

## Genome Analysis on Drought Resistance of *Hevea brasiliensis*

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*Hevea brasiliensis* (para rubber tree) plays an important role in the economy of Sri Lanka. Potential drought stress conditions due to climatic changes will have a severe effect on the yield and the survival of the rubber tree. Understanding the underlying genetic basis of drought tolerance through identification and systematic analyses of the candidate genes associated with drought tolerance of *Hevea* will help rubber breeding by marker assisted selection and transgenic improvement. This study was undertaken to generate information about the genes related to drought tolerance in *Hevea*. Biologically validated eighteen *Arabidopsis thaliana* genes with known functional pathways were used as query sequences to find orthologous *Hevea* genes from the ASM165405v1 genome assembly using the BLASTP program of the BLAST tool. Query coverage higher than 50%, bit score higher than 80 and E-value lower than  $1 \times 10^{-50}$  were taken as cut off criteria for the search. Nine *Hevea* orthologous genes were identified and they represented six functional groups involved with both physiological and molecular adaptation to drought. Highest number of candidate genes identified encodes transcription factors. Systematic analyses of the identified genes related to drought tolerance suggest that transcription regulation, phospholipid metabolism, growth control, detoxification signaling, osmolyte biosynthesis and signal transduction pathways play important roles in drought tolerance in *Hevea*. Identification and analysis of conserved regions was conducted for the identified three transcription factors using the MEME and InterPro tools respectively. Three domains were identified which shared Gene Ontology terms related to drought tolerance. The results of the research not only enrich information about the genes related to drought tolerance, but also provide new insights into understanding the drought tolerance mechanisms in rubber tree.

**Keywords:** *Hevea brasiliensis*, Drought tolerance, Orthologous genes, Transcription factors