

Phylogenetic relationships between FMO classes and the origin of YUCCA

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YUCCA proteins, a flavin monooxygenases (FMO), are important plant enzymes involved in the biosynthesis of one of the key hormones, auxin [1]. It is believed that these genes originated as a result of horizontal transfer from bacteria to plant genome [2]; though it is not clear at what stage of plant evolution it occurred: in multicellular algae or land plants. To clarify the early evolution of YUCCA genes, we reconstructed phylogenetic relationships between sequences of flavin monooxygenases, the protein superfamily to which YUCCA belongs. The analysis of active sites, domain composition and similarity of spatial structures of different FMO groups was performed. The analysis made it possible to distinguish three clades on the tree of FMO and YUCCA proteins: Yucca proteins, classic FMOs and a new group called “type II FMO-B”, which, apparently, have a unique ability to catalyze both oxidizing heteroatom-containing compounds (characteristics of FMO) and Baeyer–Villiger oxidations of ketones (characteristics of Baeyer–Villiger monooxygenases) [3]. We demonstrated that *Klebsormidium nitens* kfl00109_0340 protein, which previously was a candidate for the function of YUCCA enzymes in Charophyta [4], belongs to this new class of enzymes. The results support the hypothesis of horizontal transfer of the ancestral YUCCA genes from of bacterial genomes to the genomes of the ancestor of land plants. In addition, according to our analysis using Riebel et al. data [3], the “type II FMO-B” group of proteins is probably a new family of proteins, interesting for biocatalysis and includes proteins of bacteria, fungi, algae, higher plants. Therefore, further research for experimental verification of the functional properties of type II FMO-B is required.

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References

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