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Analysis of ras Gene Mutation in Human Oral Tumours by Polymerase Chain Reaction and Direct Sequencing

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Abstract: Genetic alterations in proto-oncogenes or tumour suppressor genes are believed to be one of the key events in the multistage process of carcinogenesis. Activating point mutations occurring in either one of the three ras proto-oncogene families are common genetic alterations in human and animal neoplasms. However, the mechanisms leading to oral cancer are not completely understood. Activation of the ras oncogene in oral carcinogenesis, although absent or rare in the western world, accounts for up to 35% of all malignancies in India and South Asia. Recognised aetiological agents of oral cancer include tobacco and alcohol. Tobacco-associated compounds such as nitrosamines are linked with carcinogenesis in humans. In the present paper, point mutations of ras genes were analysed in human oral cancers. DNA obtained from the tissue was amplified by polymerase chain reaction and then analysed by direct DNA sequencing in order to detect possible mutations at codons 12, 13 and 61 of H-ras, K-ras and N-ras. The DNA sequencing analyses revealed that there were no mutations at the hotspots of the three ras genes. These results indicate that ras gene mutation may not play an important role in the development of oral tumours in western samples.

Key Words: Oral tumour, PCR, Direct sequencing, Tobacco-specific nitrosamines

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