Computational identification and characterization of conserved miRNAs and their putative target genes in Eclipta prostrata

Souvagyalaxmi Sahoo, Rashmi Rekha Samal, Sangita Dixit

PII:	S2452-0144(18)30036-0
DOI:	doi:10.1016/j.genrep.2018.03.020
Reference:	GENREP 242
To appear in:	*Gene Reports*
Received date:	14 October 2017
Revised date:	19 March 2018
Accepted date:	30 March 2018

Please cite this article as: Souvagyalaxmi Sahoo, Rashmi Rekha Samal, Sangita Dixit , Computational identification and characterization of conserved miRNAs and their putative target genes in Eclipta prostrata. The address for the corresponding author was captured as affiliation for all authors. Please check if appropriate. Genrep(2017), doi:10.1016/j.genrep.2018.03.020

Computational identification and characterization of conserved miRNAs and their putative target genes in *Eclipta prostrata*

Souvagyalaxmi Sahoo[1]*, Rashmi Rekha Samal[1], and Sangita Dixit[2],
Tectona Biotech Resource Centre, Bhubaneswar, Odisha-751002

Abstract

MicroRNAs (miRNAs) are an abundant class of newly identified endogenous small non coding RNAs of ~22 nucleotides long molecules. They play a vital role in many biological and physiological processes of both plants and animals. The conserved nature of miRNAs provides functional role in mostly post-transcriptional regulation, gene expression and silencing the target genes. The theory based on approach of finding homologous sequences of known miRNAs both within a single genome and across genomes of related organisms. In this study, an attempt was made to identify potential miRNAs in *Eclipta prostrata* GSSs sequence through computational means. A total of 84 GSS sequences of *E.prostrata* were assembled and resulted in 7 contigs and 28 singletons, homology searched against the non-redundant 4802 known mature miRNAs of Viridiplantae plant kingdom resulted in identification of 8 potential miRNA candidates belonging to 7 different miRNA families. A majority of conserved miRNAs have been characterized by computational approaches using psTargetServer resulted in 5 potential target genes. The result concluded by obtaining eight potential miRNAs of *E.prostrata* that is evolved functional annotation and evolutionary relationship with other species.

Key words: *Eclipta prostrata;* miRNAs; GSS; Viridiplantae; psTargetServer.

Eclipta prostrata belongs to family of Asteraceae is widely used within the history of many medicinal systems of the world. This herbal plant has anti-inflammatory, hepatoprotective, antibacterial, antifungal properties and also anti-aging agent in Ayurveda. But there have no report in potential miRNA of this plant. In the present study, we have identified a total of 8 miRNAs of *E. prostrata* belonging even different families from 84 GSSs for the first time using in silico approach. Our results showed that most of the conserved miRNAs targets transcription factors as well as genes involved in signal transduction, and various metabolic processes, which are expected to provide miRNA mediated gene regulation in such an important plant. As an approach was made by developing the conceptual hypothesis describes its vital relationship and influential role in gene regulating network and transcriptional process but its further validation requires experimental approach at the expression level