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# Expression of the $S_{fa}$ -allele in homozygote genotypes ( $S_{fa}S_{fi}$ ) indicates a mutation in the stylar part of the $S_f$ haplotype as origin of self-compatibility in almond

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**Abstract.** The  $S_f$  allele shows two different expressions: an active form ( $S_{fa}$ ) inducing self-incompatibility and an inactive form ( $S_{fi}$ ) inducing self-compatibility. Their interaction was studied in several hetero/homozygous genotypes ( $S_{fi}S_{fa}$ ) in order to establish if self-compatibility was dominant as previously suggested. The seedling genotype was determined by PCR amplification of genomic DNA with universal and specific primers and the phenotype by pollen tube growth. The results showed full self-incompatibility of the  $S_{fi}S_{fa}$  genotypes as a result of the recognition of any kind of  $S_f$  pollen ( $S_{fi}$  or  $S_{fa}$ ) by the style, where  $S_f$ -RNase was produced due to the presence of the  $S_{fa}$  allele. These results confirm the allelism of the  $S_f$  allele with the series of  $S$  alleles of self-incompatibility and that a mutation in the stylar part of the  $S_{fa}$  haplotype has led to the self-compatibility of the  $S_{fi}$  form. The recognition of the  $S_{fi}$  pollen by the  $S_{fa}$  style confirms that the presence of the  $S_{fi}$  haplotype does not ensure self-compatibility, and that in these hetero/homozygous genotypes the expression of  $S_{fa}$  is dominant over that of  $S_{fi}$ .

**Keywords.** *Prunus amygdalus* Batsch – Self-compatibility – Breeding –  $S_f$  allele – Allele expression – Allele recognition.

**L'expression de l'allèle  $S_{fa}$  dans les génotypes homozygotes  $S_{fi}S_{fa}$  indique une mutation dans la partie stylaire du haplotype  $S_f$  comme l'origine de l'auto-compatibilité chez l'amandier**

**Résumé.** L'allèle  $S_f$  montre deux formes d'expressions différentes: une forme active ( $S_{fa}$ ) qui confère l'auto-incompatibilité et une forme inactive ( $S_{fi}$ ) qui induit l'auto-compatibilité florale. Leur interaction a été étudiée chez quelques génotypes hétéro/homozygotes ( $S_{fi}S_{fa}$ ) pour établir si l'auto-compatibilité est dominante comme a été suggéré antérieurement. Le génotype des semis a été déterminé par l'amplification PCR de l'ADN génomique avec des amorces universelles et spécifiques et le phénotype a été évalué par l'étude de la croissance du tube pollinique dans le style. Les résultats ont montré que les génotypes  $S_{fi}S_{fa}$  sont complètement auto-incompatibles due à la reconnaissance des deux formes de pollen  $S_f$  ( $S_{fi}$  ou  $S_{fa}$ ) au niveau du style, où  $S_f$ -RNase est produite par la présence de l'allèle  $S_{fa}$ . Ces résultats confirment l'allelisme de l'allèle  $S_f$  avec la série d'allèles  $S$  de l'auto-incompatibilité florale chez l'amandier et indiquent qu'une mutation dans le style de l'haplotype  $S_{fa}$  a généré l'auto-compatibilité de la forme  $S_{fi}$ . La reconnaissance du pollen  $S_{fi}$  dans le style  $S_{fa}$  confirme que la présence du haplotype  $S_{fi}$  n'assure pas l'auto-compatibilité, et que l'expression du  $S_{fa}$  chez ces hétéro/homozygotes est dominante sur le  $S_{fi}$ .

**Mots-clés.** *Prunus amygdalus* Batsch – Auto-compatibilité – Amélioration –  $S_f$  allèle – Expression d'allèle – Reconnaissance d'allèle.

## I – Introduction

Self-compatibility (SC) has been considered a priority objective in almond (*Prunus amygdalus* Batsch) breeding (Socias i Company, 1990). After confirming that SC was a transmissible trait (Socias i Company and Felipe 1977) it was attributed to the presence of the  $S_f$  allele, allelic to the series of S alleles of self-incompatibility (SI) (Socias i Company 1984), being inherited as a Mendelian trait (Socias i Company and Felipe 1988). In almond, it was firstly established that SC is due to the lack of RNase activity of the  $S_f$  allele (Bošković *et al.*, 1999). However, Kodad *et al.* (2009; 2010) reported that three local Spanish cultivars with the  $S_f$  allele were self-incompatible (SI), denominating as  $S_{fa}$  the active form of the  $S_f$  allele, showing a SI expression, whereas the denomination  $S_{fi}$  has been suggested for the inactive  $S_f$  allele showing a SC expression (Fernández i Martí *et al.*, 2009). The two forms of the  $S_f$  allele are not only identical for the coding region sequence (C1 to C5) (Kodad *et al.*, 2009; Fernández i Martí *et al.*, 2009), but also at the alignment of their 5'-flanking regions, as shown by the construction of a fosmid library (Fernández i Martí 2010). Later Kodad *et al.* (2010) reported that some Spanish almond cultivars sharing similar S-genotype, including the  $S_{fa}$ -allele, are cross-incompatible. In almond, some cases of cross-incompatibility have been reported in combinations sharing identical S-genotypes (Bošković *et al.*, 2007; Fernández i Martí *et al.*, 2009; Socias i Company *et al.*, 2012). Thus, in this situation a question has arisen: what will be the expression of homozygote genotypes sharing the two forms of the  $S_f$ -allele? Consequently, our objective was to study the possible interaction between the two forms of the  $S_f$  allele when present in the same genotype.

## II – Materials and methods

Three almond cultivars with identical S-genotype were included as parents to obtain seedlings for analysis. 'Belona' and 'Soleta' (SC,  $S_{fi}S_{23}$ ) were used as female parents and crossed with 'Vivot' (SI,  $S_{fa}S_{23}$ ) pollen to obtain  $S_{fi}S_{fa}$  heterozygotes. The crosses were made in the spring of 2009, nuts were collected in the following fall, seeds were stratified and the germinated seedlings were placed in growing plots and later transferred to the open field for flowering.

Genomic DNA was extracted from leaves following the CTAB extraction method based on Doyle and Doyle (1987). The consensus primers AS11I (forward) and AmyC5R (reverse), designed from conserved coding regions flanking the second intron of almond S-RNases, were used, as well as specific primers for the identification of the  $S_{23}$ - and  $S_f$ -alleles. PCR products were separated in 1.5% (w/v) agarose gels. Band scoring was carried out using a standard 1 kbp DNA ladder (Invitrogen).

The phenotype of the seedlings was determined by pollen tube growth as described by Socias i Company *et al.* (2013), since this method has been shown to be an efficient method for SC evaluation (Socias i Company *et al.*, 2014). The pistils were rated according to the level where pollen tubes were observed as defined by Socias i Company *et al.* (2013). Finally, each genotype was classified according to the average rate of all the pistils observed, pooling the data of the two years of observation in order to obtain the SC classification for the genotype.

## III – Results and discussion

PCR amplification of genomic DNA of the progeny resulting from the two crosses studied was performed with specific primers to detect the presence of the  $S_{23}$  and  $S_f$  alleles as shown in Fig. 1. As expected, only two genotypes were observed in the offspring of the two crosses (Table 1). Only the 'Vivot' pollen carrying the  $S_{fa}$  allele could grow through the pistils of the 'Soleta and Belona' cultivars, despite the genetic identity of this  $S_{fa}$  allele with the  $S_{fi}$  allele of the pistils, reaching the ovule and accomplishing its fertilisation giving progeny with two possible combinations:  $S_{fi}S_{fa}$  and  $S_{23}S_{fa}$ .

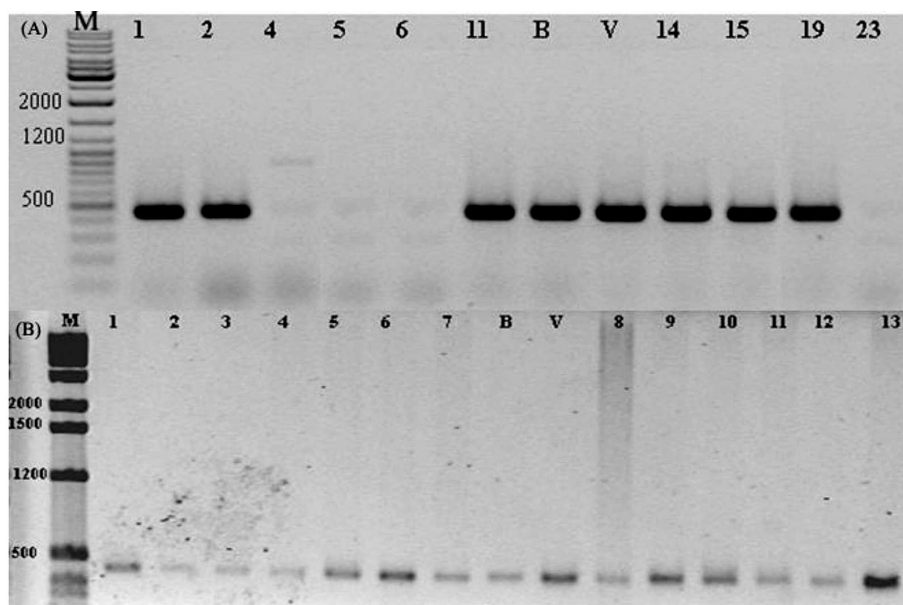


Fig. 1. Agarose gel showing S-allele fragments amplified with the *Sf*-specific primers (a) or with the *S*<sub>23</sub>-specific primers (b) of some genotypes from the family 'Belona' × 'Vivot', compared to 'Vivot' (V) and 'Belona' (B). Lanes M, 1 kbp marker ladder.

Table 1. Distribution of the *S* genotypes in the offspring of the two almond crosses studied, 'Belona' × 'Vivot' and 'Soleta' × 'Vivot'

Cross	Genotype		$\chi^2$	P
	<i>S<sub>fi</sub>S<sub>fa</sub></i>	<i>S<sub>23</sub>S<sub>fa</sub></i>		
'Belona' ( <i>S<sub>fi</sub>S<sub>23</sub></i> ) × 'Vivot' ( <i>S<sub>fa</sub>S<sub>23</sub></i> )	15	10	0.64	0.01
'Soleta' ( <i>S<sub>fi</sub>S<sub>23</sub></i> ) × 'Vivot' ( <i>S<sub>fa</sub>S<sub>23</sub></i> )	8	11	0.05	0.01
Total	23	21		

The results of pollen tube growth allowed the phenotypic characterisation of the seedlings. The seedlings of genotype *S<sub>fi</sub>S<sub>fa</sub>* were fully SI and a single one was rated as only SI. These results show that the presence of the *S<sub>fi</sub>* allele in these cases cannot be related to SC, but that the mechanisms of SI are fully active in this genotype. The homogeneity of results among all seedlings of *S<sub>fi</sub>S<sub>fa</sub>* genotype may explain the interaction between both forms of the *S<sub>f</sub>* allele. In previous studies it has been reported that the presence of the *S<sub>fa</sub>* allele in some local almond cultivars showed a self-incompatible phenotype (Kodad *et al.*, 2009; 2010; Fernández i Martí 2009) and cross-incompatibility when the two cultivars share the *S<sub>fa</sub>*-allele (Kodad *et al.*, 2010).

The full SI of the seedlings of *S<sub>fi</sub>S<sub>fa</sub>* genotype indicates that a complete recognition of both alleles takes place in the pistils of this genotype. Taking into account that the *S<sub>fi</sub>* allele does not code for any S-RNase and that the *S<sub>fa</sub>* allele codes for the *S<sub>f</sub>*-RNase (Kodad *et al.*, 2009), only a S-RNase may be present in the pistils controlling the compatibility of the incoming pollen. The incompatibility of the self-pollination of these seedlings is explained by the recognition by the *S<sub>f</sub>*-RNase of both kinds of pollen, those of *S<sub>fi</sub>* and of *S<sub>fa</sub>* genotypes. *S<sub>fi</sub>* pollen, characterized by SC, was able to grow in *S<sub>fi</sub>* pistils, but not in *S<sub>fa</sub>* pistils, where the RNase produced by the *S<sub>fa</sub>* pistils is able to recognize the *S<sub>fi</sub>* pollen, thus stopping its growth and resulting in an incompatible pollination (Fernández i Martí *et al.*, 2009). These obser-

variations, however, were in heterozygous  $S_f S_x$  genotypes, not in homozygous  $S_{fi} S_{fa}$  genotypes. Our results show that the inactivation induced by the  $S_{fi}$  genotype only takes place in the pistil part, avoiding the production of the  $S_f$ -RNase, whereas the pollen part remains completely active, as shown by the recognition of the  $S_{fi}$  pollen by the  $S_f$ -RNase, probably due to the full genetic identity of both forms. Consequently, in the  $S_{fi} S_{fa}$  genotypes, the presence of the  $S_{fi}$  allele is not a clue for SC, as generally accepted. These results confirm the hypothesis that  $S_f$  is allelic to the S alleles of SI (Socias i Company 1984) and suggest that  $S_{fa}$  is probably the original allele, being another allele of the S locus in a predominantly SI species such as almond. Consequently,  $S_{fi}$  expression may have resulted from a mutation, as first suggested by Grasselly and Olivier (1976). This mutation could have been an epigenetic change taking place in the upstream region of the  $S_f$ -RNase (Fernández i Martí *et al.*, 2014).

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