MicroRNA Expression Profiles and MiR-10a Target in Anti-benzo[a]pyrene-7, 8-diol-9, 10-epoxide-transformed Human 16HBE Cells

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Objective To screen miRNA profiles of malignantly transformed human bronchial epithelial cells, 16HBE-T, induced by anti-benzo[a]pyrene-trans-7,8-diol-9,10-epoxide (anti-BPDE), and to analyze putative miR-10a targets in 16HBE-T.

Methods A novel microarray platform was employed to screen miRNA profiles of 16HBE-T cells transformed by anti-BPDE. Microarray data for miR-10a and miR-320 were validated using quantitative real time polymerase chain reaction (QRT-PCR). The expression of a putative target for miR-10a, HOXA1, was analyzed by reverse transcription polymerase chain reaction (RT-PCR) and QRT-PCR.

Results In comparison with the vehicle-treated cells (16HBE-N), 16HBE-T exhibited differential expression of 54 miRNAs, in which, 45 were over-expressed and 9 were down-regulated. The five most highly expressed miRNAs were miR-494, miR-320, miR-498, miR-129, and miR-106a. The lowest expressed miRNAs were miR-10a, miR-493-5p, and miR-363*. Three members of miR-17-92 cluster, miR-17-5p, miR-20a, and miR-92, showed significantly higher abundance in 16HBE-T as miR-21, miR-141, miR-27a, miR-27b, miR-16 and miRNAs of the let-7 family. The putative target for miR-10a, HOXA1 mRNA, was up-regulated 3-9-fold in 16HBE-T, as compared with 16HBE-N.

Conclusion The findings of the study provide information on differentially expressed miRNA in malignant 16HBE-T, and also suggest a potential role of these miRNAs in cell transformation induced by anti-BPDE. HOXA1 is similarly up-regulated, suggesting that miR-10a is associated with the process of HOXA1-mediated transformation.

Key words: MicroRNA; Anti-BPDE; Malignant transformation; 16HBE

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