

## **Uncovering the role of the SPL transcription factors family members from the liverwort *Marchantia polymorpha*, an emerging model plant system**

The scientific goal of the project is the functional characterization of the transcription factors *SPL* (Squamosa-Promoter binding protein-Like) gene family from the dioecious liverwort *Marchantia polymorpha*. The SPL proteins were first identified in *Antirrhinum majus* based on their ability to bind GTAC core motif of the floral meristem identity gene promoter *SQUAMOSA*. Their essential role is the regulation of transition from the juvenile to adult phase and from the vegetative to reproductive phase. In addition, they control a number of other processes like leaf buds initiation, flower and fruit development or plant architecture formation. The vast majority of the SPL protein functions comes from studies on angiosperms. Presently there are no data about their roles in liverworts, the oldest living land plants. Due to their ancient origin, liverworts represent a living laboratory for studying the early morphological, anatomical and molecular adaptations needed to survive in the terrestrial environment. The easiness of culturing, wide range of genetic and molecular tools, including transformation techniques, homologous recombination, CRISPR/Cas9-mediated genome editing and access to a draft genome (<http://Marchantia.info/genome/index.php/MainPage>) are the biggest advantages of *Marchantia* as a model organism among the liverworts. In comparison to the *SPL* gene families from other plants studied to date, where the number of genes is higher than 10, the *Marchantia* genome encodes only four *SPL* genes. Therefore we hypothesize, that the liverwort *SPL* gene family may reflect an ancient archetype which in the course of evolution could give rise to all other *SPL* gene families of vascular plants. To test this hypothesis we will use combined approach utilizing the loss-of-function and gain-of-function mutant lines for each member of the *MpSPL* gene family. Phenotype characterization of each transgenic line will allow us to determine the fundamental functions of individual *MpSPL* genes. Moreover, comparison of our results with the current state of knowledge about the SPL proteins will allow us the observation, whether there is an evolutionary conservation of SPL protein functions between liverworts and vascular plants or whether in the course of evolution their roles have diverged substantially.