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Toward the Genome-wide analysis of Transcriptional and post-Transcriptional regulations in hevea

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In model plant species, the involvement of small non-coding RNAs in transcriptional and post-transcriptional regulation of gene expressions under environmental constraints is well documented. In *Hevea*, microtranscriptomic studies were carried out on several *Hevea* clones, tissues with regard to various abiotic stress. Tapping Panel Dryness (TPD) syndrome is a major physiological disease, caused by an excessive ROS production that leads to loss in natural rubber production. Previous studies also revealed that small RNA distributions can change in response to rubber harvesting stress in a TPD susceptible clone PB 260. A majority of 21-nt sRNA was observed in latex of TPD-affected trees, whereas 24-nt sRNAs were more abundant in latex from healthy trees. The shift from transcriptional to post-transcriptional regulations in response to stress could be a biological function shared between rubber clones, and needs to be further explored. Deeper analyses are under way to annotate *MIR* genes as well of Repeats Elements and Transposable Elements in the *Hevea* genomic sequences available. Partial conservation of miRNA/target justifies research programs for *Hevea* as cleavage sites of some predicted target genes by sRNA can be partially conserved in *Hevea* compared to *Arabidopsis*. Discovery of miRNA/target couples through “degradome” analysis, TE-derived siRNAs and gene-related siRNAs can lead to a full comprehensive picture of post- transcriptional and transcriptional regulations of genome expression by sRNA.