

Evolutionary–developmental study of membrane proteins

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Abstract

Using a plethora of experimental approaches for phylogenetical and functional study on several membrane signalling proteins, I brought new evidences supporting a hypothesis that the molecular evolution of protein families is a highly dynamic, not conservative, process. In DREPP family of calcium-binding peripherally-associated plasma-membrane proteins I found a broad flexibility in protein-membrane binding manners coupled with a many independent duplication of this Euphyllophyta-clade specific plant gene. In three families of auxin transporting proteins, PIN-FORMED, LAX and PILS, I showed that emergences of these proteins are uncorrelated and placed on different levels of the plant kingdom phylogenetic tree. However these proteins ensure very fundamental plant morphogenetic processes, like cell differentiation, organ formation or tropisms, with strong effects of their deleterious mutations, I found many gene radiations and losses on a all taxonomic levels in these families, evidencing that key and shared physiological processes may be realised by genes touched by a recently undergoing evolution. Evolutionary-developmental synthesis of a functional and phylogenetic data must be done with caution due to high risk of phylogenetic analysis artefacts and inappropriate generalisations of functional observation acquired on a limited number of model organisms.

Keywords

Arabidopsis thaliana, *Nicotiana tabacum*, *Chara braunii*, *Klebsormidium flaccidum*, DREPP, developmentally regulated plasma membrane polypeptide, PCaP1, PCaP2, plasma membrane-associated cation-binding protein, MAP18, microtubule-associated protein, peripherally-associated membrane proteins, auxin transport, PIN, PIN-FORMED, AUX1, LAX, PILS, PIN-LIKES, PLD δ , Phospholipase D, GFP fusion, FRAP, RICS, photobleaching, correlation spectroscopy, plasma membrane, actin, microtubules, cytoskeleton, myristylation, PtdInsPs, phosphatidylinositolphosphates, membrane affinity, phylogeny, maximum likelihood, blast, grid computing, ImageJ macro, deconvolution, PSF, point spread function, R-package, linear mixed-effect models, evolutionary-developmental biology, EVO-DEVO, plant origin, terrestrialisation.