GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Integrated miRNA-mRNA analysis of Epstein-Barr virus-positive nasopharyngeal carcinoma

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Genet. Mol. Res. 14 (2): 6028-6036 (2015)
Received September 30, 2014
Accepted February 5, 2015
Published June 1, 2015
DOI http://dx.doi.org/10.4238/2015.June.1.20

ABSTRACT. This study aims to identify the crucial miRNAs in Epstein-Barr virus-positive nasopharyngeal carcinoma (NPC) and their target genes. Gene expression profile data (GSE12452) that included 31 NPC and 10 normal nasopharyngeal tissue specimens were downloaded. Differentially expressed genes (DEGs) were identified using significance analysis of microarrays. The underlying function of DEGs was predicted via Gene Ontology and Kyoto Encyclopedia of Genes and Genomes pathway enrichment analyses. The miRNA sequencing dataset GSE14738 was also downloaded, and expression levels of miRNA were calculated by the number of reads mapped to each miRNA. The selected miRNAs were integrated into the miRecords

database to obtain their target genes. Target genes associated with DEGs were used to construct the interaction network via Cytoscape. A total of 1437 DEGs between NPC and control were identified, most of which were enriched in cell cycle and extracellular matrix-receptor interaction signaling pathways. Furthermore, 112 miRNAs were considered upregulated in NPC samples. A total of 2228 relationships between 39 miRNAs and 1247 target genes were obtained, of which 182 relationships between 32 miRNAs and 97 target genes were chosen to construct an interaction network. The interactions between DEGs and the let-7 or miR-29 families appeared strongest in this network, where *CDC25A*, *COL3A1*, and *COL1A1* were regulated by several let-7 family members, while *COL4A1* and *COL5A2* were regulated by several miR-29 family members. The let-7 and miR-29 families may be related to the development of NPC by regulating the genes involved in cell cycle and ECM-receptor interaction.

Key words: Epstein-Barr virus-positive nasopharyngeal carcinoma; Differentially expressed genes; Typical miRNAs; Target genes