

Identifying GATA Factors in *Physcomitrella patens*

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GATA factors are a class of transcriptional regulators whose members are characterised by the presence of either one or two highly conserved type IV zinc finger DNA-binding domains fitting the consensus sequence $Cx_2Cx_{17-18}Cx_2C$ followed by a basic tail region. These zinc finger proteins bind specifically to promoter elements containing the DNA sequence motif GATA.

GATA transcription factors are ubiquitous with representatives in all eukaryotic kingdoms. In plants these proteins are implicated in control of light-responsive transcription. Indeed, many plant light-regulated genes have been shown to contain a GATA motif within their promoter sequence. In *Arabidopsis thaliana* a family of over 25 GATA factors have been identified and characterised. This project addresses the role of GATA factors in the moss *Physcomitrella patens* and provides an opportunity for comparative genomics using the power of homologous recombination in this model organism.

We have identified a moss GATA factor from the *Physcomitrella* EST Programme (PEP). This gene has been partially characterised and has been shown to be single-copy. Additional candidates have been identified from the BASF EST collection and we are in the process of characterising these genes. Phylogenetic analysis indicates significant homology between *Arabidopsis* and *Physcomitrella* GATA factors, and I have attempted to identify sub-groups of homology. An additional 'LLMALS' motif has been identified at the C-terminal end of some of these proteins.

We intend to fully characterise these genes and carry out RT-PCR experiments to create an expression profile for each gene to determine whether they are differentially regulated. Knockout constructs will also be made to functionally characterise these genes by analysing the phenotypes of knockout *Physcomitrella* mutants. These studies should provide an insight into the role of this class of transcriptional regulators in moss. In addition, we are also characterising *Arabidopsis* GATA knockout plants which will be used for comparative genomics studies with *Physcomitrella* GATA factors. This approach may indicate whether functionality is conserved between similar genes from *Arabidopsis* and *Physcomitrella* and could reveal important evolutionary clues as to how this family has diverged in the transition from primitive to higher plants.

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