

Transcriptional regulation of lipid metabolism in *Camelina sativa*

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<https://camregbase.org/>

Project Goals

The main goals of this project element of this large project is to define the transcriptional networks that control tissue-specific and whole plant carbon allocation in *Camelina* (this correspond to Project Element 3 of the entire project) and the specific goals are:

- a) Develop a High-Resolution Transcriptome for *Camelina* Seed Development
- b) Characterize and Identify Targets of *Camelina* Seed Oil TFs
- c) Manipulate TFs and Metabolic Genes for Pathway Discovery and Seed Oil Metabolic Engineering

Camelina is an annual oilseed plant that is gaining momentum as a biofuel winter cover crop. Understanding gene regulatory networks (GRN) is essential in deciphering plant metabolic pathways, such as lipid metabolism. In *Camelina*, a collection of gene expression datasets enabled characterizing the expression of >4,600 TFs in >130 RNA-seq samples¹. We collected lipid-related genes (LRGs) and expression data from CamRegBase¹. The LRGs were classified according to the information provided by AraLip², and the expression data was used to identify genes highly co-expressed with TF genes. By combining these two analyses, we identified 350 TFs highly co-expressed with LRGs. We ranked these TFs based on their expression in seeds and on the number of LRGs co-expressed and selected the top 22 for further validations after discarding low expressed paralogous genes. Potential target genes for these *Camelina* TFs potentially involved in the control of lipid metabolism were further studied by DNA affinity purification sequencing (DAP-seq). Enrichment analyses of targets supported the co-expression predictions and predicted TFs associated with seed fatty acid elongation, and synthesis and degradation of triacylglycerols (TAGs). We expressed these 22 TFs in *Camelina* transgenic plants driven by the soybean glycinin promoter, and the analysis of oil by NMR of T₂ seeds provided some preliminary evidence of effects on fatty acid accumulation. The results to be presented highlight the importance of the integration of multiple layers of information to guide predictive biology toward the discovery of TFs regulators of metabolic processes.

References

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