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**Rice miRNA classification and target gene prediction**

Up till now, there are 592 pre-miRNAs with their 718 mature products deposited in *miRBase.org* (release 21, in June 2014), out of which 578 pre-miRNAs have been mapped to the rice genome (MSU 7.0). After BLAST to the rice genome, we obtained the genomic coordination of 7 pre-miRNAs, including well-known *OsMADS* gene regulator osa-miR444 family.

Because conservation may bring great distinctions to the evolutionary stability and target divergence for miRNAs, the miRNA classification by conservation was performed both for pre-miRNAs and MaMiRNA (mature miRNA), aided by miRNA family classification provided by *miRBase.org*. If there’s any other plant miRNAs in the same miRNA family, then the pre-miRNA in question is considered as conserved pre-miRNA. Meanwhile, canonical mature miRNAs as well as those non-canonical ones originated from conserved precursors, which have corresponding counterparts in other plant species are classified as the conserved MaMiRNAs. After classification, 191 of 592 pre-miRNAs are classified to be conserved pre-miRNAs and 220 of 718 MaMiRNAs are classified to be conserved mature miRNAs. The conserved miRNAs are the center of our downstream analysis, for most well-studied miRNAs are conserved.

It is inevitable to study target genes in order to understand the function of rice miRNAs, as the miRNAs play important roles in plant gene regulatory pathways either by translational inhibition or post-transcriptional mRNA cleavage which requires the high complementarity between the target gene and miRNA. We obtained targets for conserved miRNAs through bioinformatics prediction as well as published experiment validation results (*citation*). Compared with bioinformatics prediction, experiment validation is more reliable and the resulted targets are more biologically relevant to miRNAs. Here experiment validation is done through degradome (5’-RACE), and genes with clear degradome signals are taken as bona fide targets of miRNAs. And we utilized *psRNATarget* to predict potential miRNA targets. Finally, we obtained 823 targets, of which 46 targets are found in degradome validated data, and these targets formed 2113 interaction with MaMiRNAs (miRNA:target interaction).