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When crops grow up: determining regulatory control of floral transitions within *Brassica napus*

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Background:

The transition to flowering is a key agronomic stage within crop development that impacts yield. Its regulatory control has been extensively studied within the model species Arabidopsis thaliana, however, our knowledge of the underlying gene regulatory networks within crops such as Brassica napus is still limited. Furthermore, different cultivars of Brassica napus need to undergo varying degrees of vernalisation prior to flowering, yet the mechanisms and networks that cause these differences are not understood.

Objective:

Elucidation of gene regulatory networks controlling the regulation of key floral pathway integration gene SUPRESSOR OF OVEREXPRESSION OF CONSTANS 1 (SOC1) within two different cultivars - a spring-type and a semi-winter type cultivar of B. napus.

Methods:

Plants were grown under controlled conditions and transcriptome from the apex tissue was sampled at various time points until the floral transition. The transcriptome data was used to generate detailed expression time series for all genes expressed within the apex. Reciprocal BLAST was used to generate gene mappings between Arabidopsis and B. napus cultivars. Curve registration was used to compare species at different developmental time scales, which applies stretch and shift factors to expression time series (Calderwood et al., 2021). Differential Gene Expression analysis was performed to compare development across time points for each plant. The Casual Structure Inference (CSI) algorithm was used to generate Gene Regulatory Networks (GRNs) for SOC1 copies within different cultivars.

Results and further steps:

Curve registration reveals that development within B. napus follows a path parallel to Arabidopsis, however, different genes have different ‘stretch’ and ‘shift’ factors which can be grouped into distinct modules. Differential gene expression analysis for the spring type cultivar ‘Stellar’ shows a steady divergence from the initial timepoint as the plant develops. However, similar analysis for the semi-winter cultivar ‘Zhongshuang-11’ shows that, following vernalisation, it returns to a transcriptomic state similar to its pre-vernalisation timepoints. Following this anomaly, it proceeds to flower, with steady divergence observed in further timepoints. Further comparison using curve registration between Stellar and Zhongshuang-11 shows that transcriptomic development of Stellar follows parallel to Zhongshuang-11 following vernalization, confirming previous results.

Using the time series data, we inferred GRNs for SOC1. Preliminary GRN analysis suggests that all copies of SOC1 are co-regulated within the spring type Stellar, whilst in the semi-winter Zhongshuang-11 these gene copies diverged, shedding light on the regulatory changes that may drive adaption. Further experiments are being conducted to gather data for the spring type cultivar ‘Stellar’ treated with cold to confirm if this divergence indicates a regulatory difference between two cultivars with regards to floral transition or a consequence of vernalisation.

Reference:

Calderwood, A., Hepworth, J., Woodhouse, S., Bilham, L., Jones, D., Tudor, E., Morris, R. (2021). Comparative transcriptomics reveals desynchronisation of gene expression during the floral transition between *Arabidopsis* and *Brassica rapa* cultivars. *Quantitative Plant Biology*, 2, E4. doi:10.1017/qpb.2021.6