



# Identification and functional analysis of drought responsive lncRNAs in tea plant

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## ABSTRACT

Long noncoding RNAs (lncRNAs) are a class of non-coding RNAs that are more than 200 nucleotides in length. Emerging evidence suggest that lncRNAs by regulating gene expression can act as key regulators of diverse biological processes in plants. The identification of differentially expressed lncRNAs associated with drought tolerance/susceptibility is important to study and understand the complex regulation of drought responses of the tea plant. In this study, we identified 21,241 lncRNAs based on computational analysis of publicly available RNA-seq data of *Camellia sinensis*, among them 1395 lncRNAs were identified as drought specific. Some of these drought specific lncRNAs acts as target mimic of known mRNAs or putative targets for many already reported abiotic stress responsive microRNAs (miRNAs). One hundred and thirty two lncRNAs of tea were predicted to act as potential endogenous target mimics (eTMs) for 136 transcripts, which includes stress responsive transcription factors (TFs) such as GAMYB, RAP2-7 and MYC2. KEGG pathway analyses of the genes for which 132 lncRNAs act as eTMs showed highest number of genes in purine and thiamine metabolism pathways. This study gives an overview of the drought responsive lncRNAs and their possible functional roles in tea during drought stress conditions.

## 1. Background

Tea plant (*Camellia sinensis*) belonging to the family Theaceae is an evergreen woody perennial plant grown in different agro-climatic zones. Tea is the source of one of the most popular non-alcoholic beverages of the world. Besides numerous health benefits, tea is also endowed with pleasant flavor with mildly stimulating effects that make it the most preferred beverage worldwide. Tea has anti-carcinogenic, antimicrobial, anti-inflammatory, antioxidant activities for which it can be used as an effective disease preventive agent (Soni et al., 2015). Tea plants being perennial shrubs can grow under diverse climatic conditions and are subjected to many biotic and abiotic stresses. The growth and yield of plants are affected by drought as it become the major limiting factor due to global climate change and growing water scarcity (Boyer et al., 2013). The onset of drought significantly affects many morphological, physiological, biochemical and molecular processes in plants. Drought stress caused leaf size reduction, stem extension and reduced root growth which results in altered water use efficiency of the plants (Farooq et al.,

2009). In order to understand the reprogramming/differences in gene expression of plants during stress conditions, an emerging class of gene regulatory molecule viz. long non-coding RNAs (lncRNAs) gained wider attention and their roles in plant development and stress responses are evident (Xu et al., 2017; Begcy and Dresselhaus, 2018; Shuai et al., 2014; Wang et al., 2018; Chekanova, 2015; Shafiq et al., 2016; Liu et al., 2015). This study was carried out to identify drought responsive lncRNAs and to conduct differential expression analysis using publicly available RNA-seq datasets.

lncRNAs are a class of noncoding RNAs that have more than 200 nucleotides in length and lack protein-coding potential. These might be transcribed from intragenic, intergenic, exonic, intronic, or from both the strands and are often capped, spliced and polyadenylated (Ma et al., 2013). Some of them undergo an alternative form of post-transcriptional modification that distinguishes them from other types of transcripts (Quinn and Chang, 2016). The first discovered lncRNA was a eukaryotic lncRNA H19, which was identified in mouse (Bartolomei et al., 1991). Subsequently, with the advent of high throughput sequencing

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