

Hot and cold potatoes: designing temperature resilient crops for the future. PhD Opportunity: The James Hutton Institute and the University of Dundee, UK.

Background: Plants exhibit a range of responses to changes in temperature but the molecular mechanisms are unclear. One challenge is to understand temperature responses in crops, to enable the design of genotypes that can withstand adverse environments. This will increase marginal land use for food production and ultimately increase global food security.

Research question: Can the prediction and validation of *cis*-regulatory elements (CREs) in gene promoters establish a regulatory code for temperature responses in Potato?

Project Outline: Arabidopsis has 3644 transcripts regulated by heat stress and 6061 by cold stress [1,2]. The heat-regulated transcripts include transcription factors that bind heat shock elements (HSE) in the promoters of heat shock proteins. It is the sequence specificity and combinatorial association of TFs and their CREs that gives rise to a transcriptional regulatory code for temperature responses. Modeling approaches have identified aspects of the *cis*-regulatory code for salt stress responses [3], but the code for temperature stress responses is still unknown. This project will use existing data from Arabidopsis and Potato to model a transcriptional code for temperature responses, and then design synthetic promoters to test the model's ability to predict temperature responsive expression.

We have two parallel sets of data (i) microarray data for genes regulated by heat stress in potato [4], and (ii) RNA-sequencing data from Arabidopsis exposed to cold stress. Computational tools will be applied to identify significant CREs in the promoters of genes within clusters in these datasets. Next, association rule mining [5] will be used to identify combinations of CREs, designated as *cis*-regulatory modules (CRMs), that are predictive of specific gene expression patterns resulting from changes in temperature. Finally, *in-vivo* candidate CRMs will be experimentally validated using a number of methods, including the design of synthetic promoters containing candidate CRMs. Validated CRMs will be used to search for novel components of temperature response pathways in potato, that has the potential to lead to the identification of new temperature resilient genotypes.

Supervisors: This project is principally supervised by Dr Sue Jones (The James Hutton Institute) and Professor John Brown (University of Dundee).

The Student: This project would suit a student from either a biological or computer science background, as the proportion of computing vs biology can be adapted to suit the applicant.

Career opportunities: *Bioinformatics has one of the greatest skills shortages within the sciences, with specific skills gaps in genomics and computing. This PhD is an excellent opportunity to gain the interdisciplinary skills essential for a career in bioinformatics.*



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Funded studentship starting Oct 2016:
Further details FindAPhD

<http://www.findaphd.com/search/ProjectDetails.aspx?PJID=67784&LID=1374>



References: [1] Barah P, et al. BMC Genomics. 2013;14:722. [2] Barah P, et al. Front Plant Sci. 2013;4:532. [3] Zou C, et al. Proc Natl Acad Sci 2011;108:14992. [4] Hancock RD, et al. Plant Cell Environ. 2014;37:439 [5] Czibula et al. Evol Bioinformatics. 2012;8:181.