Abstract

Studying homologous processes in related species of the same taxon provides functional evolutionary comparisons of developmental processes. The *TRANSPARENT TESTA GLABRA 1* (*TTG1*) gene network regulates proanthocyanidin, anthocyanidin, seed coat mucilage production as well as trichome and root hair patterning in *Arabidopsis thaliana*. It involves the same set of genes or closely related paralogs that control additional factors specific for the respective differentiation process. I established *Arabis alpina* as a second genetic model system to analyse epidermal patterning in the light of evolution.

A. alpina has dendritic trichomes and positionally cued root hair pattern like *A. thaliana*. It is diploid, self-compatible and in the Brassicaceae family (26-40 million years apart), making it a suitable Evo-Devo model to *A. thaliana*. Using available sequence information, I identified the known *A. thaliana* genes regulating trichome and root hair development in the genome of *A. alpina* by sequence similarity and synteny. This has laid the foundations for a comprehensive study of evolution of the *TTG1* gene regulatory network. A detailed analysis of the five *TTG1* dependent traits showed not only similarities but also striking phenotypic differences between *A. alpina* and *A. thaliana* like trichome formation at later stages of leaf development and root hairs formation at non-root hair positions.

I applied forward genetics in combination with candidate gene approach to uncover the mechanistic behind trichome and root hair development in *A. alpina*. Towards this end, I searched for EMS mutants affecting the pattern and morphology of trichomes and root hairs in *A. alpina*. This revealed numerous trichome and root hair mutants reminiscent of the ones in *A. thaliana* but also a few novel mutant phenotypes. A comparison of two Aa*ttg1* alleles with their corresponding backgrounds revealed that AaTTG1 is involved in the regulation of all five TTG1 dependent traits. The role of Aa*TRIPTYCHON* as negative regulator of trichome initiation, *AaGLABRA 2* as downstream target of MYB-bHLH-WD40 complex, Aa*STICHEL* in trichome branching, Aa*CROOKED*, Aa*GNARLED* and Aa*SPIRRIG* in trichome growth is conserved in *A. alpina*. Unlike *A. thaliana* the non-redundancy of Aa*GLBRA 3* to Aa*ENHANCER of GLABRA 3* in regulating trichome and root hair patterning in *A. alpina* emphasizes the elusive differences that can be identified on comparing homologous processes in related species. The evolutionary conservation paired with striking phenotypic differences of *TTG1* dependent traits makes *A. alpina* an attractive Evo-Devo model. Further analysis on the retrieved trichome and root hair mutants of *A. alpina* will cast a new light on the evolution of plant epidermal patterning at a functional level.