

## EXPLORING *MARCHANTIA* TRANSCRIPTOME TO IDENTIFY GENES CONTRIBUTING TO SEXUAL REPRODUCTION USING mRNA-SEQ

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### Background

Liverworts belong to the earliest diverging lineage of land plants and thus occupy a critical position in land plant evolution. Hence, studying liverworts can help us to understand the genetic mechanisms that allowed plants to evolve from their aquatic algal ancestors and thereby adapt to a terrestrial environment. Any comparative evolutionary study of land plants cannot be completed without taking liverworts into account. But unfortunately, the accessible sequence information for this liverwort is still scarce. *Marchantia polymorpha* is one of the most extensively studied, widespread, dioecious liverwort, which is emerging as a model plant appropriate for carrying out molecular and developmental genetics studies.

### Aims

The aims of this study are to elucidate the genetics and molecular pathways implicated in reproductive development of *Marchantia* and to present a comprehensive survey of conservation and evolution of key genes involved in reproductive development from lower plants to present day plants.

### Methods

We employed next-generation Illumina sequencing and de novo transcriptome assembly to report a comprehensive transcriptome profile at six distinct developmental stages of *Marchantia* gametophyte - vegetative male (VM) and female (VF) thalli, immature reproductive male (IMM) and female (IMF) and mature reproductive male (MM) and female (MF) reproductive structures.

### Result and Discussion

To the best of our knowledge, this is the first report revealing a non-redundant set of 46 533 transcripts

expressing in at most one of the tissues taken into consideration. Interestingly, a substantial number of potentially novel liverwort genes were identified in this study and ~57% of the assembled transcripts have not yet been annotated. Expression analysis reported 1447 transcripts were specifically expressed in VM, 218 in VF, 65 in IMM, 95 in IMF, 496 in MM and 688 in MF respectively. The explicitly specific expression profiles between VM and VF reveal that entirely different molecular mechanisms work underneath carrying maleness and femaleness despite the high morphological similarity between VM and VF. In-silico data is further validated by Real time PCR for selected transcripts which showed significant difference between developmental stages or between male and female tissues. We performed comparative genomic analysis between algae, liverwort, moss, spike-moss, monocots and dicots and have identified 3471 transcripts encoding for 85 Transcription Factors families, 24 of which were actually identified to originate as *Marchantia* evolved and 6 of them play roles in plant sexual reproduction.

### Conclusion

Hereby, we demonstrate the transcriptome repository of six landmark stages of the liverwort development. Given large quantity of sequence information generated in this study, we have successfully identified novel sequence information which is important for sexual reproduction in *Marchantia polymorpha*. Additively, the expression data produced will assist us further in building a deeper understanding of underlying regulatory networks. This information will act as a valuable genomic resource for further molecular and developmental studies as well as for isolation and characterization of functional genes involved in sex differentiation and sexual reproduction of this liverwort.