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# Computational identification of miRNA and their expressed targets from *Carica papaya*

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## Abstract

Next Generation Sequencing (NGS) exhibited rapid developments through its high speed sequence annotation and assembly tasks which has changed the perspectives of genome era. NGS brings the great power to make several new biological observations and discoveries from genomes and helped in the growth of allied areas including Metagenomics, *De novo* sequencing, Amplicon Analysis, Transcriptomics and Small RNA profiling. *Carica papaya* small RNA sequencing helps in the understanding the role of known miRNA and identification of novel miRNA. Functional genomics often begins with studying the gene expression patterns and identification of potential targets that relies on the assumption of small RNA and the mRNA (target) sequence complementarity. The identification of Known miRNA sequences are searched through against the current miRBase version and sequences with less than 2 mismatches with known miRNAs in miRBase was considered and 1724 known miRNA depicted. Computational algorithms predict miRNA targets on the basis of the presumed mode of miRNA–mRNA interactions and also depend on the conservation of their binding sites. The mirDeep prediction software is used to predict new miRNAs where 11 novel miRNA are estimated. In addition, the functional studies of small RNAs can rely on conventional genetic strategies. Intriguingly, the advent of fast and cost effective NGS platforms in the recent past has enabled the proliferation of new ideas regarding the application of characteristic gene structures to different species.

## References

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