

IN BRIEF

Apical Bud Formation and Dormancy Induction in Poplar

The period of winter dormancy in woody perennial plants growing in the temperate



Dormant poplar buds develop in autumn after the perception of a critical short-day signal.

www.plantcell.org/cgi/doi/10.1105/tpc.107.190810

zone is initiated during bud development in autumn. Regulation of autumnal bud development involves orchestrating the processes of bud formation, acclimation to dehydration and cold stress, and the acquisition of dormancy. **Ruttink et al. (pages 2370–2390)** conducted a large-scale study of bud formation and dormancy in poplar (*Populus tremula* × *Populus alba*) involving transcript and metabolite profiling over a 6-week period from short-day induction to complete dormancy. The gene expression and metabolite profiles revealed the temporal sequence of events during bud formation and the induction of dormancy. Sets of marker genes were identified that distinguished the processes of bud formation, dormancy, and acclimation to cold and dehydration. Metabolite profiles were consistent with the approach of dormancy, acquisition of cold tolerance, and accumulation of storage compounds. In addition, genes differentially expressed during bud development were compared with those associated with dormancy induction in poplar cambium

and in *Arabidopsis* seeds. A large set of genes was found to be associated with dormancy induction in all cases, suggesting that a common molecular mechanism underlies the process in different plant organs. This study provides a comprehensive and detailed picture of molecular regulation of bud development and dormancy. In addition, climate change is expected to modify the synchronization of bud formation and acclimation to dehydration and cold. These data provide an important reference frame for future functional studies of genes and for genetic approaches to assess adaptation of trees to climate change.

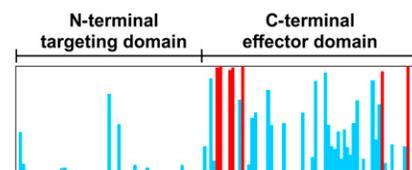
Adaptive Evolution among Plant Pathogenic Oomycete RXLR Effector Genes

Oomycete plant pathogens deliver effector proteins inside host cells, which enable parasitic colonization by modulating plant defense signaling pathways. Effectors are defined by the conserved motif RXLR (Arg, any amino acid, Leu, Arg), which is implicated in delivery of the effector into host cells. Effector proteins have a modular structure, wherein the N-terminal domain contains the signal peptide and RXLR motif that function in secretion and targeting, and the C-terminal region carries the effector activity that acts inside the plant cell. This modular structure suggests that the two

www.plantcell.org/cgi/doi/10.1105/tpc.107.190811

domains might be under different selection pressures. **Win et al. (pages 2349–2369)** used the draft genome sequences of three oomycete plant pathogens, *Phytophthora sojae*, *Phytophthora ramorum*, and *Hyaloperonospora parasitica*, to generate genome-wide catalogs of RXLR effector genes and determine the extent to which these genes are under positive selection. These three fungi carry highly complex and diverse sets of RXLR effector genes that appear to have undergone rapid evolution. Robust evidence of positive selection, acting mainly on the C-terminal region, was found in over two-thirds of the examined paralog families of RXLR genes. This work provides strong support for the idea that

RXLR effectors are modular and that distinct selection pressures have acted on the N-terminal and C-terminal modules.



Posterior probabilities from a multiple sequence alignment of five paralogous effector genes from *P. ramorum* reveal sites under positive selection (shown in red) mainly in the C-terminal effector domain.

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Plant Cell 2007;19;2322

DOI 10.1105/tpc.107.190811

This information is current as of September 22, 2020

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