

In silico analysis of mRNA:miR-3099 interaction

ABSTRACT

Introduction: MicroRNAs (miRNA) are small non-coding RNAs and have crucial role in gene expression and protein synthesis regulation, especially in nervous system and brain development. A novel miR-3099 was found highly express throughout embryogenesis especially in the developing central nervous system. Moreover, miR-3099 was also expressed upon neuronal differentiation in in vitro system suggesting that miR-3099 is a potential regulator during neuronal development. Therefore, objective of this study is to predict target genes of miR-3099 via in-silico analysis. These analyses will predict potential downstream targets for miR-3099 and their relationship to signalling pathways with special focus on neuronal function and brain development.

Methods: Four different prediction software, miRDB, miRanda, TargetScan and DIANA micro-T, were employed to identify the candidate target genes of miR-3099. The predicted downstream targeted genes were selected based on the database criteria, prior to BioVenn clustering to identify the common targeted genes. The targeted genes that were predicted by at least three different databases were subjected to DAVID bioinformatics analysis to understand the biological process and function of these targeted genes.

Results: Based on the analysis, a total of 1676 predicted genes were targeted by miR-3099. Of these, 73 genes were predicted by three software and 22 genes were predicted by all the four software. Majority of the targeted genes were annotated as involved in positive regulation of transcription activity and were identified as related to neuronal and brain development. Hence, the predicted downstream targets of miR-3099 warrant further investigation to validate the in silico analysis.