

## IN SILICO AND FILOGENETICS ANALYSIS OF THE MEDIATING PROTEIN DIFFERENTIATION CELLULAR IN FRUCTIFICATION

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The vegetal fructification is a process that requires hormonal and genetic control, in *Arabidopsis thaliana* the FRUITFULL (FUL) is one of the proteins that is associated to induce the sepals and petals development together with AP1 and GA, and with the fruit formation. The aim of this work is by *in silico* analysis search for sequences homology to FUL protein in plant non-models and by phylogenetic analysis to understand the relationship of this protein. The protein sequences were obtained in the *A. thaliana* database and others database (TIGR-MAIZE and RICE-SGN-Micro-Tom and *Medicago truncatula*) using an Evalue of  $1.0 \times 10^{-15}$ . Functional domains were searched; multiple alignments were done using ClustalW and a Neighbor-joining analysis with PAUP. Were found two functional domains in all the sequences analyzed, MADS\_MFE2\_like and K-box. The phylogenetic tree has two branches, one composed only by dicots sequences and the other one formed by monocots sequences. In the dicots there are probably an orthologous between *A. thaliana* and tomato. Furthermore, the results suggest possible gene duplication between tomato and *M. truncatula* as it was found only one sequence in *S. tuberosum*. These results suggest that the FUL protein might be functionality active in all the plants and might be associated to the fructification where such event is still not well known.

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