

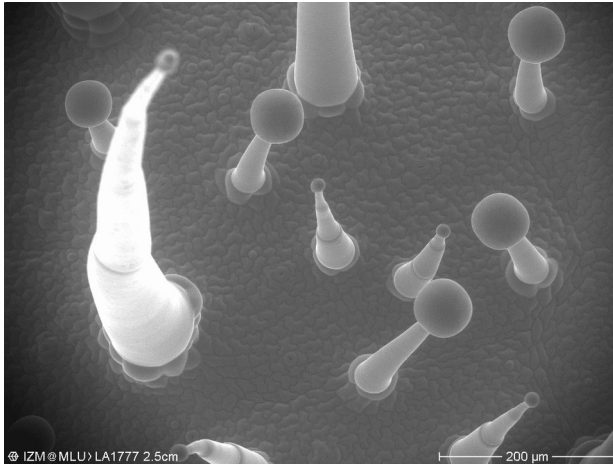
# Identification of functionally conserved plant gene family members by phylogenomic approaches

Benedikt Athmer & Alain Tissier

Leibniz Institute of Plant Biochemistry (IPB), Weinberg 3, D-06120 Halle (Germany)



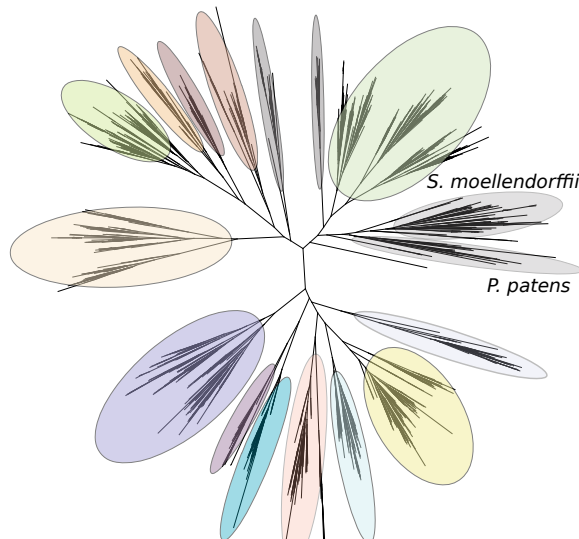
## Introduction



Type VI glandular trichomes of *Solanum habrocaites*.

- Our research focus on glandular trichomes (GT) of *Solanaceae* species, mainly tomato and tabaccum
- GT synthesize a plenty of secondary metabolites (e.g. alkaloids, terpenoids, ...)
- Plants possess large multigene families. Many of them are sparsely characterized and involved in biosynthetic pathways:
  - Cytochrome p450's (~250 in *A. thaliana*, third largest family)
  - UDP-Glycosyltransferase (~130 in *A. thaliana*)

## Objectives



Preliminary phylogenetic (ML) tree of UDP-glycosyltransferases proteins from 11 genomes. Basic land plants form independent clusters whereas higher plants scatter into many different clusters.

- Phylogenomics will be used to improve annotations and identify evolutionary important genes involved in basic processes (e.g. hormone synthesis, signaling ...)
- Species representing important evolutionary stages will be included: green algae, basic land plants (mosses) and flowering plants (monocots & dicots)
- Conserved genes will be characterized in *Arabidopsis* using reverse genetics & metabolomics