

Abstract

A study aimed at identifying putative drought responsive genes that confer tolerance to water stress deficit in tea plants was conducted in a 'rain-out shelter' using potted plants. Eighteen months old drought tolerant and susceptible tea cultivars were each separately exposed to water stress or control conditions of 18 or 34% soil moisture content, respectively, for three months. After the treatment period, leaves were harvested from each treatment for isolation of RNA and cDNA synthesis. The cDNA libraries were sequenced on Roche 454 high-throughput pyrosequencing platform to produce 232,853 reads. After quality control, the reads were assembled into 460 long transcripts (contigs). The annotated contigs showed similarity with proteins in the *Arabidopsis thaliana* proteome. Heat shock proteins (HSP70), superoxide dismutase (SOD), catalase (cat), peroxidase (PoX), calmoduline- like protein (Cam7) and galactinol synthase (Gols4) drought- related genes were shown to be regulated differently in tea plants exposed to water stress. HSP70 and SOD were highly expressed in the drought tolerant cultivar relative to the susceptible cultivar under drought conditions. The genes and pathways identified suggest efficient regulation leading to active adaptation as a basal defense response against water stress deficit by tea. The knowledge generated can be further utilized to better understand molecular mechanisms underlying stress tolerance in tea.