Phenotypic and transcriptional plasticities in response to drought in black poplar

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Context

Drought severity and frequency are increasing with climate changes, and threatening plant survival. It is acknowledged that phenotypic plasticity is a key lever in plant response to environmental fluctuation, but little is known concerning transcriptional plasticity in water fluctuating conditions.

This project explore relationships between ecophysiological and transcriptional responses including their plasticities to identify genes involved in drought tolerance.

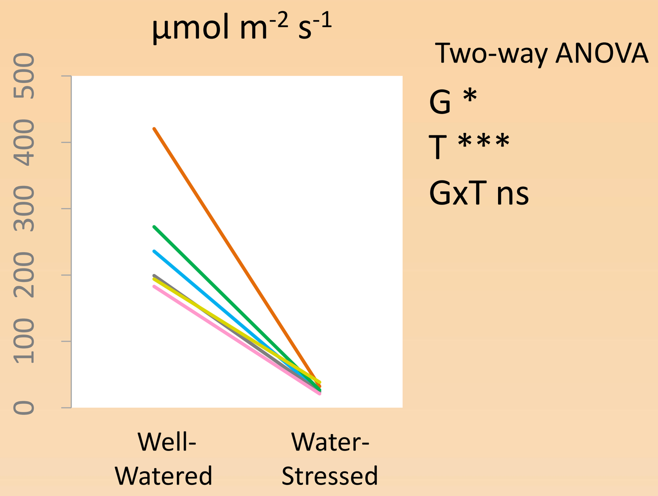
Six poplar genotypes were tested for progressive water stress. Ecophysiological traits (hydraulic and physiological traits, growth, development, leaf architecture) were monitored until predawn leaf water potential reached -2 MPa. At this time, leaves exclusively developed during drought were sampled to explore transcriptional regulations by RNAseq.

Drought affects ecophysiological and transcriptional responses of poplar genotypes

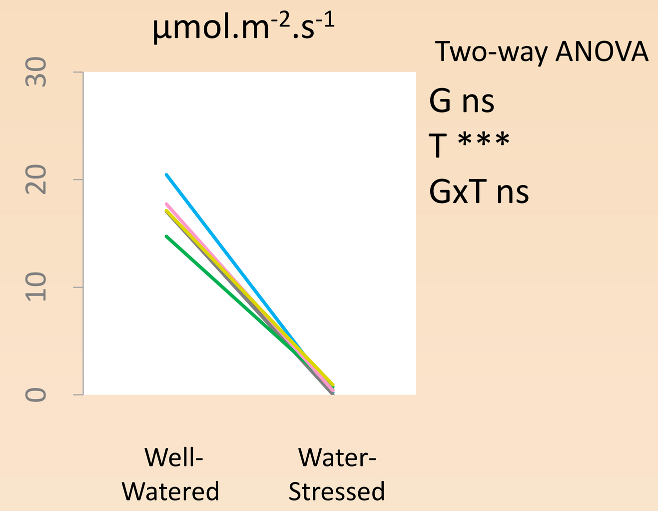
Water fluxes and physiological variations

Genotypes: ALL29, ERS05, SPM12, SPM28, SPM40, STR10

Stomatal conductance

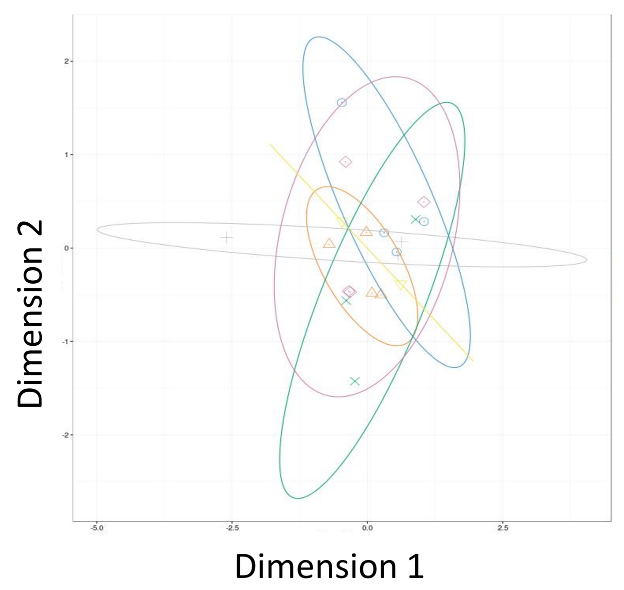


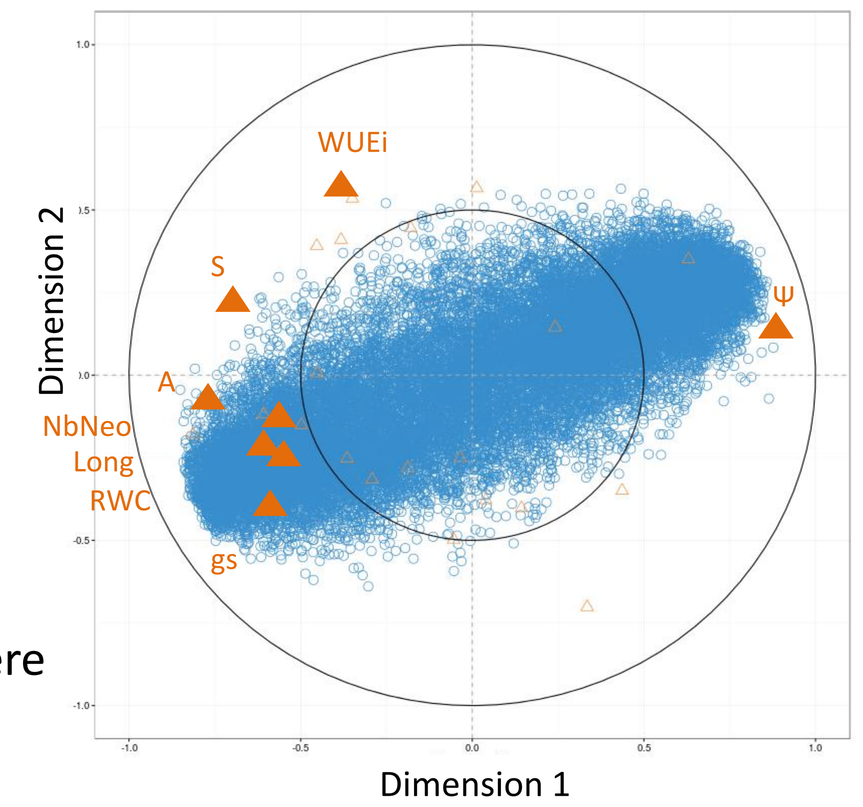
Net assimilation rate



Drought poplars limited water loss by closing stomata. Primary metabolism was stopped because of the lack of water fluxes.

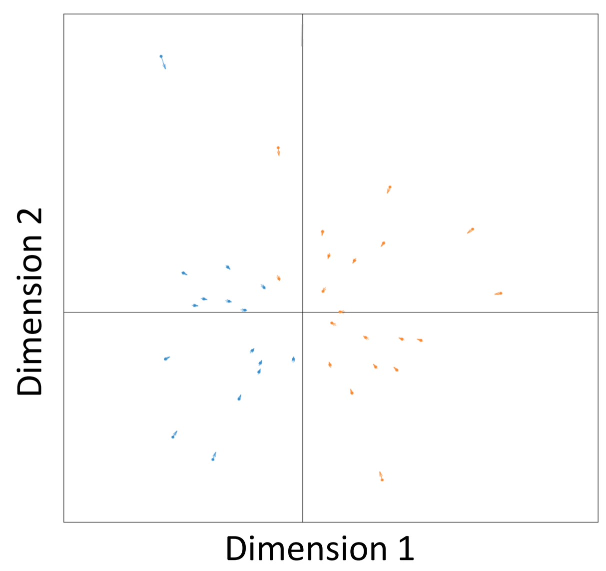
Genotype effect





Responses to drought were specific of six poplar genotypes.

Water treatment effect



Drought was enough strong to induce particular responses.

Canonical Correlation Analysis on ecophysiological and transcriptional responses to water treatment of six poplar genotypes.

-The two data sets were correlated mainly by water treatment (Dim.1).

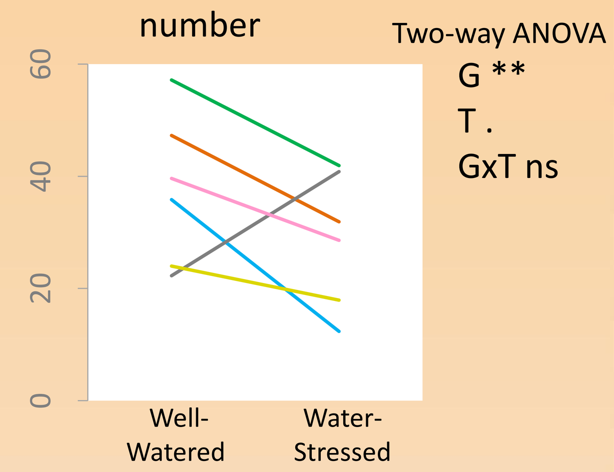
-Poplar genotypes responded similarly to drought (Dim.2) by limiting water loss (low leaf water potential *Ψ*, stomatal conductance *gs* and foliar senescence *S*). Leaf dehydration occurred (Relative Water Content *RWC*) followed by a decrease of growth and development (low net assimilation *A*, longitudinal growth *Long*, production of new leaves *NbNeo* and intrinsic Water Use Efficiency WUE_i).

- Transcripts were distributed along the first axes by their differential expression.

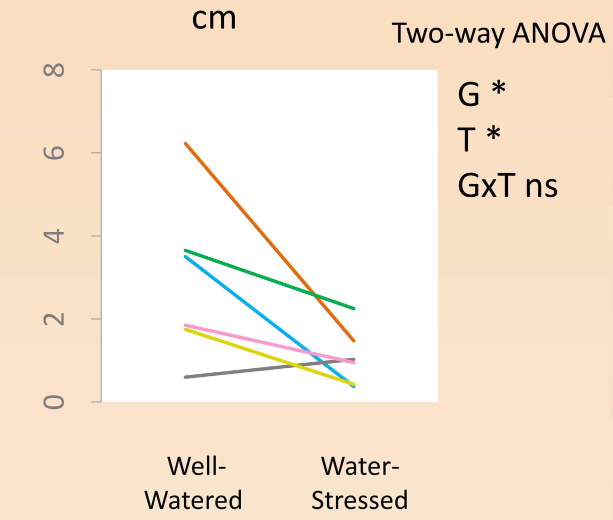
Growth and development variations

Genotypes: ALL29, ERS05, SPM12, SPM28, SPM40, STR10

Production of new leaves



Branch longitudinal growth

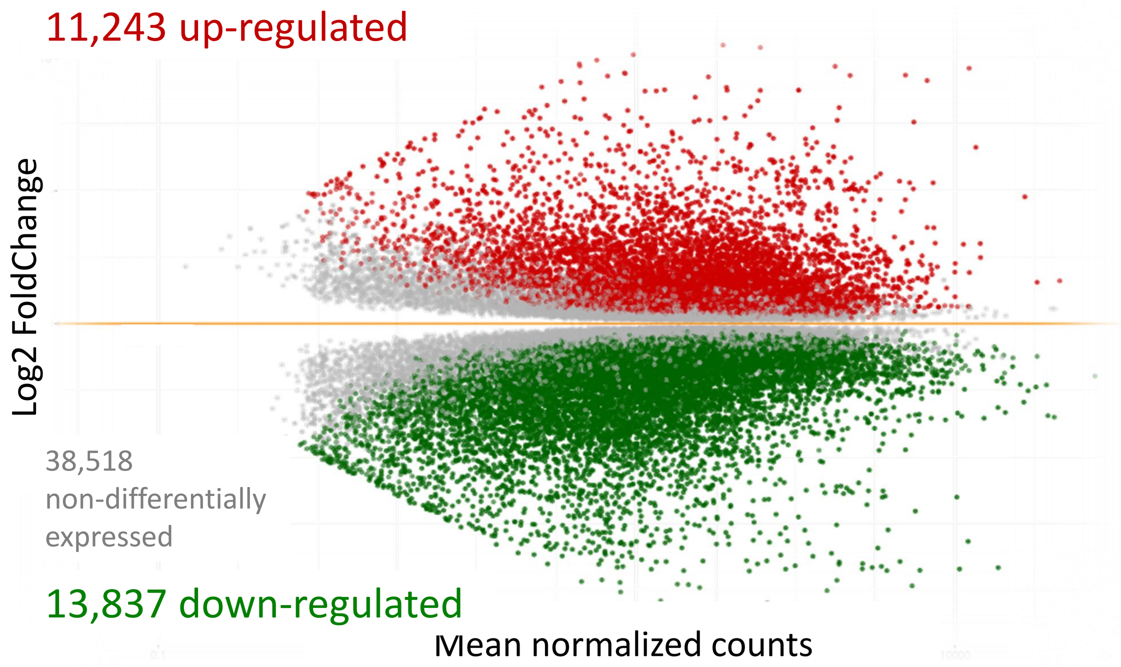


Drought induced a decrease of leaf production and growth except for SPM12 genotype.

Focus on … Leaf transcriptional data

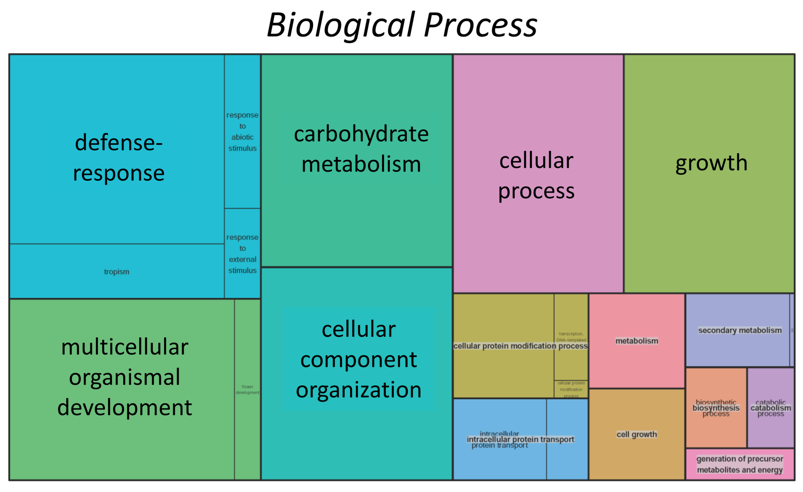
Differential expression of leaf transcripts in response to drought.

63,598 *P.nigra* transcripts were mapped on *P.trichocarpa* reference transcriptome (73,013 transcripts). 39.4% of transcripts are differentially expressed (Log2 Fold Change) in response to drought. False Discovery Rate = 0.1‰.

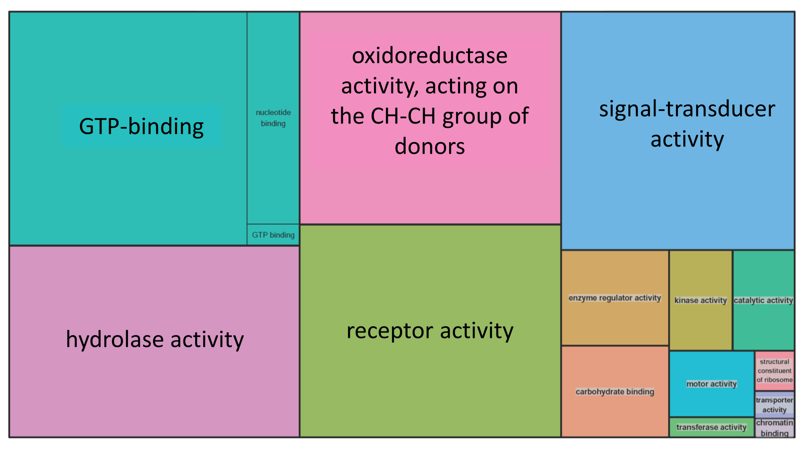


Transcriptional plasticity

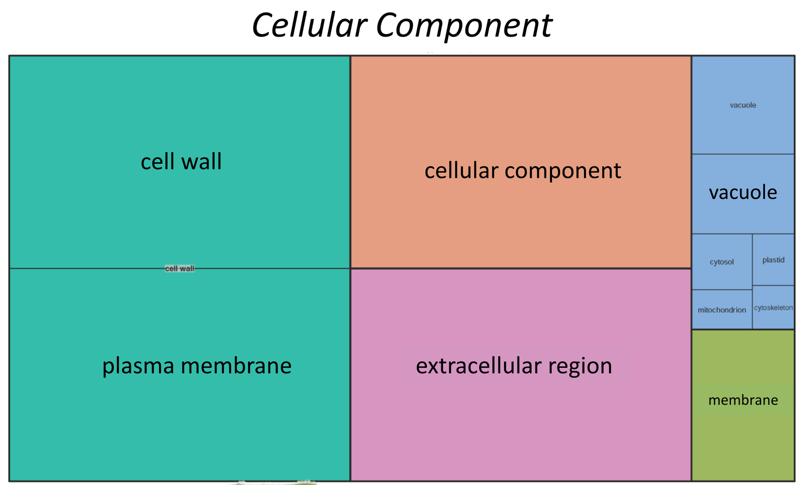
Biological Process



Molecular Function



Cellular Component



Plasticity Calculation

Relative Distance of Plasticity Index

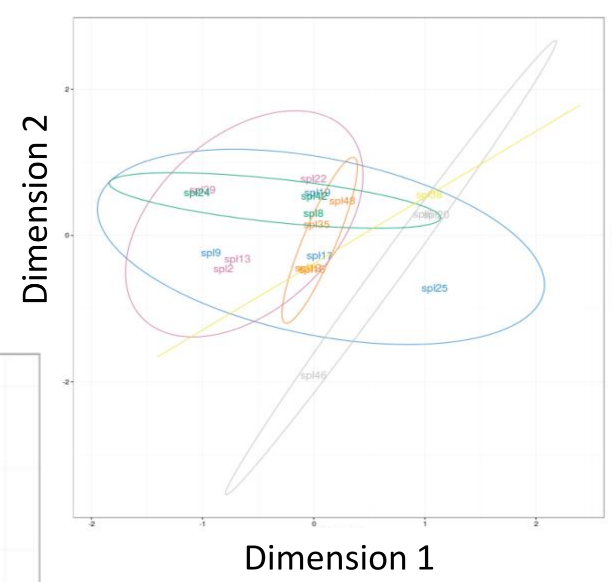
Valladares et al. 2006

$$RDPI = \frac{\Sigma\,|xij - xi'j'|\,/\,(xij + xi'j')}{n}$$

1 WS tree
1 WW tree
Paires number

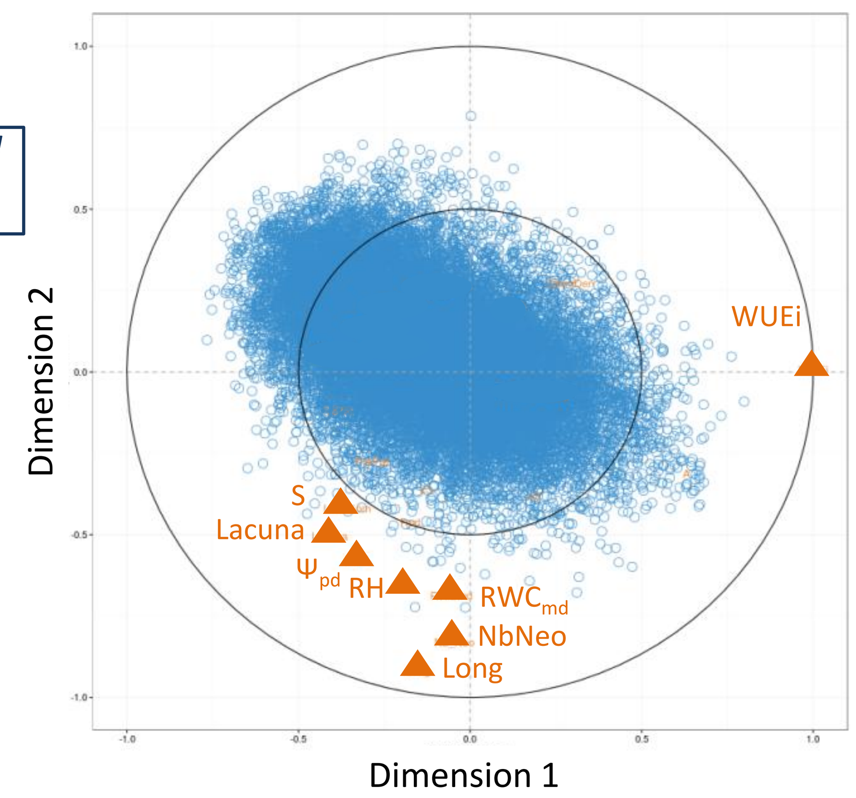
ALL29, ERS05, SPM12, SPM28, SPM40, STR10

Genotype effect



Over-represented Gene Ontology ←

N.B. Polygon size depends on Khi² test's significativity. Go terms of the same class are grouped with similar color.



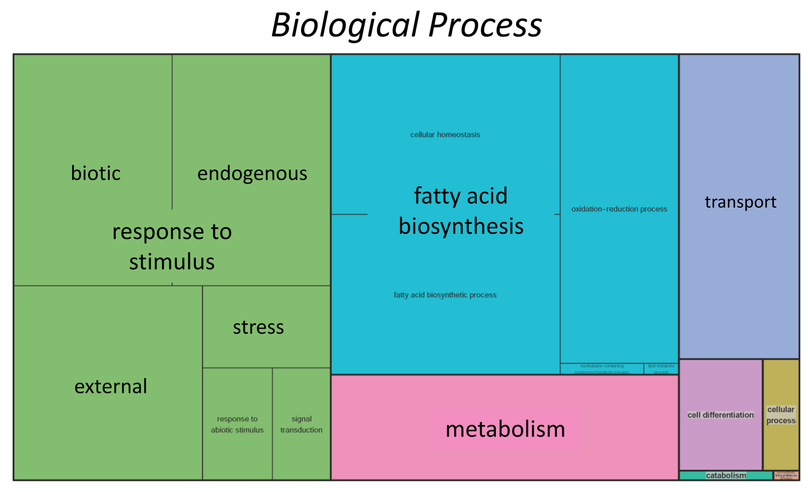
→ *Over-represented Gene Ontology*

Canonical Correlation Analysis on ecophysiological and transcriptional plasticities of six poplar genotypes.

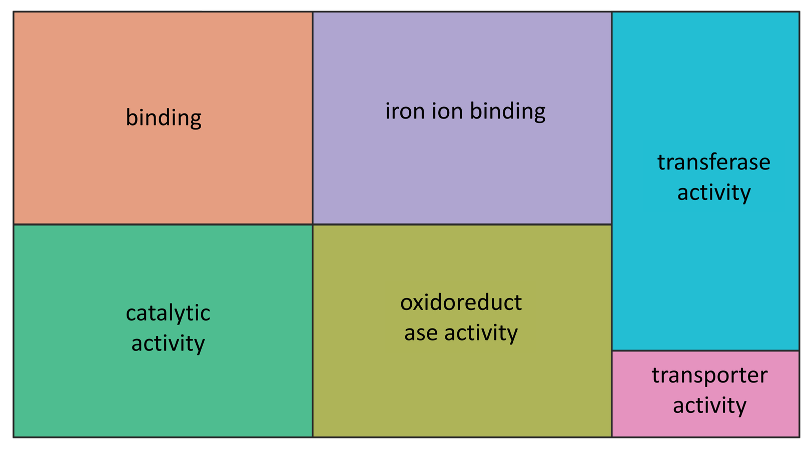
-In water fluctuating environment, poplars responded by modulating ecophysiological and transcriptional plasticities. Many traits were particularly impacted characterizing leaf hydraulic status (leaf water potential Ψ_{pd}, intrinsic Water Use Efficiency *WUEi*, Relative Water Content *RWC*, Relative Humidity *RH*), growth and development (production of new leaves *NbNeo*, foliar senescence *S*) and leaf architecture (lacuna proportion *Lacuna*).

-Informative transcriptional plasticity concerned two anti-correlated transcripts groups with a total of 1,624 transcripts.

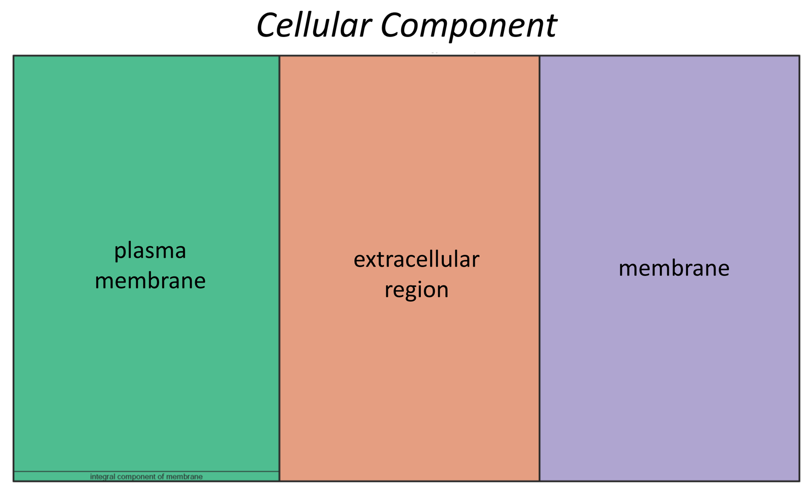
Biological Process



Molecular Function



Cellular Component



Conclusions

-Ecophysiological strategies in response to severe drought were similar among poplar genotypes.
-There is no correlation between expression level of transcripts and their plasticities.
-Genotypes can be characterized thanks to their ecophysiological and transcriptional plasticities.
-Transcripts were identified for their particular plasticity in response to fluctuating water supply.
Some of them will deserve additional in-depth attention.

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