# FINALREPORT



UHS10549

## Physiological analysis of phloem molecules in cereal cultivars under salinity stress

#### **PROJECT DETAILS**

UHS10549
PHYSIOLOGICAL ANALYSIS OF PHLOEM MOLECULES IN CEREAL CULTIVARS UNDER SALINITY STRESS
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#### Summary

Micro RNA (miRNA) are small RNA strands that are involved in the regulation of gene expression, and thus act as secondary messengers. We aimed to identify 2 miRNAs, commonly found in plants, in phloem sap of wheat collected by aphid stylectomy.

We also aimed to identify by mass spectrometry, the profile of proteins found in the sap and compare the profiles between salt stressed and control barley plants.

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#### Conclusions

Aphid sytlectomy, although an established way of obtaining pure phloem sap from cereal plants, when combined with highly sentivity tools of mass spectrometry and PCR, can be used to identify important molecules that act as messangers and regulatory molecules in a plants repsonse to environmental cues and physiological changes.

#### Recommendations

Further research is needed to expand the analysis of miRNAs and protein in the phloem sap of cereal plants under different environmental conditions, and at different developmental stages. The knowledge gained from these analyses could be further tested experimentally and any lead molecules incorporated into breeding strategies to exploit and enhance their beneficial effects in stress response.

#### Achievement/Benefit

#### **Overview of project achievements**

The presence of 2 miRNAs was successfully demonstrated in samples of 100 nanolitres or less of phloem sap collected from wheat plants by aphid stylectomy. To our knowledge, this is the first time that miRNAs have been shown to exist in the phloem sap of cereal plants and represents a significant step in our knowledge of the plant response to environmental stresses and stimuli.

Proteins were identified by mass spectrometry in similar samples of phloem sap collected from salt stressed and control barley plants. Expected and novel differences in the profiles of the identified proteins were found in the samples from salt stressed plants. This data represent an important resource for further targeted investigation of proteins in the phloem that may control responses in cereal plants to salt stress and other stresses.

#### **Other Research**

Many different applications to this technology are possible to investigate other important regulatory molecules that may travel along the vascular network of cereal plants. These include important sugars and metabolites, lipids, and metal/protein complexes. Some of these molecules under currently under investigation in the Stangoulis laboratory.