

## BINDING OF MICRORNA WITH MRNA OF GRF GENES IN COMPLETELY SEQUENCED PLANT GENOMES

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MicroRNA (miRNA) is a class of small non-coding RNAs that play an important role in gene expression. miRNAs control the growth and development of plants by changing the expression of transcription factors. Therefore it is important to determine the miRNAs, which target a family of growth-regulating factors (*GRF*).

The nucleotide sequences of *GRF* genes in *Arabidopsis thaliana*, *Glycine max*, *Hordeum vulgare*, *Medicago truncatula*, *Oryza sativa*, *Solanum lycopersium*, *Sorghum bicolor*, *Triticum aestivum*, *Vitis vinifera*, *Zea mays* were obtained from Genbank. The nucleotide sequences of miRNAs were received from miRBase. The free energy ( $\Delta G$ ) of miRNA binding, position and patterns of potential binding sites were calculated by RNAHybrid 2.1 program. E-RNAhybrid script was used for the calculation of  $p$ -value and  $\Delta G/\Delta G_m$  (%) value, where  $\Delta G_m$  is binding energy of miRNA with perfect complementary sequence. The  $\Delta G/\Delta G_m$  value was used as comparative criterion of the miRNA and mRNA interaction force.

We found that among 338 miRNAs of *A. thaliana* only miR396 was shown to have strong binding sites with mRNAs of *GRF* genes. Among nine *GRF* genes mRNAs of *GRF1-4* and *GRF7-9* were targets for miR396 with  $\Delta G/\Delta G_m$  value varied from 85 to 90%. miR396 binding sites were located in the protein-coding sequence of *GRF* mRNAs and encoded RSRKHVE or RSRKPVE heptapeptide. Analysis of miR396 interactions with *GRF* orthologs in other plant organisms has shown the similarity of characteristics of miRNA binding sites. It was found that among 554 miRNAs of *G. max* only miR396 had binding sites in the mRNA of 18 *GRF* genes. Among 719 miRNAs of *M. truncatula* only miR396 associated with four genes of *GRF* family. Among 661 miRNAs of *O. sativa* miR396 binds to mRNA of nine *GRF* genes. 36 *GRF* genes are targets for miR396 among 321 miRNAs in *Z. mays*. In *V. vinifera* among 185 miRNAs only miR396 bound to 18 *GRF* genes, in *S. bicolor* among 242 miRNAs only miR396 targeted 10 *GRF* genes, in *H. vulgare* among 67 miRNAs only miR396 had binding sites in mRNAs of five *GRF* genes. mRNAs of three *GRF* genes had binding sites only for miR396 among 44 miRNAs of *S. lycopersium*, and among 42 miRNAs of *T. aestivum* only miR396 bound to four *GRF* genes.

Our results reveal that in studied plants miR396 binding sites were located in the coding sequence of mRNA and their nucleotide sequences were conserved. The interaction sites between miR396 and *GRF* mRNAs encoded RSRKHVE or RSRKPVE heptapeptide. In all cases, the criterion of binding efficiency of miRNA to mRNA is the  $\Delta G/\Delta G_m$  value was more than 80%. The high  $\Delta G/\Delta G_m$  value indicates the strong control of *GRF* family genes expression by of miR396 and the high selectivity of the miRNA targets.