

### **T13: Studies on pattern and polarity in Arabidopsis roots**

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The Arabidopsis root displays astonishing developmental flexibility despite nearly constant lineage relationships. This organ is therefore particularly well suited to study mechanisms of plant development.

Auxins, with indole-3-acetic acid as the major active form, have diverse roles in plant growth and development that have hitherto been difficult to disentangle. Mutants in auxin transport and response suggest that this distribution is required for patterning. Re-distribution of the auxin concentration peak by laser ablation and by polar auxin transport inhibitors correlates with changes in multiple cell fates and cell- and organ polarity. Thus, auxin and its transport machinery play major roles in organising pattern and polarity in the distal root tip. The role of auxin transport proteins of the PIN and AUX1 families in pattern formation is currently being investigated and a tight link between polarity at the cellular level and pattern formation at the organ level emerges. This link is further substantiated by our studies on the *ORC/SMT1* gene, that links cell polarity to sterol biosynthesis and PIN protein localisation.

The *HOBBIT* gene is required during early embryonic development in the founder cell of the root meristem, and it is expressed throughout development in a cell-cycle dependent manner. The HOBBIT protein likely is a component of the Anaphase Promoting Complex, and we have used the requirement of the *HOBBIT* gene for correct cell fate determination as an opportunity to investigate how cell division and cell fate may be linked in plants, possibly involving the regulation of auxin responsiveness.

Downstream of auxin as a patterning cue, separate distal domains need to be specified in the root tip. The *PLETHORA1*, *PLETHORA2*, *FEZ* and *SOMBRERO* genes are required for proper development of the columella and lateral root cap and current evidence suggests that they act downstream of auxin signaling. The PLETHORA genes encode putative transcription factors.

The *SCARECROW* gene has previously been shown to be required for an asymmetric division that separates endodermis and cortical parenchyma in the ground tissue of the root. Besides this role in radial patterning, we now show that *SCARECROW* is cell-autonomously required in the quiescent center to maintain (in a non-cell-autonomous fashion) the stem cell status of the surrounding initial cells of the root, using a combination of different domain-specific ectopic expression methods. Thus, also this gene contributes to distal specification, and radial and apical-basal patterns appear to be connected in the root tip.