Abstract

Understanding the Evolution of miRNA Biogenesis Machinery in Plants with Special Focus on *Oryza sativa*

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Abstract:

Statement of the Problem: The miRNA biogenesis process is an intricate and complex event consisting of many genes/TFs that work in an equally complicated and regulated fashion so as to give rise to mature functional forms of miRNAs under ever changing conditions of development and stress. Most of these genes have been studied in *Arabidopsis* however, their orthologs and functions have not been explored in other plant species. The study will enhance our understanding of the evolution of the miRNA biogenesis and its integration with the molecular schema of the cell.

Methodology: Manual curation of all the information present in the literature domain regarding miRNA biogenesis genes and compiled the knowledge of biogenesis process based on experimentally verified direct evidences only. The conservation pattern of these genes in other plant species ranging from dicots to monocots and lower organisms was identified. And then characterization of the orthologs identified in *Oryza sativa* on the basis of comparative genomics such as transcriptome and epigenomics.

Findings: miRNA biogenesis process is an intricate and complex event consisting of many proteins working in a highly coordinated fashion. Most of these proteins have been studied in Arabidopsis; however, their orthologs and functions have not been explored in other plant species. In the present study, we found a total of 98 genes involved in miRNA biogenesis in Arabidopsis. The conservation pattern of these proteins was identified in other plant species ranging from dicots to lower organisms, and we found that a major proportion of proteins involved in the pri-miRNA processing are conserved. However, nearly 20% of the genes, mostly involved in either transcription or functioning of the miRNAs, were absent in the lower organisms. Further, we manually curated a regulatory network of the core components of the biogenesis process and found that nearly half (46%) of the proteins interact with them, indicating that the processing step is perhaps the most under surveillance/regulation. We have subsequently attempted to characterize the orthologs identified in Oryza sativa, on the basis of transcriptome and epigenetic modifications under field drought conditions in order to assess the impact of drought on the process. We found several participating genes to be differentially expressed and/or epigenetically methylated under drought, although the core components like DCL1, SE, and HYL1 remain unaffected by the stress itself. The study enhances our present understanding of the biogenesis process and its regulation.

Conclusion: The study hereby highlights the knowledge regarding the presence of miRNA biogenesis proteins in various other plant species other than Arabidopsis especially rice. The characterisation of these rice orthologs in contrasting varieties of rice indicates towards functionality of these orthologous loci and the fact that they are differentially regulated under stress conditions. These genes are subject to epigenetic regulation and are integral part of

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various yield and development related QTLs. The process is part of a beautifully constructed biological system that keep all its processes in a synchronized fashion in order to cope with every developmental or stress cue.

About Reseach Topic:

The study identifies the missing nodes in the thorough understanding of the miRNA biogenesis process in plants. miRNAs being major/significant regulators of growth and development need meticulous and exhaustive understanding of their biogenesis and function. Hence, the study highlights the areas that demand further investigation in order to improve our knowledge of the miRNA biogenesis process and the evolution of these genes.

The lack of knowledge of function and regulation of the biogenesis proteins and the yet-to-be-identified proteins involved in biogenesis in many plant species (e.g. SNC1, XRN2, RICE1&2, etc.) offer exciting avenues of research with a solid base to build on. It also identifies and curates the current yet scattered knowledge regarding the role of biogenesis proteins in plant development (besides miRNA production) such as AGO1 in yield. HEN1, HST, SE, etc. are genes that showed QTL traits not only in yield but also in other development and stress related QTL trats, indicating their role in multiple biological processes.

These results can help in future manipulation of these proteins/genes to improve miRNA biogenesis process as well as agricultural traits for the benefit of human population. Finally, it presents a new template for teaching how curation of available information is carried out and utilized to yield an exciting research project.