

Transcriptomic analysis in rice during stress conditions using R/Rstudio

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Abiotic and biotic factors such as heat, drought and salinity contribute a major proportion of crop yield losses. They pose a serious threat to global food security and any attempts to eradicate poverty to achieve fair, sustainable societies. Rice is the most important cereal crop and staple food eaten by more than half of the world's population in every meal, particularly in Asia. Stress tolerance traits are multigenic and the candidate genes are poorly known.

The majority of transcriptome sequencing (RNA-seq) expression studies in plants remain underutilised and inaccessible due to the use of disparate references and the lack of skills and resources to analyse and visualise these data. Our group at the Earlham Institute has identified and curated the metadata of over 70 RNA-seq experiments (from more than 2,000 samples) in different abiotic and biotic stress conditions in rice cultivars.

The student will be trained in R and will carry out comprehensive exploration of this large expression dataset, compare and sort the information based on the associated literature. The student will then reanalyse the whole dataset using common criteria and pipelines in order to visualise the result in a holistic way. The results of the comparative transcriptome analysis will identify novel diversity in rice varieties with superior adaptation to future climatic scenarios resulting from global warming.

This project will provide advanced training in data and statistical analysis, therefore previous experience in R would be desirable. These are areas for which we experience a shortage of skills and can directly have an impact on the agricultural industry and the global need for food security.