

miRNAs BINDING TO mRNAs OF RICE MYB GENES

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Motivation and Aim: Transcription factors (TF) play a key role in gene expression regulation. 2025 transcription factors of *Oryza sativa L. ssp. indica* are included in 63 families. The family of MYB TF genes plays a key role in the plant growth, development and stress reactions. Expression of transcription factor genes is controlled by miRNAs binding with mRNAs of genes and blocking translation. So it was important to study which miRNAs bind to mRNAs of *O. sativa* MYB genes, which genes are targets for each miRNA family and calculate free energy of miRNA-mRNA interaction.

Methods and Algorithms: The binding sites of osa-miRNA in mRNA of 136 gene of MYB family was revealed using the program MirTarget, which defines the location of the miRNA with mRNA binding sites, calculates the free energy hybridization (ΔG , kJ/mole) and the ratio $\Delta G/\Delta G_m$ (%), where ΔG_m equal to the free energy of miRNA binding with fully complementary nucleotide sequence. The binding sites of miRNA with mRNA selected by $\Delta G/\Delta G_m$ equal or above to 85%.

Results: At present 661 miRNAs and 136 MYB TF genes are known in the genome of rice. It was found that only 173 miRNAs bind to mRNAs of *O. sativa* MYB genes with value of score ranging from 85% to 96% and only 86 genes are controlled by miRNAs. Osa-miR2102-5p has the largest number of target genes. It bound to mRNAs of 23 genes with value of score from 86 to 91%. Osa-miR5075 bound to mRNAs of 11 genes with value of score equal 86-93%. In the genome of rice some miRNAs bound to mRNAs of one or several genes. Six miRNAs of osa-miR159a-f family bound to mRNAs of OsIBCD015177, OsIBCD018450, OsIBCD021789 genes with value of $\Delta G/\Delta G_m$ equal 87-96%. All ten miRNAs of osa-miR439a-j family bound to mRNAs of only one gene OsIBCD007874 with the same value of $\Delta G/\Delta G_m$ equal 85%. Six miRNAs of osa-miR164a-f family bound to mRNAs of OsIBCD014655, OsIBCD001147, OsIBCD000203 and OsIBCD028679 genes with values of $\Delta G/\Delta G_m$ equal 87-96%. Osa-miR169a-e bound to mRNAs of five genes (OsIBCD015070, OsIBCD022880, OsIBCD003079, OsIBCD032138 и OsIBCD008009) with score equal 85-87%. Osa-miR159 bound to mRNAs of three genes (OsIBCD015177, OsIBCD018450, OsIBCD021789) with value of score ranging 87-96%. Osa-miR1846d-3p bound to mRNAs of OsIBCD018922, OsIBCD023878, OsIBCD026910 and OsIBCD035359 genes. All rice miRNA binding sites are located in the protein-coding part of MYB TF family mRNAs.

Conclusion: As a result of study of *O. sativa* MYB TF gene family there was found that: 1) some target genes have more than one miRNA binding site, beginnings of which are located successively through one-three nucleotides that increases probability of translational process control by miRNA binding; 2) not all MYB family genes are targets for miRNA; 3) nucleotides of miRNA binding sites encode oligopeptides of MYB proteins in different reading frames. Results obtained show that osa-miRNAs can regulate expression the most of MYB genes and influence the plant productivity and resistance.