

Signalling the way forward: understanding plant adaptation to environmental change

Supervisory team:

Rothamsted supervisor: Dr Richard Haslam (Rothamsted Research)

Academic supervisor: Dr Simon Scofield (Cardiff University)

Dr Louise Michealson (Rothamsted Research), Prof John Harwood (Cardiff University)

Collaborators: Dr Kirsty Hassall (Rothamsted Research), Dr Claudia Jonak (AIT, Austria)

Host institution: Rothamsted Research (Harpenden)

Project description:

Plants respond to abiotic stress with a wide range of effective protective responses. Key signalling events and transcriptional responses to environmental perturbation have been widely reported. However, responses at the metabolic level are less well understood. One clear example is the metabolic stress response involving lipid remodelling. Plants regulate pathways of fatty acid synthesis, lipid assembly and trafficking for remodelling of membranes in response to stress. For instance, temperature stress triggers lipid-dependent signalling cascades (e.g. phospholipids, sphingolipids, diacylglycerol), which control gene clusters and activate adaptation. Levels of fatty acid synthesis and desaturation are regulated to maintain membrane function and plants undertake complex remodelling of plasma phospholipids (phosphocholine) and thylakoid galactolipids (e.g. monogalactosyl diacylglycerol) via a network of induced lipase and acyltransferase activities. Some metabolic changes associated with adaptation produce toxic metabolites (e.g. free fatty acids), which can be dealt with by incorporation into triacylglycerol. Collectively these changes to the cellular lipidome (the totality of lipids in cells) enable plants to adapt and survive in variable climates. Although all plants share the ability to remodel their cellular lipidome in response to abiotic stress, the capacity in different species and cultivars often varies.

Currently, our understanding of lipid responses to abiotic stress largely comes from model species such as *Arabidopsis*, but there is now interest in using extremophile species, adapted to challenging climates, to dissect the mechanisms of plant lipid signalling and remodelling. *Eutrema salsugineum* ('salt cress') is highly resilient to abiotic stress (temperature and salinity). Moreover, as a member of the Brassica family and closely related to *Arabidopsis* it is a platform for understanding stress tolerance. The genome of *Eutrema* is fully sequenced and transformation methods have been established. The similarity between genomes of *Eutrema* and *Arabidopsis* allows a direct comparison between genes and their function, rendering most of the experimental procedures developed for *Arabidopsis* highly adaptable. The central aim of the proposed project is to clarify the biochemical processes and functional significance of stress induced lipid metabolism. Using both *Arabidopsis* and *Eutrema*, we will focus on the mechanistic response to temperature stress.

Current and predicted climate variability has critical effects on food production, therefore the fundamental understanding developed in the proposed work will establish knowledge-based strategies to address crop temperature resilience.

