

Characterizing MIKC* MADS-box genes in the moss *Physcomitrella patens*

The notion of an increased size of the MIKC* MADS transcription factor family in a moss – *Physcomitrella patens* – as compared to angiosperms, and the establishment of the role of MIKC* proteins in pollen development in *Arabidopsis*, have led to the assumption that this gene family may be conservedly involved in gametophyte development in land plants and that its expansion in moss was linked to a developmentally more complex haploid phase.

Analysis of the gene family in *Physcomitrella* revealed a close relationship between members of this family, the size of which is probably the result of 2 whole genome duplications and the subsequent retention of most of the paralogues. In this study, evidence for partially differing expression characteristics even between the most similar paralogues was found. These results and the retention of the genes during evolution point to an at least partial functional divergence. A lack of observable phenotypic changes in single gene replacement mutants constructed and analysed in this work is therefore very likely only partially due to the potential redundancy in the gene family. Although expression analysis supports a function of MIKC* genes during the gametophytic phase in *Physcomitrella*, indications are that they might also be expressed in sporophytes. Although it must be seen with reservations regarding the methodology, observed expression patterns are generally not restricted to certain organs or developmental phases and apparently somewhat variable for the gene family members investigated here. Therefore it is proposed, that MIKC* gene function does not influence morphological development in a direct way, but may rather be involved in regulating physiological aspects of plant life. Consequently, an immediate link between gene family size and morphological complexity is also unlikely. A complex gametophyte may nonetheless favour a larger family size of physiologically relevant genes, because of the necessity to cope with all vegetative functions and to withstand environmentally imposed difficulties or simply because it offers more niches for gene “speciation”. The observation of expression in antheridia, rhizoids, and maybe also sporophyte feet might be an indication for an involvement in the regulation of substance transfer in-between cells or between cells and the environment. Such a function could have made MIKC* genes very important for the establishment and evolution of land plants.