**Study the Gene Expression Profiles of GPX (Glutathione Peroxidase) and CAT (Catalase) Genes in Newly Developed Rubber (*Hevea brasiliensis*)Genotypes**

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Sri Lanka is a leading natural rubber producer and is renowned for producing quality latex products in global market. Rubber (*Hevea brasiliensis)*is considered as one of the major export agricultural crops in Sri Lanka. A physiological disorder termed Tapping Panel Dryness (TPD) is considered as a crucial constraint to the industry which severely reduces yield by 15 % - 20 % annually. Plants produce Reactive Oxygen Species (ROS) at high concentrations within cells under oxidative stress and ROS accumulation contributes occurrence of TPD. Accumulated ROS are detoxified by the antioxidants present in cells. Current research was performed to study the expression of CAT and GPX genes responsible for producing two such antioxidants, catalase and glutathione peroxidase respectively. Gene expression studies facilitate breeders for early selection of promising clones expediting the conventional breeding process of rubber that takes more than thirty years to complete due to its perennial nature. Four genotypes of 2011 HP selections were selected for the experiment which were established in 2018 at Eladuwa estate, Yatadola as an Estate Collaborative Trial. RRISL 2006 recommended clone was selected as the control. RNA extraction and cDNA synthesis were performed in order to perform the quantitative PCR. 2-ΔΔCT method was used to analyze the quantitative gene expression. According to quantitative PCR data, both CAT and GPX genes were upregulated in all selected genotypes (2011 HP 42, 2011 HP 202, 2011 HP 297 and 2011 HP 300) with reference to control clone under low soil moisture conditions. Gene expression profiles provide a unique opportunity for early screening of genotypes that are capable of self-recovering and less susceptible to TPD incidence. Altogether, the study provides insights on features of CAT and GPX genes in rubber, which might be utilized for additional functional analysis to extrapolate their precise involvement in abiotic stress responses.

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