



Research paper

Is HIF1- α deregulated in malignant salivary neoplasms?

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ABSTRACT

Background: There is significant controversy in the literature regarding the relationship between hypoxia and salivary gland neoplasms (SGNs).

Objective: The current study aims to investigate levels of hypoxia markers in both benign and malignant salivary neoplasms.

Patients and methods: The current study sample is comprised of a total of 62 samples. HIF-1 α expression was evaluated by immunohistochemistry. Additionally, HIF-1 α mRNA and miR-210 levels were assessed using qRT-PCR.

Results: No differences in HIF-1 α expression were observed among the control group, benign and malignant SGNS. Similarly, HIF-1 α mRNA levels were similar between benign and malignant SGNS. Also, there was no difference in miR-210 expression between case and control groups.

Conclusion: The angiogenic markers, miR-210 and HIF-1 α , do not appear to distinguish malignancy in salivary glands.

1. Introduction

Head and neck cancers are associated with poor survival rate (Fonseca et al., 2012; de Oliveira et al., 2009; De Paula et al., 2009). In the case of salivary gland neoplasms (SGNs) a broad spectrum of phenotypic heterogeneity and are divided into five categories, according to the World Health Organization (WHO) (El-Naggar et al., 2017). Prognosis of SGNS is also related to the anatomical location of the neoplasia (Guzzo et al., 2010; Cerda et al., 2014). Recently, a large number of studies have attempted to evaluate the role of hypoxia in cancer development and prognosis (Guimaraes et al., 2016; Fraga et al., 2012). Hypoxia-inducible factor 1- α (HIF-1 α) is a marker of hypoxia and is activated under hypoxic conditions (Wang and Semenza, 1993).

miRNAs are a class of single-stranded noncoding RNAs 21–22 nucleotides in length which regulate gene expression through the

inhibition of RNA translation or degradation of target messenger RNA (mRNA) (Bartel, 2009). Recent evidence has suggested that miR-210 plays a crucial role in the cellular response to hypoxia. HIF-1 α can promote isoform-specific stabilization of miR-210 by binding to the Hypoxia Responsive Element (HRE) present in the proximal promoter of miR-210 (Corn, 2008). Similar to HIF-1 α , hypoxia induces miR-210 expression, which regulates cellular proliferation, DNA stability, mitochondrial metabolism, apoptosis and angiogenesis (Dang and Myers, 2015). Furthermore, the miR-210 expression is also significantly up-regulated in other types of cancer, including non-small cell lung cancer (Zhu et al., 2016).

Although the first choice treatment for malignant SGNS is surgery (Green et al., 2016), adjuvant therapy has historically been determined based on data from studies focused on squamous cell carcinomas of the upper aerodigestive tract (Cerda et al., 2014). Importantly, there are

Abbreviations: SGNS, Salivary gland neoplasias; HRE, Hypoxia Responsive Element

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conflicting reports with regards to the relationship between hypoxia and clinical behavior or treatment responsiveness in patients diagnosed with SGNs (Wijffels et al., 2009). Recent studies have demonstrated that hypoxia might promote an increase in radioresistance (Harada, 2016), specifically via miRNA-mediated modulation of the hypoxic response (Gu et al., 2016). These data suggest that the use of chemoradiation might be a valuable alternative treatment option for patients presenting with radioresistant neoplasias (Cerdeira et al., 2014). Considering the controversial literature regarding the relationship between hypoxia and SGNs, the current study aimed to investigate levels of hypoxia markers in both benign and malignant salivary neoplasms.

2. Methods

2.1. Study design

A retrospective cross-sectional study was designed to evaluate the expression of the main hypoxia targets in SGNs.

3. Patients

Ethical approval for this study was obtained from the relevant Institutional Review Board. A total of 62 samples were included from the databases of the glandular tumor surgery services from 2010 to 2016. Samples were divided into three groups according to the world health organization classification of head and neck tumors (El-Naggar et al., 2017).

Group 1 ($n = 16$) was comprised of glandular tissue without neoplasia. Samples were obtained from mucocele excisions. The inclusion criteria for this group were histopathological diagnosis of mucocele.

Group 2 ($n = 22$) was comprised of patients with Pleomorphic Adenoma. The inclusion criteria for this group were histopathological diagnosis of pleomorphic adenoma.

The group 3 ($n = 24$) was comprised of one sample of Acinar Cell Carcinoma, two samples of Adenocarcinoma not otherwise specified, nine samples of Adenoid cystic carcinoma, ten Mucoepidermoid Carcinoma samples and two Myoepithelial Carcinoma samples.

4. Immunohistochemistry

Immunohistochemical reactions were performed from paraffin blocks of 49 patients. Including 13 controls (normal salivary gland samples), 16 benign tumors (Pleomorphic adenoma) and 20 malignant neoplasms (Acinar Cell Carcinoma $n = 1$, Adenocarcinoma not otherwise specified $n = 2$, Adenoid cystic carcinoma $n = 8$, Mucoepidermoid Carcinoma $n = 10$ and Myoepithelial Carcinoma $n = 2$). Protein expression of HIF-1 α was evaluated through immunohistochemical reactions performed on 3.0 μm thick sections. The sections were deparaffinized with xylene and rehydrated with graded alcohol solutions. Antigen retrieval was conducted in an electric pressure cooker at 121 $^{\circ}\text{C}$ for 10 min in Trilogy buffer (Trilogy, Cell Marque, CA, USA). Endogenous peroxidase activity was blocked with 2 baths of 0.3% hydrogen peroxide for 15 min each. Samples were then incubated overnight with primary mouse monoclonal antibodies against HIF-1 α (Clone H1a67; Sigma-Aldrich, MO, USA) at 4 $^{\circ}\text{C}$ at a dilution of 1:200. The samples were then incubated with a secondary biotinylated link and streptavidin-biotin-peroxidase complex using the LSAB kit (Dako Labs, Glostrup, Denmark), followed by incubation with the 3'-diaminobenzidine-tetrahydrochloride (Cat.No.32750, Sigma-Aldrich, MO, USA). Counterstaining was performed using Mayer's hematoxylin (Cat. no. 109249, Merck, MA, USA). The samples were then dehydrated, and slides were mounted in ERV-mount (EasyPath, Brazil). Kidney samples were used as positive controls. Negative controls were performed by replacing the primary antibody with phosphate buffered saline (PBS). Ten microscopic fields of tumor parenchyma were photographed to quantify the staining at microscope FSX100 (Olympus, Center Valley,

PA, USA). Cells were then counted using ImageJ software (Rueden et al., 2017). The ratio of positive cells to the total number of cells counted was used to quantify the staining.

5. RNA isolation and real-time PCR

Validation of the immunohistochemical results was performed with qRT-PCR. Samples of 24 patients, including 10 controls (normal salivary gland samples), 7 benign tumors (Pleomorphic adenoma) and 7 malignant neoplasms (Acinar cell carcinoma $n = 1$, Adenoid cystic carcinoma $n = 2$, Mucoepidermoid Carcinoma $n = 2$, Myoepithelial carcinoma $n = 2$) were used for qRT-PCR. RNA was isolated using Trizol (Thermo Fisher Scientific, Waltham, MA, USA), according to the manufacturer's protocol. Total RNA was treated with DNase I, Amplification Grade (Invitrogen, cat number 18068015, Carlsbad, CA, USA) and 1.5 μg of RNA were reversely transcribed with the SuperScript[®] First-Strand Synthesis System for qRT-PCR (Invitrogen, cat number 11904018, Carlsbad, CA, USA). Each reaction for SYBR Green-based qRT-PCR (total volume 20 μl) contained 10 μl of SYBR Green master mix, 0.25 μM of both forward and reversed primers, 1 μl of cDNA (66 ng/reaction) and 8.5 μl H₂O. Non-Template Control (NTC) was included for each assay. The thermal cycling conditions were as follows: 95 $^{\circ}\text{C}$ for 10 min, followed by 40 cycles of the following steps: 95 $^{\circ}\text{C}$ for 15 s and 60 $^{\circ}\text{C}$ for 1 min. The specific primers/probes (Life Technologies, Carlsbad, CA, USA) were described previously (Guimaraes et al., 2016). Specifically, the following primers were used for HIF1 α : 5'-TCTGCAACATGGAAGGTATTGC-3' and 5'-CTGAGGTTGTTACTGTTGGTATCA-3. Beta-Actin was used to normalize HIF1 α gene expression and was amplified using the following primers: 5'-TGCCGACAGGATGCAGAAG-3' and 5'-CTCAGGAGGAGCAATGATCTGA-3'. qPCR was performed on a StepOne Real-Time PCR System (Life Technologies, Carlsbad, CA, USA).

For miR-210 (ID: Hs04231470_s1, Life Technologies, Carlsbad, CA, USA), a TaqMan assay was performed according to the manufacturer's protocol. RNU44 was used as an endogenous control for mi-210 analysis (ID: 001094, Life Technologies, Carlsbad, CA, USA). All reactions were done in triplicate. Normal salivary glands were used as a control group. The following reaction steps were used for amplification: 95 $^{\circ}\text{C}$ for 10 min, 95 $^{\circ}\text{C}$ for 15 s and 60 $^{\circ}\text{C}$ for 1 min. The C_q values of endogenous controls were subtracted from the C_t values of the respective targets to calculate the ΔC_q . The ΔC_q values from each experimental group were averaged and converted to log base 2 using equation $2^{-\Delta\Delta\text{C}_q}$ to compare expression among different samples.

5.1. Statistical analysis

Analyses were performed using SPSS (Version 18.0, IBM Software Inc., Armonk, New York, USA) and GraphPad Prism software (Version 5.0, GraphPad Software Inc., San Diego, CA, USA). The Kolmogorov-Smirnov and Shapiro-Wilk Tests were carried out to evaluate data distribution. These analyses revealed that the data were non-parametrically distributed; therefore, the Mann-Whitney and Kruskal-Wallis tests were performed. All data are given as means \pm S.D. $p < .05$ was considered statistically significant.

6. Results

Considering all individuals, 35 (56%) were male, and 24 (44%) were female (Table 1). There is a significant association between hypoxic markers such as HIF-1 α and miR-210 and angiogenesis (Dang and Myers, 2015; Zhang et al., 2017) (Fig. 1). However, the impact of hypoxic markers in SGNs still unknown. Qualitative analyses of HIF-1 α immunorexpression is presented in Fig. 2(A–G). Most of the groups presented weak staining for HIF-1 α . The staining was not homogeneous considering the histological types. Quantitative analyses of HIF-1 α immunorexpression and mRNA is shown in Fig. 3 (A and B respectively).

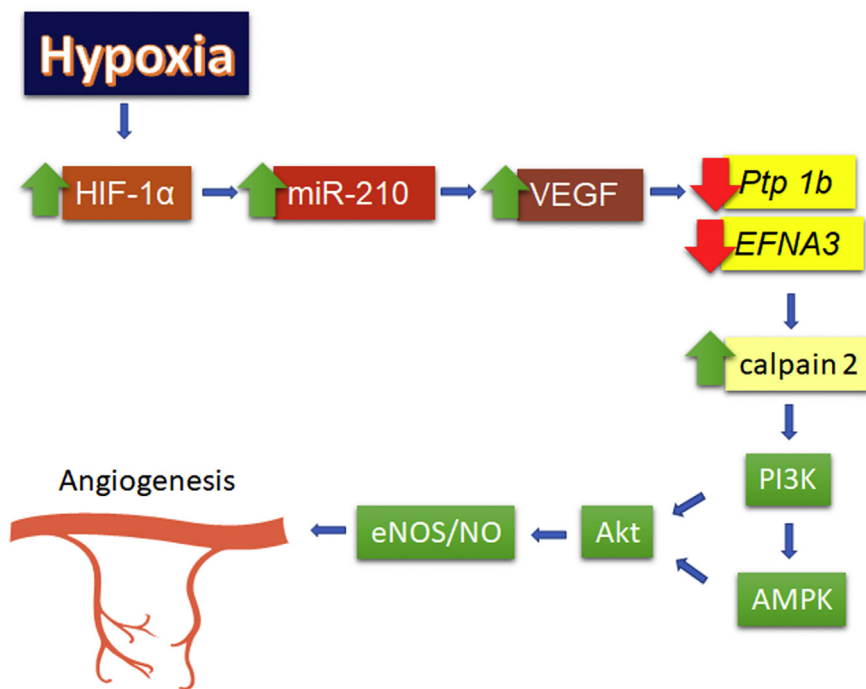


Fig. 1. Schematic representation of angiogenesis induced by Hypoxia.

Hypoxia induces the increase (green arrows) of Hypoxia-inducible factor 1-alpha (HIF-1 α), miR-210 and Vascular endothelial growth factor (VEGF). Consequently, there is a transcription inhibition (red arrows) of both genes protein tyrosine phosphatase 1B (*Ptp 1b*) and Ephrin A3 (*EFNA3*). All these molecular events activate (green symbols) Phosphatidylinositol-4,5-bisphosphate 3-kinase (PI3K), 5' adenosine monophosphate-activated protein kinase (AMPK), AKT serine/threonine kinase (AKT), Nitric oxide synthases (NOS) and Endothelial NOS (eNOS) which induces angiogenesis. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

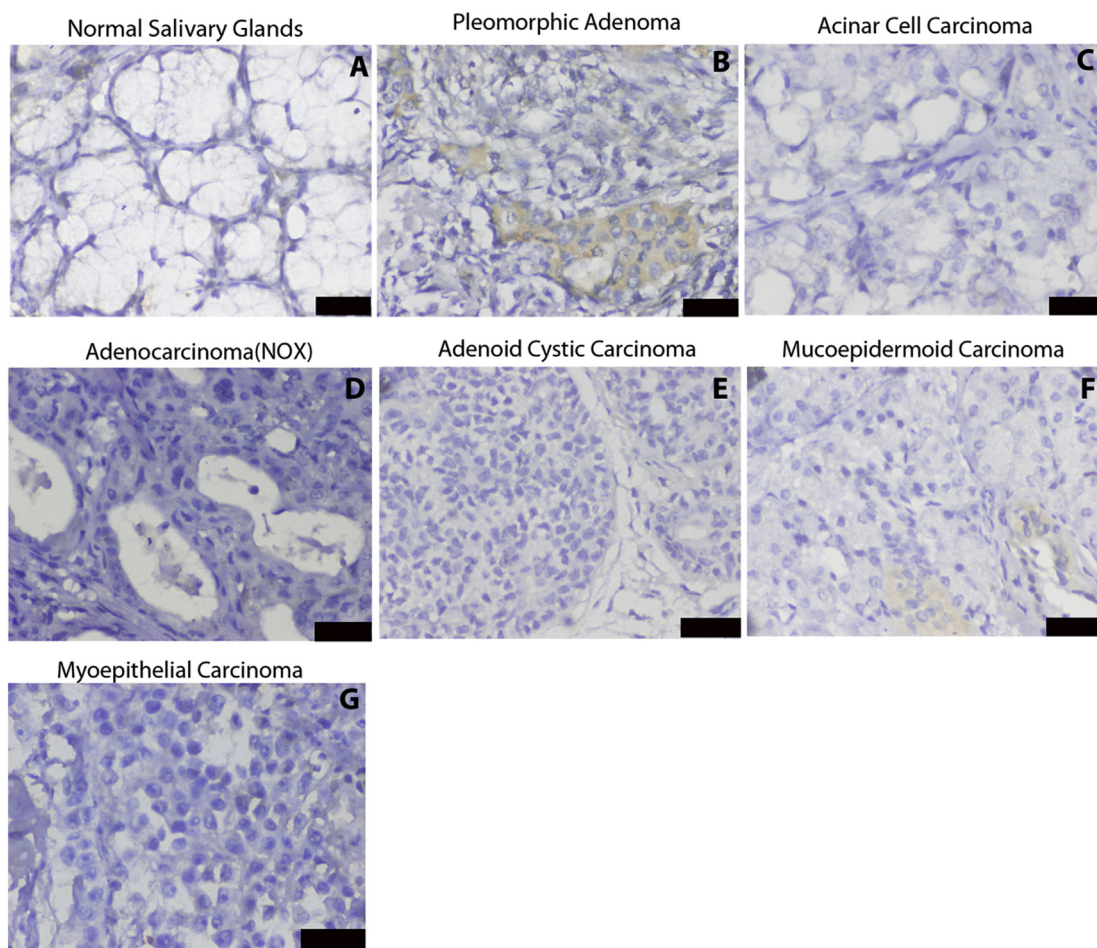


Fig. 2. Qualitative HIF-1 α immunohistochemistry in samples.

HIF-1 α expression qualitative results in Control (A), Pleomorphic Adenoma (B), Acinar Cell Carcinoma (C) Adenocarcinoma (NOX) (D), Adenoid cystic carcinoma (E), Mucoepidermoid Carcinoma (F) and Myoepithelial Carcinoma (G).

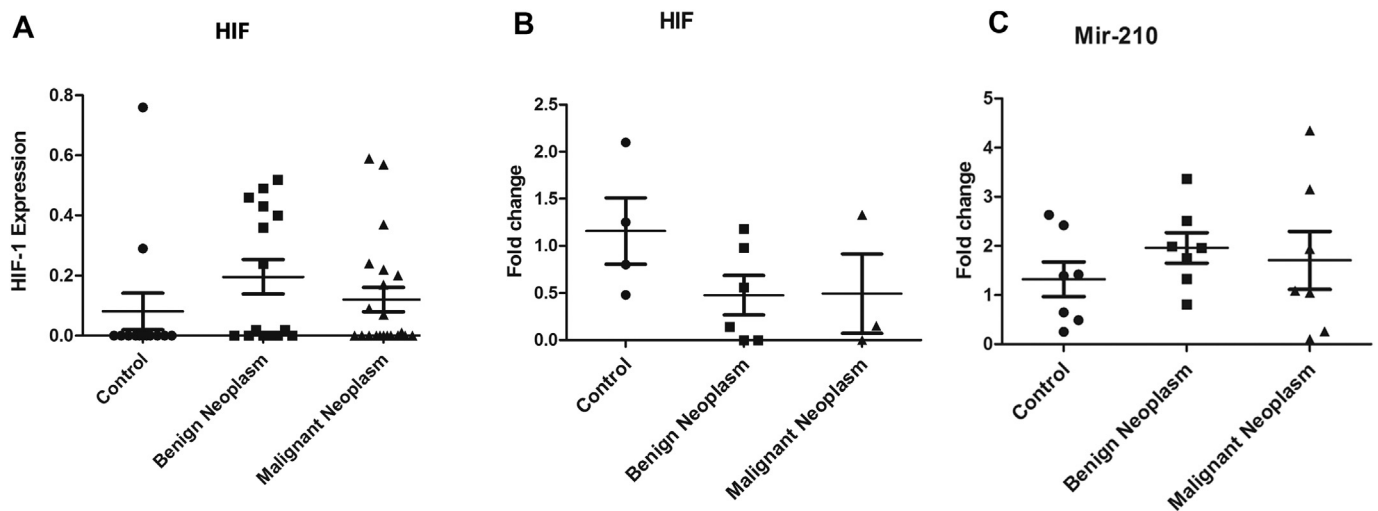


Fig. 3. Quantitative analyses of HIF-1 α immunoexpression, HIF-1 α mRNA and miR-210.

HIF-1 α immunoexpression (A), HIF-1 α mRNA (B) and miR-210 (C) in control, benign and malignant SGNS. (A). HIF-1 α expression (A) or mRNA levels (B) is not altered in SGNS, compared with control samples. No difference in expression of miR-210 is observed between groups (C).

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The current study was not sponsored by an organization that has a financial interest.

Ethical approval

Ethical approval for this study was obtained from the relevant Institutional Review Board (52767316600005146). All patients signed informed consent.

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