

## A peach germplasm collection for increasing the genetic diversity in European breeding programs

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Peach is the most important crop among the stone fruit species worldwide. The species was originated in China, spread to Persia via the Silk Road and from there throughout Europe more than 2000 years ago. The crop is also located in the Mediterranean countries where the species is very well adapted. European yearly production reached about 4,310 million tons recently, based on a large number of varieties which allow marketing of diverse types of fruits and a long harvest season. The large number of varieties released is due to active breeding programs. Most of the countries where the crop is relevant have a high activity on breeding. However, European breeding programs are hampered by the low intraspecific genetic diversity, which is due to the self-compatibility of the species along with the low number of genotypes introduced and thus used for breeding. In 2009, four research institutions which carried out peach breeding programs in Aragon, Catalonia, Valencia and Murcia started a new peach germplasm collection aimed at enlarging the peach genetic diversity available for breeding.

The plant material was introduced from germplasm collections located in China, Central Asia, Iran and the USA (National Germplasm Repository of Davis). Sanitary status was assessed by molecular diagnosis of known diseases caused by virus, viroid, bacteria and phytoplasm pathogens. Healthy plant material was grafted and maintained in quarantine conditions. The new germplasm collection was established in two areas: Zaragoza as high chilling and Murcia as low chilling requirements. Pomological and molecular data are being gathered and a public data base constructed. The descriptors used are from the National Center for Genetic Resources from the INIA. Introduced budwood and seeds resulted in more than 250 new genotypes from 15 countries. The molecular analysis of a subset of the collection with 21 SSR markers evenly distributed in the genome resulted in a high number of alleles ( $A=9.5$ ) and low observed heterozygosity ( $H_o=0.38$ ). Variability was further assessed by geographic origin. Population structure analysis revealed the existence of 8 subpopulations explained, in some cases, by the geographic origin of the genotypes. As a result of