*les dossiers*
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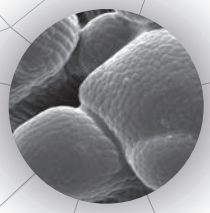
*Expertise of the scientific community in the Occitanie area (France)*

# COMPLEX SYSTEMS
## *From biology to landscapes*



Number 23
February 2019

# Analysis of regulatory networks of genome expression controlling stress adaptation

Gene expression is regulated by different mechanisms under genetic and epigenetic control. The first level depends on the epigenome dynamics and involves the condensation of chromatin bound to histone marks that determine the accessibility of the genomic sequence to transcription protein complexes. The second level is gene transcription regulation, which includes cytosine methylation-driven epigenetic regulation of promoters, as well as transcription activation regulation by cis- (regulatory box) and trans-regulatory elements. The third level concerns post-transcriptional regulation involving noncoding microRNAs that cleave target gene transcripts or inhibit their protein translation. Finally, post-translational modifications affect protein activity.

The BURST* team (AGAP joint research unit [UMR]) studies these mechanisms using omics data (transcriptomics, microtranscriptomics, degradome analysis and metabolomics), biology-type network analysis and validation using functional genomics approaches. These data are integrated and represented using bioinformatics tools such as Mixomics, weighted gene co-expression network analysis (WGCNA), etc. Analyses at this level generate a more comprehensive understanding of the regulation of perennial species under stress, while identifying the adaptive mechanisms involved and allele combinations that could enhance prebreeding programmes.

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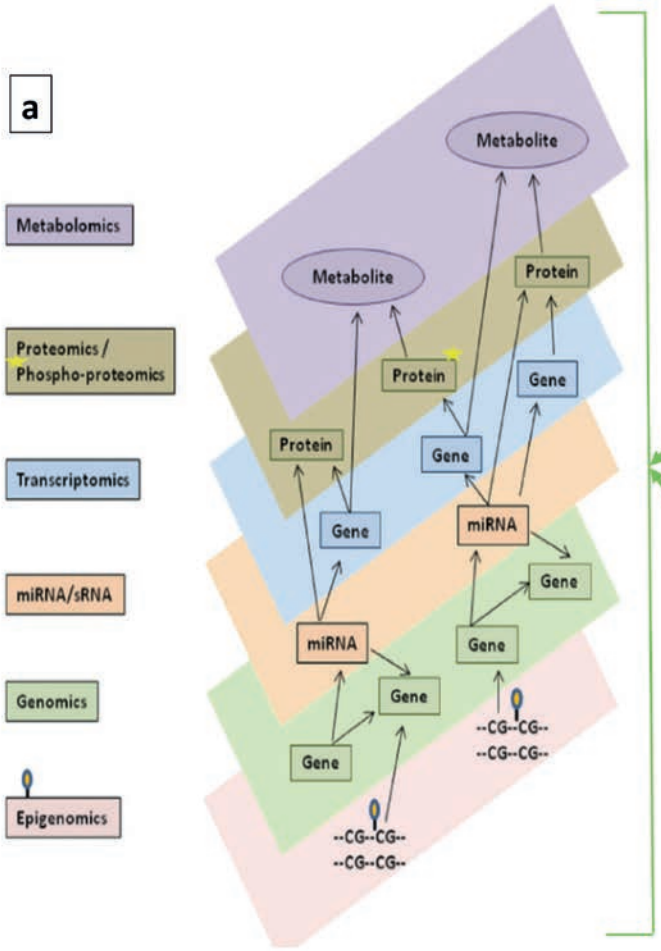
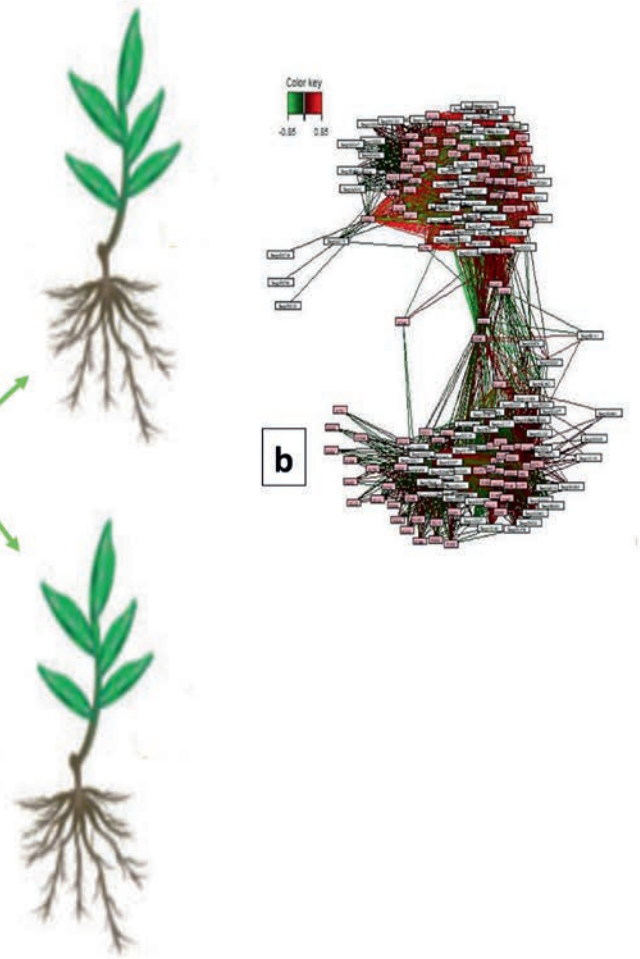
* Adaptation to abiotic stress in perennial species (BURST)




▲ *A. Integrative diagram of various levels of global genome to phenotype analyses and linkages with genetic analyses of traits of agronomic value.* From Shakhawat, 2015.




▲ *B. Integration of transcriptomics (white) and metabolomics (pink) data in eucalyptus (Favreau, in prep).*