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Risk of tongue and buccal mucosa cancers may vary with FAS and FASL SNPs, in a gender dependent way

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Background: Several reports have linked FAS (CD95 receptor) and FASL (CD95 ligand) aberrations with human cancers, including those of Head and Neck. However, expression pattern of these proteins vary among various tissues. Hence, we hypothesized that the role(s) of FAS and FASL together or independently may be specific to the site of the oral cancer and gender.

Objective: To test the hypothesis, we examined whether the promoter region polymorphisms of FAS (-1377 G>A; rs2234767 and -670 A>G; rs1800682) and FASL (-844 T>C; rs763110) have any association with cancers of tongue and buccal mucosa in males and females.

Materials and Methods: A case-control study of 535 oral cancer and 525 normal subjects were performed. Polymorphic variants were determined by subjecting genomic DNA isolated from peripheral blood to PCR-RFLP technique.

Results: We report a significant association between the FASL-844 T>C polymorphism and increased risk for buccal mucosa cancer in females. Protective effect of the combined genotypes of FAS -1377 GA and FAS -670 GG against tongue cancer (OR=0.28; P≤0.01) and increased risk of the cancer with the co-occurrence of FAS -1377 AA and -670 GG genotypes in males (OR=4.4; P≤0.03) was noted. In females, combined genotypes of FAS -1377GA and FAS -670 AA increased risk of buccal mucosa cancer (OR=3.27; P≤0.01). Increased susceptibility towards tongue cancer was observed in male carriers of the FAS -1377 AA + FAS -670 GG + FASL -844 CC variants. Our investigations also revealed gender bias in the distribution of the SNPs between normal males and females.

Conclusion: SNPs of the FAS and FASL might be associated with tongue and buccal mucosa cancers differentially and in a gender dependent manner.

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