

ABSTRACT

Non-coding RNAs (ncRNAs) are the emerging players of post-transcriptional gene regulation (PTGR). MicroRNAs (miRNAs) are small ncRNAs, which regulate gene expression by inhibiting translation or by degrading messenger RNAs (mRNAs). On the other hand, long non-coding RNAs (lncRNAs) are the transcripts responsible for the up-regulation and down-regulation of transcription. Although the genome of many plant species is available, yet the roles of these ncRNAs in PTGR remain elusive. In this study novel miRNAs have been predicted computationally along with the computational prediction of lncRNAs followed by miRNA-lncRNA interaction. Novel miRNAs are computationally predicted from the genome of *Medicago truncatula*, *Brassica oleracea* and *Hordeum vulgare*. lncRNAs are predicted from the coding DNA sequence of *Brassica oleracea*, *Hordeum vulgare* and *Phaseolus vulgaris*. To corroborate the computational prediction, few randomly selected miRNAs of cauliflower and pigeon-pea along with lncRNAs of cauliflower, pigeon-pea and french beans are experimentally validated by qRT-PCR. Targets of these miRNAs and lncRNAs on mRNAs are predicted using psRNATarget server and network models of interaction between miRNAs and mRNAs of different plant species is built. Few abundant targets are selected and experimentally validated through a modified version of 5' RLM-RACE. Five targets of cauliflower and three targets of pigeon pea are validated in this study. In this study, different miRNA families were analyzed based on their targets. Four different Viridiplantae families (Brassicaceae, Fabaceae, Poaceae and Solanaceae) are considered for the analysis. Along with that interaction between these plant-derived miRNAs are human mRNA and lncRNA has been studied. The target human mRNAs are involved in different types of cancer, neurological disorder, auto-immune disorder and immune deficiency disorder and the lncRNAs are involved in various diseases including cancer, neurological disorder and immune disorder. Findings of this dissertation will surely enhance the knowledge of non-coding genome of the representative plant species and their roles in PTGR, which may improve the agricultural traits of this economically important crop. Along with that the cross-kingdom interaction between plant-derived miRNAs and human mRNAs may provide new insight into the field of nutrigenetics and nutrigenomics.

KEY WORDS: Viridiplantae, microRNA, long non-coding RNA, post-transcriptional gene regulation, psRNATarget server, quantitative-real time PCR, U6 snRNA, GAPDH, cross-kingdom