

Acclimation of Populus to wind: kinetic of the transcriptomic response to single or repeated stem bending

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Lise Pomies, Mélanie M. Decourteix, Jérôme J. Franchel, Bruno B. Moulia, Nathalie Leblanc-Fournier. Acclimation of Populus to wind: kinetic of the transcriptomic response to single or repeated stem bending. IUFRO Genomics and Forest Tree Genetics Conference, May 2016, Arcachon, France. IUFRO, 1 p., 2016. hal-02739238

$\begin{array}{c} {\rm HAL~Id:~hal\text{-}02739238} \\ {\rm https://hal.inrae.fr/hal\text{-}02739238v1} \end{array}$

Submitted on 2 Jun 2020

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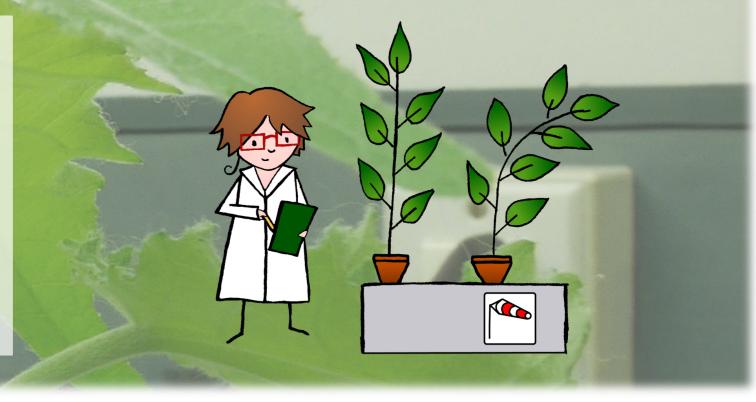
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Acclimation of Populus to wind: kinetic of the transcriptomic response to single or repeated stem bending.

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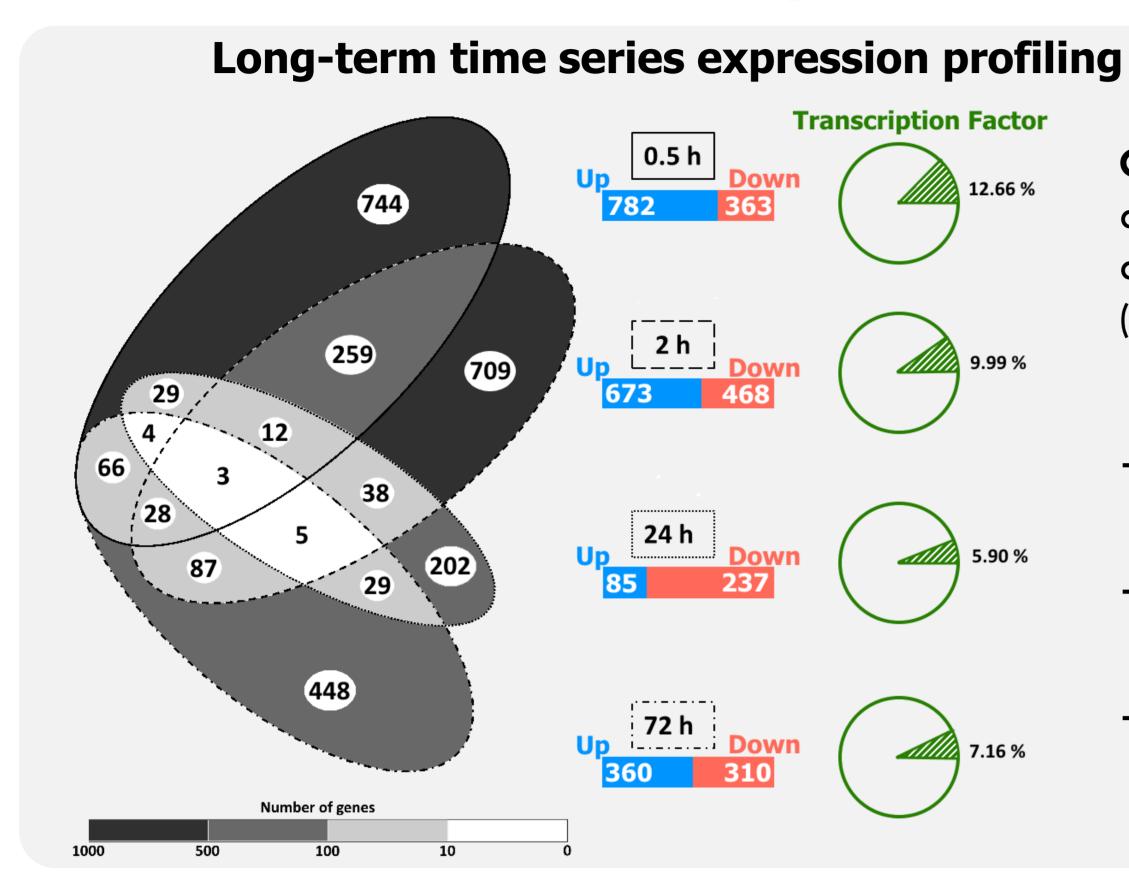
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Storms are the 1st cause of damages to European forests. Trees are sensitive to stem bending due to chronic wind. After 1 bending, they respond by modifying their growth during several days [1]. However, repeated stem bending induce a reduction in tree responsiveness, a phenomenon called accommodation [2][3]. Due to climate changes, strong wind may be more frequent [4]. How will trees acclimate or not to such new wind regimes?

First global and kinetic picture of molecular responses to stem bending



Gene expression modifications were assessed at 0.5 h, 2 h, 24 h and 72 h after a transitory controlled bending (with Affymetrix microarray).

- → 2,633 differentially expressed genes (DEG)
- \rightarrow 75.6% of DEG are detected at 0.5 h and 2 h after the bending
- → Many DEG are detected at several time points.

Identification & characterization of temporal patterns in gene expression

k-means clustering

⇒40 different temporal patterns (clusters)

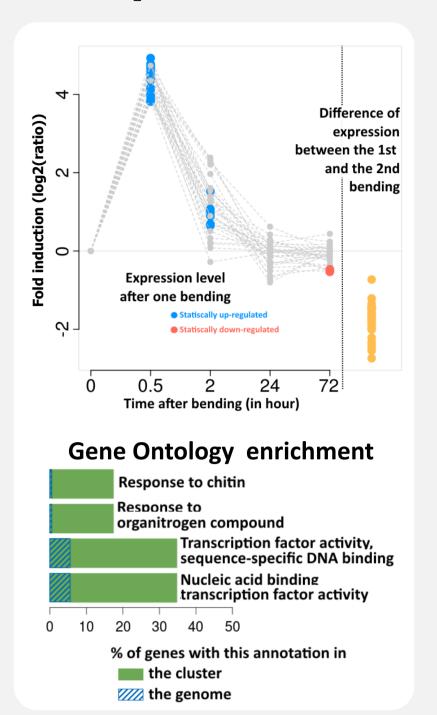
Gene Ontology (GO) enrichment in each cluster

⇒Temporal patterns are assigned

a biological function

Example: Cluster 4

31 genes up-regulated 0,5h after 1 bending with a transcription factor activity GO affiliation.



Refinement of the early time course analysis for the biological processes involved

Refined time course analysis using Q-PCR \rightarrow 6 extra time points between 0,5 h and 24 h for representative genes of each cluster

Chosen genes represent the temporal patterns and the GO annotations of the cluster.

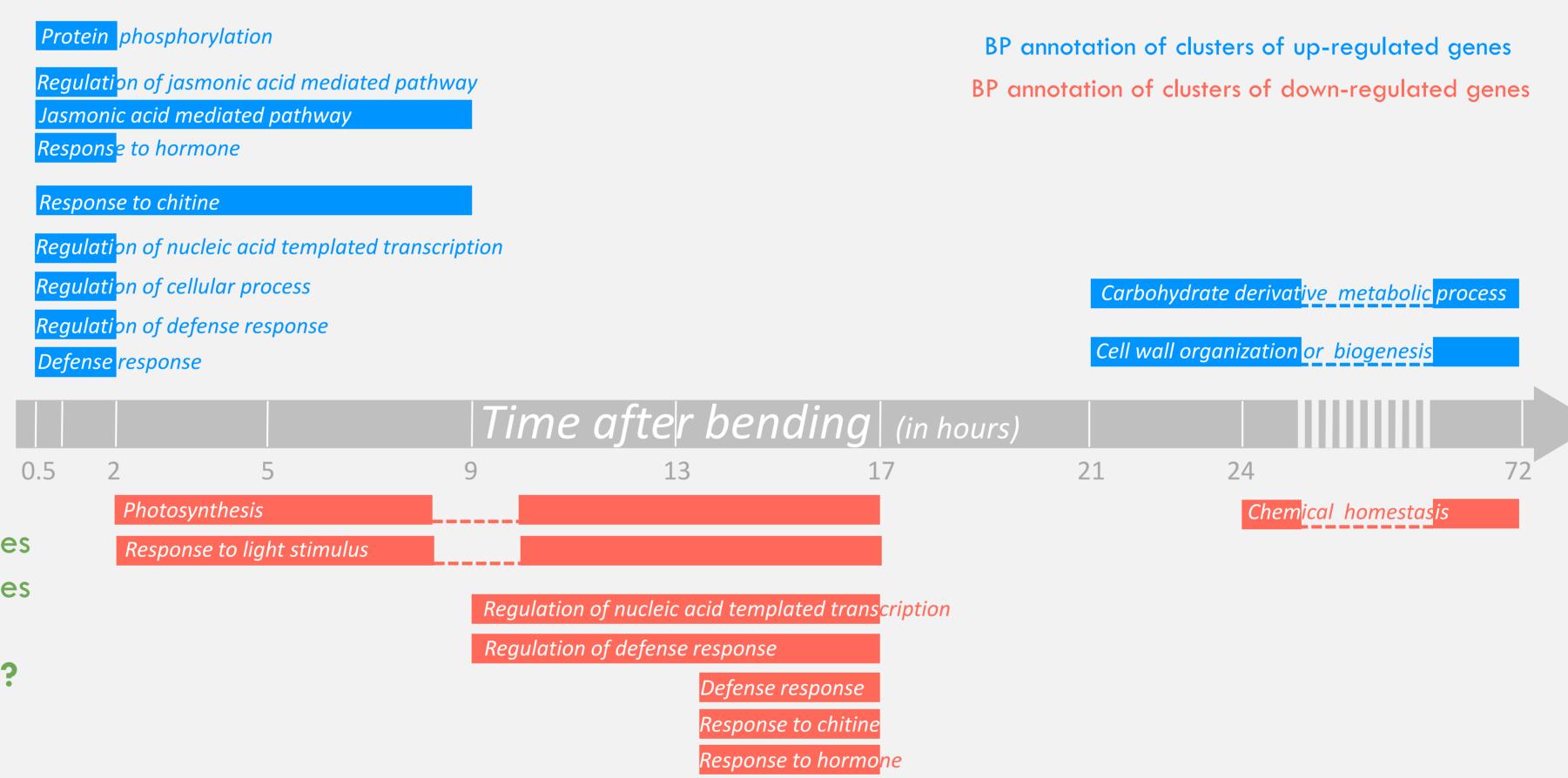
•Early regulated genes are related to "stress response":

- Transcription factors families (e.g. fig. A);
- -Jasmonic acid and ethylene signaling (e.g. fig. B).

•Some early up-regulated genes are down-regulated in later stages (see PtaJAZ2 fig. B)

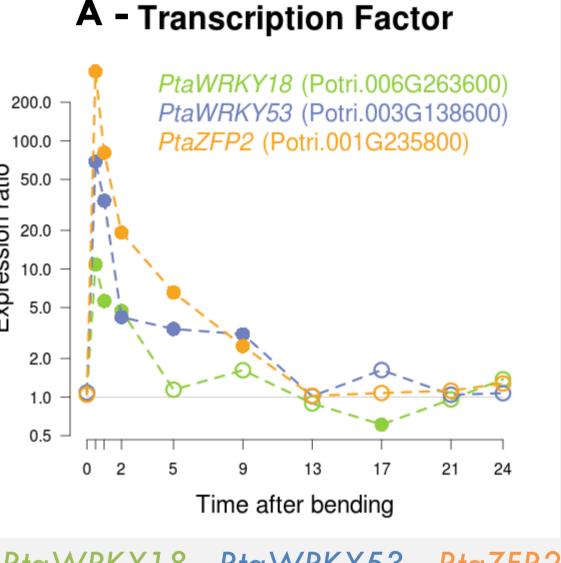
→ negative feedback mechanism?

•Late up-regulated genes (21 h -72 h), seem to be linked to a remodeling of cell wall-related processes.

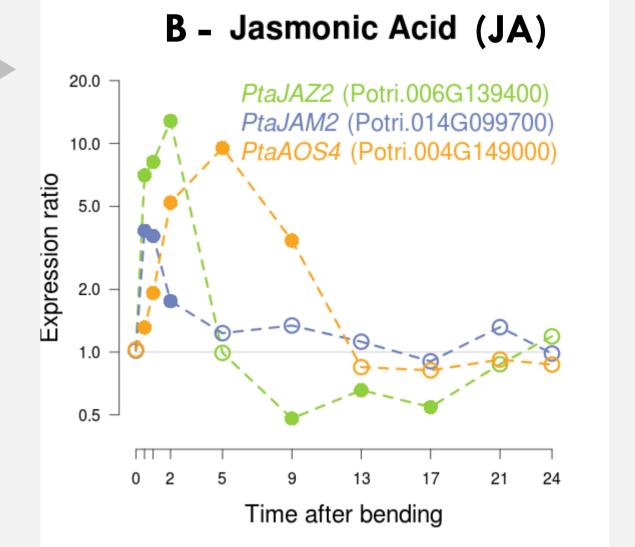


Regulation of jasmonic acid mediated signaling pathway

Jasmonic acid mediated signaling pathway



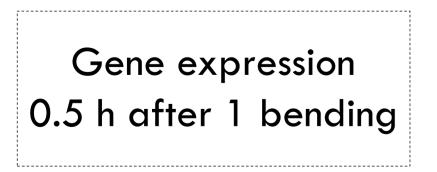
PtaWRKY18, PtaWRKY53, PtaZFP2 (C2H2): transcription factors



PtaJAZ2, PtaJAM2 JA-induced transcription factors, negative regulator of JA responses PtaAOS4, allene oxide synthase, JA biosynthetic pathway

Toward a better understanding of the accommodation process

Objectives: to investigate the extent of the molecular accommodation and to identify potential molecular actors.

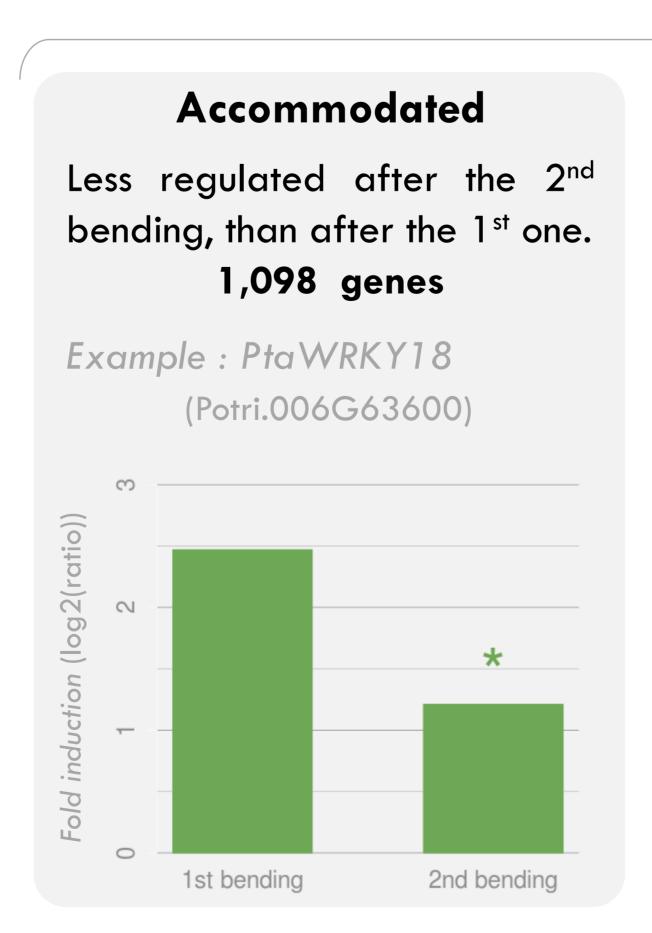


VS.

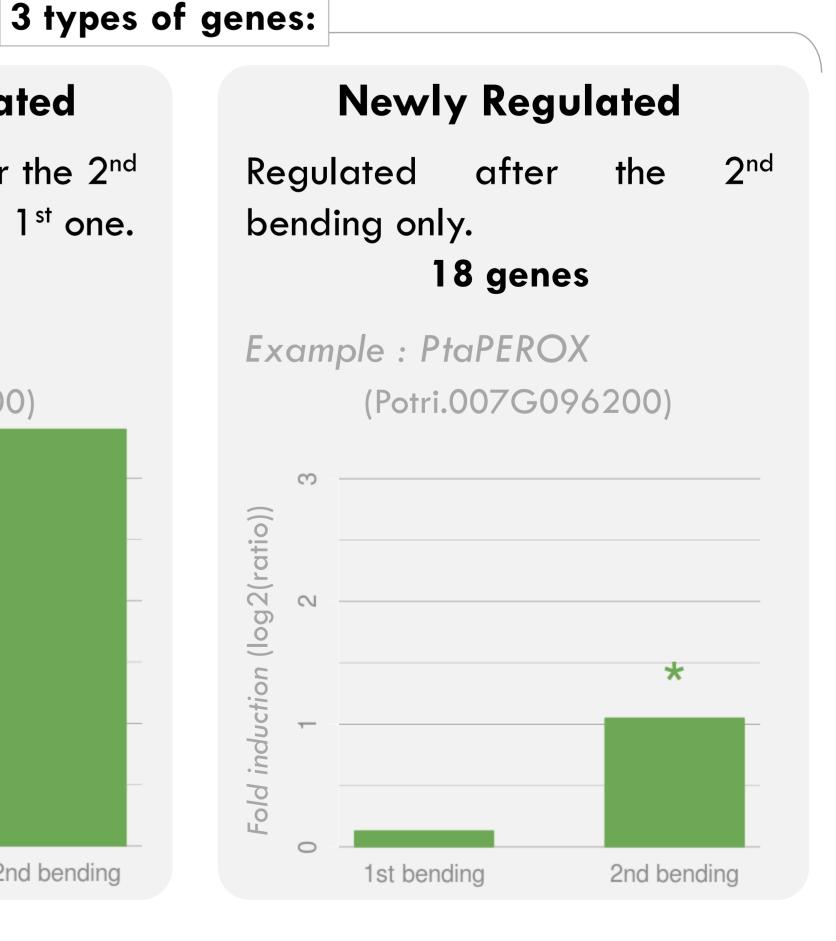
Gene expression 0.5 h after 2 bending (24 h interval)

96% of the early regulated genes after a 1st bending are less regulated after a 2nd bending

This mechanism may allow the plant to avoid over-reaction to successive bending.



Non Accommodated Equally regulated after the 2nd bending, than after the 1st one. 44 genes Example : PtaHRD (Potri.006G021000) (log2(ratio)) Fold induction 1st bending 2nd bending



Perspectives: We are currently working on new methods of gene network inference to understand the fine regulation of this mechanical signaling pathway.

