

Selected transcriptome profiles of oral cancer suggestive of field cancerisation using second generation sequencing

Type: Meeting Abstract

Content:

Objectives: To characterize differential gene expression between oral cancerous tissues and the normal mucosal tissues of oral cancer patients and oral mucosal tissues of cancer free patients using second generation sequencing. **Methods:** Five fresh frozen oral cancer tissue samples from smoking patients, with 2 samples of proximal normal were included in this study. An additional 8 samples consisting of normal oral mucosal tissues from the alveolar mucosa of non-cancer patients who had their wisdom tooth removed where 4 were smokers and another 4 were non-smokers was also included. The tissues and socio-demographic information were obtained from the Malaysian Oral Cancer Data and Tumour Bank System (MOCDTBS) at the Oral Cancer Research and Coordinating Centre (OCRCC). Manual macrodissection was used to obtain >70% tumour or normal epithelial tissue. High quality poly A+ RNA was extracted from the macrodissected tissues and second generation sequencing was done using the Illumina Genome Analyzer. Validation of second generation sequencing was done using commercial and custom microarrays. **Results:** Among the differentially expressed genes, KRT76 which encodes a filament protein that is responsible for the structural integrity of epithelial cells was the most down-regulated gene when comparing all tumours to all normals (excluding proximal normals). KRT76 is the second most down-regulated gene when comparing differential expression between proximal normal and normal non-cancer samples. Further comparison of all tumors against all normals, including the proximal normals, still indicates down-regulation of KRT76, but to a much lesser degree. A similar pattern was also observed for other down-regulated genes such as the KRT2, KRT3, ANKS1B, CPLX2, FGB, HIST1H3A, HIST1H3G, HIST1H4I, LOR and ZFH2. **Conclusions:** This pattern of partial cancerisation of proximal normal samples is suggestive of the possible presence of 'field cancerisation'. **Relevance:** The "field cancerisation" theory was postulated by Slaughter whereby the occurrence of multiple independent primary tumours was explained by the fact that the upper aerodigestive tract is chronically exposed to carcinogens. Various conventional molecular methods including microarray based technologies have been applied. Nevertheless, there have been no reports utilizing second generation sequencing to elucidate differentially expressed genes in relation to 'field cancerisation' in oral carcinogenesis. Using second generation sequencing to discover genes involved in 'field cancerisation' may be useful in predicting the outcome of different management strategies for oral cancer patients.

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