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In silico characterization of Wall-Associated kinases (WAKs) in *Populus trichocarpa*

Kévin Tocquard

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HAL Authorization

In silico characterization of Wall-Associated Kinases (WAKs) in *Populus trichocarpa*

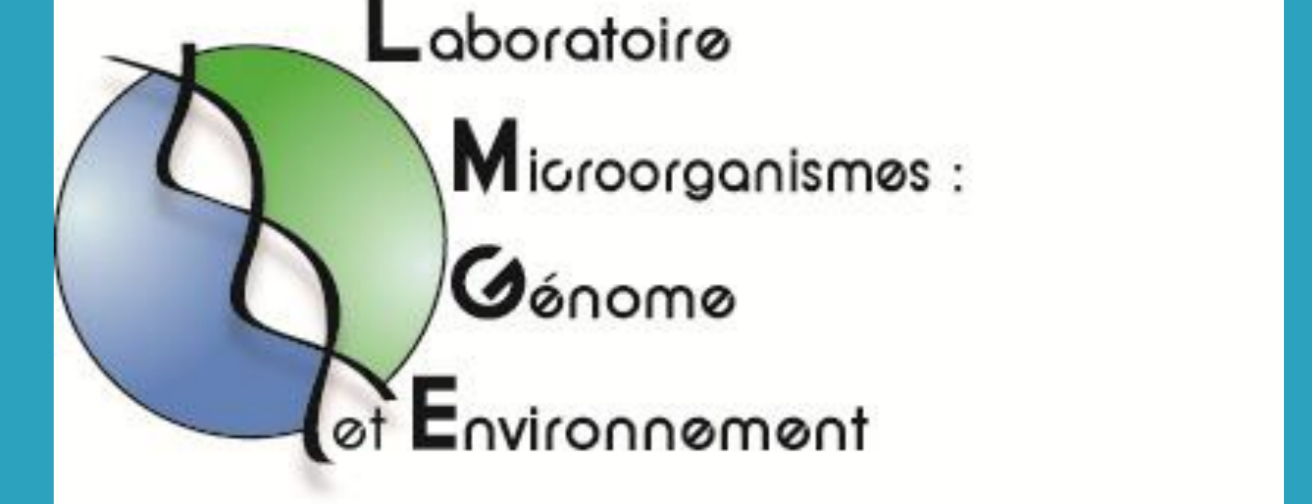
Tocquard Kévin

Supervisors

Pr Roedel-Drevet Patricia
Dr Venisse Jean-Stéphane

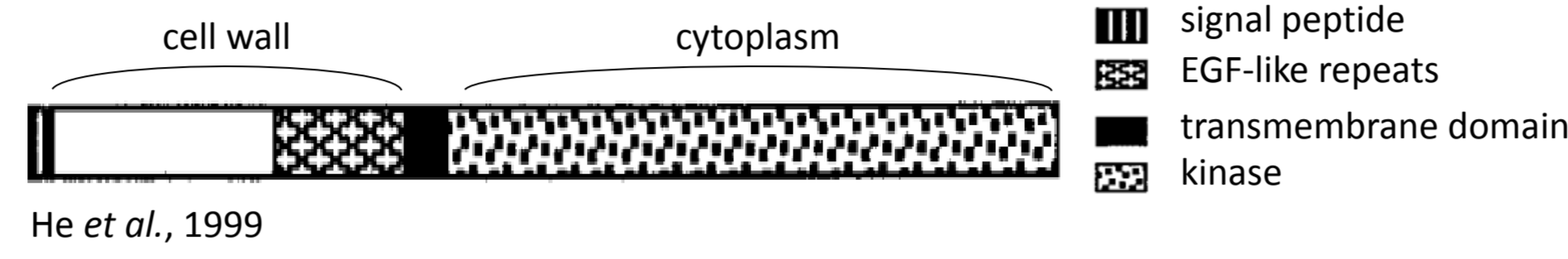


Collaborations



Introduction

The wall-associated kinases (WAKs) are a set of receptor-like kinases (RLKs) involved in signaling pathways. WAKs have been described exhaustively in two herbaceous models, *Arabidopsis thaliana* and *Oryza sativa* (27 et 125 members, respectively). Various studies suggested that WAKs are able to bind pectins of the plant cell wall through a specific protein domain located in their extracellular region.

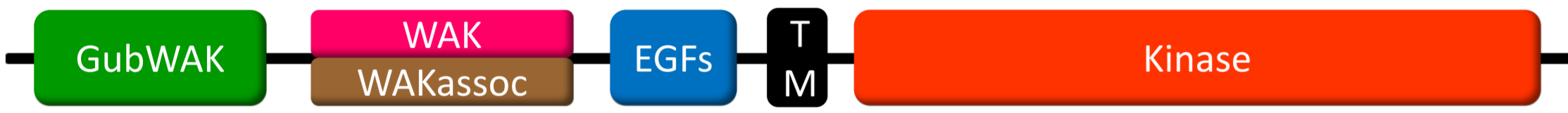


In woody species, WAKs, as receptors, may play a decisive part in development and in response to environmental constraints. The main characteristic of trees is wood production through secondary growth and perennialism, which implies short-term and long-lasting responses in continually changing environmental conditions. In addition, environmental stresses can induce specific modifications in secondary cell wall characteristics, notably G layer deposition in the tension wood, which requires cellular communications between the apoplasm and the cytoplasm. The involvement of WAKs as potential mediators of the reaction wood formation in response to gravitropic stimulus has been proposed.

Retrieval and sorting of *PtWAK* sequences

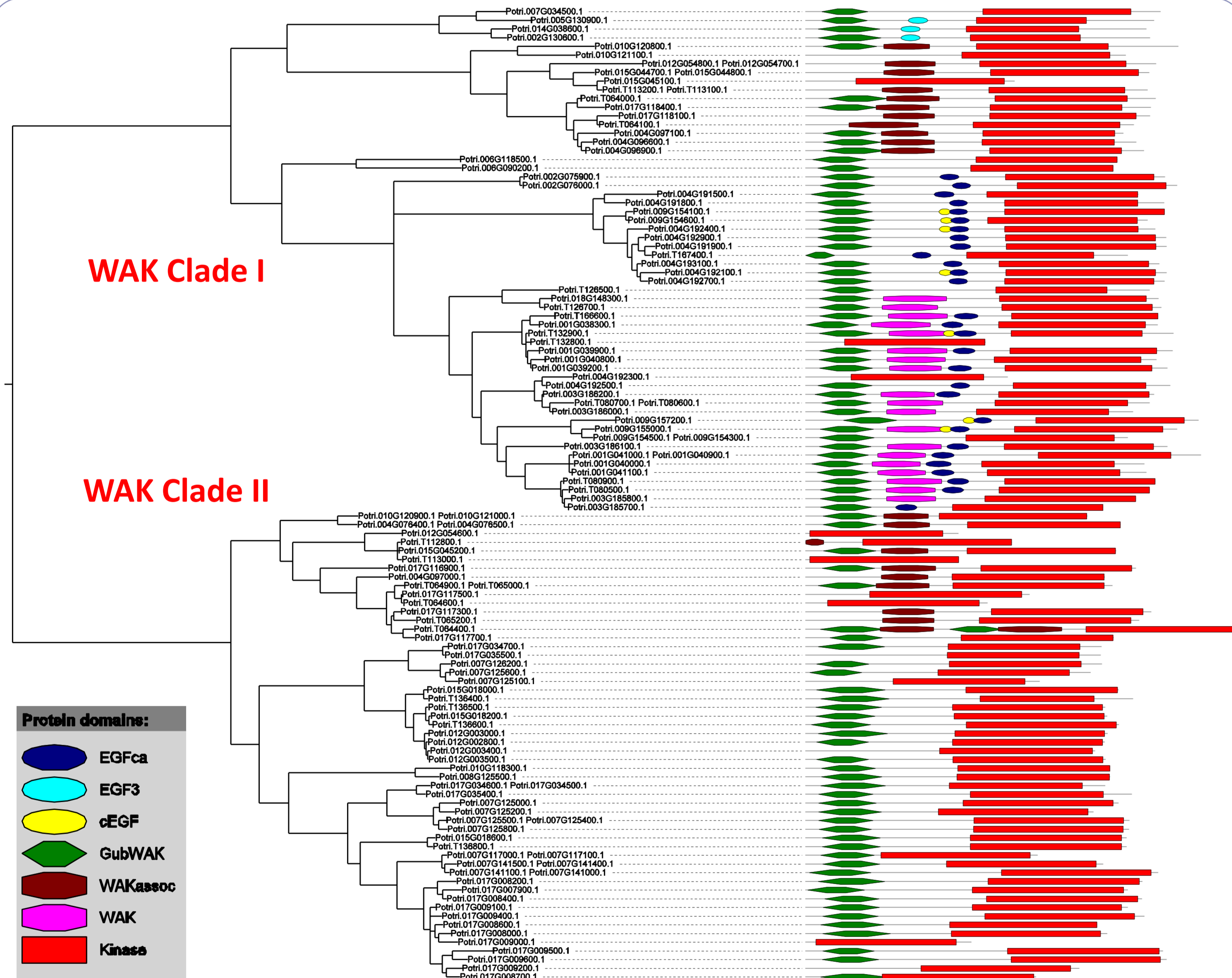
Protein domains

- GubWAK : adhesion site of WAKs to pectin
 - WAK : unknown function
 - WAKassoc : unknown function
 - EGFs : potentially involved in protein-protein interaction
 - TM : Transmembrane domain
 - Kinase : phosphorylating domain
- Extracellular → Intracellular



Group	Specifications	Gene number
<i>PtWAK</i> -RLK (Receptor-like kinase)		119
<i>PtWAK</i> -RLCK (Receptor-like cytoplasmic kinase)		32
<i>PtWAK</i> -RLP (Receptor-like protein)		22
<i>PtWAK</i> short genes		2
Total number of WAKs		175

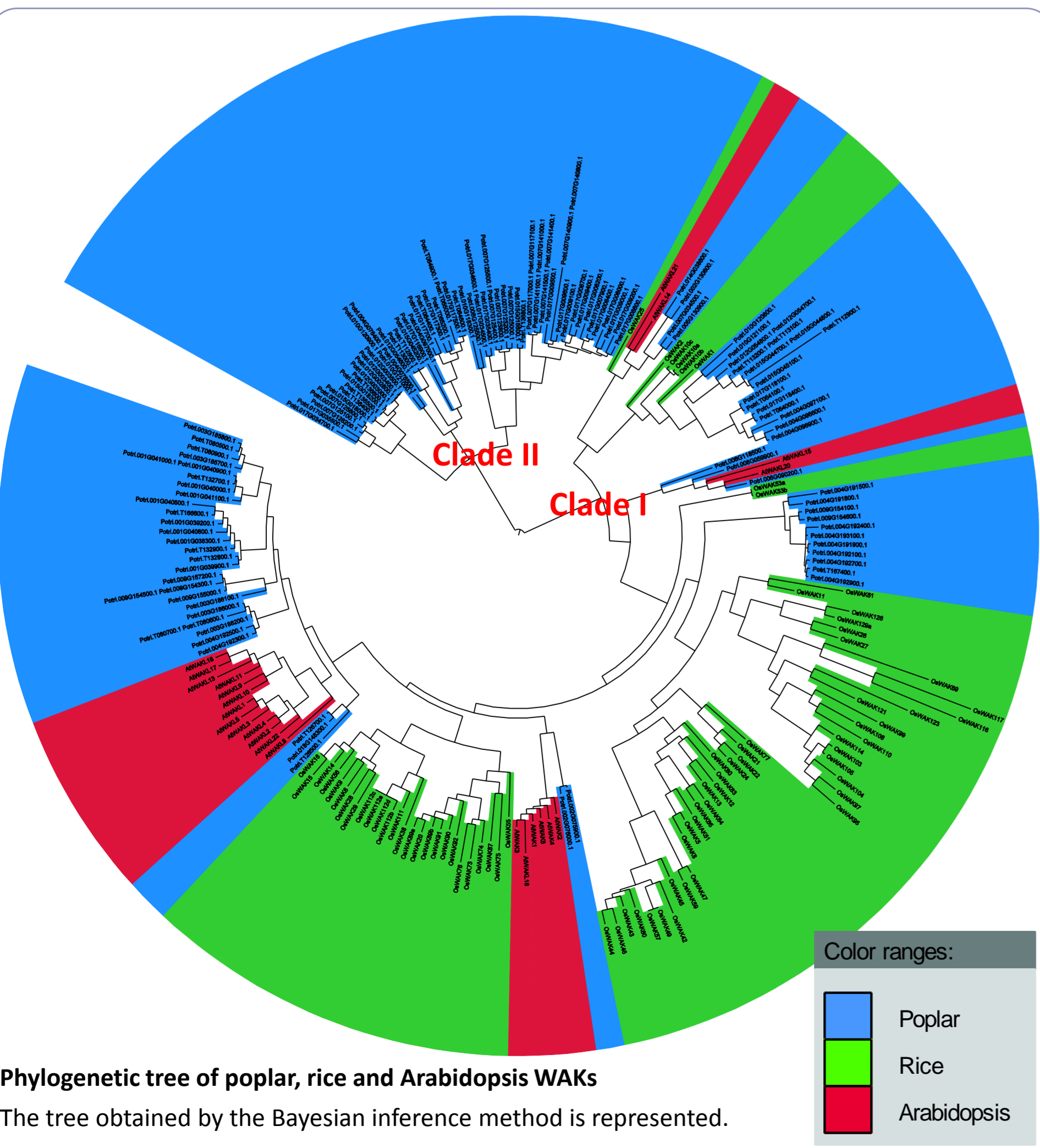
Phylogenetic analyses



Phylogenetic tree of poplar WAKs

The protein domain architecture is indicated on the right of the phylogeny. Bar length and color shapes are proportional to the number of amino acids and the prediction of domain length, respectively. The tree obtained by the Bayesian inference method is represented.

➤ Although the phylogenetic analysis is calculated on the kinase domain, some monophyletic groups preferentially contained one type of extracellular domain combination, suggesting a parallel evolution between the intracellular kinase domain and extracellular domains of *PtWAK*-RLK.

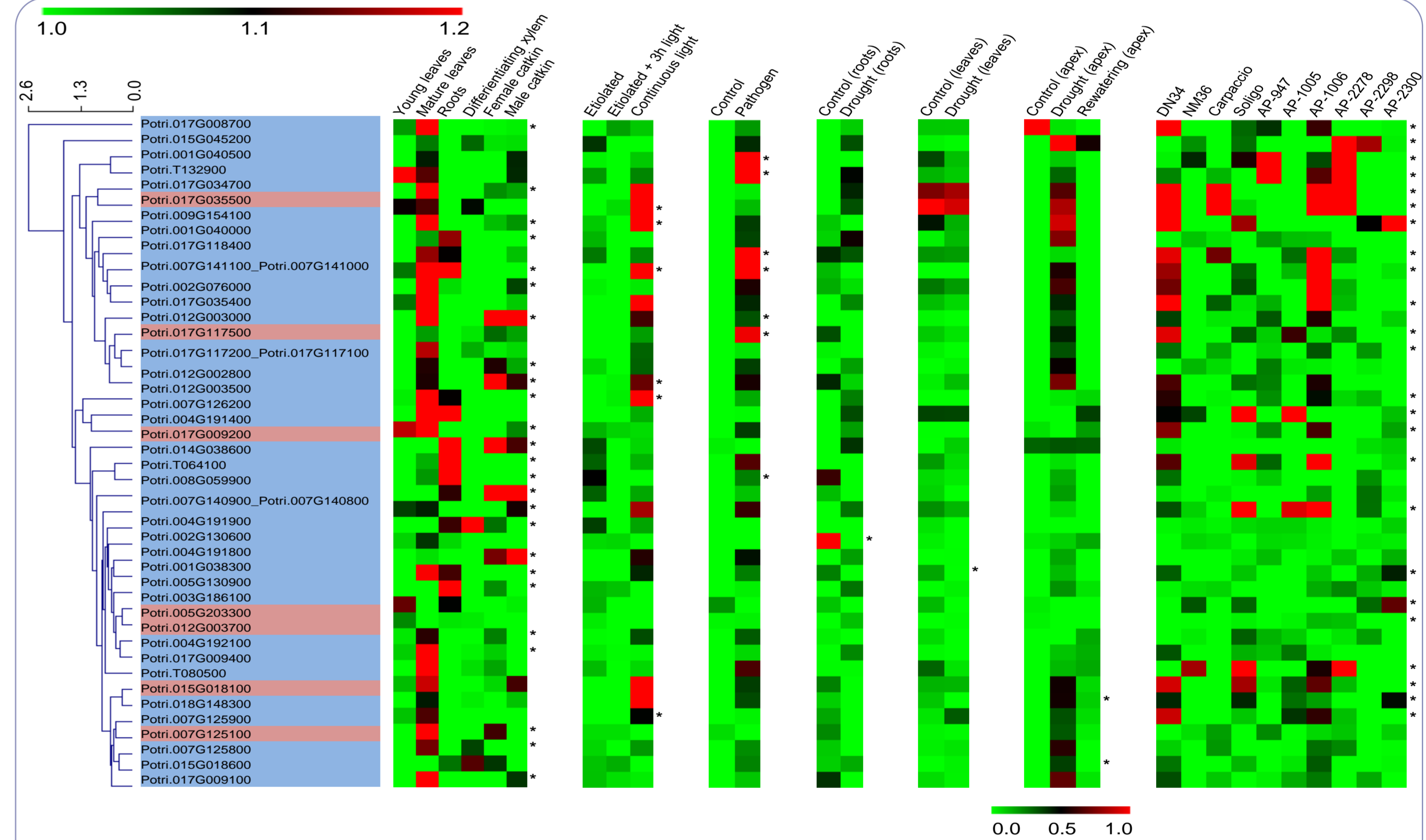


Phylogenetic tree of poplar, rice and Arabidopsis WAKs

The tree obtained by the Bayesian inference method is represented.

➤ Two monophyletic clades are markedly differentiated (i.e. WAK Clades I and II). A phylogenetic analysis of poplar, rice and Arabidopsis WAKs was also carried out. WAK clade I contains members from the three species while WAK clade II contains only *PtWAK*s. This suggests that the evolution of sequences in the WAK clade I occurred in the monocot-dicot common ancestor, while the sequence in the WAK clade II evolved independently in poplar.

Transcriptomics data analyses



Clustered heatmap showing expression patterns of significant tissue/condition/genotype specific expressed in poplar

Only *PtWAK*s showing differential expression in at least one tissue/environmental condition/genotype are displayed (42 *PtWAK*s). Scale from 0.0 to 1.0 corresponds to drought experiment in the apex; scale from 1.0 to 1.2 is for all the Affymetrix array experiments. An asterisk indicates significant tissue/environmental condition/genotype effect on *PtWAK* expression according to Welch's t-test/one-way ANOVA for two or more samples followed by adjusted Bonferroni correction (* $p < 0.05$). Hierarchical clustering was performed for *PtWAK*s according to their expression patterns.

'Carpaccio', 'DN34' and 'Soligo' are *Populus canadensis* genotypes, 'NM36' is *P. nigra* × *P. maximowiczii* while 'AP-947', 'AP-1005', 'AP-1006', 'AP-2278', 'AP-2298' and 'AP-2300' are *P. balsamifera* genotypes. Blue- and red-shaded *PtWAK* names belong to *PtWAK*-RLK and *PtWAK*-RLCK gene groups, respectively.

➤ Twenty-five *PtWAK*s showed a differential expression in at least on tissue, mainly an over-expression in mature leaves, roots and flowers, 16 *PtWAK*s were significantly affected by changing environmental conditions, and 24 were modulated differentially between poplar genotypes.

➤ Interestingly, *PtWAK* that showed a modulated expression after pathogen attack and *PtWAK* that are modulated during developmental/growth processes belong to WAK clade II (specific to poplar) and WAK clade I (shared with Arabidopsis and rice), respectively. This is in accordance with what have been shown for the global receptor-like kinase (RLK) family, suggesting that members of a gene family developed in a species-specific way correspond to species-specific needs.

Conclusion

WAKs features described above make WAKs appealing candidates to investigate new communication networks that may relay the cell wall status to the cytoplasm. The cell wall is an essential compartment affected by many biotic constrains such as pathogen attacks or developmental processes but also by abiotic stresses such as drought and various mechanical stimulations.

Our study provides new insights into the WAK gene family in *Populus*. Our findings may be a starting point for a study of the physiological roles of WAKs in cellular regulatory networks in woody species.

References

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