

# Population genomics of apricots unravels domestication history and adaptive events

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## Abstract

Among crop fruit trees, the apricot (*Prunus armeniaca*) provides an excellent model to study divergence and adaptation processes. Here, we obtain nearly 600 *Armeniaca* apricot genomes and four high-quality assemblies anchored on genetic maps. Chinese and European apricots form two differentiated gene pools with high genetic diversity, resulting from independent domestication events from distinct wild Central Asian populations, and with subsequent gene flow. A relatively low proportion of the genome is affected by selection. Different genomic regions show footprints of selection in European and Chinese cultivated apricots, despite convergent phenotypic traits, with predicted functions in both groups involved in the perennial life cycle, fruit quality and disease resistance. Selection footprints appear more abundant in European apricots, with a hotspot on chromosome 4, while admixture is more pervasive in Chinese cultivated apricots. Our study provides clues to the biology of selected traits and targets for fruit tree research and breeding.

## Biograph :

Dr Veronique Decroocq is a senior scientist with extensive expertise in plant breeding, genetics and genomics, both for forest and fruit trees. She received her Ingenieur diploma in Agronomy from the University of Lille (France) in 1988. In 1994, she completed her

PhD. in Genetics and Plant Molecular Biology, jointly between the University of Paris XI Orsay (France) and Wageningen Agricultural University (The Netherlands). Between 2015 and 2017, Dr Decroocq worked as a postdoctoral research scientist at the CSIRO (Canberra, Australia) on genetic engineering of Eucalypts.