Genetic Diversity and Self-incompatibility Studies in Sweet Cherry

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Genetic Diversity

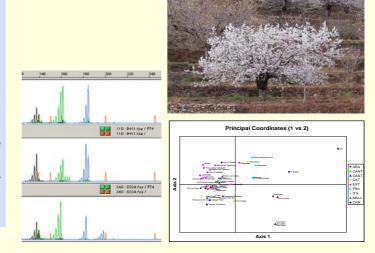
At the CITA de Aragon a sweet cherry collection with more than 100 accessions, that includes modern cultivars, antique accessions and local varieties, is conserved. Part of the work of this collection includes its maintenance and characterization. As part of this work we carry out molecular characterization (using SSRs and SNPs) and genetic diversity studies of all the plant material conserved. We also carry out the collection of local varieties within the framework of a project that aims to conserve the local diversity.

<u>Cachi AM</u>, López-Corrales M, Arbeloa A, Gella R, <u>Wünsch A</u>. (In press). Molecular Diversity of Local Spanish Sweet Cherry Cultivars by SSR and S-Locus Analysis. Acta Horticulturae.

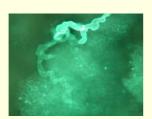
Wünsch A, Hormaza JI (2002) Molecular characterization of sweet cherry (*Prunus avium* L.) cultivars using peach (*Prunus persica* L. Batsch.) SSR sequences. Heredity 89(1): 56-63

Wünsch A, Hormaza JI (2002) Cultivar identification and genetic fingerprinting of temperate fruit tree species using DNA markers. Euphytica 125(1): 59-67

<u>Wünsch. A</u> (2009) 'Cross-transferable polymorphic SSR loci in *Prunus* species'. Scientia Horticulturae, 120:348-352.









S-locus genotyping and diversity

Due to self-incompatibility, sweet cherries need the availability of compatible pollen to ensure fruit set and therefore it is relevant to determine cultivar cross-compatibility for correct orchard establishment. Sweet cherry cultivars are cross-incompatible when their S-genotype is the same and are, accordingly, classified into the same Incompatibility Group. The S-locus, being multi-allelic, can also be used as a genetic marker for cultivar identification and the study of genetic diversity. As part of our research we investigate the S-genotype of local varieties and cultivars by molecular and pollination techniques, as well as the S-locus diversity in local and wild cherries from Spain.

Wünsch A, Hormaza JI(2004). Molecular evaluation of genetic diversity and S-allele composition of local Spanish sweet cherry (*Prunus avium* L.) cultivars. Genetic Resources and Crop Evolution 51: 635-641

Wünsch A, Hormaza JI (2004) Cloning and characterization of genomic DNA sequences of four self-incompatibility alleles in sweet cherry (*Prunus avium* L.). Theoretical and Applied Genetics 108 (2): 299-305.

 $\frac{\hbox{W\"unsch A}, \hbox{ Hormaza JI}(2004). \hbox{ S-Allele identification in sweet cherry cultivars by PCR analysis. Plant Breeding 127: 327-331.}$

<u>Cachi AM, Wünsch A.</u> S-genotyping of sweet cherry varieties from Spain and S-locus diversity in Europe. Euphytica, under review.

Self-compatible varieties

Self-compatibility is a primary objective of sweet cherry breeding. In Spain some local varieties are self-compatible. This trait is being characterized to develop tools that allow early selection and to complete our understanding of the self-incompatibility system. Self-compatibility in one of these varieties, 'Cristobalina', is caused by a mutation of a modifier unlinked to the S-locus, genetically mapped in sweet cherry linkage group 3. Work is on course to further characterize this trait in these accessions and to identify markers for early selection and the genes involved.

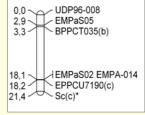
<u>Cachi AM, Wünsch</u> A (2011) Characterization and mapping of non-S gametophyte self-compatibility in sweet cherry (Prunus avium L.). Journal of Experimental Botany 62: 1847-1856.

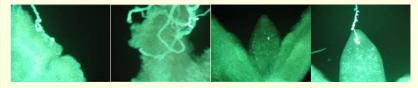
<u>Cachi AM</u>, Hedhly A, Hormaza JI, <u>Wünsch A</u> (2013) Pollen tube growth in the self-compatible sweet cherry genotype, 'Cristobalina', is slowed down after self-pollination. Annals of Applied Biology, doi: 10.1111/aab.12079.

Wünsch A, Hormaza JI (2004) Genetic and molecular analysis in Cristobalina sweet cherry, a spontaneous self-compatible mutant. Sexual Plant Reproduction 17: 203-210.

Wünsch A, Tao R, Hormaza JI (2010) Self-compatibility in 'Cristobalina' sweet cherry is not associated with duplications or modified transcription levels of S-locus genes. Plant Cell Reports 29:715–721.







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