

Genome wide profiling of tongue and cheek cancer using high resolution array based CGH

Meeting Abstract Content.

Introduction: Tongue and cheek cancer have different behaviors. In order to understand these behaviors, there is a need to look into the chromosomal alterations and gene pathways that maybe associated with oral cancer at these sites. Therefore, the objective of this study is to determine the differences in chromosomal aberrations and gene pathways involved in tongue and cheek cancer using high resolution array CGH.

Methods: A genome wide screening with array CGH (SurePrint G3 CGH 1x1M microarray) was performed using gDNA from 20 snap frozen fresh tissues consisting of 12 tongue and 8 cheek oral squamous cell carcinomas (samples from the Malaysian Oral Cancer Data and Tumour Bank System [MOCDTBS] coordinated by OCRCC-UM). Cytosure Software was used to detect the chromosomal aberrations and candidate genes related to the selected regions. Pathway analysis was done using MetaCore™ software for selected genes.

Results: The mean number of chromosomal aberrations per tumour for tongue cancer (22 ± 24.97) was higher than cheek cancer (8.38 ± 11.98). The most common amplified regions in tongue cancers were 8q24.22 (33.33%), 8q24.3 (33.33%), 11q13.1 (33.33%), 11q13.2 (33.33%), 12q13.13 (33.33%), 14q32.33 (33.33%) and for cheek cancer the most common amplified region was 22q12.3 (25%). For the deleted regions, the most common for tongue cancer were 2q21.1 (16.67%), 6q21 (16.67%) and for cheek cancer were 2q22.1 (25%), 7q35 (25%), 19q13.33 (25%). The most significant pathway based on $p < 0.001$ involved in tongue cancer is cell adhesion ECM remodeling pathway. Among the genes involved in amplified region, were EGFR, MMP1, MMP10, MMP12, MMP3, MMP7 and MMP9. For cheek cancer, the cancer associated significant pathway was apoptosis and survival (the role of CDK5 in neuronal death and survival). An oncogene located at 8p12 was identified in this pathway is NRG1.

Discussion: This study showed a different pattern of chromosomal aberrations in tongue and cheek cancer with different significant gene pathways. Tongue cancer behaves more aggressively than cheek cancer which may be due to the involvement of ECM remodeling pathway, where MMP family which are the proteolytic enzyme that degrade various component in the extracellular matrix would favor invasion and metastasis.

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