The Physcomitrella EST programme (PEP)

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The 3 year BBSRC-funded programme, to sequence Physcomitrella ESTs and to offer a service to the plant community for functional analysis of higher plant genes by gene targeting in moss, will complete this year. The achievements of the programme will be discussed; these include linkage of PEP to the NIBB EST collection, resulting in a total of around 60,000 ESTs being available in the public domain; added value to the PEP programme, by construction of a BAC library, by David Lightfoot and colleagues at SIU, Illinois), which is now available for library screening as filter grids (http://www.moss.leeds.ac.uk) and progress towards a phenotypic screen service for identifying altered phenotypes.

This talk will draw attention to posters detailing work emanating from PEP resources to be presented at this meeting i.e. Lomas et al. on bioinformatic analysis (poster P10); Panvisavas et al. on analysis of Rho-GTPase genes in Physcomitrella (poster P15); Deeks et al. on analysis of the mago-nashi gene in Physcomitrella (poster P3).

The Centre for Plant Sciences at Leeds is one of the largest group of plant scientists in the UK (http://www.plants.leeds.ac.uk). Research specialisms at Leeds are allowing a unique combination of expertise to be linked through PEP and applied to fundamental plant functional genomic analysis. We are focussing on tip growth and incorporating approaches looking at roles in development for the cell wall (see talk by Lee et al., T21); intracellular organelles, initially through peroxisomes in collaboration with Dr Alison Baker and extracellular stimuli, initially through light responses involving GATA transcription factors in collaboration with Prof. Phil Gilmartin.