

Webinar « Photosynthesis and Metabolism »

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Repeated evolution of furanocoumarin biosynthesis in plants

Furanocoumarins (FCs) are phenolic allelochemicals and show a scattered distribution in plants with a chemotaxonomical tendency toward Apiaceae, Fabaceae, Rutaceae, and Moraceae. Even though these four plant families are phylogenetically distant each other, they use the common precursor and intermediates to produce the FC backbone. This raises a question how the FC biosynthetic pathway has emerged and spread in plants. Here, we have carried out molecular identification of FC biosynthetic enzymes from different plant taxa and these FC biosynthetic genes/enzymes were subjected to phylogenetic analysis. Firstly, umbelliferone dimethylallyltransferase (UDT) genes, which are located at the first committed reaction step, were isolated from Apiaceae and Moraceae. Phylogenetic tree analysis and comparison of exon-intron structures strongly suggested that Apiaceous and Moraceous UDTs are derived from different ancestors each other. Moreover, in Moraceae, we identified CYP71F112 as a marmesin synthase gene at the biosynthetic step next to UDT. Phylogenetic analysis demonstrated that CYP76F112 has been acquired in Moraceae through a taxon-specific molecular evolution. These results support that the FC biosynthetic pathway has been emerged repeatedly in plants. We will also discuss factors which might have promoted the repeated emergence of FCs.

