



Category: Bioinformatics

## Meaningful interpretation by reanalyzing the publicly available dataset: A case study of *Salvia miltiorrhiza*

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### Abstract

MicroRNAs are a newly discovered class of non-protein small RNAs with 22-24 nucleotides and evolutionary conserved post-transcriptional regulatory RNAs, which shows an enormous role in several biological and metabolic process. Plant derived miRNA entered into the body fluid and regulated the expression of host mRNA. *Salvia miltiorrhiza* is an important medicinal plant known for its potent cardiovascular and anticancer activity and hence, it was selected to identify the cross kingdom regulatory mechanism between medicinal plant and human. In this study, total 8 highly stable putative novel miRNA were predicted from the publically available ESTs of *Salvia miltiorrhiza*, out of which 2 miRNA were found to be regulating 32 target genes in human. Functional annotation, gene ontology and network analysis were carried out based on their significance and find out the association with the prominent disease like cancer and cardiac diseases. The network analysis showed the some important network protein like SOCS2, CD274, STAT3, TRAF3, and CXCL2 with their associated pathways. The predicted miRNA have a significant potential role in cytokine, Apoptosis and EGFR receptor signalling pathways and its biological regulation. It may be further validated using in-vivo experiment for broader picture into their miRNA epigenetic mechanism and action.

### References

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