P18: Proteome analysis of protonema and gametophore tissues of *Physcomitrella*

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*Physcomitrella patens* is a monoecious moss, which requires simple growth conditions for the completion of its life cycle. Moss gametophytes exist in two morphologically distinct forms: the juvenile filamentous tissue called protonema and the adult leafy tissue called gametophore. However, the molecular mechanism for the transition from the juvenile (protonema) to the adult (gametophore) stage is not precisely known.

We have constructed the protein reference map on different tissues of *Physcomitrella patens* (protonema and gametophore) to provide a basis for future proteome analyses to understand the genetic networks which control specific biological processes during development of the moss *Physcomitrella patens* and understand how these proteins function and interact with each other in cells. More than 400 protein spots from gametophore and protonema were resolved on 2-DE gels. Peptide mass fingerprints (PMF) of 90 different spots between protenema and gametophore were obtained with matrix assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometer. For protein identification using PMFs, NCBInr protein database was searched using the search engine ProFound (http://prowl.rockefeller.edu/cgi-bin/ProFound). In addition, MS-Fit program (http://prospector.ucsf.edu/ucsfhtml4.0/msfit.htm) was used for searching against [pdbEST.others.02.20.2003] database to get the matched ESTs, which were again used for public protein database search with BLASTX program (http://www.ncbi.nlm.nih.gov/BLAST/). To confirm the identities of proteins, Q-TOF was applied for the internal peptide fragment sequencing.

For the sustaining massive culture of *Physcomitrella*, we have developed a 20 litre capacity bioreactor, which provides a simple and cheap culture system.