

Title:	Genomic DNA copy number alterations from precursor oral lesions to oral squamous cell carcinoma
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Abstract:	<p>Oral cancer is a multifactorial disease in which both environmental and genetic factors contribute to the aetiopathogenesis. Oral cancer is the sixth most common cancer worldwide with a higher incidence among Melanesian and South Asian countries. More than 90% of oral cancers are oral squamous cell carcinoma (OSCC). The present study aimed to determine common genomic copy number alterations (CNAs) and their frequency by including 12 studies that have been conducted on OSCCs using array comparative genomic hybridization (aCGH). In addition, we reviewed the literature dealing with CNAs that drive oral precursor lesions to the invasive tumors. Results showed a sequential accumulation of genetic changes from oral precursor lesions to invasive tumors. With the disease progression, accumulation of genetic changes increases in terms of frequency, type and size of the abnormalities, even on different regions of the same chromosome. Gains in 3q (36.5%),</p>

	5p (23%), 7p (21%), 8q (47%), 11q (45%), 20q (31%) and losses in 3p (37%), 8p (18%), 9p (10%) and 18q (11%) were the most common observations among those studies. However, losses are less frequent than gains but it appears that they might be the primary clonal events in causing oral cancer.
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