# GENOME ANALYSIS ON DROUGHT TOLERANCE OF *Hevea brasiliensis*

A dissertation submitted to the
Faculty of Animal Science and Export Agriculture
Uva Wellassa University
In partial fulfillment of the requirements for the award of
Bachelor of Science in Palm & Latex Technology and Value Addition

by

**RAJAPAKSHA LEKAMALAGE PUNSIRINI NAYANARASI DINITHI RAJAPAKSHA**

**Department of Export Agriculture**
**Faculty of Animal Science and Export Agriculture**
**Uva Wellassa University of Sri Lanka**

**2017**

# ABSTRACT

*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 using Basic Local Alignment Search Tool (BLAST). Nine *Hevea* orthologous genes were identified and they represented six functional groups involving 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 factors, phospholipid metabolism, growth control, detoxification signaling, osmolyte biosynthesis, signal transduction pathways play important roles in drought tolerance in *Hevea.* Conserved regions identification and analysis was conducted for the identified three transcription factors using the MEME and InterPro tools respectively. Three main domains were identified. Among them Basic Leucine-Zipper domain and AP2/ERF domain were included in the functional and biological categories whereas MYC type BHLH domain was included in the biological category on gene ontology terms. 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 the rubber tree.



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