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IDENTIFICATION OF MICRORNAS AND SIRNAS INVOLVED IN SOYBEAN SEED DEVELOPMENT

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RESUMO

Non-coding RNAs (ncRNAs) are fundamental in the regulation of gene expression in the most varied biological contexts. During the seed development, microRNAs (miRNAs) can modulate the processes of embryogenesis and maturation, and their inhibition can be lethal to the embryo and compromise seed formation. In this study, we seek to identify known and novel miRNAs involved in the seed development of soybean (*Glycine max*), a legume of great nutritional and economic importance. The methodology involved the usage of different bioinformatics tools for identification of known and novel miRNAs, analysis of the expression profile, analysis of phased secondary small interfering RNAs (phasiRNAs) triggered by known miRNAs, prediction of putative miRNA targets and construction of small interfering RNAs (siRNAs) clusters. The results showed 66 known miRNAs expressed in globular, heart, cotyledon and early maturation stages of seed development. Of these miRNAs, 39 were common to all stages. Analysis of the expression profiles showed miRNAs with high expressions in all stages, such as miR482, miR1507, miR1510, miR166, miR398, miR390, miR159, and miR2118. We found that the miR396, miR156, miR167 and miR159 perform tissue-specific regulation of target genes at different tissues and stages of seed development. The search for phasiRNAs revealed that the 22-nt miR2118 is a precursor to phasiRNAs in developing soybean seeds. 228 potential novel miRNAs were identified, and most of these miRNAs showed stage-specific expression. Prediction of putative miRNA targets exhibited genes that play important roles during the seed formation. The correlation analysis of the 21-nt and 24-nt siRNAs clusters showed that all tissues are positively correlated, and the 21-nt siRNAs clusters exhibited variable expression profiles between tissues. Our findings increase the number of potential new miRNAs in soybean and provide relevant data on the expression of miRNAs in developing soybean tissues.

PALAVRAS-CHAVE: Small RNAs, seed development, soybean

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