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Identification of miRNA for expression in rice to provide resistance to RYMV

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The worldwide importance of rice, *Oryza sativa*, as food crop is well-understood. In order to maintain a consistent supply of rice globally, control of pathogens affecting crop production is matter of due concern. Rice yellow mottle virus (RYMV) is known to cause a variety of symptoms in *Oryza sativa* plants and certain symptoms account for death and hence reduce yield. Four ORFs can be identified in the genome of RYMV encoding for P1 (ORF1), Polyprotein (processed to produce VPg, protease, helicase, RdRp4); (ORF2), putative RdRp; (ORF3) and capsid/coat protein (ORF4). This research was executed to identify genome encoded miRNAs of *O. sativa* that are targeted to the genome of Rice Yellow Mottle Virus (RYMV). A consensus of four prediction algorithms (RNA22, miRanda, TargetFinder

and psRNATarget was considered, thus allowing a multitude of miRNA target prediction parameters to be implemented including minimum free energy of binding, folding energy, seed pairing, target site accessibility and multiple target sites. A phylogenetic tree was constructed to portray the evolutionary relationships between RYMV strains isolated to date. Finally, target site conservation was also evaluated which revealed a varying degree of miRNA target site conservation in the genome of RYMV. Results of this research are expected to act as precursor for the development of RYMV resistant rice varieties around the world by using recombinant expression of selected miRNAs in *O. sativa*.

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