



Research article

Genome wide identification and characterization of abiotic stress responsive lncRNAs in *Capsicum annuum*

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ABSTRACT

Long non-coding RNAs (lncRNAs) are a type of non-coding transcripts having length of more than 200 nucleotides lacking protein-coding ability. In the present study, 12807 lncRNAs were identified in *Capsicum annuum* tissues exposed to abiotic stress conditions viz. heat, cold, osmotic and salinity stress. Expression analysis of lncRNAs in different treatment conditions demonstrates their stress-specific expression. Thirty lncRNAs were found to act as precursors for 10 microRNAs (miRNAs) of *C. annuum*. Additionally, a total of 1807 lncRNAs were found to interact with 194 miRNAs which targeted 621 mRNAs of *C. annuum*. Among these, 344 lncRNAs were found to act as target mimics for 621 genes. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis revealed that out of those 621 gene sequences, 546 were tagged with GO terms, 105 Enzyme Code (EC) numbers were assigned to 246 genes and 223 genes are found to be involved in 63 biological pathways. In this report, we have highlighted the prospective role of lncRNAs in different abiotic stress conditions by interacting with miRNAs and regulating stress responsive transcription factors (TFs) such as DoF, WRKY, MYB, bZIP and ERF in *C. annuum*.

1. Introduction

The climate change scenarios and agriculture are correlated with each other in various aspects (Raza et al., 2019) as crops are more frequently exposed to abiotic stresses such as drought, cold, salinity, high temperature etc. *Capsicum* is one of the most important vegetables and a well-known spice crop. *Capsicum* fruits are rich in capsaicinoid compounds such as capsaicin and dihydrocapsaicin; vitamins A, B, C, E and are loaded with antioxidant, anticarcinogenic, antimutagenic, antiaging and antibacterial properties. It is also widely used as a coloring agent, food flavoring, cosmetic and pharmaceutical ingredient (Ferrari and Torres, 2003; Kim et al., 2014; Perla et al., 2018). Studies on effect of various abiotic stresses have been carried out in *Capsicum* during heat, cold, salinity, osmotic stress conditions. Expression patterns of important functional genes can be summarized by studying diverse lncRNAs as growing pieces of evidences are confirming that lncRNAs play a pivotal role in regulation of gene expression (Chekanova, 2015). Solving the mysteries associated with cross-links that might exist between non-coding and coding RNAs can enhance our understanding of varying

gene expression patterns in changing abiotic conditions.

Any abiotic stress imposed in a plant will show an impact on its physiology and also influences its productivity. The eukaryotic genome consists of protein-coding RNAs and noncoding RNAs (ncRNAs) and their interaction governs the expression pattern of the genes (Berretta and Morillon, 2009). Recent studies have shown that ncRNAs play major regulatory roles in various biological processes (Wilusz et al., 2009; Kim et al., 2011). lncRNA is a type of ncRNA that generally contains more than 200 nucleotides and does not exhibit any protein-coding potential (Guttman et al., 2013). lncRNAs are transcribed by RNA polymerase II and their post-transcriptional modification mechanism is similar to that of mRNAs (Guttman et al., 2009; Karlsson and Baccarelli, 2016; Wang and Chang, 2011). Numerous lncRNAs were identified in several other plant species and they were reported to play important roles in gene silencing (Bardou et al., 2014; Matzke and Mosher, 2014), plant growth including the control of flowering time (Berry and Dean, 2015; Kim and Sung, 2017; Wang et al., 2017a), organ development (Li et al., 2016), photo-morphogenesis in seedlings (Wang et al., 2014), cell differentiation (Liu et al., 2019), reproduction (Zhang et al., 2014) and aroma formation (Varshney et al., 2019). They also act as decoys that mimic the

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