

THE FLORAL INTEGRATOR *LFY*: PHYLOGENETIC ANALYSES

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Environmental and endogenous signals for the flowering control are assembled by regulators promoting the integration and convey the resulting outcome to floral meristem identity genes at the shoot apex. Among of this group there is the *LEAFY* gene (*LFY*), which is a transcription factor, involved in the flower development in *Arabidopsis thaliana*. The aim of this work is to identify *LFY* protein sequences in different plants and understand its conservation and evolutionary relationships. In order to do this, the *Arabidopsis LFY* protein was used to blast against TAIR, TIGR, SOL Genomics Network and NCBI databases using an Evalue of 1.0×10^{-15} . Multiple alignments were generated using ClustalW and Neighbor-joining analyses were done using PAUP program. The results obtained showed that all the sequences had the FLO_LFY functional domain. The phylogenetic tree revealed two great branches, one formed only by dicots plants and the second branch formed by monocots sequences and the Brassicaceae family came closer to the ancestral. There was a group at the Solanaceae family such as *Nicotiana tabacum*, *Lycopersicon esculentum* and Micro-tom. The presence of those two tomato sequences suggests possible gene duplication. It was also observed recent duplications also in the group of the monocotyledonous. So *LFY* can be functionality active in plants no-model, where such event is still not well understand.

Supported by: CNPq

Key words: Flowering, flowering pathway integrators, phylogenetic analysis, *LYF*.