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The study strategy featured floral development: first, the accurate identification of genes determining floral meristem identity, as in A. thaliana , APETALA1 (AP1) and LEAFY (LFY), and second, the genetic analysis of phenotypes aberrant for characters on the flowers, which allowed characterization of homeotic genes involved in the process.

Analysis of mutants

There are many mutations that affect floral morphology , however, his analysis is very recent. One of the evidences of these mutations is that most affect the identity of floral organs. That is, some organs develop in the place where you should do another, this fact is called homeotic mutation , by analogy with characterized mutations in Drosophila . In Arabidopsis and Antirrhinum , the two taxa model used, these mutations always affect adjacent whorls. Thus, three classes are characterized mutations, as the whorls affected:

? Function mutations in genes A, affecting the calyx and corolla, the outermost whorl. In these mutants, such as APETALA2 of A. thaliana , differentiated carpels instead of sepals, and stamens instead of petals, ie, the whorls of perianth whorls become reproductive.

? Function mutations in genes B ', affecting the corolla and stamens, intermediate whorls. We have described two mutants in A. thaliana , APETALA3 and PISTILLATA, which differ sepals and petals instead of carpels instead of stamens.

? Function mutations in genes C, affecting the reproductive whorls, that is, the stamens and carpels. The mutant in A. thaliana for this group is called AGAMOUS, which has a phenotype change of identity of petals and stamens to carpels to sepals.

Techniques for detecting differential expression

Has cloned the DNA of genes associated with homeotic functions affected in the mutants described, in this way, the analysis of their expression during flower development shows tissue expression patterns, which generally correspond to the predicted by the ABC model.

The nature of these genes corresponds to that of transcription factors , as expected, its structure is analogous to that of a family of factors in yeast andanimal cells called MADS family (the term is an acronym of the various factors described above). MADS These factors have been detected in all plant species investigated, although not ruling out the involvement of other elements of regulation of gene expression .

Genes function A

In A. thaliana , the function A is represented mainly by two genes, APETALA1 (AP1) and APETALA2 (AP2) 17 Ap1 is a MADS-box gene type, while AP2 is a representative of the family of AP2 domain genes, to which he its name, which consists of transcription factors specific to plants. 18 AP1 gene function acts as A, hence the identity of sepals and petals, but is also involved in their own floral meristem . AP2 is expressed not only in the first two whorls, but in the remaining two, in developing eggs and even leaves, then there may be a post-transcriptional regulation that controls

its operation, or that have other purposes regardless of that role in determining the identity of the body .

In Antirrhinum , the orthologous gene in AP1 is squamosa (SQUA), which also has a special impact on floral meristem identity. Counterparts to AP2 areLIPLESS1 (LIP1) and LIPLESS2 (LIP2), redundant function and special interest in the development of sepals, petals, and eggs.

In Petunia hybrida have described three genes similar to AP2 , namely P. APETALA2A hybrida (PhAP2A) PhAP2B And PhAP2C . PhAP2A has high homology to AP2 in Arabidopsis , both in sequence and expression pattern, suggesting that they are orthologous. PhAP2B and PhAP2C are, however, slightly different proteins, although they belong to the family of transcription factors like AP2 , also expressed by different, although close to being complementary, compared to PhAP2A . In fact, mutants for these genes do not offer the usual phenotype, the characteristic of the null alleles of genes function A. 20 However, a mutant known to function in Petunia has long been known mutant blind (bl), although its gene has not been cloned yet.

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