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Transferring knowledge of the floral transition from Arabidopsis to *B. oleracea* using gene expression dynamics

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Background:

Flowering time genes and their regulation have a strong impact on successful reproduction and life cycle adaptation in plants. However, the regulation of these genes is very complex and mainly studied in the model species *A. thaliana*. For crops with a polyploid background, like *B. oleracea*, it is not clear whether the same gene networks exist. Moreover, transcriptomic studies to understand this developmental process in *B. oleracea* are still limited.

Objective:

Therefore, we aim to investigate the extent to which the knowledge from *Arabidopsis* can be transformed to *B. oleracea* through comparative developmental studies. This study identifies similarities and differences in gene expression at equivalent time-points, suggesting differences in the underlying gene regulatory networks (GRNs). Different organisms such as *A. thaliana* and *B. oleracea* develop at different rates, and one challenge in making useful comparisons is in determining equivalent time-points and how to transfer knowledge between species.

Methods:

To address this challenge, we developed a Bayesian approach based on statistical model comparison, which finds the optimal alignment of gene expression dynamics by inferring temporal shifts and stretches. We compute the Bayesian Information Criterion to compare the support for a non-registered model (in which two gene expression dynamics are considered to be different) versus a registered model (in which expression profiles are considered the same) (Kristianingsih et al. In preparation). We developed an R package, “greatR” (https://CRAN.R-project.org/package=greatR), to make the approach widely available.

Results:

Our approach has been used to compare gene expression profiles during the floral transition of *Arabidopsis* to *B. rapa* (Calderwood et al. 2021) and *Arabidopsis* to *B. oleracea*. Similar to what has been found between *Arabidopsis* and *B. rapa*, there is not one, but many different ‘developmental progressions’ of gene expression running at different rates between *Arabidopsis* and *B. oleracea*. Different optimal registration parameters are required for different genes, indicating that there is no single common developmental time during floral transition based on gene expression between Arabidopsis and B. oleracea. Additionally, through curve registration, we found that most of the key floral genes in B. oleracea show similar dynamics to those in *Arabidopsis*. This suggests that the GRN of floral transition in *B. oleracea* can be understood as modules of genes with highly similar regulatory relationships as in *Arabidopsis*.

Conclusions:

Taken together, using our approach, we could gain an understanding of the differences in regulation of the floral transition between *Arabidopsis* and *B. oleracea*. This data provides a knowledge foundation in *B. oleracea* and could be taken forward and used for future breeding strategies of *B. oleracea* crops.

References:

Calderwood, A. *et al.*, (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