

Evaluating the Effects of Deregulated miRNAs by Human Papilloma Virus on Gene Expression Profiles of Squamous Cell Carcinomas of the Head and Neck

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Abstract

Background and aim: Human Papilloma Virus plays an important role in some of human malignancies and causes alterations in normal expression levels of cellular microRNAs. In this paper, we evaluated the effects of such changes on Head and Neck Squamous Cell Carcinoma tumor samples at gene expression profile level.

Methods: in this descriptive-analytical study, gene expression profiles of 36 tumor samples were compared in two groups: with or without virus. Differentially expressed genes among the two groups were judged in terms of their ability in segregating the tumor samples and also their overlap with Gene Ontology Biological Function categories. Furthermore, using hierarchical clustering analysis and Gene Set Enrichment Analysis methods, the effect of confirmed cellular targets of 11 reported cellular microRNAs on the gene expression profiles of our samples was assessed.

Results: Unlike unsupervised methods, differentially expressed genes, including 47 and 7 unique induced and suppressed genes, respectively, discriminated perfectly the two sample sets in a hierarchical clustering analysis ($P=0.0001$). These genes were primarily engaged in regulation of cell cycle (FDR adjusted $P\leq 0.05$). Targets of induced cellular microRNAs were found enriched in virus-positive set (FDR adjusted $P\leq 0.05$). Among analyzed cellular miRNAs, hsa-miR-155-5p and hsa-miR-221-3p change the gene expression profile of tumor samples significantly (FDR adjusted $P\leq 0.05$).

Conclusion: deregulating expression levels of cellular microRNAs, HPV is capable of affecting the gene expression profiles of Head and Neck Squamous cell Carcinoma tumors. It is suggested to confirm the results of this study using experimental methods.

Keywords: Human Papilloma Virus, Squamous cell carcinoma of the head and neck, microRNA, Gene Expression Profiling