MicroRNA16 Inhibit Lung Cancer Cell Proliferation

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ABSTRACT

MicroRNAs (miRNAs) are small endogenous RNAs, approximately 18-24 nucleotides that can down-regulate various target gene products by translational repression or by directing mRNA degradation. miRNAs exhibit diverse biological functions in metabolism, differentiation, proliferation, and cell cycle. Recent studies have shown that aberrant expression of miRNAs in various human cancers, suggesting that they may play an important role in cancer development. In this study, we investigated and identified the miRNA candidates related with non-small cell lung carcinoma (NSCLC) by using homemade miRNA microarray and cell line model (normal human bronchial epithelial cell: BEAS-2B; lung cancer cell: CL1-0 and CL1-5). The results revealed that 13 out of 354 human miRNAs tested are more than 3-fold changed between BEAS-2B and lung cancer cells, such as miR16, miR23a, miR127, miR494, miR638, and so on. Furthermore, we detected the miRNA expression in different lung cancer cell lines by miRNA stem loop RT-PCR. We also found that the low expression level of miR16 in CL1-0, CL1-5, A549, CRL-5802, CRL-5806, H2981 and HTB54 lung cancer cells compared with that of BEAS-2B cells. To study the biological functions of miR16 in lung cancer cells, we constructed a miR16 over-expression system in CL1-5 cells and analyzed the cell proliferation. We demonstrated that over-expression of miR16 can inhibit lung cancer cell proliferation. Through 2-D electrophoresis analysis, we find out the proteins NYGGF4 and ALDOA will be reduced after miR16 over-expression. Finally, we also suggest that miR16 might regulate cell proliferation through down-regulated NYGGF4 and ALDOA gene expression.

Keywords : MicroRNA ; miR16 ; lung cancer ; invasion ; migration

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