BINDING OF miR396 FAMILY WITH mRNA OF GROWTH-REGULATING FACTORS IN RICE AND MAIZE

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Motivation and Aim: microRNAs (miRNAs) are involved in plant growth and development by regulating post-transcriptional gene expression. miR396 family directly regulates growth processes in plants via targeting growth-regulating factor (*GRF*) genes family. It is important to identify the interaction characteristics of miR396 family with mRNA of *GRF* genes in rice and maize.

Methods and Algorithms: Gene nucleotide sequences of *Oryza sativa* and *Zea mays* were obtained from GenBank (http://www.ncbi.nlm.nih.gov). miRNAs nucleotide sequences were received from miRBase (http://www.mirbase.org). The free energy (ΔG) of hybridization of miRNA and mRNA, the position of potential binding sites, and the interaction schemes were calculated by using the RNAHybrid 2.1 software (http://bibiserv.techfak.uni-bielefeld.de/rnahybrid/). The E-RNAhybrid software (http://sites.google.com/site/malaheenee/software/) was used to compute the $\Delta G/\Delta Gm$ value and p-value. The $\Delta G/\Delta Gm$ value was used as comparative criterion of the miRNA and mRNA interaction force.

Results: We found that among 661 miRNAs of *O. sativa* only osa-miR396a-i are shown to have strong binding sites with mRNAs of nine *GRF* genes. These miRNAs bound with mRNAs of *GRF* genes with various degree of prediction reliability and distributed into five groups: miR396a,b; miR396c; miR396d,e; miR396f; and miR396g,h,i. The $\Delta G/\Delta Gm$ value for miR396 binding sites in mRNAs of *Os02g0701300, Os06g0116200, Os02g0776900, Os03g0729500, Os02g0678800, Os03g0674700, Os11g0551900, Os04g0600900* and *Os12g0484900* genes ranged from 75.9% to 100% of the maximum free energy, which indicates a strong interaction of these miRNAs with the mRNA of the *GRF* gene family. osa-miR396a-i binding sites in mRNA of these *GRF* genes are located in the protein-coding sequence, are highly homologous and encode the same RSRKHVE heptapeptide. We have also investigated miRNAs and *GRF* genes as their targets in maize. Our results reveal that among 321 miRNAs of *Z. mays* only zma-miR396 family bind to the mRNA of 36 *GRF* genes with various degree of prediction reliability. By their different binding ability zma-miR396 family may be distribute into five groups: miR396a,b; miR396c; miR396d,e; miR396f; miR396g,h. zma-miR396 binding sites in mRNA of *GRF* genes in *Z. mays* are located in the protein-coding sequence, are highly homologous and encode RSRKHVE heptapeptide. In all cases, the free energy of zma-miR396a-h binding with mRNAs of 36 *GRF* family members in maize varied from 78.8% to 100% of the maximum free energy, which shows a high rate of interaction. All paralogs of *GRF* genes in *Z. mays* bind all members of miR396 family.

Conclusion: Our results show that miR396 binding sites are located in the protein-coding sequence of the mRNA, and they are highly conserved in rice and maize. We suggest the expression of growth-regulating factors, that affect the productivity of rice and maize, is under strong miR396 family control.