



Oncogenic drivers in 11q13 associated with prognosis and response to therapy in advanced oropharyngeal carcinomas



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ABSTRACT

Objectives: To identify potential molecular drivers associated with prognosis and response to treatment in advanced oropharyngeal squamous cell carcinomas (OPSCC).

Materials and methods: Thirty-three OPSCC biopsies from untreated Brazilian patients were evaluated for human papilloma virus genotyping, genome wide copy number alterations and gene expression profiling. Data were integrated using CONEXIC algorithm. Validation with TCGA dataset and confirmation by RT-qPCR of candidate genes were performed.

Results: High-risk HPV positive cases, detected in 55% of advanced OPSCC, were associated with better outcome. Losses of 8p11.23-p11.22, 14q11.1-q11.2 and 15q11.2, and gains of 11q13.2 and 11q13.2-q13.3 were detected as recurrent alterations. Gains of 3q26.31 and 11q13.2 and losses of 9p21.3 were exclusively detected in HPV-negative tumors. Two clusters of expression profiles were observed, being one composed mostly by HPV positive cases (83%). HPV-positive enriched cluster showed predominantly immune response-related pathways. Integrative analysis identified 10 modulators mapped in 11q13, which were frequently cancer-related. These 10 genes showed copy number gains, overexpression and an association with worse survival, further validated by TCGA database analyses. Overexpression of four genes (*ORAOVI*, *CPT1A*, *SHANK2* and *PPF1A1*) evaluated by RT-qPCR confirmed their association with poor survival. Multivariate analysis showed that *PPF1A1* overexpression and HPV status are independent prognostic markers. Moreover, *SHANK2* overexpression was significantly associated with incomplete response to treatment.

Conclusion: The integrative genomic and transcriptomic data revealed potential driver genes mapped in 11q13 associated with worse prognosis and response to treatment, giving fundamentals for the identification of novel therapeutic targets in OPSCC.

Introduction

In the last decades, several epidemiological studies have revealed

decreased incidence of head and neck squamous cell carcinomas (HNSCC) in oral cavity and larynx as a consequence of lower exposure to the tobacco products. Nevertheless, an increasing incidence of

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oropharyngeal squamous cell carcinomas (OPSCC) mainly associated with oncogenic human papillomavirus (HPV) has been reported [1–6].

In general, HPV-positive OPSCC is associated with good prognosis, presenting better survival in comparison with HPV-negative cases [7–11]. De-escalation of radiation and chemotherapy for HPV-positive cases has been proposed and tested in different clinical trials aiming to avoid overtreatment and long-term toxicities [8,12,13]. However, accurate identification of cases with good prognosis and treatment-responsive tumors are critical findings, since distant metastasis may occur in a set of HPV-positive OPSCC [8,14]. In contrast, few advances have been made for treatment of HPV-negative OPSCC patients and a large number of them will present loco-regional recurrence [9].

The molecular mechanisms underlying oropharyngeal carcinogenesis have been investigated and potential biomarkers were reported, however the data are still unclear and controversial [15–19]. The integration of genomic and transcriptomic analysis can be used to identify cancer-driver genes and disrupted pathways, which can be drug targetable [20]. This strategy has revealed functionally relevant drivers involved in the carcinogenic process in different tumor types, including oral carcinoma [21], ovarian cancer [22], penile carcinoma [23,24], uterine leiomyoma [25] and leiomyosarcoma [26].

Integration of genomic, transcriptomic and epigenomic data of 279 HNSCC, including oral (n = 172, 62%), oropharyngeal (n = 33, 12%) and laryngeal (n = 72, 26%) carcinomas was reported by The Cancer Genome Atlas (TCGA) [27]. Distinct genetic alterations were observed between HPV-positive HNSCCs (68% in oropharynx) and HPV-negative cases. Recurrent deletions and truncating mutations of *TRAF3* found in HPV-positive tumors were associated with anti-viral immune response. Conversely, HPV-negative HNSCCs presented loss of 9p21.3 (including *CDKN2A* gene) and co-amplifications of 11q13 and 11q22, which contain genes implicated in cell death/NF- κ B and Hippo pathways [27]. A distinct genetic subgroup of HPV-negative tumors is also being reported, characterized by low frequency of copy number alterations (CNA), wild-type *TP53*, mutation in *HRAS* and *CASP8* and more favorable prognosis [13].

Nevertheless, prognostic and predictive biomarkers in advanced OPSCC are still limited and need to be further investigated. In this study, we integrated DNA CNA and gene expression analyses to identify drivers in advanced OPSCC according to HPV status. *In silico* functional analysis was performed to identify genes and pathways associated with oropharyngeal carcinogenesis, which can reveal potential drug targets.

Patients and methods

Patients and samples

Fresh-frozen tumor biopsy samples from 40 OPSCC patients naive of treatment were obtained from A.C. Camargo Cancer Center and Barretos Cancer Hospital, Brazil. Eligibility criteria included patients harboring locally advanced clinical stages III, IVA and IVB according to AJCC (7th Edition). The follow-up time ranged from 0.5 to 190 months (mean of 53 months). The study was approved by the Human Research Ethics Committee from both Institutions (A.C. Camargo Cancer Center #1249/09 and Barretos Cancer Hospital #139/2008). All patients provided written informed consent. Patients underwent curative therapy according to standard clinical protocol taking into account the medical decisions for each patient, which included induction chemotherapy (IC) followed by radiotherapy with concurrent chemotherapy (CT-RT), and upfront surgical resection followed by radiotherapy with or without chemotherapy. Pretreatment risk stratification was defined as low, intermediate and high, based on HPV status, smoking history and tumor/node stage [7].

Treatment and response assessment

The majority of patients included in this study were treated by IC

followed by CT-RT (n = 24). Patients were treated with a combination of docetaxel, cisplatin and 5-fluorouracil (TPF) as IC followed by radiotherapy and weekly carboplatin or cisplatin concurrent to radiotherapy. Cetuximab was employed in eight cases as concurrent therapy to radiation (one case received IC before). Six patients were treated by surgery followed by adjuvant therapy (RT or RT+CT); one patient deceased surgery and one patient lost the follow-up before completing the treatment (supplementary Table S1). Six patients were treated only by surgery followed by adjuvant therapy (RT and or CT), one patient deceased soon after surgery and one patient lost the follow-up before treatment begins.

Nucleic acids extraction and HPV genotyping

OPSCC samples (80% of tumor cells) and surrounding normal tissues were macrodissected for DNA (Qiagen DNeasy Blood & Tissue Kit; Qiagen, Valencia, CA) and total RNA extraction (RNeasy MiniKit; Qiagen, Valencia, CA). The Linear Array HPV Genotyping Test Kit (Roche Molecular Systems, Inc., Branchburg, NJ, USA) was used for HPV detection.

CNA analysis by array-based Comparative genomic Hybridization

OPSCC (n = 33) and normal commercial DNA (Promega) samples were differentially labeled (Genomic DNA Enzymatic Labeling Kit; Agilent Technologies) and the hybridized on Agilent Human CGH 180K Oligo Microarrays. Genomic data were extracted by Feature Extraction 10.1.1.1 software (Agilent Technologies) and analyzed using the Nexus Copy Number software (v.6.0, Biodiscovery, El Segundo, CA, USA). CNA was defined as exceeding the significance threshold of 1×10^{-6} and containing at least five consecutive altered probes per segment. The thresholds were defined as the average \log_2 CGH fluorescence ratio for copy gains ≥ 0.6 , high copy number gains ≥ 1.4 , losses ≤ -0.6 and homozygous losses ≤ -1.25 . Genomic variants detected in control individuals from worldwide populations and classified as common ($> 1\%$) according to DGV database (<http://dgv.tcag.ca/dgv/app/home>) were excluded. Alterations detected in at least 20% of the cases were selected for further analysis. The unsupervised hierarchical clustering analysis was performed using complete linkage and Euclidian distance.

Gene expression microarray

Total RNA from OPSCC (n = 33) and surrounding non-neoplastic oropharyngeal tissues (n = 3) were labeled and hybridized using the Two-Color Human GE 4x44K microarray platform (Agilent Technologies), following the manufacturer instructions. Data processing, quality control filtering and normalization (Lowess) were performed using the Feature Extraction v.10.1.1.1 software (Agilent Technologies) and an in-house pipeline. Gene expression analysis was performed using R version 2.15 (<http://www.bioconductor.org/>) and BRB ArrayTools software (v.4.4.0). An unsupervised hierarchical clustering analysis was employed with the most variable probes (interquartile range > 0.1) using complete linkage and Euclidian distance. Transcriptomic variations among clusters were identified by significance analysis of microarray (SAM) (false discovery ratio $< 1\%$).

The CNA and expression microarray data are available at the Gene Expression Omnibus (GEO) (GSE111395).

Integrative analysis

Paired CNA and gene expression data of 33 OPSCC was integrated using Copy Number and EXpression In Cancer (CONEXIC) algorithm to identify drivers, which results in a ranked list with high scores modulators [28]. In this analysis, unbalanced expressed genes are correlated with the expression of group of genes (modules), and genomic regions

with significant alterations indicate a greater possibility of the gene has some adaptive advantage on the tumor phenotype. Parameters used in this analysis were described elsewhere [25]. Mann–Whitney test (Prismv.5.0, GraphPad Software, La Jolla, CA) was applied to analyze the relationship between gene expression and CNA.

External data validation and in silico functional analysis of driver candidates

Driver candidates were validated in 78 OPSCC available in the TCGA public database (SNP arrays and RNAseq), using cBio Cancer Genomics Portal (<http://www.cbioportal.org/public-portal/index.do>) assessed in February 2018). Ingenuity® Pathway Analysis (IPA v2.3; <http://www.ingenuity.com>) and KOBAS (v.3.0; <http://kobas.cbi.pku.edu.cn/>) software was additionally used to highlight enriched canonical pathways modulations.

Data validation by reverse transcription quantitative polymerase chain reaction (RT-qPCR)

Thirty OPSCC (23 array-dependent and 7 independent samples) and four non-neoplastic oropharyngeal tissues were assessed to evaluate the *ORAOV1*, *CPT1A*, *PPF1A1* and *SHANK2* transcript levels by RT-qPCR (primer sequences are showed in supplementary Table S2). *HMBS* and *HPRT1* were selected as reference genes using geNorm algorithm (tested in combination with *ACTB*, *GAPDH* and *GUSB*) [29]. Robotic pipetting was carried out using QIAgility (QIAGEN) in a total volume of 12.5 µL containing Power SYBR Green PCR Master Mix (Applied Biosystems), 20 ng of cDNA and 200 nM of each primer. All samples were analyzed in duplicate. Normalized relative gene expression was obtained according to Pffaf method [30].

Statistical analysis

Fisher exact test was used to associate the clustering analysis and copy number alterations with clinicopathological features. Transcript levels were evaluated according to CNA and response to therapy using Mann–Whitney test. High expression levels were defined as at least two-fold in tumor tissues compared to normal tissues. Overall and disease-free survival probabilities were calculated using Kaplan-Meier method and statistically compared with log rank. Multivariate analysis was applied using Cox proportional hazards including all variables with *p* value < 0.1 in the univariate analysis. Receiver Operating Characteristic (ROC) curve was applied to verify the predictive value of the variables in relation to response to treatment, defined by the Area Under the ROC Curve (AUC). Statistical analysis was performed with GraphPad Prismv5.0 (GraphPad Software Inc., La Jolla, CA) and SPSS v.21.0 (SPSS; Chicago, IL).

Results

HPV infection status and prognosis

Clinical and pathological features of the Brazilian patients included in this study are presented on Table 1. Fifty-eight percent (23/40 cases) of the advanced OPSCC were HPV-positive, being HPV16 the most prevalent subtype (19 cases; 1 HPV16/18; 1 HPV16/33; 1 HPV18 and 1 HPV33) (supplementary Table S1). Tonsil was the most common affected site by HPV (57%) (Table 1). Longer overall survival was observed for HPV-positive compared to HPV-negative cases (*p* = 0.008, supplementary Fig. S1A). Risk stratification based on HPV status, smoking history and tumor/node stage [7] was performed. High-risk patients (*n* = 15) showed shorter survival compared with low (*n* = 15) and intermediate-risk patients (*n* = 10) (*p* = 0.013, supplementary Fig. S1B).

Table 1
Patient distribution according to the demographic and clinical variables and 11q13 amplification status.

Characteristics	Number of patients (%) ^a , <i>N</i> = 40	11q13 amplification ^b (%), <i>N</i> = 33	<i>p</i> value
Gender			
Female	2 (5)	0/2 (0)	0.542
Male	38 (95)	11/31 (35.5)	
Age			
Median (interquartile range)	55.5 (47.8–62.3)		
< 60 years	26 (65)	6/20 (30)	0.714
≥ 60 years	14 (35)	5/13 (38.5)	
Anatomic site			
Base of the tongue	16 (40)	4/14 (28.6)	1.000
Soft palate	1 (2.5)		
Tonsil	23 (57.5)	6/19 (31.8)	
HPV infection status			
Negative	17 (42.5)	7/15 (46.7)	0.163
HPV16	19 (47.5)	4/18 (22.2)	
Other HPV (18/33)	2 (5)		
Co-infection (HPV16 and HPV18/33)	2 (5)		
Tobacco consumption			
No	9 (22.5)	1/8 (12.5)	0.218
Yes	31 (77.5)	10/25 (40)	
Alcohol consumption			
No	14 (35)	1/10 (10)	0.109
Yes	26 (65)	10/23 (43.5)	
Clinical T stage			
T1	1 (2.5)	7/23 (30.4)	0.696
T2	7 (17.5)		
T3	21 (52.5)		
T4	11 (27.5)	4/10 (40)	
Clinical N stage			
N0	11 (27.5)	2/9 (22.2)	0.681
N1	5 (12.5)	9/24 (37.5)	
N2	18 (45)		
N3	6 (15)		
Stratification risk ^c			
Low	15 (37.5)	4/20 (20)	0.065
Intermediate	10 (25)		
High	15 (37.5)	7/13 (53.8)	
Treatment response (RXT + CT)			
Stable disease/ progression	3 (9.7)	5/9 (55.6)	0.097
Partial	7 (22.6)		
Complete	21 (67.7)	4/19 (21.1)	
Not available ^d	9	5	
Clinical outcome			
Free of disease	25 (62.5)	8/19 (42.1)	0.278
Local recurrence	11 (27.5)	3/14 (21.4)	
Distant Metastasis	4 (10)		
Death			
No	26 (65)	5/20 (25)	0.270
Yes	14 (35)	6/13 (46.2)	

^a Risk stratification according to Ang et al. [7].

^b Nine patients not submitted to concurrent radiotherapy and chemotherapy (CT-RT).

^c Amplification in at least one gene located in 11q13; *p* value: Fisher exact test.

Genomic and transcriptomic analyses in OPSCCs

Fig. 1 summarizes the genomic and transcriptomic analysis approaches and the main results. Recurrent CNAs included losses of 8p11.23-p11.22, 14q11.1-q11.2, 15q11.2 and gains of 11q13.2 and 11q13.2-q13.3. After the comparison of all significant CNA (*p* < 0.05) with DGV database, only gains of 11q13.2 and 11q13.2-q13.3 were

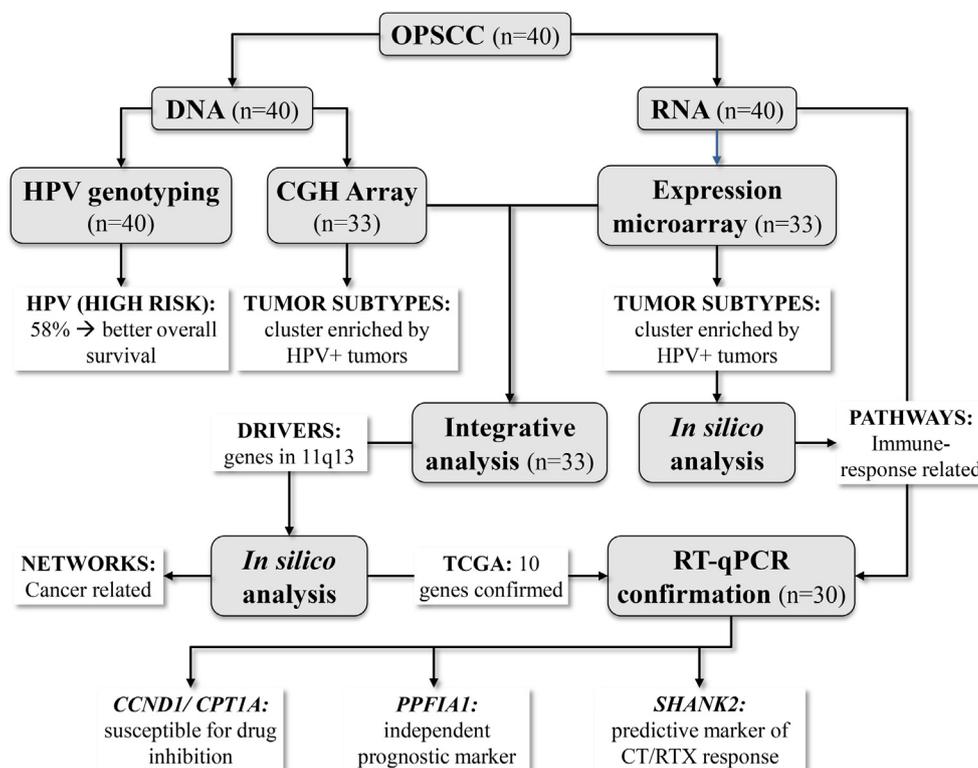


Fig. 1. Flowchart illustrating the methodologies and major findings of the study.

classified as new alterations. Genes and ORFs mapped in these regions are shown in supplementary Table S3.

CNA profiles revealed two clusters of samples, being the cluster 1 enriched by HPV-positive cases (cluster 1: 67% and cluster 2: 28%, $p = 0.038$), low/intermediate risk stratification (cluster 1: 77% and cluster 2: 25%, $p = 0.005$), complete chemoradiation response (cluster 1: 89% and cluster 2: 26%, $p = 0.004$) and lower mortality (cluster 1: 27% and cluster 2: 82%, $p = 0.008$) (Fig. 2A). CNA analysis according to HPV status revealed gains of 3q26.31 and 11q13.2 and losses of 9p21 exclusively detected in HPV-negative cases ($p < 0.05$, supplementary Table S4).

The gene expression analysis also demonstrated a cluster of samples enriched by HPV-positive cases (cluster 1: 87% and cluster 2: 44%, $p = 0.027$). A trend of low/intermediate risk enrichment (cluster 1: 85% and cluster 2: 50%, $p = 0.067$) was also observed in the cluster 1, which presented a partial overlapping with CNA cluster 1 (Fig. 2B). The comparison between these two gene expression clusters revealed 423 differentially expressed transcripts (supplementary Table S5). The pathways identified in HPV-enriched cluster were related to immune response, including interferon-gamma (IFNG) and programmed cell death-1 (PD-1) signaling (supplementary Table S6) (IPA and KOBAS v3.0). The main molecule predicted as activated by IPA upstream regulator analysis was IFNG (supplementary Table S7), which was detected as overexpressed in HPV-enriched cluster.

Integrated genomic and gene expression data

The integrative analysis using CONEXIC revealed 16 putative modulators mapped at 11q13 (*ANO1*, *CCND1*, *CPT1A*, *FADD*, *FGF3*, *FGF4*, *FGF19*, *IGHMBP2*, *MRGPRD*, *MRGPRF*, *MRPL21*, *ORAOV1*, *PPF1A1*, *PPP6R3*, *SHANK2* and *TPCN2*). Ten of 16 modulators showed statistically significant association between copy number gains and higher expression levels (Fig. 3A). Interestingly, copy number gains of these genes were associated with shorter overall survival (Fig. 3B). *In silico* analysis showed interactions between these 10 driver candidates

and their association with cell cycle, cancer, organismal injury and abnormalities (supplementary Fig. S2). In addition, interactions with recognized cancer-related molecules (calmodulin and p21) were observed, being *CCND1* and *CPT1A* susceptible for drug inhibition (arsenic trioxide and perhexiline, respectively) (drugbank: <https://www.drugbank.ca/>. Accession in February 2018).

Validation of candidate driver genes

The putative drivers were further tested using the TCGA database of OPSCC, confirming the increased gene expression levels and genomic copy number gains of 10 genes (supplementary Fig. S3A). Similarly to our data, these genomic alterations were also associated with shorter overall survival (supplementary Fig. S3B).

In 30 OPSCC samples with available tissues for RNA extraction RT-qPCR confirmed a significant association of genomic gains in 11q13 and overexpression of *ORAOV1*, *CPT1A*, *PPF1A1* and *SHANK2* genes (Fig. 4A). High expression levels of these genes were associated with shorter survival (Fig. 4B). The multivariate analysis revealed *PPF1A1* expression and HPV status as independent prognostic markers in advanced OPSCC (Table 2).

Among the four potential markers identified, significant decreased expression level of *SHANK2* was detected as predictive marker of complete response (Fig. 4C) and complete response without recurrence in at least five years (Fig. 4D) after concurrent radiotherapy and chemotherapy ($p = 0.010$ and $p = 0.012$, respectively). Compared to risk stratification (low, intermediate or high) or HPV status (negative or positive), *SHANK2* relative expression presented a higher performance in predicting concurrent CT-RT complete response (AUC = 0.733, AUC = 0.646, AUC = 0.833; respectively) (Fig. 4C) and complete response without recurrence (AUC = 0.659, AUC = 0.606, AUC = 0.811; respectively) (Fig. 4D).

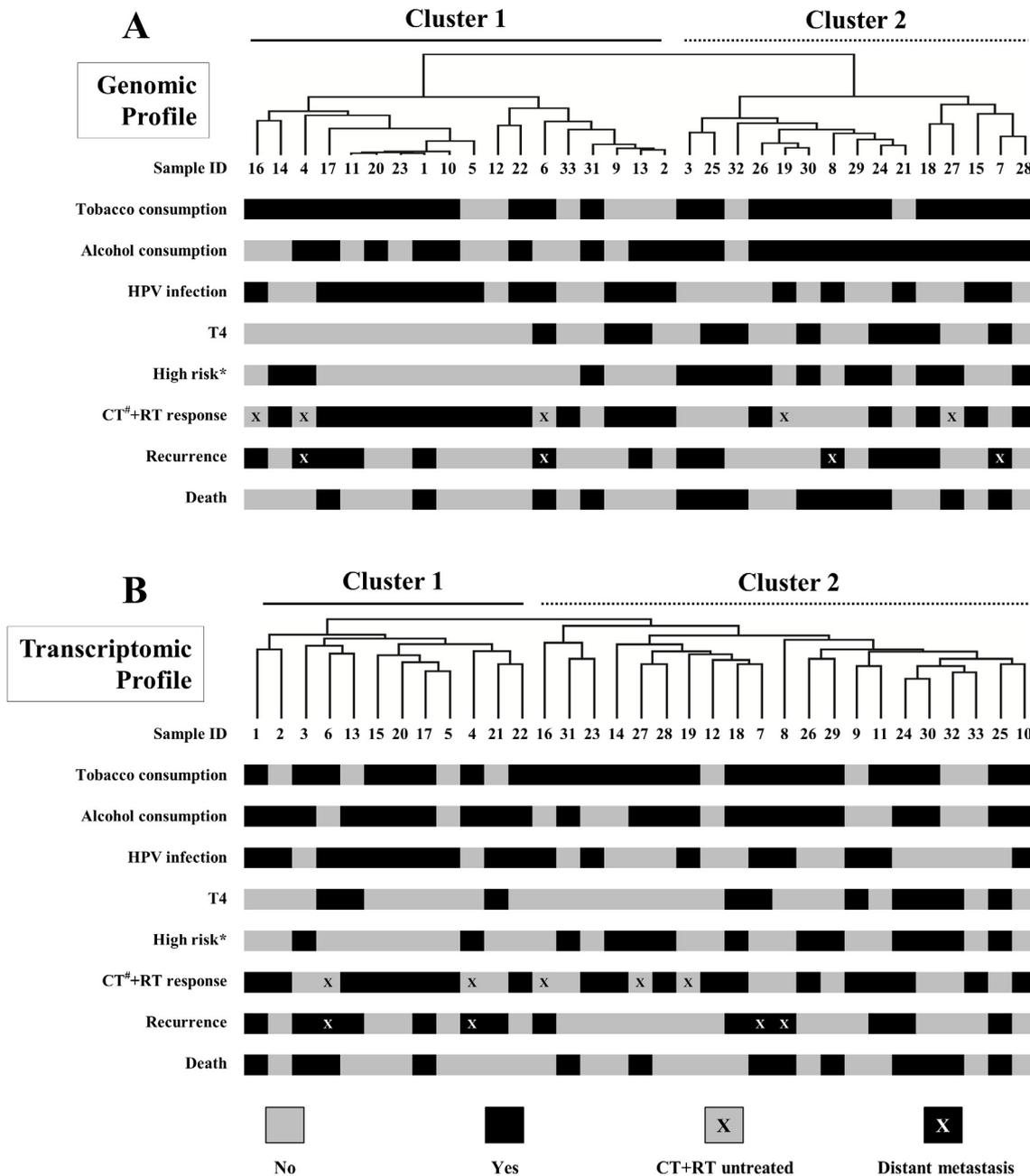


Fig. 2. Unsupervised hierarchical clustering analysis of (A) array-CGH and (B) global gene expression data according to the clinical features. CT: chemotherapy; RT: radiotherapy; *Risk stratification (Ang et al. [7]), #Patients submitted to induction chemotherapy followed by concurrent platinum/cetuximab and radiotherapy or only concurrent platinum/cetuximab and radiotherapy.

Discussion

This study was designed to reveal potential drivers in locally advanced OPSCC, aiming to identify new therapeutic targets and biomarkers. About half of OPSCC cases were positive for high-risk HPV, which was associated with improved survival, corroborating previous reports [7,8,10,11,31,32]. Among the HPV positive cases, 95% (22/23) were HPV16/18, similar to recent findings described in HNSCC [33]. Moreover, worse prognosis was observed for high-risk patients (according to HPV, TNM and smoking), supporting the hypothesis that the clinical course of HPV-positive tumors is modified by tobacco usage [7]. Curiously, the distribution of HPV infection was uneven between the patient recruitment centers. Tumors collected from Sao Paulo (the largest metropolis in Brazil) presented 77% (23/30) of positivity compared to 0% (0/10) in the Barretos cohort (an inland city in Brazil

southeast). The Brazilian OPSCC patients were recently characterized as having 4% of HPV positivity compared to 59% and 31% in USA and Europe, respectively [34]. However, the predominance of HPV in Brazilian patients can drastically differ due to geographic heterogeneity of our population, which can vary socioeconomically, in alcohol-tobacco consumption and in sexual behavior.

Significant recurrent gains of 11q and two clusters based on CNA similarities were observed, being the cluster 1 enriched by HPV-positive tumors. Particularly, gains of 11q13.2 (*LRP5*, *PPP6R3* and *SAPS3* genes) were exclusively detected in HPV-negative samples. Amplification of 11q13 is commonly reported in different tumors, including HNSCC [20,27,35–38], particularly in HPV-negative tumors [39,40] and OPSCC [15]. Mutually exclusive amplifications of 11q13 (*CCND1* and *FADD*) and 11q22 (*BIRC2* and *YAP1*) were detected in HPV-negative HNSCC [27]. These data emphasizes that distinct molecular alterations

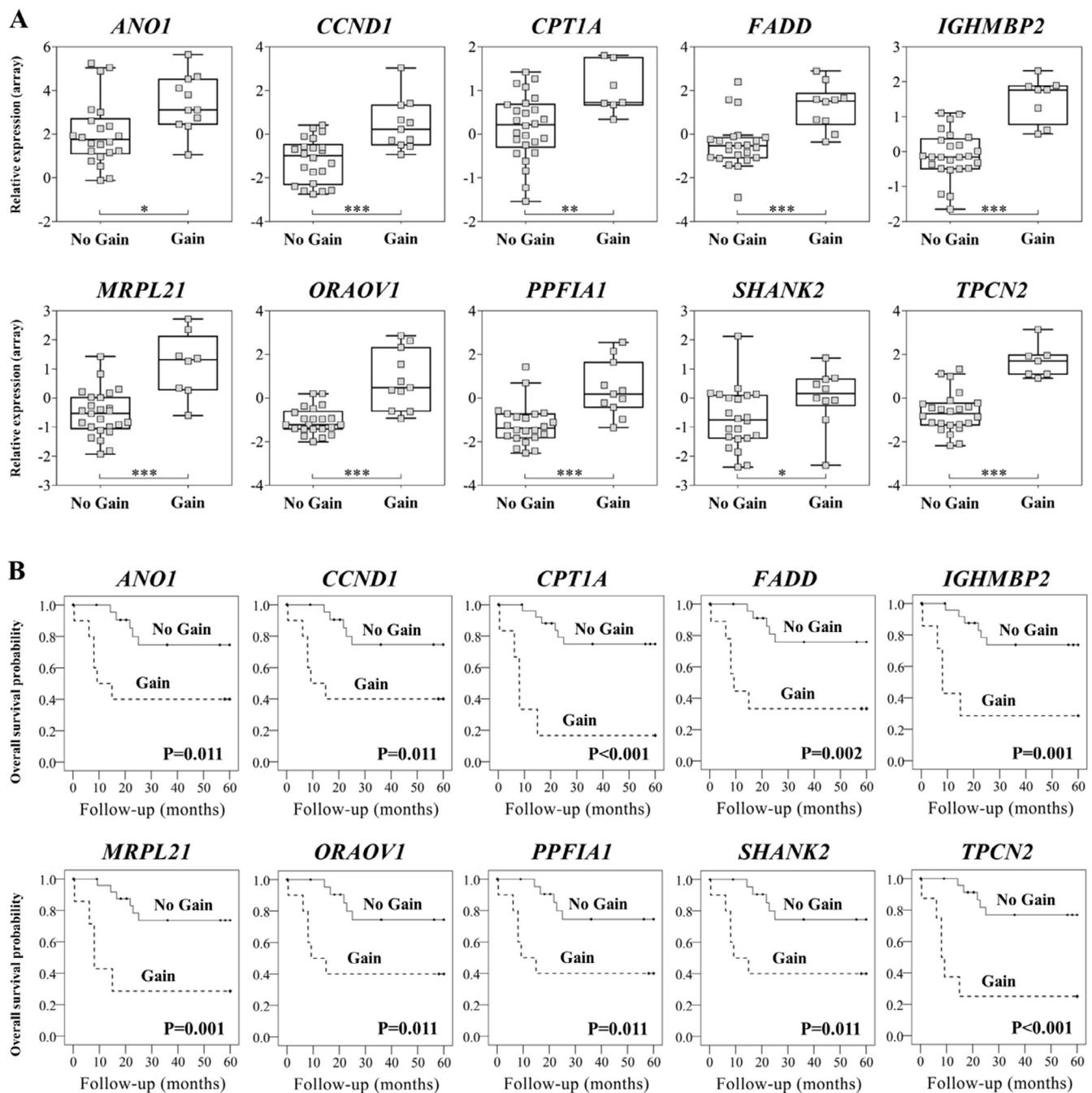


Fig. 3. A. Association of DNA copy number gains with expression levels of ten genes identified as driver candidates in OPSCC. B. Overall survival analysis according to DNA copy number gains in 10 candidate driver genes. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$ (Mann-Whitney test); Overall survival analysis performed by Kaplan Meyer method with log rank test.

drive the oropharynx carcinogenesis according to the HPV status.

Large-scale gene expression analysis also showed distinct clusters according to HPV status. HPV-enriched cluster presented predominantly immune response-related genes, mainly involving negative regulators of T-cell immune function, as cytotoxic T-lymphocyte-associated antigen 4 (CTLA-4) and programmed death 1 (PD-1) and its ligand PD-L1 immune checkpoints pathway members. The PD-1/PD-L1 and CTLA-4, have shown promising clinical success as a cancer immunotherapy target [41]. Nonetheless, many factors influence in the response to immunotherapies, as the degree of tumor lymphocyte infiltration and the checkpoint proteins levels [13]. A previous study showed that 70% of HPV-positive HNSCCs presents PD-L1 positive immunostaining [42]. The authors reported increased transcript levels

of *IFNG* in oropharyngeal tumors HPV+/PD-L1+, suggesting that IFN- γ might induce PD-L1 in tumor cells. In our study, IFN- γ was highly overexpressed in the HPV-positive enriched cluster and was predicted by IPA as the one of the main upstream regulator. Tumor infiltrating lymphocytes overexpressing PD-1 presented better clinical outcome, mostly in head and neck tumors HPV-positives [43]. Furthermore, CD8+ tumor infiltrating lymphocytes showing high expression levels of PD-1 were found more frequently in HPV-negative tumors with compromised IFNG secretion. These patients presented worse prognosis. Conversely, HPV-positive tumors presenting low PD-1 expression in T cells were associated with better response to immunotherapy (anti-PD-1) and outcome [43]. In melanoma, the immunostaining positivity for MHC (Major Histocompatibility Complex) class II molecules was

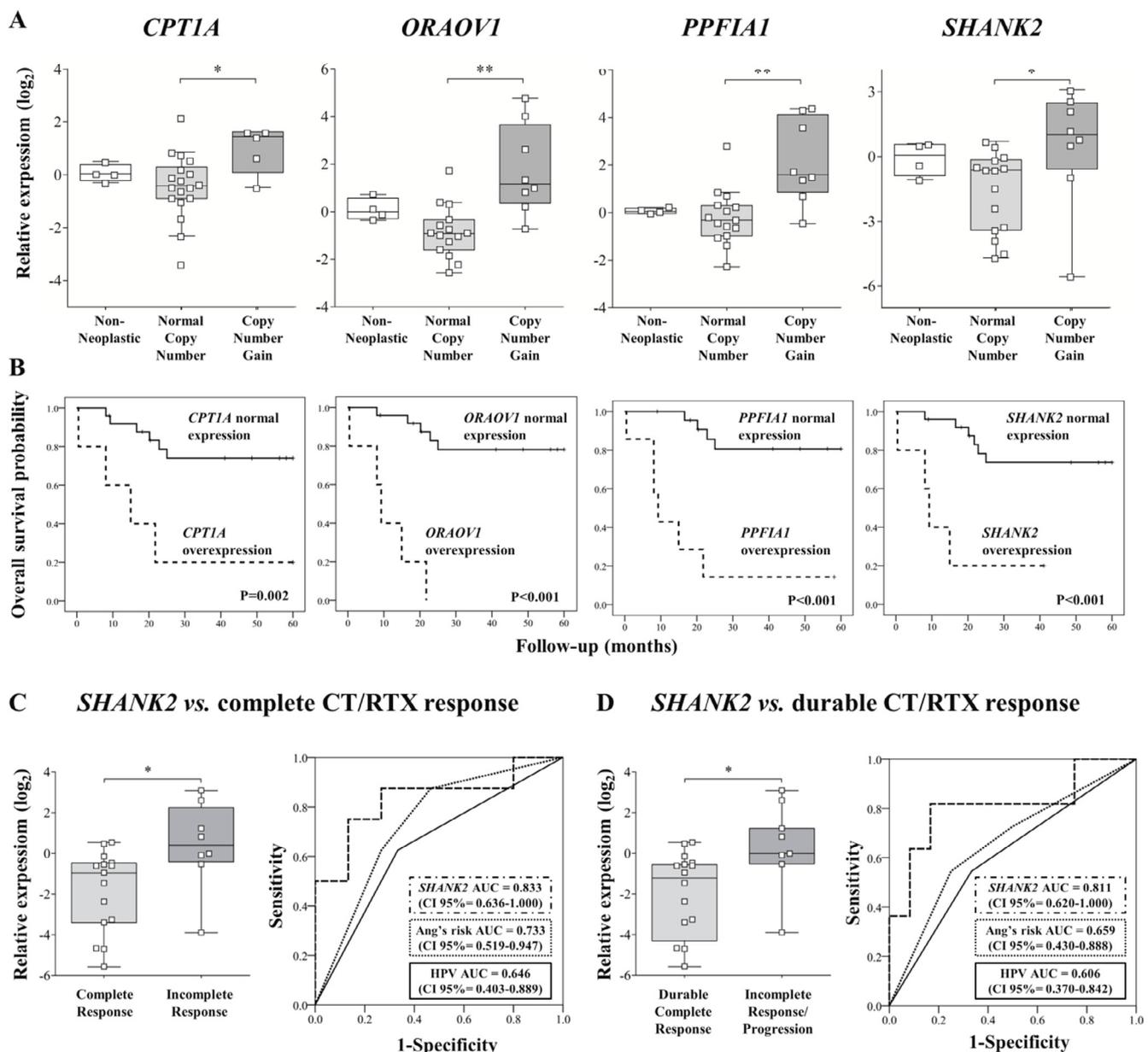


Fig. 4. A. Relative gene expression analysis using RT-qPCR in non-neoplastic samples and OPSCC with two copies (normal) and 11q13 copy number gains. B. Disease-free survival curves of tumors in normal range of expression and overexpression of the genes assessed by RT-qPCR (p value obtained from log rank test). C and D. Expression level of *SHANK2* (RT-qPCR) as a predictive marker of complete response (C) and durable complete response (D) to concurrent radiotherapy and chemotherapy, comparing HPV status and risk stratification (Ang et al. [7] $p < 0.05$; $** p < 0.01$ (Mann Whitney non-parametric test); AUC: area under the ROC (receiver operating characteristic) curve.

associated with therapeutic response and better clinical outcome in anti-PD-1-treated patients [44]. In our study, overexpression of MHC class II genes was detected in HPV-related cluster (supplementary Table S4). Overall, our findings give additional evidence that PD-1/PD-L1 is a target for new therapeutic strategies in OPSCC, particularly in HPV-positive cases.

Correlation between CNAs mapped in 11q13.2-11q13.3 and corresponding genes expression levels was previously described in HNSCC [21]. In our study, 10 cancer-related genes (*ANO1*, *CCND1*, *CPT1A*, *FADD*, *IGHMBP2*, *MRPL21*, *ORAOV1*, *PPF1A1*, *SHANK2* and *TPCN2*) mapped in 11q13 showed copy number gains and overexpression. These findings were further validated using the TCGA, suggesting that other genes besides *CCND1* may confer an advantage to OPSCC cells [45]. Moreover, gains involving these genes were associated with worse survival in our study and in TCGA, thus supporting their relevance in

OPSCC outcomes.

Further analysis using RT-qPCR confirmed an association among *ORAOV1*, *CPT1A*, *PPF1A1* and *SHANK2* overexpression and shorter survival. A meta-analysis comprising 15 publically available microarray gene expression data assessing 140 normal and 277 HNSCC samples revealed a list of 181 differentially expressed genes. *ANO1* and *FADD* (both mapped in 11q13) were overexpressed in at least 30% of the TCGA samples (528 HNSCC), and associated with higher risk of recurrence and death [46]. Gains of 11q13.2, including *CPT1A*, were also associated with worse survival in patients with esophageal carcinoma [47]. *CPT1A* (*Carnitine palmitoyl transferase 1A*) gene encodes a rate-limiting enzyme for fatty acid transport inside the mitochondria for β -oxidation. Fatty acid oxidation is essential for ATP production in metabolic stress conditions and particularly in cancer [48]. Enzymes involved in fatty acid oxidation, such as *CPT1*, are promising targets for

Table 2
Univariate and multivariate analysis of OPSCC overall survival.

Variables	Univariate analysis		Multivariate analysis	
	HR (CI _{95%})	p value	HR (CI _{95%})	p value
HPV infection				
No	1		1	
Yes	0.3 (0.1–1)	0.056	0.1 (0.02–0.56)	0.001
Ang's risk stratification				
Low/Intermediate	1			
High	3.7 (1–14.5)	0.056	–	–
CPT1A expression				
Normal range	1			
Overexpression	6 (1.7–21.9)	0.006	–	–
ORAOV1 expression				
Normal range	1			
Overexpression	18.3 (4.1–80.9)	< 0.001	–	–
PPFIA1 expression				
Normal range	1		1	
Overexpression	11.9 (3.2–44.1)	< 0.001	30.9 (5.3–179.6)	< 0.001
SHANK2 expression				
Normal range	1			
Overexpression	7.6 (2–28.1)	0.003	–	–

HR: hazard ratio; CI_{95%}: confidence interval of 95%. p value: Cox proportional-hazards regression.

cancer therapy [48] and might be considered as a potential target in OPSCC. Interestingly, CPT1 enzyme can be pharmacologically inhibited by perhexiline [49].

Although increased expression levels of *ORAOV1* (*oral cancer overexpressed 1*) have been reported in several tumors [50–52], its biological function is not completely characterized. In oral carcinomas, reduced *ORAOV1* expression was associated with delayed cell growth *in vitro* and inhibition of tumor growth and angiogenesis *in vivo* [51]. A protective response to reactive oxygen species was related to *ORAOV1* overexpression, a common feature of many cancers [53], including HNSCC [54]. Despite the small sample size and number of events (10 patients died during a 5-year follow-up), *PPFIA1* overexpression was identified as an independent prognostic marker (independent of the HPV status and/or tobacco consumption). *PPFIA1* was reported as the highest up-regulated gene associated with copy number gains of 11q13 in HNSCC cell lines [55]. In breast cancer cells, the silencing of *PPFIA1* promotes inhibition of migration and invasion [56]. Overall, our data suggest that *PPFIA1* acts as an oncogene in OPSCC, although its function in these tumors requires further studies.

SHANK2 overexpression was associated with incomplete response to therapy, being able to distinguish treatment-unresponsive from responsive tumors more efficiently than HPV status. *SHANK2* is a member of scaffold protein family involved in excitatory synapses in the central nervous system. In oral carcinomas, co-amplification and overexpression of *SHANK2* and *CTTN* was reported, suggesting a cooperative role of these proteins on tumor cell motility and invasiveness [57]. Amplification and overexpression of *SHANK2* was also associated with poor prognosis in esophageal squamous cell carcinoma [58]. In oral carcinomas, *SHANK2* was described as one of seven prognostic markers evaluated by DNA methylation [59]. These findings suggest that CNA and/or epigenetic mechanisms may result in *SHANK2* increased expression and consequent HNSCC aggressiveness. To our knowledge, the association between genes mapped in 11q13 and chemoradiation response was not previously reported. The role of these genes in oropharyngeal carcinogenesis, particularly in tumor aggressiveness and their ability to predict therapy response, should be further investigated.

Considering that only locally advanced OPSCC biopsies obtained from patients subsequently treated with specific therapeutic strategies were included in our study, the major limitation was the small sample

size (n = 40). Nonetheless, with the addition of an independent sample set (n = 78) from TCGA (not treatment-standardized), we were able to confirm the potential clinical relevance of genes mapped in 11q13.

In conclusion, we described a higher frequency of HPV infection than previous Brazilian OPSCC reports, which varied greatly according to the geographic region and tobacco-alcohol consumption. HPV-positive tumors showed an immune response-related gene signature, which can have an impact on immunotherapy response prediction leading to a more precise treatment indication. In addition to *CCND1* previously described, novel driver genes including *ORAOV1*, *CPT1A*, *PPFIA1* and *SHANK2* genes mapped in 11q13 presented a role in the prognosis and chemoradiation response prediction, regardless of the HPV status.

Conflict of interest statement

None declared.

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Authors' contributions

SRR and LPK conceived and designed the experiments; MCBF, MH and LARR conducted the experiments; MCBF, FAM, LARR, SAD analyzed the data; SRR and LPK contributed with reagents/materials; SRR, LPK and SAD supervised the study; CALP performed the histopathological evaluation; URN, ALC and LPK selected the cases and obtained the clinical data; MCBF, SAD and SRR wrote and edited the manuscript. All authors read and approved the final version of the manuscript.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <https://doi.org/10.1016/j.oraloncology.2018.06.010>.

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