

# Study of the origin of the genes controlling flower development

Castro, Beatriz M.K.; Gonçalves, Carlos A.X.; Ortega, J. Miguel

*Laboratório de Biodados, Universidade Federal de Minas Gerais*

Flowers are recent innovations in the evolutionary history of plants. The only extant plants that develop flowers are the angiosperms. They constitute the most diverse and cosmopolite group of plants, due to their great evolutionary success. Their main evolutive strategies are (i) the pollen dispersion by the male parts, (ii) the protection of the ovules by the female parts and (iii) the envelopment of the seeds by the fruit. In order for the flower to be formed, a complex regulatory network with different genes controls the floral development. Most of these genes belong to the MADS-box family. The main controller of this network is the LEAFY gene. During evolution, new genes can arise and enable new molecular activities, thus allowing for the development of more complex regulatory systems. This work had the objectives of (i) constructing a pathway to describe the floral development of *Arabidopsis thaliana*, a model species of the angiosperm group; (ii) grouping their orthologues with SeedServer software and (iii) investigate the evolutionary origin of the genes present on this system, by determining the Lowest Common Ancestor (LCA), clade which originated all current species carrying each gene, using Genesis webtool. The results demonstrated that the first MADS-box to appear during evolution was the AP3 gene, on origin of the eukaryotes. Other early genes of this family were AP2 and CO, which originated on the green plants (Viridiplantae). LEAFY only appeared later, among the green algae (Streptophyta). SEP1, SEP2, SEP4, AG and API all arose on the land plants (Embryophyta), whereas SEP3 and SPV only originated recently, on the clade of the vascular plants with seeds (Spermatophyta). These results show that the genes that comprise the complex regulatory network for the floral development appeared on different clades during the evolutionary history of the plants, with the main regulator of the system originating among aquatic organisms. However, most of the MADS-box genes appeared during the conquest of the terrestrial environment by the plants, along with their independence of water for fecundation and the development of the seed for the protection of the embryo. Other genes involved in the flower formation pathway, are only found on the clade of the angiosperms (Magnoliophyta) and non-basal angiosperms (Mesangiospermae). Thus, flowering comprises genes originated along the all clades of plant evolution, but depending on some genes as recent as the origin of the flower.