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Multiple Deletions in Chromosome 3p are Associated with the Development of Head and Neck Squamous Cell Carcinoma

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KEY WORDS Head and neck squamous cell carcinoma; chromosome 3; tumor suppressor gene(s); loss of heterozygosity; microsatellite size alteration.

ABSTRACT Detailed deletion mapping was done in the chromosomal 3p21.2-22 and 3p12-13 regions, showing high deletions in our previous study, using 13 highly polymorphic microsatellite markers in 25 primary head and neck squamous cell carcinoma (HNSCC) to narrow down the candidate tumor suppressor genes' (TSGs) loci. Deletions in the different regions of chr.3p were seen to increase significantly with the progression of the clinical stages as detected by the fractional regional loss (FRL) index analysis. Five discrete areas with the following order of deletion frequency i.e. D3: 3p21.31 > D2: 3p21.32 > D1: 3p21.33 > D4: 3p21.2-21.1 > D5: 3p12.1, had been identified. Among these regions, the onset of deletions during progression of the tumor i.e. from stage I to stage IV, was suggested to occur in the following order i.e. D3 → D1& D2 → D4 & D5. The deletion in the D5 region was significantly associated with the progression of the clinical stages. Microsatellite size alterations (MAs) were seen to be high in and around the highly deleted regions. Also loss of normal copy / interstitial alterations of chr.3 in the late stages of the tumor as well as rare biallelic alterations around the highly deleted regions were seen in our samples. The Human Papilloma Virus (HPV) infection was found to be associated with the MAs in D3 region, whereas nodal involvement of the tumor was correlated with the deletions in D1, D2, D4 and D5. Thus, this study indicates that multiple tumor suppressor genes (TSGs) may be present in chr.3p whose differential deletions are associated with the development of HNSCC.

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