Furry and the RAM molecular network in *Arabidopsis thaliana*

How cells of single-celled organisms such as yeast, or the complex organisms of multicellular plants and animals acquire their shapes has been a question that fascinated biologists for a long time. The study of morphogenesis greatly accelerated in the molecular genetics era with the advent of mutants displaying abnormal shapes or aberrant development. Their investigation paved the way towards a molecular-level understanding of the underlying processes. One such mutant of the fruit fly *Drosophila melanogaster,* an early model for animal genetics and development, displayed abnormally branched and multiplied structures such as hairs and bristles, and was therefore named *furry*. Subsequent studies identified the *Furry* gene to encode a large, novel protein of unknown function. Over time, reports accumulated on proteins similar to Furry present in organisms ranging from single-celled yeast, through other models such as the nematode *Caenorhabditis elegans,* to mammals. In all organisms studied, loss of Furry function caused distinct defects in morphology, such as for instance improper cell shape or patterning of neural tissue. Further research lead to the realisation that Furry acts as a component of a larger molecular network, named RAM, composed of several other conserved protein types, and that RAM networks typically control vesicular trafficking in individual cells to carry out their morphogenetic roles.

In contrast to the relatively advanced understanding of RAM networks in many organism types, the existence of a potential RAM network in plants is only beginning to be elucidated. The model plant *Arabidopsis thaliana* possesses genes encoding homologues of Furry as well as other components of RAM networks, but only scarce experimental data has been obtained so far. Preliminary experiments show that RAM network components are required for normal plant growth, having roles in development controlled by the plant hormone auxin and being essential for fertility. In this project, the molecular and developmental functions of Furry and the RAM network will be studied in *A. thaliana* by approaches including advanced genetic engineering, fluorescent live imaging, developmental studies of mutants, and proteomics. The anticipated outcome of the project is the understanding of how a RAM molecular network similar to those known from other organisms acquired a function in shaping the plant body to enable its normal function, likely through the regulation of plant cell’s intracellular trafficking pathways. The project will fill an important knowledge gap in the field of plant cell biology and development, and valuably contribute to the wider biological study of morphogenesis.