The epigenetic factors in adaptations to terrestrial environments of early land plants

One of the most significant events in the history of the Earth, with tremendous repercussions for the evolution of organisms and ecosystems, was the colonization of terrestrial environments by plants ~470 million years ago. The transition from an aquatic life to a terrestrial one involved the evolution of a number of specialized cells, tissues and organs required for survival and reproduction. Plant adaptations to life on land include the development of many structures — a water-repellent cuticle, stomata to regulate water evaporation, specialized cells to provide rigid support against gravity, specialized structures to collect sunlight, alternation of haploid and diploid generations, sexual organs, a multicellular embryo protected by parental tissue, a vascular transport system, and rhizoids, roots and root hairs essential for the absorption of morphological diversity, including the establishment and perpetuation of developmental programs involved in plant adaptations to life on land remains limited.

Bryophytes (liverworts, mosses, and hornworts) comprise the earliest diverging land plant lineages. Fossil record and experimental evidence strongly suggests that liverworts are among the first plants that colonized terrestrial environments, and they have thus been considered as living laboratories in which to evaluate morphological adaptation associated with the transition to life on land. Up to the date only few liverworts species possess ability to live in the both, aquatic and terrestrial environments, thus being a perfect objects to study the adaptation on morphological and molecular levels. In some liverworts species the submerged and terrestrial forms exist in one population, suggesting that the adaptation to aquatic and land environments is drive by differences in expression and epigenetic factors like RNA editing and DNA methylation. The process of RNA editing is often considered as main player during the early stages of colonization of terrestrial environments, which limits the mutational impact of UV radiation and restore ancestral state of mRNA transcripts. The preliminary studies reveal also differences in amount of methylated DNA, which can lead to different picture of transcriptomes individuals living in aquatic and terrestrial environments. The comparative studies on changes in gene expression, RNA editing and DNA methylation can point out the genes which play main role in the early stages the colonization of terrestrial environments.

The main aim of this project is to better understand the processes behind the early stages of the adaptations to terrestrial environments, which could appear before evolution of specialized cells, tissues and organs. The analyses will be conducted on six common liverworts species representing three main evolutionary lineages: complex thalloids (*Marchantia polymorpha* and *Riccia fluitans*), simple thalloids (*Aneura pinguis* and *Pellia endiviifolia*) and lately divergent leafy liverworts (*Calypogeia neesiana* and *Scapania undulata*). All these species appear in the natural environments in the both, aquatic and terrestrial microhabitats, sometimes even these forms grow sympatrically (*Aneura pinguis, Pellia endiviifolia*).

The state of art molecular methods, including sequencing genomes, transcriptomes and methylomes form single individuals will reveal molecular picture of water-land transition process during single plant generation. Comparison obtained results between different liverworts evolutionary lineages enable to identify the set of genes impacted by habitat transition that are shared by all liverworts. Finally, the outcome of this project lets us better understand the initial stages of terrestrial environments colonization by plants.