Distal cis-regulatory elements regulate tissue-specific water-deficit response

Maud Fagny, Johann Joets, Olivier Turc, Claude Welcker, Anthony Venon, Harry Belcram, François Tardieu, Sylvie Coursol, Clémentine Vitte

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Introduction

Understanding the molecular bases of crops response to environment is crucial for adapting cultivated varieties to climate change. Crops response to environment is mainly driven by developmental modifications and determined by a complex interaction bet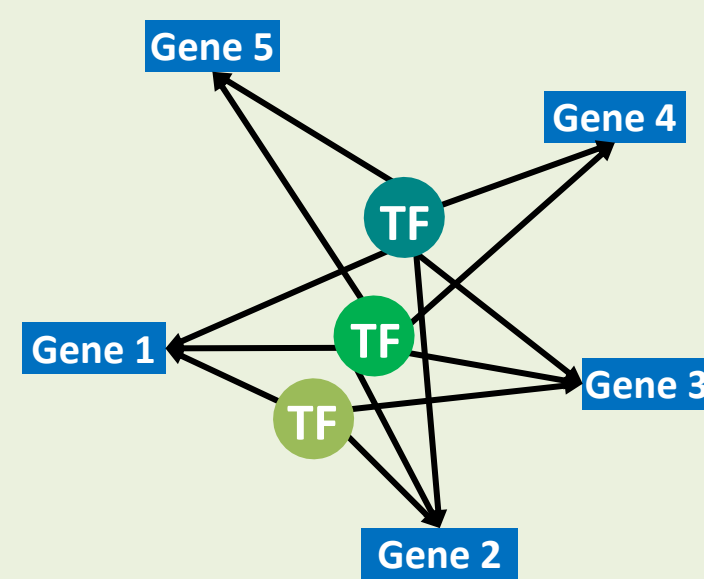ween genetic background and environment. However, these GxE interaction remain largely unknown. Distal *cis*-regulatory elements (dCRE), including enhancers and silencers, are key players in the spatio-temporal coordination of gene expression during development and in response to environment. They activate complex genome-wide regulatory networks. While annotating dCRE in a genome is now largely feasible, identifying the target genes of these elements in non-model species is challenging. Functional biology experiments are costly, and dCRE can target different genes in different cell types, and not necessarily the closest genes. For these reasons, the contribution of dCRE-articulated regulatory networks to crops response to the environment remains poorly understood. **Here we aim to address two questions: (1) What role plays the dCRE in the regulating gene expression in response to water deficit in crops? (2) Are the regulatory networks of some tissues more impacted by water deficit than others?** Using maize and its response to water deficit as a model, we investigate the extent of the gene regulatory network rewiring in response to environment in several tissues. We first generated RNA-Seq data from seven tissues of the inbred line B73 grown in two watering conditions. Using the NetZoo software suite, we integrated these data with genomic and DNA methylation data to model the tissue- and condition-specific regulatory networks between transcription factors binding the dCRE and their potential target genes.
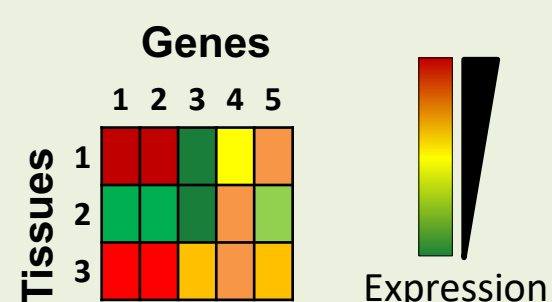
Methods

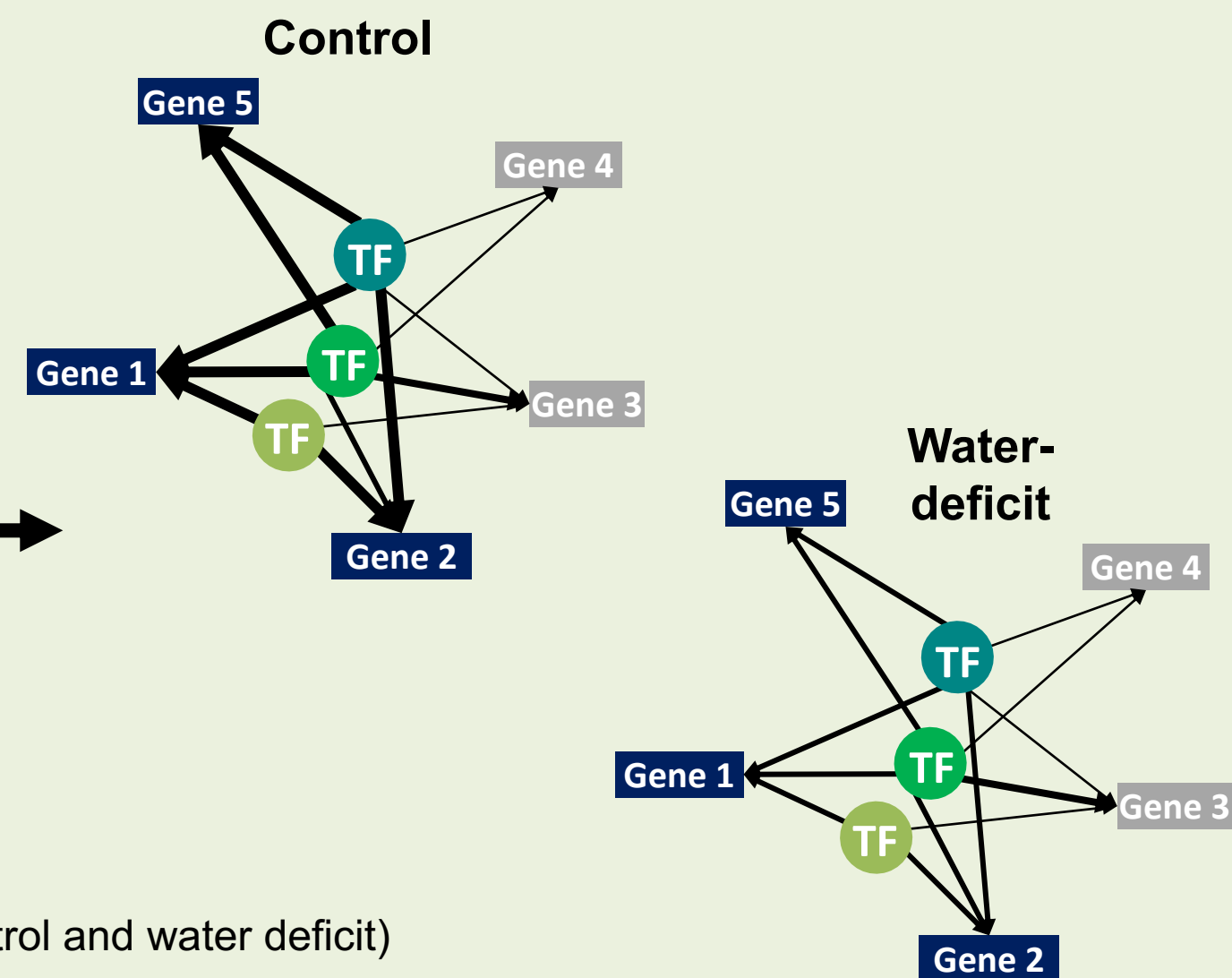**Annotation of TFBS & Potential target genes**

« Prior » GRN

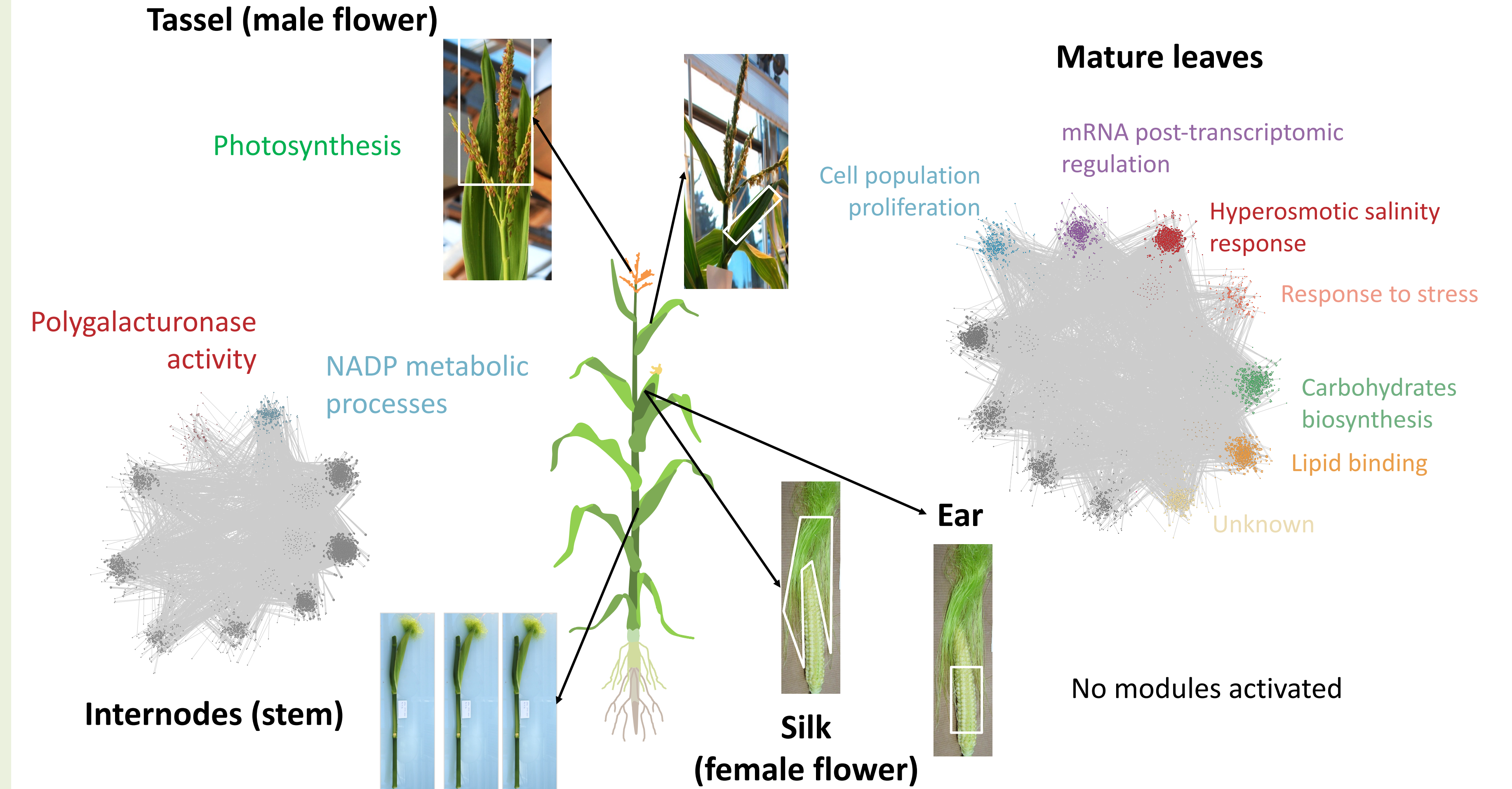**Tissue-specific networks**
(NETZOOPY - https://netzoo.github.io/)

Control

Water-deficit

Gene
Potential target genes

Gene
Non-target genes

Gene
True target genes

TFBS = transcription factor binding sites
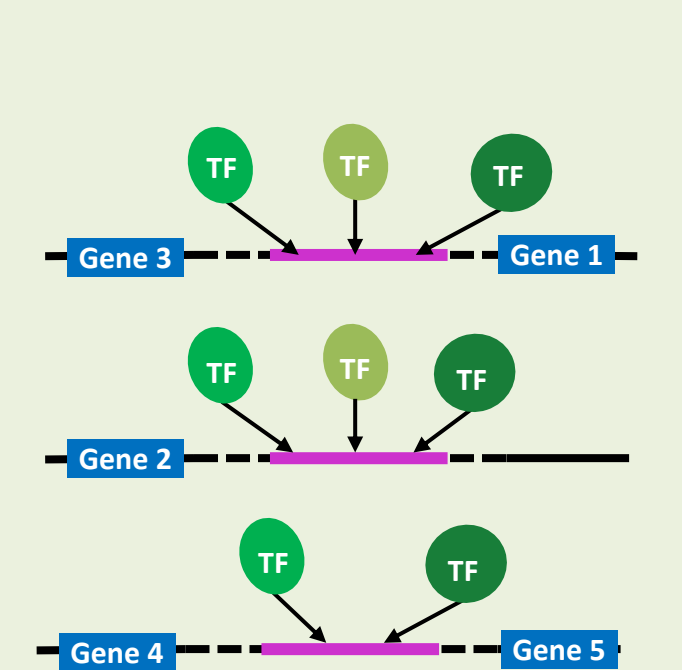
Co-expression data

Genes

Expression

B73 (model maize line)
- ✓ 7 tissues
- ✓ 2 watering condition (control and water deficit)

Results

Tassel (male flower)

Photosynthesis

Polygalacturonase activity

NADP metabolic processes

Internodes (stem)

Mature leaves

Cell population proliferation

mRNA post-transcriptomic regulation

Hyperosmotic salinity response

Response to stress

Carbohydrates biosynthesis

Lipid binding

Unknown

Ear

Silk (female flower)

No modules activated

Conclusions

We show that gene regulatory network inference methods are efficient tools to identify target genes of dCRE involved in maize response to water deficit. This varies across tissues in terms of both magnitude of regulatory network rewiring and categories of biological functions activated. Maize response to water deficit involves, at the molecular level, a profound rewiring of the gene regulatory networks articulated by dCRE. Mutation at these elements could thus play a crucial role in determining tolerance to water deficit in maize.

Fundings