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PHYTOPROT

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Is a database of clusters of plant proteomics evolved, help to the number of protein which increases regularly in plant, can promote study and production of functions of different protein, delineating characteristics sequences, differentially orthologues forms from paralogues, building phylogenetic reconstructions and also functional annotation by homology protein sequences can predict in that clustering. In this clustering databases while taking the complete proteome of *Arabidopsis thaliana* and all the available sequence from the other databases are grouped and compare into clusters which make a resulting database called PHYTOPROT. The protein sequence of *Arabidopsis thaliana* are retrieved from EMBL proteome site http://www.ebi.ac.uk/proteome and other plants protein sequence information from SWISS-PROT and TrEMBL databases. Before the end of 2003 a new sets of comparisons will be to PHYTOPROT. It will consist of the *Arabidopsis thaliana* proteome (released by the TIGR Institute in July 2002) compared against itself, which should be useful for the study of the numerous multigenic families in this plant. One clusters database can be queried at http://genoplant-info.infobiogene.fr/phytoprot .