mRNA Biomarkers for Detection of Oral Squamous Cell Cancer

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Abstract

Objectives: Cancer is one of the main causes of death in the world. Changes in the expression of CK19 and CEA genes in peripheral blood of OSCC patients were examined for early diagnosis. Methodology: The participants were 36 patients and 36 normal individuals. CK19 and CEA of blood serum were measured through Real-Time PCR. The relationship of the biomarkers with tumor staging and cancer development was examined. Results: Comparison of the two groups of participants using t-test indicated no significant difference in terms of mean age. CK19 marker was positive in 19 participants of the patient’s group (n=36), which meant the sensitivity of the marker was 53%. In addition, the marker was positive in eight participants of the normal group (n=36). CEA marker was positive in 26 participants of the patient’s group (n=36), which meant the sensitivity of the marker was 72%. Moreover, the marker was positive in 11 participants in the normal group (n=36). Conclusion: In general, the study introduced a screening test for early diagnosis of OSCC. To have evidence with more reliability, future studies should be carried out with larger sample groups.

Keywords: Oral squamous cells carcinoma- early diagnosis- CK19- CEA
tumors [1, 13].

Carcinomaembryonic antigen (CEA) is a glycoprotein of the cell membrane that acts as a tumor marker for diagnosing cancers. It is effective on the adhesiveness of cell and it is usually synthesized during embryo development and stops functioning shortly before child-birth [4]. The increase of serum level of CEA is a prognostic of the disease. Still, using more than one marker and carrying out molecular tests to examine mutations are more effective treatment methods [2].

Materials and Methods

Totally, 36 patients at Cancer Institute, Tehran University of Medical Sciences diagnosed as suspect OSCC cases and 36 volunteer healthy individuals (after being examined by a specialist) took part in the study.

By patient we refer to an individual at 1, 2, or 3rd stage of the disease –i.e. without distance recurrence metastasis, who has received no medical intervention (e.g. chemotherapy, radiotherapy or surgery). The participants in both groups were identical in terms of age and gender.

Pleural fluid sample (10ml) was taken from all the participants. The top 2ml sample was removed from the study due to the risk of contamination with epithelial cells. The rest of the samples were immediately sent to a lab for RNA extraction. The volume of sample was determined based on the sensitivity of RT-PCR technique.

RNA extraction

The process was carried out using RNeasy Midi Kit (Qiagen Cat no. 75144). At first, red blood cells (if any) were lysed by lysis buffer. After centrifuge, the cell mass was rinsed with PBS accurately and the total mRNA was extracted through the extraction process.

cDNA development

The process was carried out using Viva 2-steps RT-PCR Kit (Cat no.RTPL12). The main elements needed for reverse transcription were provided in RT Primer Mix framework and the reserve transcription was done in a kit.

Quality and quantity of RNA and cDNA were checked at the end of each stage using Nanodrop Spectrophotometer (Bio-Tek, USA).

Designing special primer in AlleleID6

The special primer for each marker was designed in AlleleID6 and ordered to the producer. Table 1 lists the parameters and required volumes for the final Real-time reaction.

Real-time RT-PCR

HotTaq EvaGreen qPCR Mix (Cat No.BT11101- Sina Colon Co.) was used. The elements of RT-PCR were:

a. Pattern sequence (2µl);

b. Master mix (4µl);

c. The primer prepared based on the optimum concentration determined in set up tests; and

d. Distilled deionized water to increase the solution volume to 20µl.

Temperature and time period of the reaction were determined based on the instruction on the kit. The results of each reaction were interpreted based on Amplification and melt curves.

Data analyses

Means scores of the two groups were compared using t-test and the percentage of positive markers in the two groups of the participants was compared using the Two-sample binomial test in SPSS (20) (p<0.05).

Results

Findings

The participants included the patients (n = 36) and normal groups (n = 36). The results of t-test showed no significant differences in terms of mean age –i.e. age was not a confounding factor Table 3.

RT-PCR results

CEA marker in the patient’s group was positive in 26 cases, which means 72% sensitivity. A number of the positive cases in the normal group was 11 out of 36. Comparison of the positive cases in the two groups using two-sample binomial test indicated a significant difference between the two groups (P-value=0.025).

CK19 markers in the patient’s group were positive in 19 patients, which means 53% sensitivity. A number of positive cases in the normal group was eight out of 36. Comparison of the positive cases in the two groups using two-sample binomial test indicated a significant difference between the two groups (P-value = 0.011) Figure1.

Difference between the markers in the two groups

The relative level of difference between the markers in the two groups of patients and normal individuals was measured for CEA-mRNA and CK19-mRNA through ΔΔct method. Two to the power of ΔΔct yields the difference between the markers. As the results showed, the number of primary copies of CEA marker in the patient’s group was 2.14 times of the normal group. In addition,
the number of primary copies of the CK19 marker in the patient’s group was 1.52 times of the normal group Figure 2.

**Discussion**

OSCC is the eighth prevalent cancer in men and fifteenth prevalent cancer in women [14]. It encompasses tumors of lips, tongue, gum, palate, saliva glands, tonsils, oropharyngeal, nasopharynx, and hypopharynx. More than 90% of oral cancers are OSCC and about 9% are saliva glands, sarcoma, and lymphoma carcinoma [14].

Since the five years, survival rate is directly related to the stage of disease at the time of diagnosis, early preventive and intervention treatments not only attenuates the severity of the disease but also stops the progress of the disease. Thereby and given the growing prevalence of oral cancer and that the disease is the cause of death of many, early diagnosis of the disease is imperative [15].

Biomarkers have drawn a great deal of attention for early diagnosis of cancer recently [11]. In fact, the biomarkers are key tools to study, follow up, and diagnose cancer [16].

In addition, tumor markers provide a way to supervise effectiveness of therapeutic measures [17]. Detailed knowledge of biomarkers of different disease including cancer is one of the key requirements in medicine. One of the main usages of the biomarkers is to determine the stage of cancer [18]. Methods for early diagnosis of OSCC were examined in this paper.

CK19 is a member of the large family of intermediate strand protein (Keratin family). There are more than 20 polypeptides in the family and their main role is to preserve the integrity of epithelial cells. They are one of the key markers in diagnosing and controlling tumors [1].

CEA is a glycoprotein of the cell membrane and a tumor marker for diagnosing cancers. It plays a role in adhesiveness of cells; it is normally synthesized during embryo development and stops functioning shortly before childbirth [2]. Increase in serum level of CEA is a prognosis of the disease progress. Still, surveying more than one tumor marker simultaneously and carrying out molecular tests to spot mutation is a more reliable way to diagnose and treat cancers [1].

In a study on 60 cases with OSCC and 20 normal cases, the VEGF-A levels of serum and tissue were determined through ELISA and immunohistochemistry methods respectively using antibodies against VEGF-A. The expression of VEGF-A mRNA was analyzed through PCR method and the results indicated 50 times increase in the expression [19]. CEA-mRNA and CK19-mRNA of the biomarkers were surveyed and the results showed an increase of the biomarkers in OSCC cases.

Surveys by Zhu G et al. (2004) of the expression of CK19-mRNA and CEA-mRNA in the peripheral blood of NSLC patients showed a positive expression rate of 50% for CK19-mRNA, 40% for CEA-mRNA, and 43% for the both. They concluded that CK19-mRNA and CEF-mRNA were proper biomarkers to diagnose micro-metastasis. Similar results were obtained by a recent study on OSCC [20].

Guo Y et al. (2009) surveyed the expression of CEA mRNA, CK20, and CK19 of peripheral blood in lung carcinoma patients through nested RT-PCR. They reported the positive expression of 41% of CK20, 36.1% of CK19 and 48.2% of CEA mRNA; in addition, 73.5% of the samples had at least one positive marker that was related to metastasis (P<0.05) [21].

There were 72% positive CEA mRNA marker and 53% positive CK19 mRNA marker in OSCC cases. In this regard, there was a significant difference between the patients and normal groups.

In summary, the results introduced

![Figure 2. Difference in Expression of CEA, CK19 Genes in the Patients Group and Normal Group](image-url)
References


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