Bioinformatics Analysis of Next Generation Sequencing Data of Small RNAs in *Arabidopsis Thaliana*

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ABSTRACT: Next generation sequencing technologies have a substantial impact on a broad range of biological applications. Small RNAs are 21–24 nucleotides in length and are known to play a major role in the activation of mRNAs and genomic DNAs. Next generation sequencing is used to reduce the size of sample components, reagent costs, and enables massively parallel sequencing reactions. *Arabidopsis Thaliana* is the model organism chosen for analysis of small RNAs through Avadis NGS software. *A. thaliana* genome is maintained by the Arabidopsis Information Resource (TAIR). In this work, we have performed the in-silico based preliminary experiment using NGS dataset of small RNAs in *Arabidopsis Thaliana*. To start with we worked on Avadis NGS software, a comprehensive data mining and visualization platform. Several steps such as Import samples, Alignment, Quality Inspection, Filter, and Quantification were followed and we observed the active regions of microRNA, through which we identified the corresponding accession ID of the gene coding microRNA and finally the accession of the miRNA. Thereafter, the sequences of the mature miRNA were downloaded from miRBase database which were further analyzed in psRNA Target tool with default settings, as a result we observed the target gene of miRNA. The obtained results could be further validated with experimental approaches. © 2014 iGlobal Research and Publishing Foundation. All rights reserved.