

Structural characterization of MADS-box genes in the moss *Physcomitrella patens*

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MADS-box genes play important roles in the formation of flowers within angiosperms, as well as in the formation of reproductive structures within gymnosperms. In contrast, almost nothing is known about the function of MADS-box genes within more basal tracheophytes such as ferns, or within non-vascular plants. Therefore, we decided to study the function of MADS-box genes within the moss *Physcomitrella patens*, which is the only land plant known so far that offers the possibility to efficiently knock out genes via homologous recombination.

The MADS-box genes of *P. patens* represent MIKC-type genes previously known only from seed plants and ferns. By comparison of sequence similarities and by studying exon/intron structures the *P. patens* MADS-box genes can be divided into two types, termed MIKC^c- and MIKC^{*}-type. The MIKC^c-type genes of *P. patens* *PPM1*, *PPM2* and *PpMADS1* have nearly identical structures as the MIKC^c-type genes from higher plants. They share a very similar exon/intron structure, the conserved pattern of hydrophobic aminoacids within K-domains, as well as the diagnostic length of the fifth and sixth exon of 42 bp. The I-domain is placed on one exon.

In contrast, the MIKC^{*}-type genes *PPM3*, *PPM4*, *PpMADS2* and *PpMADS3* differ from this conserved structure by longer I-domains distributed on four or five exons, respectively. It was shown that the MIKC^{*}-type genes are not restricted to the moss *Physcomitrella patens*. Also *LAMB1* from the lycopod *Lycopodium annotinum* shows this longer I-region consisting of four exons instead of one. That *LAMB1* belongs to the MIKC^{*}-type genes is also supported by phylogeny reconstructions, with the MIKC^{*}-type genes forming a clade supported by high bootstrap values. Due to the isolation of MIKC^c- and MIKC^{*}-type genes from *P. patens* and from *L. annotinum*, the last common ancestor of mosses and lycopods about 450 MYA must have had at least one MIKC^c- and one MIKC^{*}-type gene.

Evidence was gained that gene networks similar to those known from higher plants may also exist in mosses. This is supported by the appearance of regulatory promoter elements, the high number of at least five MADS-box genes of MIKC^c- and MIKC^{*}-type each, and the existence of K-domains in the predicted gene-products, which are necessary for protein dimerization.