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Systems genetics of drought-related traits in maize

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Objective and strategy

The evolution of maize yields under drought is of particular concern in the context of climate change and human population growth. To better understand the mechanisms associated with the genetic polymorphisms underlying the variations of traits related to drought tolerance, we used a systems genetics approach integrating high-throughput phenotypic, proteomics and genomics data acquired on 254 half-sibs maize hybrids grown under well watered (WW) and mild water deficit (WD) conditions (Fig. 1).

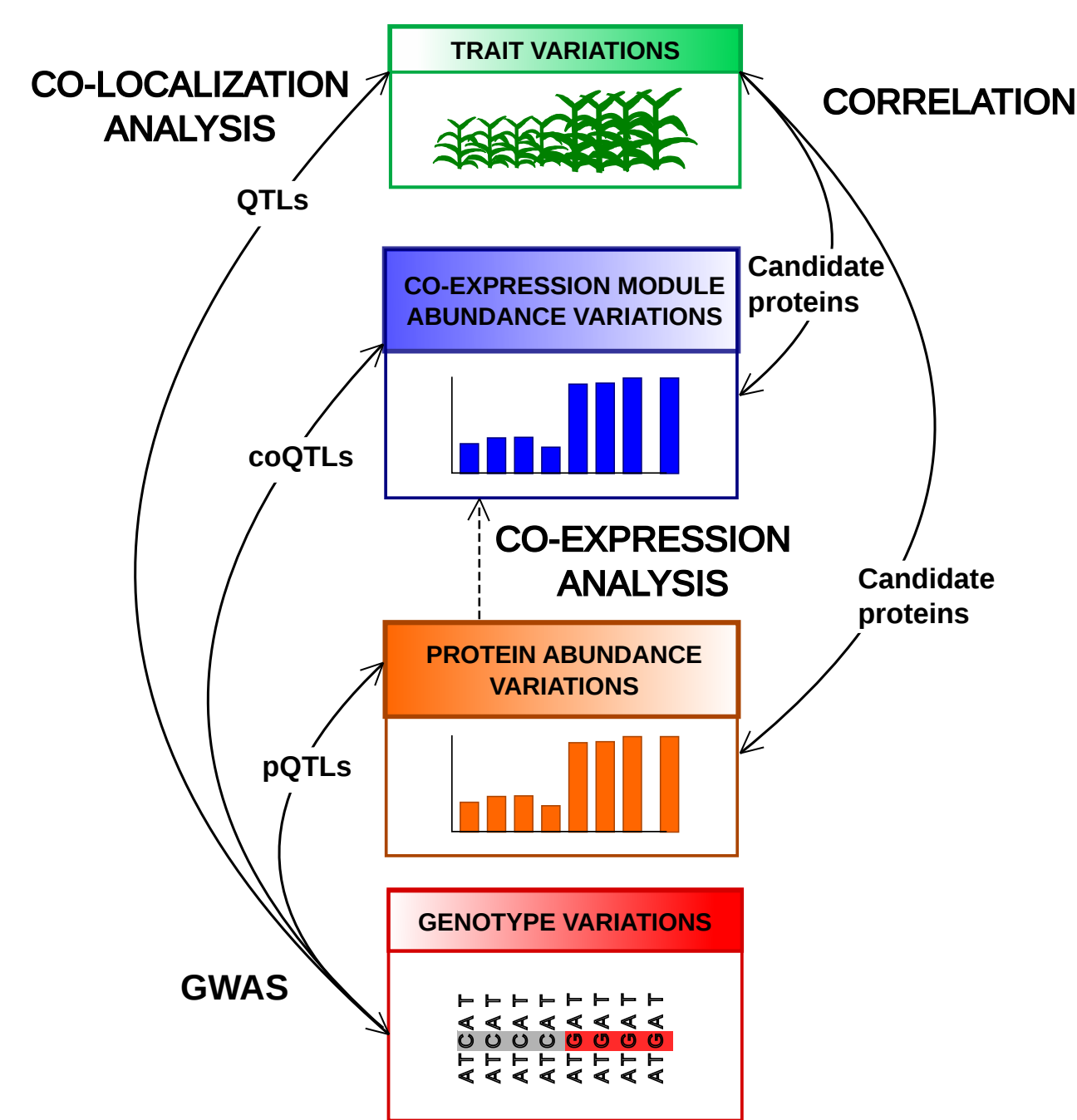


Fig. 1: Schematic representation of the systems genetics approach. Protein abundances were first analyzed by using genome wide association study (GWAS) and co-expression networks. Then, they were integrated with phenotypic data measured for drought-related trait in the same conditions through correlation analysis and search for QTL/pQTL co-localizations.

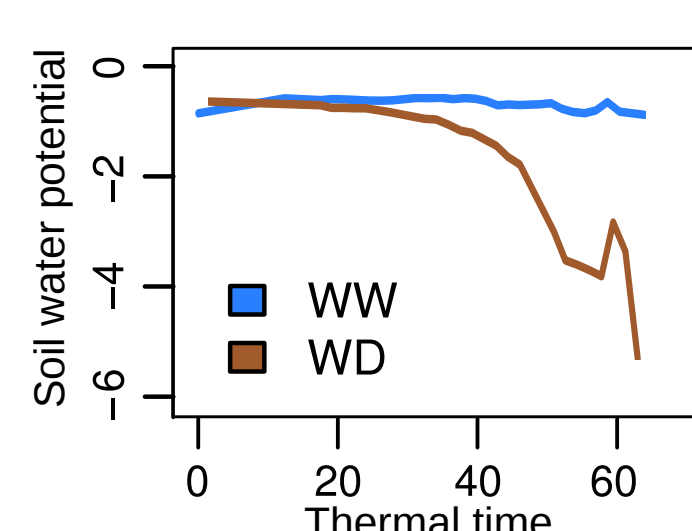
Experimental pipeline



254 genotypes grown in PhenoArch (Montpellier, France)



1,016 leaf samples (254 genotypes x 2 conditions x 2 replicates) taken at the pre-flowering stage



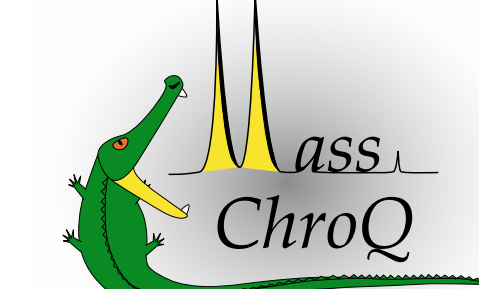
Ecophysiological parameters measured during plant growth



Mass-spectrometry-based proteomics analysis



Protein identification and inference using X!TandemPipeline [1]



Peptide quantification using MassChroQ [2]



GWAS using FaST-LMM [3] (961,971 SNPs tested)



Data analyses using R

Water deficit has extensively remodeled the proteome

- About 75% of the 1,950 quantified proteins showed significant abundance changes in response to water deficit (Fig. 2). These included several stress and drought-response proteins.

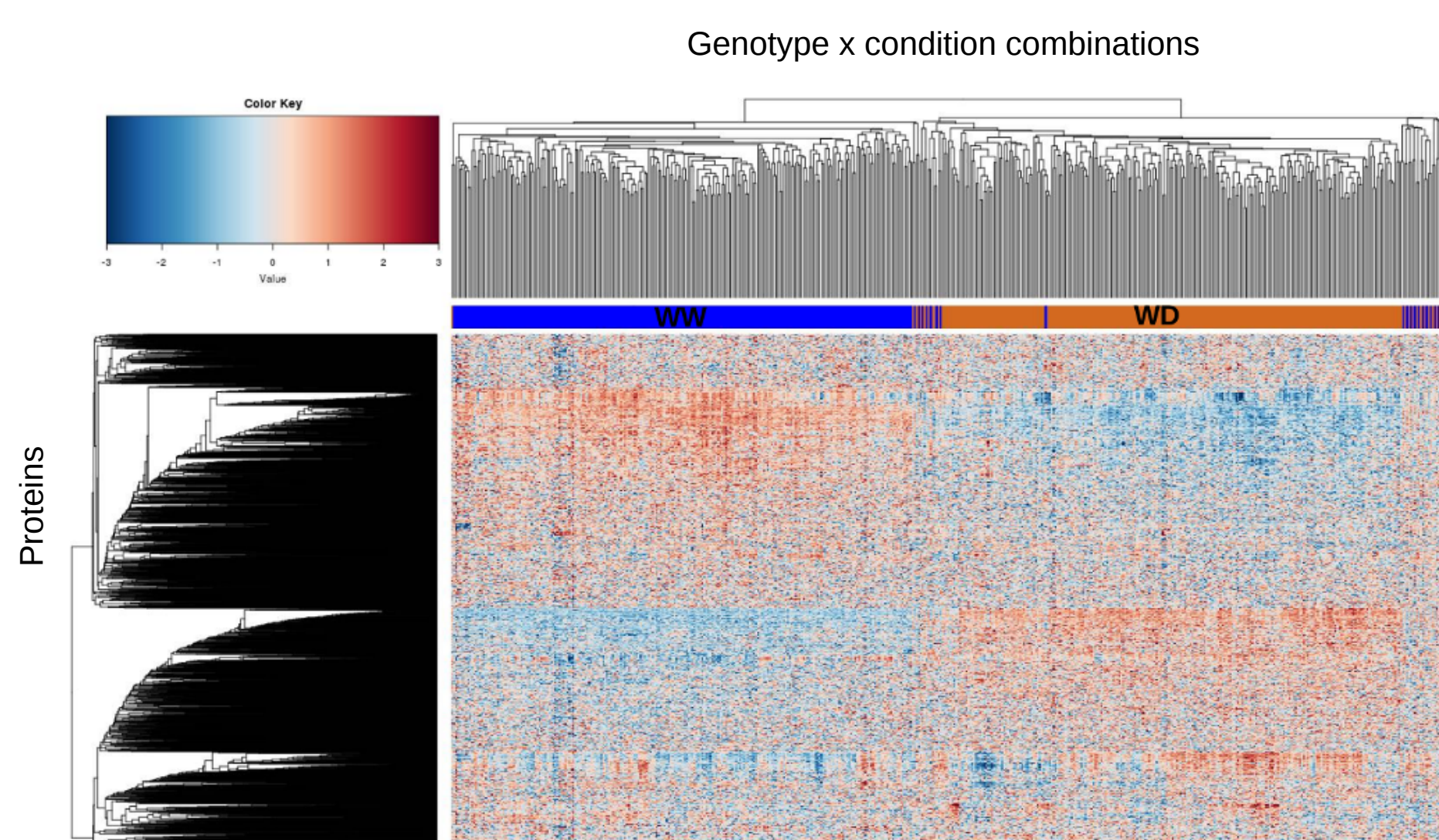


Fig 2: Heatmap representation of protein abundances showing that water deficit has extensively remodeled the proteome.

- 29,004 pQTLs were detected by GWAS for 95% of the 3,900 (=1,950 proteins x 2 conditions) molecular phenotypes. Only 8.4% of the pQTLs detected in the WW condition had a co-localizing pQTL in the WD condition, suggesting that water deficit has deeply impacted the genetic regulation of protein expression (Fig. 3).

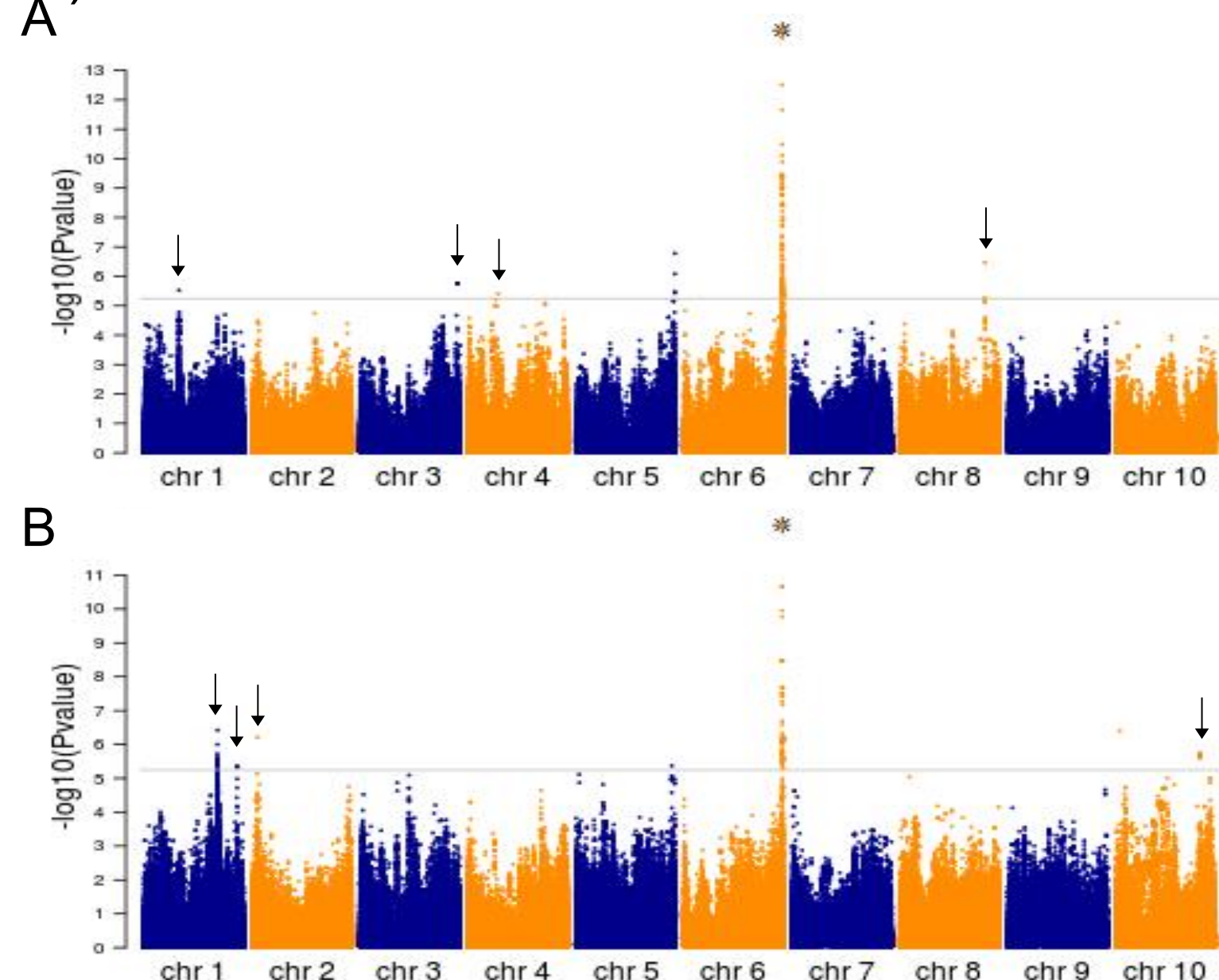


Fig 3: Example of the Manhattan plots obtained in the WW (A) and WD (B) conditions for a same protein. Black arrows indicate pQTLs detected in only one of the two conditions. Stars indicate the position of the protein encoding gene.

Identification of genomic regions involved in multi-scale genetic control

- Co-expression networks were built from protein abundances in each environment, showing that stress proteins were specifically co-expressed under WD (Fig. 4).

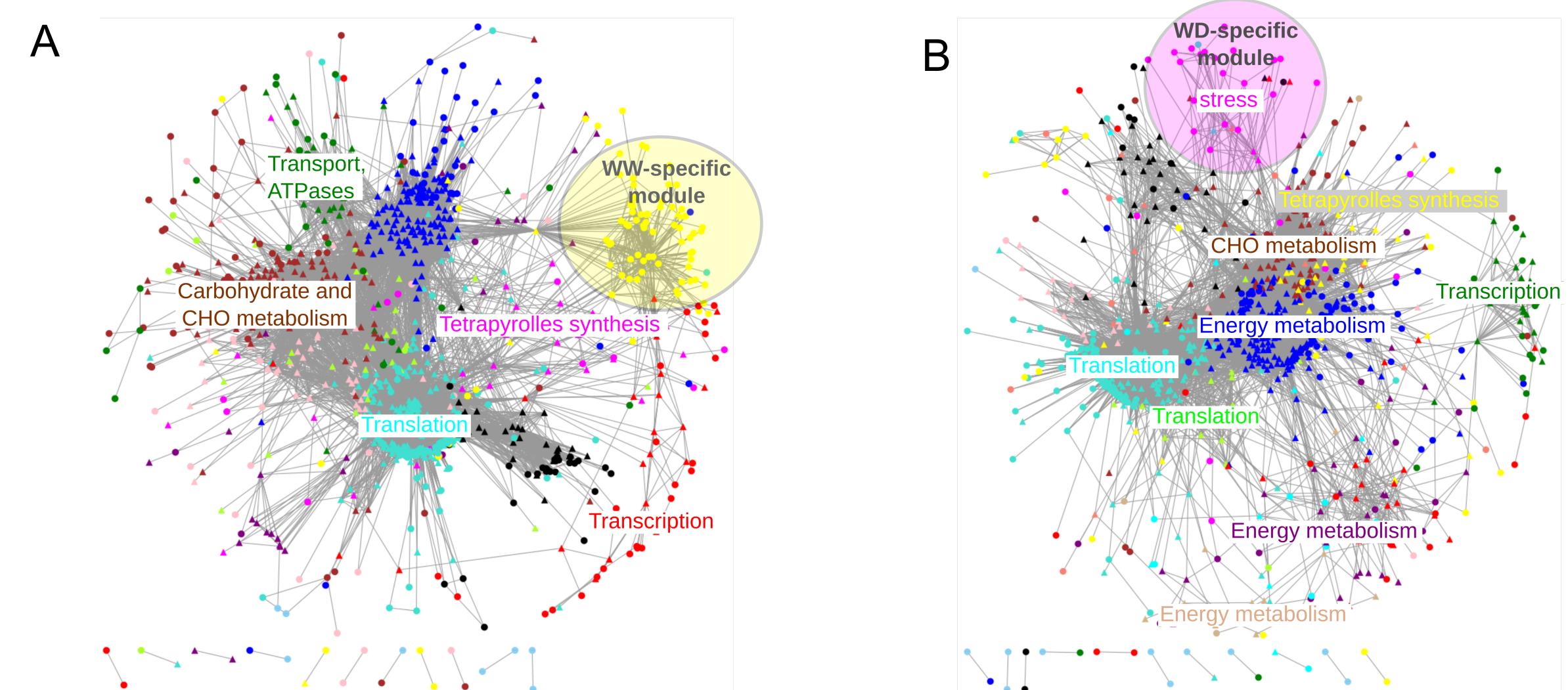


Fig. 4: Representation of the co-expression networks in WW (A) and WD (B). Functional enrichments and condition specificities are indicated.

- 369 co-expression QTLs (coQTLs obtained by submitting the abundance values representing each co-expression module to GWAS) were detected. Co-localizations between QTLs, pQTLs, and coQTLs indicated the presence of genomic regions involved in the genetic control of traits at different levels of biological complexity and highlighted promising underlying candidate genes (Fig. 5).

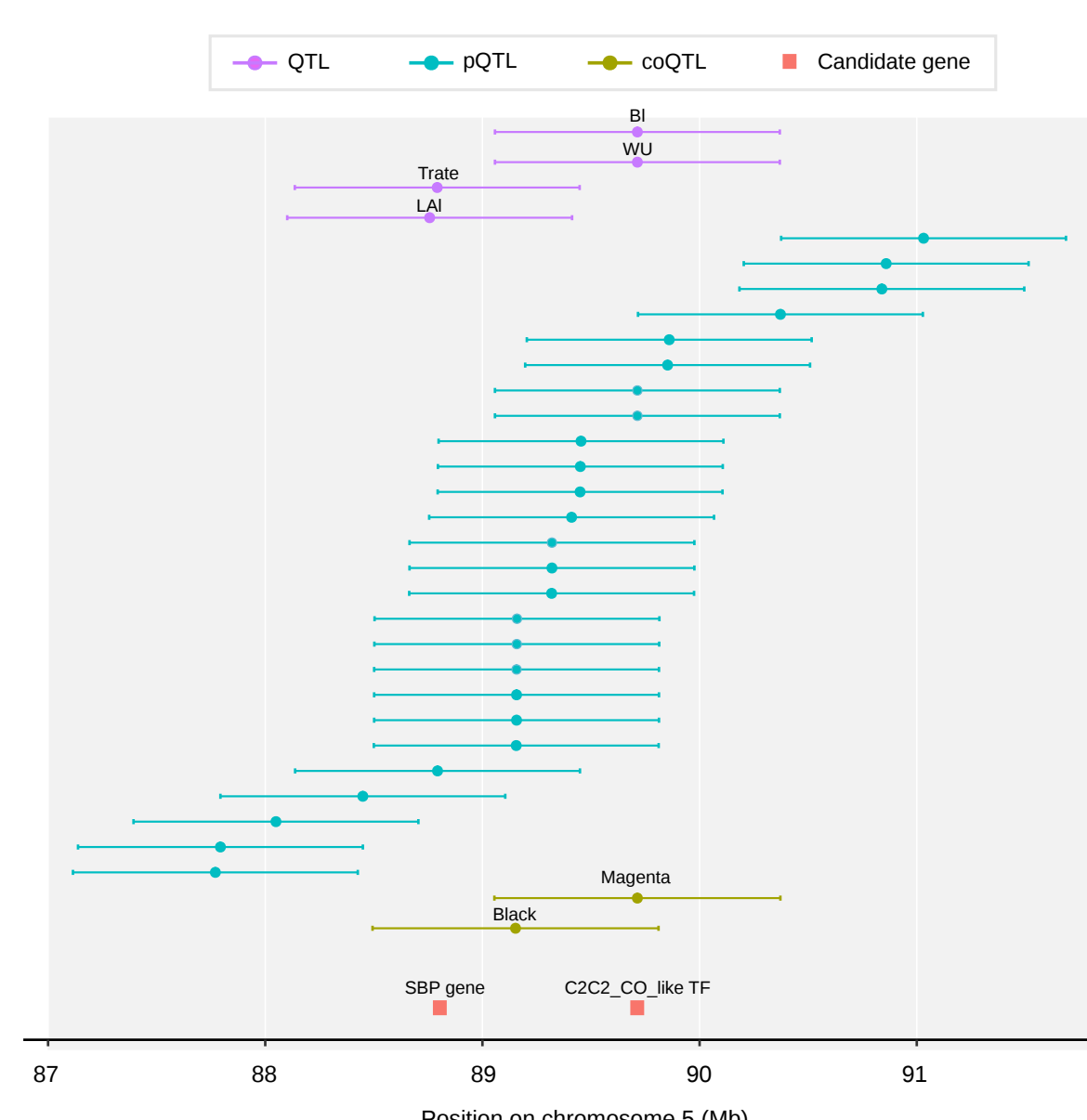


Fig. 5: Detailed view of the QTLs, pQTLs, coQTLs and promising candidate genes detected in a region of chromosome 5 representing a hotspot of protein expression regulation. Dots represent the SNPs determining the position of the QTLs and horizontal bars represent the linkage disequilibrium-based window around each SNP.

Conclusions

By using a systems genetics approach including MS-based proteomics data, we highlighted several original results. We showed that water deficit, even mild, induced a strong proteome remodeling and a reprogramming of the genetic control of the abundance of many proteins, notably those involved in stress and drought responses. We identified close co-localizations between QTLs and pQTLs in the WD condition, thus highlighting environment-specific pleiotropic loci associated to the co-expression of drought-responsive proteins and to the variations of phenotypic traits. These findings bring several lines of evidence supporting candidate genes at many loci and provide novel insight into the molecular mechanisms of drought tolerance.