

Evaluation of Mitochondrial DNA Content in Saliva of Oral Squamous Cell Carcinoma and Leukoplakia as Non-invasive Biomarker

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Abstract: Mitochondria are key organelles in eukaryotic cells principally responsible for multiple cellular functions. The identification of reduced or increased mtDNA copy number has been increasingly reported in human cancers.

Oral squamous cell carcinoma is the most common malignant epithelial neoplasm affecting the oral cavity. They may be preceded by oral potential malignant lesions (OPMLs) that may last for many years. Tumor progression in epithelia has been classified as normal, hyperplastic (non-dysplastic), dysplastic, carcinoma in situ and invasive carcinoma. Malignant transformation of cells into cancer arises due to long term accumulation of genetic and epigenetic events. Almost half of the patients with OSCC worldwide are diagnosed at advanced stages (III, IV). Thus, early diagnosis (at stages I/II) and referral are the key to a better prognosis, reducing the mortality from the disease. We study the present state of our knowledge regarding evaluation of mtDNA quantity levels and whether we can utilize this measurement as a diagnostic biomarker for identifying genetic predisposing in saliva of oral squamous cell carcinoma and potential malignant lesion. We describe here a rapid, simple and accurate quantitative real-time PCR method for direct synchronized analysis of mitochondrial (mtDNA) DNA in saliva samples by using tag man probe and primers.

Keywords: Mitochondrial DNA, Oral Squamous Cell Carcinoma, Leukoplakia, Non-invasive Biomarker.

Introduction:

Mitochondria are unique cytoplasmic organelles of the eukaryotic system that play a central role in regulating metabolism, cellular energy production, apoptosis¹, cell motility, transport, cell proliferation², and calcium homeostasis and are involved in free radical production³. Mitochondria have their own genome, namely mitochondrial DNA (mtDNA), which possesses hundreds to thousands of copies per mammalian cell. Human mtDNA is a 16,569 bp, maternally inherited, closed circular double-stranded molecule⁴ encoding, 2 rRNAs, 22 tRNAs demanded for mitochondrial protein synthesis, 13 proteins (total of 37 genes) necessary for oxidative phosphorylation,^{5,6} and displacement loop (D-Loop), which regulates mtDNA replication and transcription³.

mtDNA may independently duplicate and does not coincide with nDNA. MtDNA is highly susceptible to damage by environmental carcinogens because of the absence of protective histones, lack of introns, limited DNA repair capacity, and its closeness to high levels of endogenous reactive oxygen species (ROS) in the mitochondrial inner membrane as a by-product of the oxidative phosphorylation system^{3,7,8}.

The effect of mtDNA in carcinogenesis or progression to malignancy can be achieved through a number of changes in mtDNA. Point mutation or length instability of displacement loop and Coding region deletion or short deletion of mitochondria have been found involved in the breast, colorectal, gastric, thyroid

cancer and head and neck. Furthermore, specific changes in the mtDNA copy number^{1,9} have been increasingly observed in human cancers and their premalignant counterparts and have been proposed as significant oncological biomarkers¹⁰.

Oral cancers are malignant neoplasms that attack the structures or tissues of the mouth¹¹. However, this term tends to be used alternately with oral squamous cell carcinoma (OSCC), which represents the most frequent of all oral cancers. It is estimated at 96% of all cancers of the oral cavity^{12,15}. It is known that a significant ratio (up to 62%) of OSCCs come from clinically recognizable precursor oral potential malignant lesions (OPMLs), such as leukoplakia^{18,19}.

Oral leukoplakia is a lesion that presents as a white plaque in the oral mucosa^{19,20} that cannot be characterized clinically or histopathological as any other disease^{21,23}. Leukoplakia lesions are classified clinically (homogeneous or non-homogeneous)²⁴ and histologically, which may undergo sequential pathological changes from hyperplasia, mild dysplasia, severe dysplasia or carcinoma in situ and finally invasive carcinoma^{13,25,27}. The presence of epithelial dysplasia is the strongest predictive parameter²⁸ associated with an increased risk of malignant transformation of up to 31%¹⁷ and the absence of dysplasia does not allow the clinician to consider the lesion at low risk²⁸, for that dysplasia grading is not an exact predictor. Most OPMLs regress or remain unchanged and dysplasia grading has been criticized as subjective, inadequate for clinical management, and poorly reproducible²⁹. However, clinical and pathological characteristics have limited prognostic value for predicting which leukoplakia will proceed to malignancy¹⁷. There is a need for better predictive biomarkers of transformation to improve the management of patients with oral cancer¹⁰. Genetic biomarkers may be currently useful to identify lesions at a risk assessment for malignant transformation¹⁷. Our study explored the evaluation of mtDNA copy number change in bodily fluids (saliva) of OSCC and leukoplakia and whether we can utilize it as a diagnostic molecular biomarker that may have use in evaluating the malignant transformation. To test these hypotheses, we did quantitative PCR for calculating the relative ratio of the quantity of a given mtDNA-encoded gene to that of a nDNA-encoded gene of saliva samples obtained from 17 OSCC and 21 leukoplakia and a control group of 20 participants without oral cancer.

Materials and Methods:

Sample Procurement:

Damascus university approval was obtained to perform studies at the Laboratory of National Commission for Biotechnology and to acquire a salivary sample of OSCC from Damascus Hospital and Almohsaa Hospital and to acquire leukoplakia salivary sample from the Faculty of Dentistry.

Sample selection

The study sample was defined clinically by suspicion of a risk lesion and, if no risk had been considered clinically, by pathologic diagnosis of dysplasia. The sample was designed to include all submitted biopsy specimens for which the Pathology report would be expected to provide information on the possible risk of malignant transformation. The histologic diagnosis of Oral scc and OPMLs was made and agreed upon by one senior pathologists at the Department of Pathology (Faculty of Dentistry) based on World Health Organization (WHO) guidelines.

Subject:

The saliva samples used in this study were collected in a time period from 2013-2014. The patients involved in the study (n = 58) were divided into 3 groups: 1) OSCC group (n = 17); 2) leukoplakia lesion group (n = 21) and 3) a healthy control group (n = 20). Written consent forms were collected from all patients who were involved in this study. The institutional ethics committee approved the protocol for the study. Patients' data (age, tobacco and alcohol consumption, drug taking, systemic disease, tumor size, lymph node involvement, extent of metastasis, and histopathological report) were obtained from the pathological reports. We also identified all individuals with a history of any other systemic disorder, individuals suffering from acute inflammatory conditions of the oral cavity (e.g. dental abscess, pericoronitis), patients receiving chemotherapy/radiotherapy, individuals taking drugs that induce hyposalivation (e.g. anticholinergics, antihistaminics, antihypertensives and beta adrenergic blockers) and individuals using secretagogues and excluded them from the study. All saliva samples were taken before any surgical interventions or therapeutic treatments.

Sample collection:

Whole unstimulated saliva was collected from all the subjects. The subjects refrained from eating, drinking, using chewing gum, mints, etc., for at least 2 h prior to the evaluation. We instructed the subject to do two times of gargling for 15 seconds with 60 mL of de-ionized, purified water and to throw out The 60 ml gargle samples. Samples were obtained by requesting the subjects to swallow first, tilt their head forward and expel the saliva (500ml) into 2-ml sterile plastic vials for 10 min.

Processing of saliva samples:

The samples (500ml) were centrifuged at 1600 rpm for 10 minutes. The supernatant was discarded and the cell pellet (200ml) was retained and stored at -80°C until the biochemical analysis.

DNA extraction:

Salivary DNA was extracted from cell pellets using a standard laboratory inisorb spin forensic kit (stratec molecular GmbH). Briefly, the saliva sample was incubated at 56°C for 20 min under continuous shaking in 100 ml lysis buffer M, 100 ml ddH₂O, carrier RNA and 10 ml proteinase K. The sample was then transferred to a new RTA spin filter tube to which 200 ml binding buffer B6 was added, centrifuged for 1min at 12,000 rpm. A washing buffer was added and centrifuged for 30sec at 12,000 rpm. Then we added elution buffer D and centrifuged the sample for 1 min at 8,000 rpm and stored the eluted DNA at -80°C .

Standard preparation:

Genomic DNA was extracted from whole-blood samples via GeneJET, Genomic(DNA) Purification Kit (Thermoscientific, (EU) Lithuania), **Amplification** was carried out in 0.2 ml tubes containing: 12.5 Dream Taq PCR Master Mix(2x) (Thermo Scientific, (EU) Lithuania), 1 μl each primer (0.5 μM) (VbCBiotech, Vienna) (Table 1), 2 μl purified DNA and 8.5ml PCR water to make a volume of 25 μl . Thermal cycling conditions were as follows: initial denaturation and Taq polymerase activation at 95°C for 3 minutes, followed by 40 cycles of 95°C for 30 seconds, 60°C for 30 seconds, 72°C for 30second and final extension 72°C for 7 minutes. The PCR products were analyzed by electrophoresis in 2% agarose gel with ethidium bromide staining along with 50bp and 100bp ladders (Fermentase, Germany). We purified the PCR product via Exosape(Affymetrix, USA).

DNA quantification:

A nanodrop spectrophotometer was used, according to the manufacturer's instructions, to measure the total amount of extracted DNA. The conversion of the unit ng/ μl to copies/ μl was done by exploiting the software application available at this site <http://www.endmemo.com/bio/dnacopynum.php>. We performed dilution standards containing 10-fold a dilution series ($10^8, 10^7, 10^6, 10^5, 10^4, 10^3, 10^2, 10^1$ copies/ μl). All dilution standards were kept at 4°C for the duration of the study.

Real time qPCR:

MtDNA content was assessed by quantification of a unique mitochondrial fragment relative to a single copy region of the nuclear b2M using a taqman assay. A 65-bp fragment of MtDNA was amplified using the primers: hmito-F, hmito-R, and hmitoP were used as the hybridization probe, containing the FAM (6-carboxy fluorescein) as a fluorescent reporter dye and NFQ as a quencher dye at the 3' end. Nuclear content was quantified by targeting a unique region of the B2 M gene using the JOE/TAMRA™ Probes, primer limited (VbCBiotech, Vienna). For each 20 μl reaction, 3 μl of DNA was amplified containing 2 μl of each mtDNA primer (0.4 μM), 2 μl (1 μM) for nDNA, 2 μl (0.4 μM) probe, 3 ml nuclease free water and 10 master mix (Kapabiosystems, USA). The real-time PCR conditions consisted of initial denaturation and Taq polymerase activation at 95°C for 3 minutes followed by 40 cycles mtDNA-50cycles nDNA of 95°C for 3 seconds, 60°C mtDNA- 55°C nDNA for 20 seconds, and 72°C for 10second. Some measurement was repeated in triplicate and a non-template control and a positive control were included in each experiment. mtDNA to nuclear DNA (nDNA) ratios were calculated by dividing the mtDNA signal for each gene by the corresponding nuclear signal.

Table1. Primers/probes used in the study.

Product size (bp)	Oligonucleotide sequence	Primer/probe	Gene accession no
65	CTTCTGGCCACAGCACTTAAAC GCTGGTGTAGGGTTCTTTGTTTT FAM-ATCTCTGCCAAACCCC	hmito F hmMito R hmito P	Human mitochondrial genome NC_012920
95	GCTGGGTAGCTCTAAACAATGTATTCA CCATGTACTAACAATGTCTAAAATGGT JEO-CAGCAGCCTATTCTGC	hB2M F hB2M R hB2M P	Humanb2M Accession number M17987

Statistical Analysis:

The copy number of mtDNA among oscc, leukoplakia, control subject saliva specimens were compared by the parametric test ANOVA, Differences in host characteristics (Table 2) gender, age, oral health, smoking status, between patients and control subjects were assessed via spearman, Pearson correlation coefficients and Student's *t*-test for continuous variables, Within oscc patients and leukoplakia, mtDNA content by tumor stage and histopathological characteristics of leukoplakia was also compared, All statistical analyses were performed using the SPSS statistical package (version 11.5, Chicago, IL). P values < 0.05 were considered significant.

Table 2. Distribution of selected host characteristic:

variable	Cases oscc no=17(28.3%)	Leukoplakia=21(36.7%)	Control=20(35.0%)
Sex			
Male	11(64.7)	16(77.3)	12(61.9)
femal	6 (35.3)	5 (22.7)	8 (38.1)
Age			
Std±	16.9	9.7	15.7
Mean	52.8	46.3	43.7
Range	30-82	25-69	24-77
Oral health			
Good	3(17.6)	0(0)	3(14.3)
Mild	2(11.8)	13(59.1)	6(28.6)
Bad	12(70.6)	9(40.9)	12(57.1)
Smoking			
Never	5(29.4)	6(27.3)	9(42.9)
current	12(70.6)	16(72.7)	12(57.1)

Results:

We determined the ratio of copy number of mtDNA to copy number of $\beta 2$ microglobulin ($\beta 2M$) gene nDNA in cells from the saliva of 58 individuals by including the sample in the real time quantitative PCR analysis. The patients and controls were similar in distributions with regard to age, sex, oral health and smoking status (match case- control). The relative mean mtDNA copy number was significantly higher in leukoplakia patients (6900.40) than in oscc and controls (680.51, 382.16) respectively. However, there were no statistically significant differences between the cases (oscc, leukoplakia) and controls subjects ($P = 0.435$); also there were no statistically significant differences in terms of age ($P = 0.985$), gender (oscc $P = 0.616$, leukoplakia $P = 0.068$), control ($P = 0.724$), oral health ($P = 0.460$), smoking status (oscc $P = 0.749$), leukoplakia ($P = 0.534$), control ($P = 0.395$) as presented in (Table 3).

To assess the alteration of mtDNA content on tumor stage and histopathological change in leukoplakia, we examined the relative content of mtDNA/nDNA in saliva from the early stage (stages I and II) versus advanced stage (stages III and IV) OSCC and histopathological characteristics of leukoplakia. The results

showed that there were no statistically significant differences in tumor stage ($P = 0.306$), and histopathological characteristics of leukoplakia ($P = 0.324$) Table 4.

Table 3. mtDNA copy number by host characteristics of cases and control subject:

variable	oscc	leukoplakia	control	P value
Group(mean)	680.51	6900.40	382.16	0.435
Sex(mean)				
Male	842.03	303.85	413.02	
female	384.38	28009.37	324.86	
P value	0.616	0.068	0.724	
Age(P value)	0.157	0.947	0.072	0.985
Oral health(mean)	0.843	0.266	0.969	0.460
Smoking status(mean)				
Never	463.56	292.72	504.88	
current	770.90	9543.48	300.35	
P value	0.749	0.534	0.395	

Table 4. Overall saliva mtDNA copy number by histopathological characteristics

Tumor(TNM stage)	Cases no%	P value
0	3(17.6)	0.306
II	1(5.9)	
III	4(23.5)	
IVA	4(23.5)	
IVB	1(5.9)	
IVC	4(23.5)	
leukoplakia		0.324
Dysplasia	11(54.5)	
Hyperplasia	10(45.5)	

Discussion:

Mitochondria is essentially involved in many important physiological processes and cellular bioenergy including metabolism, apoptosis, signaling, cell cycle, and differentiation. Unlike nuclear DNA, mtDNA is present at a consistently high level in normal cells, and the mitochondrial genome lacks protective histones and introns and is involved in free radical production. As a consequence, the mutation rate of mtDNA is substantially greater than that of nuclear genomic DNA and copy number variations have been frequently reported in various human cancers. Previous studies showed that the increased mtDNA in human cells have long been suspected as contributor to carcinogenesis including oscc cancer⁹. However, the prognostic value of copy number variations of mtDNA in oscc cancer patients remains to be explored. In this study, we investigated relative mtDNA/nDNA copy number (match case- control) in saliva of oscc, leukoplakia and normal subject (control subjects) by using real-time quantitative PCR method. Our data showed that relative mean mtDNA content showed no significant differences in oscc, leukoplakia, and control subjects. This does not correspond with the (Jiang et al, Mondal et al, Masayeva et al, Kim et al)^{9,30,31,32} studies because they had significant difference between cancer and control subjects. Moreover, we did not find associations of mtDNA content with gender, age, oral health, smoking status, tumor stages and histological differentiation of leukoplakia. Our data corresponds with (Mondal et al)³⁰ studies that showed no relationship between mtDNA content and age of patient, but also our study does not correspond with the (Jiang et al, Kim et al)^{9,32} studies because mtDNA content was identified to be altered by aging, tumor stage and histopathological differentiation of leukoplakia. Moreover our study does not correspond with the (Jiang et al, Mondal et al, Masayeva et al, Kim et al)^{9,30,31,32} studies, which showed increased levels of mtDNA in smokers as compared with non-smokers. According to this study, diagnostic results require a surgical biopsy and this means a more accurate and golden standard in judging the nature of suspicious lesions clinically.

In conclusion, we investigated relative mtDNA/nDNA content in saliva of oscc, leukoplakia, and control subjects, demonstrated that no statistically significant differences of m DNA content exist between patient and control subjects ,and did not findan association between mtDNA and cigarette smoking, age, gender, oral health or tumor stage. Therefore, the mtDNA copy number content method is an inaccurate method for diagnosing these lesions.

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