



Category: Plant Genomics

Identification of Groundnut miRNA and their targets

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Abstract

MicroRNA (miRNA) are ~22nt small non-coding RNA molecules which play an important role in post-transcriptional gene regulation in both plants and animals. As the miRNAs are highly conserved among species, comparative genomics based homology search has played a key role in identifying new miRNAs in different species whose genomes are not yet sequenced. *Arachis hypogaea* (groundnut or peanut) is one such legume crop and being grown in more than 100 countries, ranks third worldwide among oilseeds produced. In India, it is the second largest in terms of production but stands first in terms of area of cultivation. Identifying miRNAs and their targets can be helpful in crop improvement. In the present study, we tried to identify new conserved miRNA from the 205442 ESTs through blast search, using previously known plant miRNAs. The non-protein coding sequences with homology showing no more than 3 mismatches were folded back to stem-loop structure. These were subsequently passed through strict filtration criteria to obtain new miRNAs belonging to different miRNA families, as well as their targets.

References

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