## Gene expression in human oral squamous cell carcinoma is influenced by risk factor exposure

## Abstract

Oral squamous cell carcinoma (OSCC) is a world health problem and is associated with exposure to different risk factors. In the west, smoking and alcohol consumption are considered to be the main risk factors whilst in India and southeast Asia, betel quid (BQ) chewing is predominant. In this study, we compared the gene expression patterns of oral cancers associated with BQ chewing to those caused by smoking using Affymetrix microarrays. We found that 281 genes were differentially expressed between OSCC and normal oral mucosa regardless of aetiological factors including MMP1, PLAU, MAGE-D4, GNA12, IFITM3 and NMU. Further, we identified 168 genes that were differentially expressed between the BQ and smoking groups including CXCL-9, TMPRSS2, CA12 and RNF24. The expression of these genes was validated using qPCR using independent tissue samples. The results demonstrate that whilst common genes/pathways contribute to the development of oral cancer, there are also other gene expression changes that are specific to certain risk factors. The findings suggest that different carcinogens activate or inhibit specific pathways during cancer development and progression. These unique gene expression profiles should be taken into consideration when developing biomarkers for future use in prognostic or therapeutic applications.

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## Keyword

Betel quid, Gene expression, Oral squamous cell carcinoma, Risk factors, Smoking

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