TEs in plant-microbe interaction revealed from total RNA-seq approach

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Abstract

Strategies to underpin plant-microbe interaction have benefited from RNA-seq approaches to reveal plant genes that respond to the presence of a microbe, be it a beneficial organism or a pathogen. Most studies rely on model plants and well-known interactions. In addition, most transcriptome data available is derived from mRNA-captured molecules. Towards enlarging the opportunities from a given tissue sample, a total RNA-seq approach is devised in a non-model polyploid organism such as sugarcane. A total transcriptome prepared from 10 interacting conditions reveals significant changes in TE expression and opens avenues for identifying TE indicators. The experiment explores four sugarcane cultivars submitted to different pathogenic conditions, and tissues are collected at 48 post-inoculation. Differentially expressed TEs are identified from a previously built reference sugarcane TE database. Both transposons and retrotransposons respond to the inoculation but eight elements. Helitron-derived elements are the most affected TEs. Maximus-derived elements are mostly not responsive. Downregulation of TEs is observed in two of the three susceptible cultivars, while the tolerant cultivar modulates the expression of the whole TE family assortment. Some of the identified lncRNAs are derived from previously described Transposable Elements. The work presented sheds light on a multiscale TE interactome not previously projected by classical mRNA-targeted transcriptome sequencing.

Keywords: plant, microbe interaction, sugarcane, total transcriptome

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