

3736734 SCBT/M : MAJOR : BIOTECHNOLOGY ; M.Sc. (BIOTECHNOLOGY)

KEY WORD : CATALASE / ETHYLENE / *HEVEA BRASILIENSIS* / LATEX  
OXIDATIVE STRESS / SUPEROXIDE DISMUTASE

PANIDA KONGSAWADWORAKUL : STUDIES ON DIFFERENTIAL  
EXPRESSION OF GENE POTENTIALLY INVOLVED IN THE ONSET OF THE  
TAPPING PANEL DRYNESS (TPD) IN *HEVEA BRASILIENSIS*. THESIS  
ADVISOR : JARUNYA NARANGAJAVANA, D.Agr.Sc., HERVÉ CHRESTIN,  
Ph.D., VALÉRIE PUJADE-RENAUD, Ph.D. 213 p. ISBN 974-589-149-5

Tapping panel dryness (TPD) is a disease of rubber trees characterized by the reduction or total cessation of latex flow upon tapping, due to senescence of the laticifers leading to abnormal coagulation processes. It is a worrying symptom from the economic point of view since the plants affected are no longer tapped. The purpose of the present work was to investigate whether modifications in the expression of some genes involved in the protection against oxidative stress and/or in coagulation could account for the unbalancing of the peroxidative metabolism towards deleterious effects and *in situ* coagulation, in different cases of bark dryness.

Northern blot analysis showed that moderate ethylene treatment stimulated catalase, Mn-superoxide dismutase and glutathione reductase gene expression. However, overstimulation-induced TPD trees did not respond to ethylene, both in views of catalase and Mn-superoxide dismutase mRNA level and catalase activity. The overall results led to the conclusion that the modification of catalase and Mn-superoxide dismutase gene expression in sick and healthy trees may be involved in the onset of TPD. A 1.7 kb catalase cDNA from rubber tree latex was cloned and sequenced. It was found that the catalase cDNA consisted of 1,476 nucleotides which encoded a protein of 492 amino acids with a molecular weight of 56.7 kDa. Sequence comparison showed that this rubber tree catalase cDNA was highly homologous to several other plant catalases, of which the highest score of homology was shared by the *R. communis* catalase gene CAT1, with 89 and 91 % homology in nucleotides and amino acids, respectively.