Expression of Vascular Endothelial Growth Factor (VEGF) in oral cancer patients attending National Cancer Institute Maharagama- Sri Lanka

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Background

Oral squamous cell carcinoma (OSCC) represents an important pathology of the upper digestive tract, being the sixth common cancer diagnosed around the world. Angiogenesis is involved in carcinogenesis and metastasis. Vascular endothelial growth factor (VEGF) is considered as a prime mediator of angiogenesis. Various studies examined the relationship between VEGF protein over expression with the clinical outcome in patients with oral cancer

Aim

To analyze the VEGFA gene expression in oral squamous cell carcinoma patients attending National Cancer Institute Maharagama- Sri Lanka

Methods

This is a part of an ongoing study. The gene expression was evaluated using venous blood samples of histologically confirmed primary OSCCs (n = 10), and compared with healthy patients (n =10). The blood samples collection and RNA extaection was on the ame day to maintain the quality and the quantity of the RNA. Standard precortions were taken to prevent the contamination. The RNA was extracted using purelink RNA mini kit. The RNA was immediately converted to cDNA and Quantitative PCRs were performed using the TaqMan system for the VEGFA gene and GAPDH as the housekeeping gene. Gene expression was determined using the $2^{-\Delta\Delta CQ}$ method.

Results

The relative quantification(RQ) of controls ranged from 0.66-1.48. Mean relative quantification (RQ) value of VEGFA in OSCC patents was 4.85(1.59-11.10). VEGFA mRNA was overexpressed in primary samples compared to controls (5.12-fold). VEGFA transcript level was overexpressed (4/10) which ranged from 5.2-11.1 in T3-T4 tumors. Tumors (5/10) belong to TNM classification T1 - T2 had a comparatively low RQ value range from 1.59 -4.1. Poorly differentiated (RQ-11.10) and invasive oral squamous cell carcinoma(RQ-8.03), high-level of VEGFA was observed

Conclusions

VEGFA was over expressed in aggressive OSCCs and that VEGFA expression may be an important prognostic factor in oral cancer. However advance studies are needed to develop the pattern of expression