

## Transcriptional Regulatory Network Analysis to Increase Yields in Camelina

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### Project goal:

Although metabolic regulation plays a key role in controlling carbon fixation, transport and allocation in plants, genetic control at the systems-level is superimposed on metabolism and thereby constitutes a key element controlling vegetative growth and seed development. To address the genetic controls that regulate seed and oil production, we will investigate and the transcriptional regulatory networks that impact seed oil production.

### Abstract:

Understanding control of gene expression in oil producing crops is vital towards engineering a more economically feasible crop for biofuel production. To address the genetic controls that regulate seed and oil production, we are investigating and engineering the transcriptional regulatory networks that impact seed oil production. Much of what is known regarding the regulation of seed oil genes is derived from studies in Arabidopsis, a close relative of Camelina. Using this information, we have developed a gene regulatory knowledge base for Camelina using the published and publicly available Camelina RNA-seq datasets that will contain various analytical and computational tools with a friendly user interface. The database also includes transcription factors and co-regulators classified into different families as well as lipid gene annotations and homologs in Camelina. This will serve as a useful resource for the research community for accelerated discovery in elucidating regulatory mechanisms essential to their needs.

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