Narjala et al. (2017) Can J Biotech, Volume 1, Special Issue, Page 51
https://doi.org/10.24870/cjb.2017-a38

Canadian Journal of Biotechnology

ISSN 2560-8304

Poster Presentation **OPEN ACCESS**

Category: Bioinformatics

Role of HYL1, a dsRNA binding partner of DCL1, in selecting a unique cryptic motif in plant miRNAs

Anushree Narjala[1,2], Ashwin K. Nair[1,2], Arati Ramesh[1] and P.V. Shivaprasad[1*]

[1]National Centre for Biological Sciences, 560065, INDIA

[2]SASTRA University, 613401, INDIA

Presenting author: anushreen@ncbs.res.in; *Corresponding author: shivaprasad@ncbs.res.in

Abstract

MicroRNAs (miRNAs) are small ~21nt long endogenous non-coding RNAs that are involved in post-transcriptional silencing of target mRNAs. miRNAs are processed from precursors having a stem-loop structure that are recognized and cleaved by Dicer-like1 (DCL1) with the help of dsRNA binding protein Hyponastic leaves1 (HYL1) and a zinc finger protein named Serrate (SE). Unlike animal miRNAs where miRNA foldbacks are mostly uniform, plant miRNA foldbacks are very diverse in length and structure. Processing mechanism and the nature of RNA motifs in animal pre-miRNAs are comparatively well studied (Ha and Kim, 2014) than plant miRNAs. There have been few efforts to understand the molecular signatures that affect accuracy and efficiency of miRNA processing. Bulges in the lower stem has been shown influence precision and efficiency of processing (Song et al., 2010; Werner et al., 2010; Mateos et al., 2010) and the loop length negatively influences miRNA abundance (Jagtap et al., 2014).

Through computational analysis, we find that there is a unique cryptic motif present in plant miRNAs. This cryptic motif is conserved among diverse plant groups, suggesting a conserved mechanism that selects the motif. We hypothesize that HYL1 could be responsible for observed selection for cryptic motif in miRNAs. hyl1 mutants are seen to lack precise precursor processing ability and accumulate miRNAs at much lower levels. We have identified amino acid residues in HYL1 that are likely to mediate selection of specific cryptic motif in miRNA precursors and help in precise cleavage by DCL1. As expected, these residues are present only in HYL1, but not among other RNA binding protein partners of DCL1 and other DCL proteins that produce small RNAs without a cryptic motif. Our results pave way for understanding a previously unknown determinant of plant miRNA biogenesis.

Citation: Narjala, A., Nair, A.K., Ramesh, A. and Shivaprasad, P.V. Role of HYL1, a dsRNA binding partner of DCL1, in selecting a unique cryptic motif in plant miRNAs [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 51. https://doi.org/10.24870/cjb.2017-a38