

miRNAS BINDING WITH mRNAs OF *ARABIDOPSIS THALIANA* C2H2 TRANSCRIPTION FACTOR GENES

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Motivation and Aim: Transcription factors (TF) play a key role in gene expression regulation. 2290 transcription factors of *Arabidopsis thaliana* are included in 64 families. The C2H2 family of TF genes plays a key role in the plant development. 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 *A. thaliana* C2H2 transcription factor genes, which genes are targets for each miRNA family and calculate free energy of miRNA-mRNA interaction.

Methods and Algorithms: The binding sites of ath-miRNAs in mRNAs of *A. thaliana* genes was revealed using the program MirTarget, which defines the location of the miRNA 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 miRNAs selected by $\Delta G/\Delta G_m$ equal or above to 85%. The diagrams of conservation of oligopeptides which are encoded by the miRNA binding sites are obtained by the program WebLogo.

Results: At present 337 miRNAs and 99 C2H2 TF genes are known in the genome of *A. thaliana*. It was found that only 49 miRNAs bind with mRNAs of *A. thaliana* C2H2 genes and only 59 genes are controlled by miRNAs. ath-miR5021 has the largest number of target genes. It bound with mRNAs of 18 genes with value of score from 87 to 93% and the binding sites of ath-miR5021 are encoded homological oligopeptide SSSSS. ath-miR5658 bound with mRNAs of 16 genes with value of score equal 85-96%, the binding sites are encoded homological amino acid sequence HHHHHH. ath-miR414 bound with mRNAs of ten genes with value of $\Delta G/\Delta G_m$ equal 86-92%, the binding sites are encoded homological oligopeptide DDDDD. ath-miR854a bound with mRNAs of six genes with value of $\Delta G/\Delta G_m$ equal 85-96% and the binding sites are encoded homological oligopeptide PPPPP. ath-miR5015b bound with mRNAs of five genes with values of $\Delta G/\Delta G_m$ equal 86-88%. In the genome of *Arabidopsis* some miRNAs bound with mRNAs of one or several genes. ath-miR3434 bound with mRNAs of three genes (AT1G26610, AT3G58070 and AT4G35280) with score equal 86-94%. ath-miR838 bound with mRNAs of three genes too (AT2G18490, AT4G27240 and AT5G56200) with value of score ranging 86-90%. ath-miR860 bound with mRNAs of AT1G03840, AT3G50700 and AT5G44160 genes with value of score ranging 85-94%. ath-miR5632, ath-miR5638a, ath-miR5640, ath-miR830 and ath-miR837 miRNAs have two gene targets each. The rest 37 miRNAs have only a one gene target each. All miRNA binding sites are located in the protein-coding part (CDS) of C2H2 TF family mRNAs.

Conclusion: As a result of study of *A. thaliana* C2H2 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 C2H2 family genes are targets for miRNAs; 3) nucleotides of miRNA binding sites encode oligopeptides of C2H2 proteins in different reading frames. Results obtained show that ath-miRNAs can regulate expression the most of C2H2 genes and influence the plant productivity and resistance.

Availability: miRTarget (our own program)