

S-RNase allele identification and incompatibility group assignment in apricot cultivars

S. Herrera¹, J. Rodrigo,¹ J.I. Hormaza², M. Herrero³ and J. Lora²

¹Unidad de Hortofruticultura, Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA), Instituto Agroalimentario de Aragón-IA2 (CITA-Universidad de Zaragoza), Avda. Montañana, 930, 50059 Zaragoza, Spain.

²Instituto de Hortofruticultura Subtropical y Mediterránea “La Mayora” (IHSM-UMA-CSIC), 29750 Algarrobo-Costa, Málaga, Spain;

³Pomology Department, Estación Experimental Aula Dei-CSIC, Av. Montañana, 1005, 50059 Zaragoza, Spain

Apricot (*Prunus armeniaca*) is a member of the Rosaceae originated in China. Most of the European apricot cultivars have been traditionally considered self-compatible (SC) although *S-RNase*-based-Gametophytic Self-Incompatibility (GSI), a common incompatibility mechanism found in the Rosaceae genetically determined by a locus (S) with multiple alleles, is common in the species. This locus encodes an allele-specific *S-RNase*, expressed in the style, which inhibits the growth of pollen tubes with the same S alleles. In the last years, an important renewal of plant material is taking place worldwide, with the introduction of new cultivars from different breeding programs. The use of self-incompatible (SI) cultivars as parental genotypes has resulted in an increasing number of SI new cultivars with unknown pollination requirements. In order to establish the incompatibility relationships among apricot cultivars, in this work we perform an *S-RNase* allele identification in a group of new cultivars from different breeding programs. The S-alleles of each cultivar were determined by PCR amplification of the *S-RNase* gene. The results allowed allocating the cultivars in their corresponding incompatibility groups, a highly valuable tool for fruit growers to design apricot orchards, and for breeders to choose parental genotypes in breeding programs.