Accommodation responses of poplar to successive mechanical loadings

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In their natural environment, plants are continuously exposed to highly variable wind loads, and in particular to the days-to-week scale alternation of windy and quiet periods. In response to a single mechanical load, plants usually exhibit a dramatic growth response (thigmomorphogenesis) and genes involved are being characterized. However, molecular mechanisms involved in plant acclimation to recurring and successive mechanical loadings are not well characterized. More specifically how plants avoid over-responding in to continuously changing wind conditions is unknown. Through the analysis of the short-time effects of quantified stem bending on young poplars, we demonstrated the rapid induction of *PtaZFP2* expression, a gene encoding a putative C2H2 zinc finger transcription factor. The *PtaZFP2* transcripts accumulate 10 min after a single bending and the relative abundance of *PtaZFP2* transcripts was linearly correlated with the amount of applied mechanical solicitation (Martin *et al*., 2009; Coutand *et al.*, 2009). To test the effect of successive bending, young trees were submitted either to one transient bending per day for several days or to two bendings, 1–14 days apart. Our results indicate that *PtaZFP2* mRNA accumulate to a lesser extent after two bendings than after a single one. The minimum rest periods between two successive loadings necessary to recover a response similar to that observed after a single bending, were 7 days and 5 days. This response was observed for three other early mechano-responsive genes having different functions in the plant mechanosensing pathway, such as calcium signalling or wall modifications.

These results clearly show a partial desensitization of plants to recurrent successive bendings, indicating a day-scale acclimation of sensitivity (accommodation) (Martin *et al*., 2010).

Our objectives are now to identify molecular actors involved in such mechanism by studying the regulation of early responsive gene such as *PtaZFP2* (Gourcilleau *et al*., 2011).

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