

## Evaluating epigenetic and transcriptomic adaptations to climate change in *Brassicca napus* (oilseed rape)

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### Project Description:

**Background:** The recent heat wave events witnessed over the past few years across the UK as a result of change in the global climate, represents a serious threat to agriculture. Significant loss in crop production has been observed worldwide, which is sometimes attributed to the rise of heat coupled with drought (Mittler, 2006). Oilseed rape (*B. napus*) is an economically important crop for the UK, where higher temperature at pre-anthesis period has been proven to reduce pollen fertility (Morrison, 1991) and also can have severe impact on seed moisture at post-anthesis, which in turn deteriorates the quality of oil content and composition. At the other extreme, cold temperatures in December, which may be less common in the future, have recently been positively associated with yield in oilseed rape (Brown *et al.*, 2019).

There is increasing evidence that epigenetic mechanisms, such as DNA methylation and histone modifications, alter the regulation of gene expression as a direct response to heat stress; this may influence plant growth and development. It has been shown that higher temperatures can significantly affect expression of genes related to flowering in *B. napus* (Tang *et al.*, 2019). Currently, the epigenetic mechanism of heat stress response for the UK varieties is not well understood.

**Project Aims and objectives:** the aim of this project is to provide a systems-level molecular and metabolic understanding of the impact of heat stress on yield and seed development of *B. napus* for UK-specific varieties. Such a systems biology approach will be achieved through monitoring DNA methylation and global transcriptome profiling in tandem with metabolic analysis of oilseed rape as a result of heat stress. The project is a collaboration between Cranfield University and University of Reading. The main objectives of the project include:

1. Investigating the effect of heat stress on two lines on pollination fertility and seed quality at pre- and post-anthesis periods of *B. napus*.
2. Identifying site-specific modification of DNA methylation in the *B. napus* genome susceptible to heat stress
3. Performing transcriptome profiling using RNA-Seq, to identify key differentially expressed genes as a result of heat stress.

The above objectives will lead to the development of a gene regulatory network in order to assess the epigenetic mediation effect on pollination fertility and seed quality measures. Ultimately, these results will be used to develop a machine learning model to predict the future impact of heat stress on pollination fertility and seed quality.

**References:**

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