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Identification of Viral Infection-Related Differentially Expressed Genes in Oral Squamous Cell Carcinoma

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ABSTRACT

Oral Squamous Cell Carcinoma (OSCC) represents a major global health burden, with multifactorial aetiology involving genetic, environmental, and infectious factors. Among these, viral infections have emerged as important contributors to oral carcinogenesis. Oncogenic viruses such as human papillomavirus (HPV), Epstein–Barr virus (EBV), and herpes simplex virus (HSV) have been implicated in the initiation and progression of oral malignancies. The study method involved searching for the OSCC datasets (GSE30784) in the Gene Expression Omnibus database and comparing gene expression between them and normal tissues. Total number of 2054 differentially expressed genes (DEGs) were identified using GEO2R out of which 1253 were upregulated and 1254 were downregulated. To find statistically significant genes, the adjusted P-values (adj. P) and Benjamini and Hochberg false discovery rate were used [Log FC (fold change) > 1 and adj. P-value < 0.05]. Functional annotation analysis revealed that the upregulated genes were involved with Human Papilloma virus infection(63 genes), Epstein Barr Virus infection (42 genes), Human cytomegalovirus infection (39 genes), Human T cell leukaemia virus 1 infection (37 genes), Herpes simplex virus 1 infection (35 genes), Coronavirus disease -COVID 19 (32 genes), Viral protein interaction with cytokine and cytokine receptor (29 genes), Human immunodeficiency virus 1 infection (28) and viral myocarditis (16 genes). The upregulated genes are mostly involved in the inflammatory pathways, viral oncoprotein expression, modulation of tumour suppressor genes, and alteration of signalling pathways involved in cell proliferation and invasion. The pathways may be explored further to find out the interaction of these genes related to immune responses in cancer pathogenesis.

Keywords: *Oral cancer, DEGs, functional annotations, viral response*

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