



Category: Plant Genomics

Poster Prize Winner

# Deciphering the role of a miRNA in rice domestication

Swetha Chenna and Varsha Tirumalai

National Centre for Biological Sciences, INDIA

Presenting author: [chennas@ncbs.res.in](mailto:chennas@ncbs.res.in)

## Abstract

MicroRNAs (miRNAs) are a class of 21 nt non-coding small RNAs (sRNAs) produced from endogenously expressed MIR genes. miRNAs are mostly involved in development and disease resistance. We are interested in identifying key miRNAs that are differentially expressed among wild and cultivated rice species. Analysis of sRNA datasets from two wild species (*O. nivara* and *O. rufipogon*) and one cultivated species of rice (*O. sativa* var. *indica* Pusa Basmati-1), revealed a surprisingly higher abundance of small RNAs originating from Chromosome 2 in wild rice species. This locus codes for a novel 22 nt miRNA. This novel miRNA was found to be highly abundant in flag leaf of wild species, a tissue that usually provides 70% of energy required for grain filling. This miRNA targets a group of proteins (Os03g0273200, Os01g0827300, Os01g0850700, Os11g0708100 and Os01g0842500) which are involved in secondary metabolite production, although a functional significance of this interaction has not been understood. The expression of these targets also differs across the species. Typical of 22 nt miRNAs, the identified miRNA also triggers a secondary cascade silencing by producing small interfering RNAs (siRNAs) from target mRNAs in *O. nivara*. These secondary siRNAs are observed only among wild rice species but not in cultivated rice. Currently we are using a range of genetic, biochemical and molecular techniques to understand role of this novel miRNA in domestication of rice.

## References

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