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Understanding the evolution of miRNA biogenesis machinery in plants with special focus on *Oryza Sativa*

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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 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.

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Biography

Miss Tonu Angaila Chithung studied Under Graduation in Biotechnology from St. Joseph's College, Bangalore University, India in 2016 followed by Post Graduation in Plant Molecular Biology and Biotechnology from University of Delhi, India in 2018. During the course she got the opportunity to work on dissertation thesis with the title "Characterization of miR397b, miR1425 and miR1871 in rice". Then she joined the same department as PhD student in 2019 and currently working on drought-regulated miRNAs in rice under the supervision of Prof. Saurabh Raghuvanshi.

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