

# IDENTIFICATION OF QTLs ASSOCIATED WITH SELF-COMPATIBILITY IN ALMOND

A. Fernández i Martí<sup>1</sup>, W. Howad<sup>2</sup>, R. Tao<sup>3</sup>, J.M. Alonso<sup>1</sup>, P. Arús<sup>2</sup> and R. Socias i Company<sup>1</sup>



<sup>1</sup> Unidad de Fruticultura, CITA de Aragón, Av. Montañana 930, 50059 Zaragoza, Spain

<sup>2</sup> IRTA- Centre de Recerca en Agrigenòmica CSIC-IRTA-UAB. Ctra. Cabrils Km 2, 08348 Cabrils (Barcelona), Spain

<sup>3</sup> Laboratory of Pomology, Graduate School of Agriculture, Kyoto University, Kyoto 606-8502, Japan

Although self-incompatibility (SI) is an important trait in plants from the evolutionary point of view, self-compatibility (SC) is a critical agronomic trait in order to ensure the production of an economic crop. Thus, SC has become one of the main objectives in many breeding programmes of fruit trees, such as almond, *Prunus amygdalus* Batsch

SC in almond has been so far only related with the presence of the  $S_f$  allele, allelic with the  $S$  series of SI alleles and dominant over SI. As a consequence, SC/SI has always been considered as a qualitative trait, controlled by a single multi-allelic locus, called the  $S$ -locus

However, some genotypes from the breeding cross 'Vivot' × 'Blanquerna' without the  $S_f$  allele have been recently identified as highly SC and on the other hand some seedlings carrying the  $S_f$  allele have been shown to be clearly SI after pollen tube growth and fruit set trials, thus suggesting that additional external factors or other genes not related to the  $S$  locus, possibly modifier genes located outside the  $S$  complex, may be responsible for the genetic control of SC/SI in almond (Fernández i Martí et al., 2009)

As a consequence, our goal was to better understand the SI complex in almond and to know which additional external factors may be able to modulate the SI mechanisms. Thus, a QTL approach has been undertaken using a combination of SSRs and  $S$ -locus markers for ascertaining and locate the genes involved in the SI reaction

An F1 population of 77 individuals from the cross 'Vivot' × 'Blanquerna' was studied in order to ascertain candidate factors for SI/SC control in almond

A total of 102 SSR markers were tested in the 'V × B' almond progeny to identify polymorphic markers between the two parents, pursuing a good coverage of the *Prunus* bin mapping 'T × E'. From those, 52 SSRs were selected because of their polymorphism in one or both parents and distribution over the 'T × E' *Prunus* reference map. Additionally, several specific primers for the  $S$ -locus (PaConSI/EMPC5R;  $S_f$ /SR;  $S23F$ / $S23R$ ;  $S8F$ / $S8R$ ) were included in the analysis

The maps of the parents were constructed using MapMaker/EXP 3.0 (Fig. 1). Additionally, Joinmap 3.0 was used in this study to construct an integrated map using the 53 loci (Fig. 2). And finally, quantitative trait loci effects were detected using the simple interval mapping procedure of MapQTL 4.0. QTLs with a LOD score higher than 2.0 were declared significant

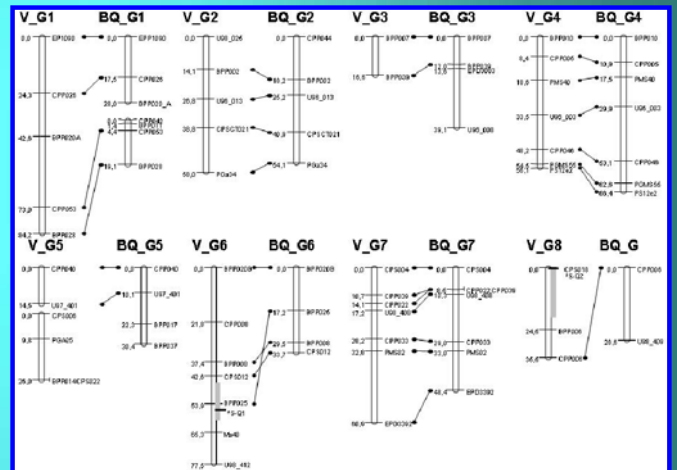


Figure 1: Anchor markers of the molecular linkage maps of 'Vivot' and 'Blanquerna' constructed using MapMaker. Two QTLs associated with SC in 'Vivot' are shown in G6 and G8. QTL positions are indicated as vertical bars, the position of the black horizontal line indicates the maximum LOD score. QTL length is plotted from LOD±1 with respect to the maximum LOD score

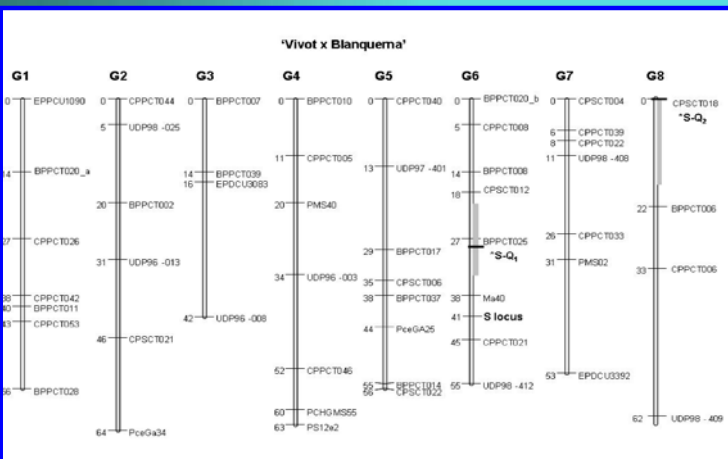


Figure 2: Integrated map of 'Vivot' × 'Blanquerna' containing 53 loci, including the two QTLs associated with SC identified on G6 and G8. The map was constructed using JOINMAP

Two significant QTLs,  $S$ -Q1 and  $S$ -Q2, were identified. The first located in the middle of the G6 (BPPCT025) and the second at the beginning of G8 (CPSC1018)

As a result of their combination, a probability of nearly 85% of identifying SC genotypes in the progeny studied was reached

These results pose a question about the monogenic nature of SI/SC in almond, so far considered as a qualitative trait. It seems that in many species, including Rosaceae, SI might act as a quantitative trait rather than as a qualitative one

Fernández i Martí A, Hanada T, Alonso JM, Yamane H, Tao R, Socias i Company R (2009). A modifier locus affecting the expression of the  $S$ -RNase gene could be the cause of breakdown of self-incompatibility in almond. Sex Plant Reprod. 22:179-186.