Highlighting molecular dynamics methods to investigate stress responses in plants

Martin Kulke

In recent decades, molecular dynamics simulations have become a valuable tool to complement experiments as a computational microscope and hypothesis generating method. Especially in highly collaborative environments, in silico studies streamline scientific throughput by providing insights into atomistic biomolecular interactions that are difficult to obtain experimentally. Using two projects in the context of plant stress responses as examples, I will highlight the molecular dynamics simulation methods we use to answer mechanistic research questions.

The first project investigates the small gaseous organic molecule isoprene, which some plants produce on hot summer days in response to heat stress. While the function of isoprene in plant tissues remains unresolved, current hypotheses include preventing oxidative stress, regulating proteins or modifying membrane physical properties in a temperature-dependent manner. Experimentally, isoprene was demonstrated to prevent leaves in direct sunlight from suffering heat burns, which suggest a strong link to chloroplasts and the photosynthetic complex. To elucidate the mechanism of isoprene, we investigated and quantified the influence of isoprene on protein structures and thylakoid membrane properties using molecular dynamics methods. Based on the results, isoprene most likely has a regulatory function and we identified several potential target proteins.

In the second project, we investigated long-distance signaling mechanisms in response to drought stress. Lipid trafficking through the phloem in particular attracted our attention as it depends on soluble lipid-binding proteins to solubilize otherwise membrane-associated lipids. One such protein, the PHLOEM LIPID-ASSOCIATED FAMILY PROTEIN (PLAFP) from *Arabidopsis thaliana*, targets the signaling lipid phosphatidic acid (PA). To understand the binding mechanism of PLAFP, we performed protein-lipid binding simulation studies leading us to propose a two-step PA-binding mechanism for PLAFP. First, the protein binds to the membrane, which induces a conformational change opening a hydrophobic pocket for lipid binding. In a second step, a PA lipid binds into the formed pocket prior to dissociation and transport.