

Functional characterization of the *SHI* gene family in *Physcomitrella patens*

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The *SHORT INTERNODES (SHI)* gene family consist of nine transcribed members, including the *STYLISH (STY)1* and *STY2* genes, in *Arabidopsis thaliana*. They are unique to plants and have a highly redundant functions in the development of the gynoecia, stamens and leaves, and severe developmental defects can only be observed in multiple mutant lines.

The SHI/STY proteins are localized to the nucleus and contain a putative Zinc-finger (ZnFn) motif and several acidic or glutamine rich regions, suggesting a function as a transcriptional activator. The proteins also have a second conserved domain, called the IGGH domain, unique to the SHI proteins.

Using Microarray and qRT-PCR we have identified several putative direct targets of STY1 action, one of which is *YUCCA (YUC)4*, a flavin monooxygenase, rate limiting in the biosynthesis of Indole acetic acid (IAA). We also have preliminary data suggesting that the STY1 protein bind to the promoter of *YUC4*.

In the moss *Physcomitrella patens* the orthologs to the *Arabidopsis SHI* genes are *PpSHI1* and *PpSHI2*. They are highly similar to each other with an 88% sequence identity at the nucleotide level, and differ at the amino acid level only in regions outside of the conserved ZnFn and IGGH domains.

We have produced single disruptants of both genes, a double disruptant, as well as several lines over expressing *PpSHI1* (*PpSHI1ox*). *PpSHI1ox* lines show an increased radial growth rate and hyper pigmentation in the older, central, protonema. They also seem to have less developed gametophores. The *PpSHI1*, but especially the double and *PpSHI2*, disruptants show a decreased radial growth and larger and more well-developed gametophores. In addition to this, the chloronemal filaments have an increased branching, which is best observed in colonies grown in low intensity light. All disruptants also show a *PpSHI1ox*-like pigmentation when grown on high concentrations of NAA.

We suggest that the *Physcomitrella SHI* genes act as transcriptional activators regulating the expression of auxin biosynthesis genes. Future studies will reveal which these downstream targets are and how their expression is altered in the different genotypes presented in this study.