

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

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Apricot (*Prunus armeniaca* L.) is a member of the Rosaceae originated in Asia. Most of the European apricot cultivars have been traditionally considered self-compatible (SC). 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) 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 cultivars from different breeding programs.



The S-alleles of each cultivar were determined by PCR amplification of the S-RNase gene by using the primers SRC-F/SRC-R that allow amplifying the first intron and identifying eight alleles. The primers Pru-C2/Pru-C4R were used to amplify the second intron of RNase in those alleles that showed similar size (S_1 and S_7 ; S_6 and S_9).

S-allele	SRc-F/SRc-R	Pru-C2/Pru-C4
S_1	407	2260
S_2	327	-
S_3	267	-
S_4	243	-
S_6	421	~1400
S_7	407	900
S_9	414	700
S_c	359	-

Some of the cultivars showed a fragment of 420 bp or 430 bp, which are close in size to the S_6 allele. To elucidate if these fragments correspond to S_6 or are different alleles, both S-alleles were cloned and sequenced and the real sequence resulted in 414 bp and 421 bp respectively.

The alignment of the 421 bp fragment in the NCBI database showed a 99% identity with allele S_{52} (KF951503). Moreover, the primers Pru-C2/Pru-C4 showed a PCR-fragment of around 1400 bp for allele S_6 and a 1386 bp for allele S_{52} strongly suggesting that S_6 and S_{52} are the same allele.

The 414 bp fragment did not show sequence similarity to any S-allele of *Prunus armeniaca*. The primers Pru-C2/Pru-C4, showed a PCR-fragment of around 700 bp. Its cloning, sequencing and alignment revealed a 99% identity with the S_9 allele.

The results allowed determining the S-genotype of 48 apricot cultivars

I.G.	S-genotype	Cultivars
I	S_1S_2	Goldrich, Hargrand
III	S_2S_6	ASF0401, Bergarouge, Moniqui
VIII	S_6S_9	ASF0405, ASF0402, Orangered ¹ , Stark Early Orange, Wonder Cot
XVIII	S_2S_3	Mayacot, Sun Glo
XIX	S_2S_9	Goldstrike, Magic Cot
XX	S_3S_9	Durobar, Flodea, Henderson, T sunami
XXI	S_7S_9	Goldbar
Self-compatible cultivars		ASF0404 (S_c), Bergecot (S_2S_c), Canino (S_2S_c), Charisma (S_7S_c), Faralia (S_6S_c), Flopria (S_9S_c), Kioto (S_c), Mitger (S_c), Paviot (S_2S_c), Pricia (S_3S_c), Soledane (S_c), Tadeo (S_c), Tom Cot (S_9S_c), Katy, (S_1S_2), Lorna ¹ (S_1S_2), Palsteyn ¹ (S_1S_2)
Unclassified		Aurora (S_9), Big Red (S_1), Early Queen (S_2), Golden Sweet (S_3), Harcot (S_4), JNP (S_9), Lilly Cot (S_3), Muñoz (S_2), Pandora (S_2), Perle Cot (S_9), Pinkcot (S_9), Veecot (S_2), Westley (S_2)

¹Cultivars in which S-RNase genotype reported herein differs from that reported in other studies.



The allele S_c was identified in 15 cultivars, which were assigned to the self-compatible group with other three cultivars previously described as self-compatible ('Katy', 'Lorna' and 'Palsteyn'). Although two alleles were identified in most cultivars, a unique allele was identified in 13 cultivars. The other 19 cultivars were assigned to 7 incompatibility groups. These results are valuable for the selection of parental genotypes in breeding programs and for an appropriate distribution of pollenizer cultivars in commercial orchards.

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