

Almond and peach tree genomes shed light on their differences

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Almonds & Peaches. Credit: CRAG

Humans have been eating peaches and almonds for thousands of years. Although at first sight the products of these trees may seem to be very different, both species are part of the *Prunus* genus, and are genetically

very similar—so much so that they can be cross-bred, and fertile hybrids can be obtained from them. Now, an international team led by researchers of the Centre for Research in Agricultural Genomics (CRAG) has sequenced the genome of one almond tree variety and compared it to the peach tree genome. The detailed comparison of both genomes provides insights into their evolutionary history, and reveals the key role played by genomic mobile elements, also known as transposable elements, or transposons, in the diversification of both species. According to the authors of the paper, the movement of the transposons could lie at the origin of the differences between the fruit of both species or the flavour of the almond.

The knowledge of the almond tree's [genome](#) will be a very important tool in the improvement of the [species](#). "For example, this information will enable us to look for more productive and more disease-resistant varieties and also rule out those that bear bitter almonds more easily," explains Pere Arús, an IRTA researcher at CRAG. Arús led the study that is now published in *The Plant Journal*, and also took part in the international consortium that ultimately sequenced the peach tree genome in 2013.

A common ancestor in the center of Asia

The comparison of the genome of the Texas almond tree variety and the peach tree genome places the divergence of both species 6 million years in the past. The results are consistent with the existing hypothesis that places the existence of a common ancestor of these *Prunus* species in the centre of Asia and the subsequent separation of both populations that occurred when the Himalayas massif was lifted. This geological phenomenon would have left both populations of *Prunus* exposed to totally different climates in which both species would evolve: the almond tree in the arid steppe of the centre and west of Asia and the peach tree in the subtropical climates of the East, in the area that is now South

China.

The differentiation: mobile genetic elements

The authors of the paper found, as was to be expected, that the genomes of the almond tree and the peach tree have a high degree of conservation, and they investigated the extent of the differences between them and whether they could be accounted for by the action of the transposons.

Transposons are pieces of DNA with the capacity to change position within a genome and proliferate, jumping from one chromosome to another, and taking up a major part of the genome. In this transposition process, these mobile genetic elements may create mutations or change the genome's local properties, thus affecting [gene regulation](#). There has been a great deal of discussion regarding the utility of these mobile genetic elements since Barbara McClintock predicted their existence almost 70 years ago and for which she received the Nobel Prize in Medicine and Physiology in 1983.

The results of the analysis of the almond tree and peach tree genomes show that approximately 37 percent of their genome is composed of mobile elements and that some of the genes that play a key role in the differentiation of both species are affected by the presence of these elements.

"In this study, we discovered that the recent history of the transposons of the almond tree and the peach tree could lie at the basis of many of the important differences between both species," explains Josep M. Casacuberta, a CSIC investigator at CRAI expert in mobile genetic elements and study co-leader. "Although increasingly, more studies have demonstrated the key role of the mobile elements in evolution, the comparison of the almond tree and the peach tree, both species with

distinct characteristics but with very closely related genomes, provides unique insights into the impact of the transposons on the initial steps in the separation of the species," says Casacuberta.

Key in the eradication of bitter almonds

Most of the *Prunus* species have a bitter and toxic seed, although there is a group of almond tree varieties that bear a sweet almond, an aspect that has been key in their domestication and their agricultural and economic interest. Previous studies identified certain genes involved in the synthesis of the compound that confers bitterness and toxicity to these seeds: amygdalin. Now, the CRAG team has discovered that in sweet almond tree crops, at least one of these genes involved in the synthesis of amygdalin is affected by transposon insertions, suggesting a key role not only in the diversification of the almond tree and the [peach](#) tree, but also in variations within the same species (bitter almond and sweet [almond](#)).

More information: Tyler Alioto et al, Transposons played a major role in the diversification between the closely related almond and peach genomes: Results from the almond genome sequence, *The Plant Journal* (2019). [DOI: 10.1111/tpj.14538](https://doi.org/10.1111/tpj.14538)

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