

T19: Moss Functional Genomics at Freiburg University

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The post-genomic era relies on a variety of high-throughput approaches for the establishment of stringent gene/function correlations. One of the most powerful tools is reverse genetics, where the targeted disruption of a specific ORF leads to a loss-of-function mutation, which in turn establishes the biological role of this specific gene. Therefore, the moss *Physcomitrella patens* has emerged as a novel tool in plant functional genomics.

This talk will concentrate on recent work in the lab, including the establishment of standardized protocols for growth (bioreactors), transformation, documentation, induction of sexual reproduction, mutant analyses, and cryopreservation.

Sequencing of normalized and subtracted cDNA collections resulted in ~ 100,000 EST sequences and a clustered database, which comprises more than 95% of the moss transcriptome (~ 25,000 genes).

Unbiased transformation at a constant production capacity of 160 transgenics per day / 800 per week resulted in ~ 75,000 tagged transgenics with an enormous rate of developmental and metabolic deviations from the wild type.

As *Physcomitrella* is rich in secondary metabolites and in very long and unsaturated fatty acids promoting human health, a variety of novel genes like elongases and desaturases were identified. Likewise, functional knockout of the *apr* gene revived an old route of sulfate assimilation in plants.

The *Physcomitrella* genome is about three times as big as the *Arabidopsis* genome and is distributed on 27 chromosomes. To fully understand – and exploit - land plant diversity it should be sequenced as soon as possible.

Acknowledgements

This work was supported by BASF Plant Science, Deutsche Forschungsgemeinschaft, the Federal State of Baden-Württemberg, Fonds der Chemischen Industrie and Freiburg University.