IN *Eriobotrya japonica* LINDL.

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Loquat (*Eriobotrya japonica* Lindl.) is an underutilized fruit tree species that is acquiring increasing importance in some areas of the world. Recently, crop intensification has resulted in a reduction of productivity in some regions. The main difficulty to overcome this problem is the scarce knowledge on the reproductive biology of this species. It has been previously shown that loquat has a pollen-pistil incompatibility system and that the behaviour of the pollen tube growth with inhibition in the style is typical of gametophytic self-incompatibility (GSI). GSI is controlled by a single polymorphic locus, *S*-locus, based in pistil RNases with multiple alleles. In order to study the incompatibility mechanism, degenerated primers have been used to identify RNases associated to self-incompatibility in loquat. The sequences of the primers were generated by comparing conserved sequences of *S*-RNases in several species of the Maloideae subfamily, to which loquat belongs. Loquat *S* genotypes were detected by fragment and PCR analysis and *S* alleles were cloned and sequenced. The nucleotide and deduced amino-acid sequences obtained were compared with sequences of other species of the Maloideae and the results obtained show that loquat sequences contained structural characteristics of Maloideae *S*-RNases. The good correspondence between microscopic studies of pollen tube growth in controlled crosses and the *S* genotypes identified in some cultivars have allowed to define the first incompatibility groups in loquat. Both inter-incompatibility between cultivars with the same *S* genotypes and inter-compatibility between groups with different allelic number have been observed. These results will contribute to the choice of the most appropriate pollinator cultivars providing an adequate orchard management of this species.