
LTR-RTs as intermediate of the stress response in plants?

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Résumé

Retroviral-type LTR elements are major components of plant genomes. LTRs (Long Terminal Repeat) represent promoter/regulatory capsules that can drive the production of chimeric cotranscripts with adjacent genes in response to their own specific expression patterns. Large-scale reprogramming of gene expression via LTR-driven cotranscripts was evidenced in mammalian studies but is still largely inchartered in plants. Plant LTR retrotransposons can be activated by stress and may be involved in the host response to specific stimuli. An abundance of LTR-gene associations, over-represented in stress conditions, were revealed in the tobacco. We have identified many cotranscripts originating from the LTRs of several tobacco retrotransposons. These cotranscripts extend into downstream adjacent sequences, including genic sequences. In many cases, cotranscripts are orientated opposite to the adjacent gene, suggesting a possible repressive impact on gene expression. Our experimental analysis confirm that 3'LTRs can drive the synchronous expression of these cotranscripts in conditions where retrotransposons are transcriptionally activated, such as microbial elicitors or wounding. The retrotransposon response to stress and associated cotranscript production varies depending on the element. In parallel, new cotranscripts were also searched by massive 454 sequencing of expressed 3' LTRs / flanking junctions for several retrotransposons. A preliminary analysis detected a large number of new Tnt1 cotranscripts produced in stress conditions. The complete analysis of these data will allow to confirm the correlation between LTR-RT template expression and cotranscript production, and to evaluate if cotranscription targets specific types of genes. Our aim is to evaluate how the production of chimeric cotranscripts can alter the transcription profile of adjacent genes.

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