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Protein prenyltransferases regulate the multicellular thallus development of liverwort *Marchantia polymorpha*

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Motivation and Aim: Protein prenylation plays a crucial role in the development of all multicellular organisms. Multicellularity transition is one of the major events in the evolution of living organisms. Considering that in Plant kingdom the multicellularity transition occurred several times independently the study of protein prenylation role in the development of plants allow us to find out new data on the multicellularity regulation. In this study, the role of three different prenyltransferases in the development of liverwort *Marchantia polymorpha* was studied.

Methods and Algorithms: Knockout lines of *M. polymorpha* protein prenyltransferases' genes were obtained via CRISPR/Cas9 technology. Complement lines were developed using pMpGW301-305 plasmids. Expression pattern were detected by CLSM. Proteome analysis were performed by MS.

Results: Mutant lines of *Δplp* and *Δggb* demonstrated callus-like phenotype with undifferentiated cells, formed solid structures, whereas *Δera1* knockout plants could form wild type dorso-ventral thallus phenotype. However, that *ΔRabggb* mutant plants were viable and remained the WT phenotype. The complementation of KO *M. polymorpha* resulted in the recovering of WT phenotype. The proteome analysis of *Δplp* and *Δggb* mutant plants allowed us to find out the correlation in the protein expression in these two lines comparing to WT.

Conclusion: Therefore, we showed the influence of protein prenylation on the development of the multicellular thallus of *M. polymorpha*. The following study of the expression of found genes will allow us to determine new gene pathways involved in multicellularity regulation.

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