

HPV-related Oropharyngeal Squamous Cell Carcinoma: p16^{INK4A} Immunohistochemistry or HPV Genotyping?

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Abstract. *Background:* Infection with high-risk human papillomavirus (HPV) is linked to a sub-group of squamous cell oropharyngeal tumors (OPSCC). *Our aim was to compare an HPV Polymerase Chain Reaction (PCR) assay and p16^{INK4A} expression status by immunohistochemistry (IHC) as a surrogate marker. Materials and Methods:* This was a retrospective study considering patients affected by squamous cell oropharyngeal tumors. All included samples were processed for IHC for p16^{INK4A} and tested by PCR for detection of HPV DNA and HPV genotyping. *Results:* A total of 84 patients affected by squamous cell oropharyngeal tumors were included and tested. A significant positive correlation was found between HPV PCR and p16^{INK4A} IHC but the agreement was poor (k coefficient of 0.25). In fact, the sensitivity of p16^{INK4A} IHC positivity in detecting HPV PCR positivity was low (28.21%, 95% confidence interval=16.54% - 43.78%). *Conclusion:* Positivity of p16^{INK4A} by IHC had a low sensitivity in detecting HPV DNA and our results suggest the need at least to test p16^{INK4A} IHC- negative samples using HPV PCR to increase detection accuracy and provide valuable information for the clinical management of these patients.

Head and neck squamous cell carcinomas (HNSCC) are the sixth most common type of cancer worldwide,

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accounting for 633,000 new cases annually (1-3). Common events in head and neck carcinogenesis are loss of heterozygosity (LOH), hypermethylation, deletion, and mutation of the *p16* gene locus (4). Therefore, loss of p16^{INK4A} expression defines a sub-group of patients with oropharyngeal cancer (OPSCC) including those of the base of the tongue and tonsils, including lingual tonsil and Waldeyer's ring with worse clinical outcome (5). Historically, tobacco and alcohol consumption are the primary known risk factors for development of HNSCC; recently, it has become evident that infection with high-risk human papillomavirus (HPV) is etiologically linked to a sub-group of HNSCCs (6, 7). Viral DNA is detected in about 20% of HNSCCs, the strongest association being found in OPSCC, in which HPV prevalence has been estimated at between 25% and 50% (8, 9), where carcinomas of the tonsils are particularly associated with HPV infection, most frequently with HPV16 (10). Recent studies indicated that in HNSCC, patients with HPV-infected tumors have a more favorable prognosis compared to patients whose tumors are HPV-negative (11).

Most of the acquired data on HPV-driven carcinogenesis comes from the uterine cervix model in which E6 and E7 proteins play the principal role in the malignant transformation, interacting with retinoblastoma protein (pRb; 12, 13). The retinoblastoma protein is a nuclear phosphoprotein that regulates growth in the G₁ phase of the cell cycle. pRb exerts its growth-inhibitory effects by binding to and inhibiting critical regulatory proteins, including members of the E2F family of transcription factors; E2F activation is necessary for the G₁-S transition (14). E2F selectively associates with hypophosphorylated pRb, and phosphorylation of pRb appears to release E2F from an inhibitory complex, enabling it to promote the transcription necessary for cell progression into late G₁ and

S phase (15, 16). In quiescent cells, pRb is hypophosphorylated and associates with E2F. When quiescent cells are exposed to mitogenic signals, cyclin-D associates with and activates the cyclin-dependent kinases 4 and 6 (CDK4 and CDK6, respectively), which phosphorylate pRb during the G₁ phase, causing release of E2F (17). Therefore, the free and active E2F promotes the transcription of genes that encode proteins essential for cell-cycle progression. The main inhibiting factor of this pathway is p16^{INK4A}, which associates with CDK4 and CDK6 and inhibits their kinase activity (17). Expression of p16^{INK4A} causes accumulation of hypophosphorylated pRb and consequent G₁ cell arrest (18).

HPV infection leads to the association between viral protein E7 and pRb. This interaction results in release of active E2F and stimulation of cells to S-phase entry, even in the absence of active cyclin-D-CDK4/6 complexes (19). To counteract E2F activation, HPV-infected cells overexpress p16^{INK4A}.

In analogy with female genital (or cervical) carcinogenesis, HPV testing has been widely recommended in OPSCC, but there is no consensus on which test is considered the ‘golden standard’ (20) among the numerous detection methods available either as single tests or combinations (21).

However, although recent publication of Guidelines for Head and Neck Cancer and College of American Pathologists protocol for the Examination of Specimens From Patients With Carcinomas of the Pharynx suggest p16^{INK4A} immunohistochemistry (IHC) as a screening method for HPV detection (22, 23), some questions remain regarding the accuracy of the test when used alone, without confirmatory molecular detection of HPV-DNA.

In the present study, we aimed to compare two different commonly used HPV detection methods: an HPV Polymerase Chain Reaction (PCR) assay, and p16^{INK4A} expression status by IHC as a surrogate marker.

Materials and Methods

Participants and study design. In this retrospective study we included all consecutive patients from January 2000 to December 2014 affected by primary, previously untreated OPSCC from the Institute of Anatomic Pathology of Udine University Hospital and from the Institute of Anatomic Pathology of University Politecnica delle Marche. Where available, in the majority of cases, we preferred diagnostic small biopsy, otherwise we used excision biopsy. We considered as exclusion criteria HNSCC localized on lips, buccal mucosa, hard palate, tongue margins and all cases with insufficient paraffin-embedded tumor tissue (FFPE) for performing HPV PCR and p16^{INK4A} IHC, or cases where HPV PCR was not feasible. The included cases were revised by two independent pathologists (MO and LM) who confirmed the diagnosis. Clinicopathological information regarding the age of the patients, tumor staging according to the TNM classification (23), treatment performed and follow-up were gathered from clinical files.

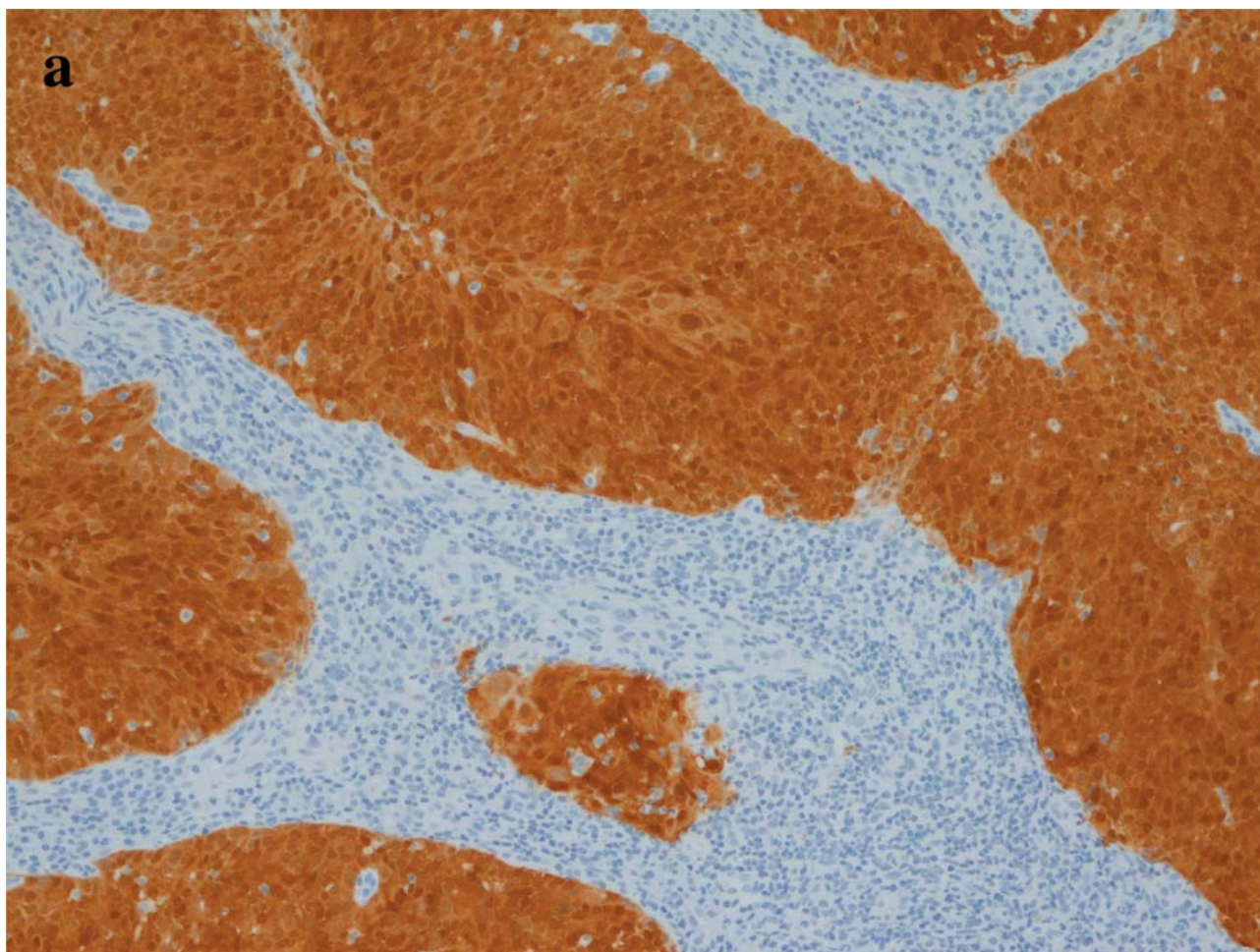
Table I. Population features.

Characteristic	84 patients
Age at diagnosis, years	
Median	57
Range	40-83
Sex, no. (%)	
Male	64
Female	20
Site of tumor origin, no. (%)	
Base of tongue	34 (40.5%)
Pharynx	26 (30.9%)
Retromolar trigone	12 (14.3%)
Tonsils	10 (11.9%)
Cervical lymph nodes	2 (2.4%)

Table II. Results of the different detection methods for human papillomavirus (HPV) infection in our series.

p16 ^{INK4A} immunostaining	
Positive	13 (15.5%)
Negative	71 (84.5%)
HPV DNA, no. (%)	
Negative	45 (53.5%)
Positive	39 (46.5%)
HPV-16	34 (85%)
HPV-39	3 (7.5%)
HPV-31	1 (2.5%)
HPV-11	1 (2.5%)
HPV-positive tumor site of origin, no. (%)	
Base of tongue	16 (41%)
Pharynx	11 (28.2%)
Tonsils	6 (15.4%)
Retromolar trigone	4 (10.3%)
Cervical lymph nodes	2 (5.1%)
HPV+p16 ^{INK4A} +	11 (13.1%)
HPV+p16 ^{INK4A} -	28 (33.3%)
HPV-p16 ^{INK4A} -	43 (51.2%)
HPV-p16 ^{INK4A} +	2 (2.4%)

Tissue microarray (TMA). Haematoxylin and eosin-stained sections were carefully examined to select representative regions from each selected donor block. TMAs were made using a microarrayer semi-automated instrument (Galileo TMA CK4500; Integrated Systems Engineering SRL, ISENET, Milan, Italy). A cylindrical, thin-walled needle (inner diameter of 1.5 mm) was used for coring tissues and for transferring cored samples into array cavities in the recipient block. We performed three core biopsies from each tumor sample in order to obtain good representativity of the tumor. From the recipient block, we obtained 4-µm-thick sections.

Figure 1. *Continued*

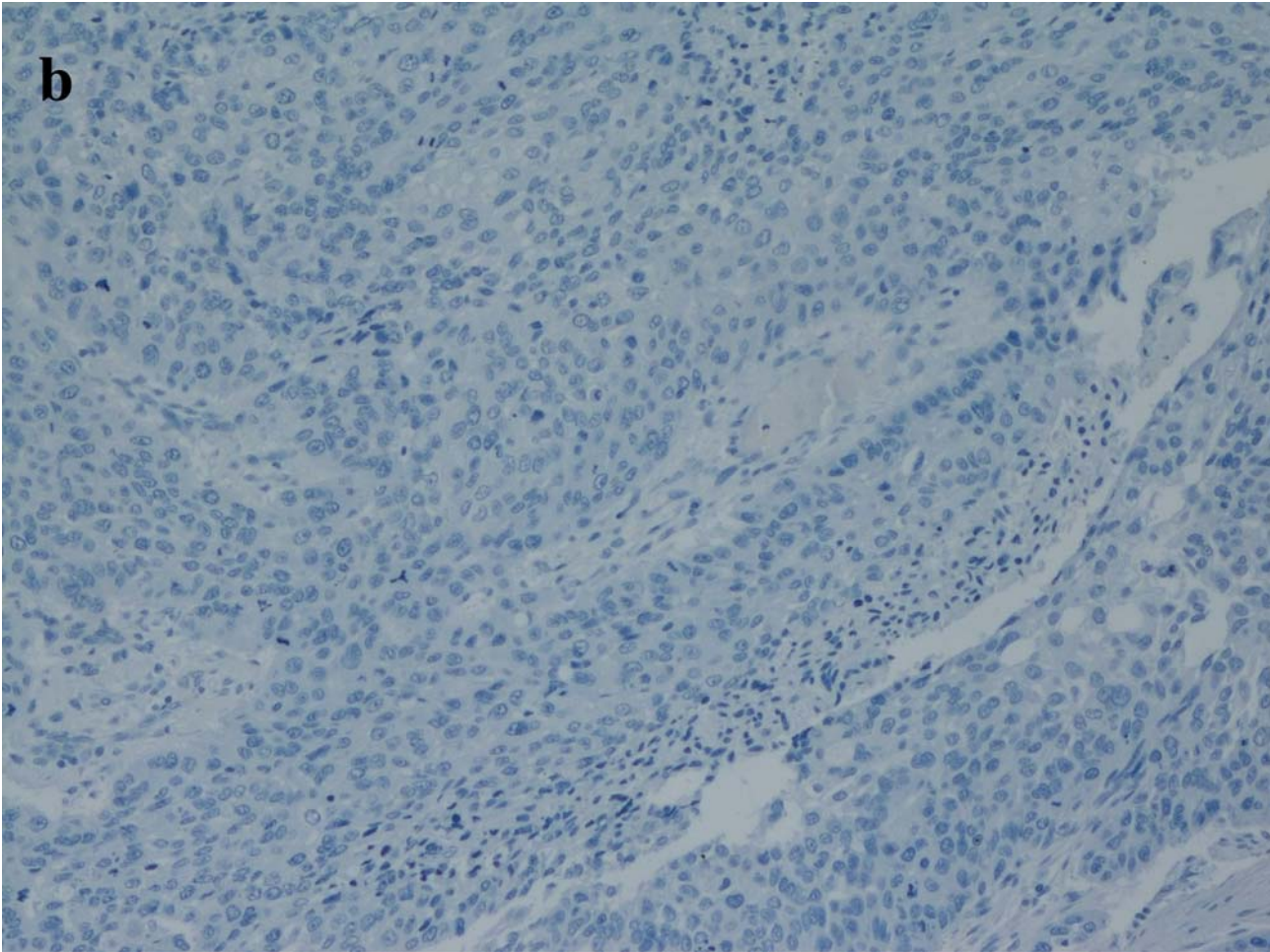
IHC for p16^{INK4A} and scoring of results. Tissue sections were cut at 4- μ m-thick; for antigen retrieval and deparaffinization, slides were heated for 20 min at 98°C in Target Retrieval Solution low pH (code K8005; DAKO, Glostrup, Denmark) with PT-link (DAKO). The slides were then incubated at room temperature in hydrogen peroxide for 10 min to block endogenous peroxidase activity. A fully automated immunohistochemistry kit, CINtec[®] Histology Kit (code 9517; CINtec[®] Ventana Medical Systems, Roche S.p.A., Segrate, Milan, Italy), was used for the qualitative detection of the p16^{INK4A} antigen according to the instruction manual. Cervical cancer sections known to be HPV-positive were used as a positive control and omission of primary antibody was used as a negative control. Among the 84 cases, 50 had sufficient tissue on the FFPE block to perform TMA, while the other 34 samples had an insufficient tumor area to be cored. For these samples, p16^{INK4A} staining was performed on the entire section. Tumors were classified as p16^{INK4A}-positive (strong, diffuse, nuclear and cytoplasmic staining in >70% of carcinoma cells), or as p16^{INK4A}-negative, following College of American Pathologists (CAP) guidelines (24).

IHC evaluation was carried out independently by two pathologist (MO and LM). Each pathologist was blinded to the results obtained

by the other and to the results of the HPV test. Cases with discordant results were re-evaluated to determine a consensus.

DNA extraction. Genomic DNA was extracted from FFPE tumor samples using QIAamp[®] DNA FFPE Kit (code 56404; Qiagen, Milan, Italy) according to the manufacturer's protocol. The extracted DNA was suspended in 30 μ l of sterile water.

PCR for detection of HPV DNA and HPV genotyping. Viral DNA was detected with the HPV Sign[®] Q24 Complete Real-Time PCR assay (code 979990; Diatech Pharmacogenetics, Jesi, Italy) according to the manufacturer's instructions using RotorGene Q Real-Time PCR platform (Qiagen, Milan, Italy). This assay allows detection of the most clinically relevant HPV genotypes. The presence and integrity of DNA in all samples was verified by β -actin gene amplification, which acts as an internal control. HPV-positive samples were genotyped by pyrosequencing assay according to the instructions of the HPV Sign[®] Q24 Complete Real-Time PCR kit. The obtained sequences were compared with the genotype-specific sequences available in the public database using IndentiFire software (Diatech Pharmacogenetics, Jesi, Italy).

Figure 1. *Continued*

Statistical analysis. Statistical analysis was performed using R language and environment for statistical computing (version 3.1.2), from the R Foundation for Statistical Computing, Vienna, Austria (<http://www.R-project.org/>). The correlation between immunohistochemical p16^{INK4A} staining and HPV DNA was evaluated by Chi-square test. Furthermore, the agreement between detection methods was assessed by Cohen's k coefficient. We considered Cohen's k coefficient values of less than 0.4 as indicating poor agreement, values between 0.4 and 0.75 as fair to good agreement and values over 0.75 as excellent agreement. In addition, we evaluated the accuracy p16^{INK4A} staining positivity in predicting HPV DNA positivity.

Results

In our registers, we found 94 patients affected by primary previously untreated OPSCC (81 from Udine and 13 from Ancona); 10 cases were excluded because HPV PCR was not feasible. The reform the total number of cases analyzed was 84.

The age of the patients at the time of diagnosis ranged from 40 to 83 years, with a mean age of 57 years (Table I).

The primary tumor location was mainly the base of the tongue (40.5%), and pharynx (30.9%) (Table I).

p16^{INK4A} is normally weakly- expressed in restricted basal-parabasal layers of oral squamous epithelium, whereas it is generally overexpressed in OPSCC. The protein expression in positive OPSCCs was diffusely distributed in the nuclei and cytoplasm of almost the entire cancer cell population. In the evaluation of our cases, tumors were classified as 13 cases (15.5%) with p16^{INK4A}-positive staining (strong, diffuse, nuclear and cytoplasmic staining in >70% of carcinoma cells) (Figure 1a), and 71 cases (84.5%) with p16^{INK4A}-negative staining (Figure 1b), following CAP guidelines (24). In our cohort, six cases exhibited focally weak-to-moderate p16^{INK4A} staining in fewer than 70% of carcinoma cells (Figure 1c), categorizing these cases as negative.

HPV-DNA was found in 39 out of 84 cases of OPSCC (64 male and 20 female patients) and HPV 16 was the most frequent genotype detected (Table II), as described in the literature for Italy (25).

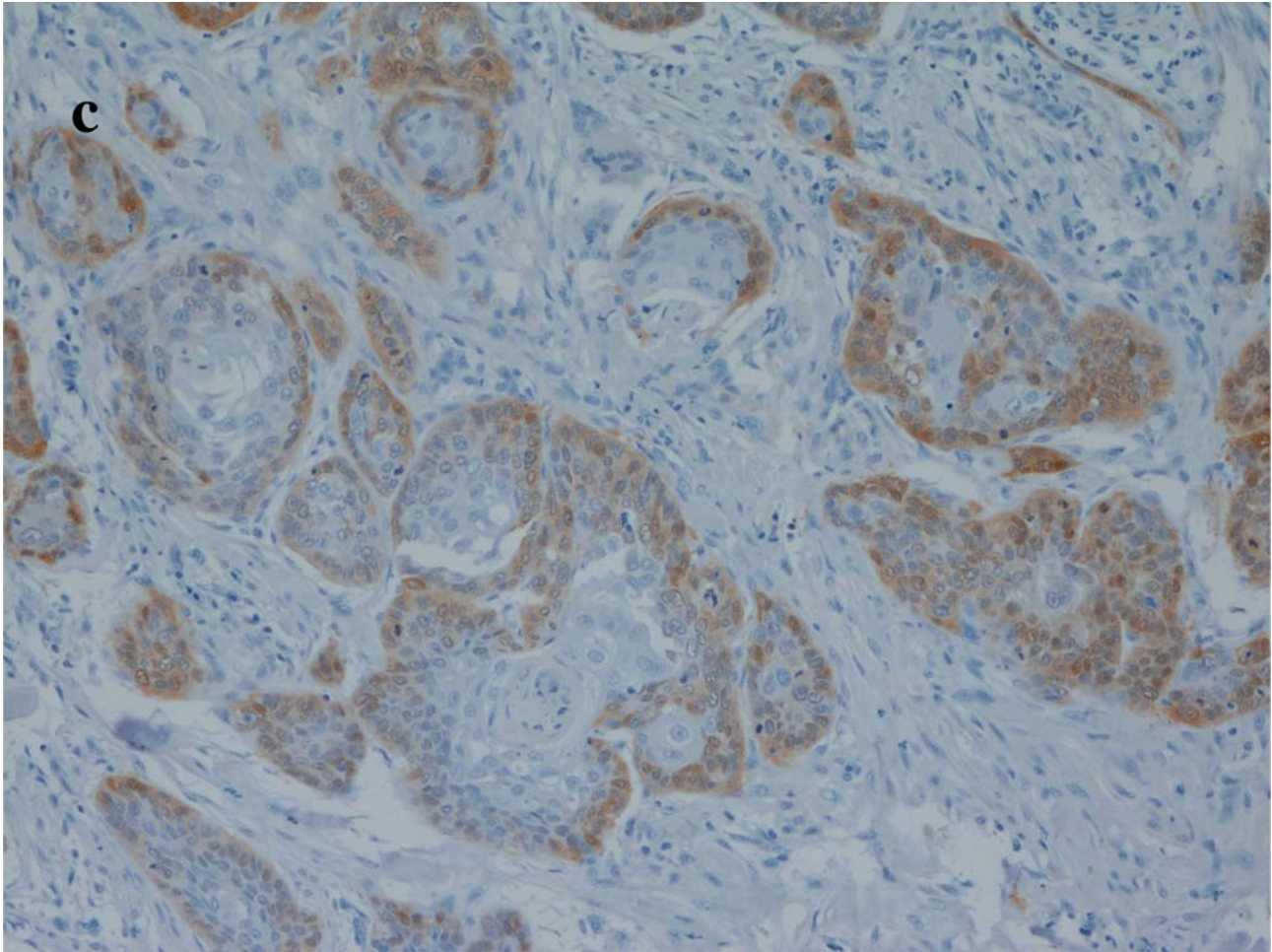


Figure 1. Representative examples of immunohistochemical staining of tissue sections for p16^{INK4A}: a: strong and diffuse p16^{INK4A} staining in tumor cells ($\times 10$), b: negative p16^{INK4A} staining in tumor cells ($\times 10$), c: focally weak to moderate p16^{INK4A} staining in fewer than 70% of carcinoma cells, categorizing such cases as negative ($\times 10$).

The majority of tumors (51.2%) were both HPV- and p16^{INK4A}-negative. Out of the HPV-positive tumors, 11/39 (28.2%) were p16^{INK4A}-positive, while only 2/45 (4.4%) of the HPV-negative tumors were p16^{INK4A}-positive (Table II). What is interesting to note is the high number of tumors (28/39, 71.8%) that were HPV-positive but p16^{INK4A}-negative (Table II). The tumor site for which HPV genotype detection was higher was the base of the tongue, with 16 cases (41%) (Table II). HPV-positive p16^{INK4A}-negative cases that were analyzed for expression of p16^{INK4A} by TMA were also analyzed over the entire section in order to be sure that the negativity in p16^{INK4A} was not due to the coring of a small area not representative of the whole tumor. The data obtained confirmed that in all cases, the neoplasm was homogeneously negative for p16^{INK4A}.

We found a significant correlation between p16^{INK4A} staining and HPV DNA ($p < 0.05$). However, Cohen's κ

coefficient of 0.25 shows a poor agreement between the two tests. In addition, sensitivity of p16^{INK4A} staining in predicting HPV DNA was 28.21% (95% confidence interval=16.54-43.78%), the specificity was 95.56% (95% confidence interval=85.17-98.77%), the positive likelihood ratio was 6.35 (95% confidence interval=1.59-25.27), the negative likelihood ratio was 0.75 (95% confidence interval=0.61-0.92), and accuracy was 64.29% (95% confidence interval=53.62-73.7%).

Discussion

In the present study, we found a significant positive correlation between HPV PCR and p16^{INK4A} IHC but the agreement was poor. In fact, the sensitivity of the p16^{INK4A} IHC against the HPV PCR was low (28.21%, 95% confidence interval=16.54-43.78%).

The *p16* gene (CDKN2a/INK4a) functions as a negative regulator of the cell cycle through its inhibition of CDK4/6 and subsequent blockage of the cyclin-dependent phosphorylation of the Rb. In oral epithelial pre-cancer and cancer, the *p16* gene is frequently inactivated via the following events: LOH, hypermethylation, deletion, mutation (4); this inactivation and loss of p16^{INK4A} expression defines a subgroup of patients with OPSCC with worse clinical outcome (5). p16^{INK4A} protein overexpression has been proposed as surrogate marker of HPV infection initially in cervical cancer (26), and subsequently the same concept was applied for squamous cell carcinomas from sites other than the uterine cervix (27), and especially in head and neck cancers (28).

However, the overall low specificity of p16^{INK4A} IHC for the diagnosis of high-risk HPV infection in recent series of patients (29) is certainly very different to what was observed for the cervix, in which virtually all SCCs are associated with high-risk HPV and p16^{INK4A} overexpression. In the HNSCC, more heterogeneous causative factors, such as as lifestyle (tobacco and smoke) and molecular profiles, contribute to the pathogenesis of the disease (30); therefore p16^{INK4A} overexpression may derive from different mechanisms other than HPV infection (31).

In our study, only 11 cases (13.1%) with HPV positivity on PCR overexpressed p16^{INK4A}, undermining the usefulness of p16^{INK4A} as a diagnostic surrogate for HPV infection in the oropharynx, which was the site previously was seen to have the highest concordance between IHC and PCR results (32).

In head and neck tumors, up to now, the only consistent clinical predictors for disease specific survival of patients with SCCs is TNM stage (33, 34). In spite of the histological homogeneity (most head and neck cancer cases are of SCC), there is a wide biological heterogeneity, and this contributes to a lack of consistency in treatment planning and in tumoral treatment response. The better characterization at a molecular level may better define homogeneous groups of patients for prognosis, as well as for responsiveness to treatments (35). The growing evidence of the prognostic significance of HPV status in OSCC (36, 37), indicating that HPV is associated with a better prognosis and an increased radiosensitivity, suggests that it can be used as a molecular marker in OPSCC.

Despite clinical advances, there exist no commercially available, validated, and universally accepted tests for the determination of tumor HPV status, nor any guidelines. With our study, we underline the need for a consensus on the methods to be used for HPV detection in OPSCC (20, 38) and we re-inforce the idea, proposed by other authors (29), that the gold standard for the identification of HPV infection in OPSCC should be the molecular method, at least for those with negative p16^{INK4A} immunostaining.

The main limit of this study was its retrospective design and the inclusion in the study of tumor tissue embedded in

paraffin 10 years before the analysis; in fact in 10 samples, HPV PCR detection was not feasible. However, the wide number of cases analyzed was the main strength of our study. Furthermore, we need prospective studies in this field and a consensus is mandatory for the cut-off used to define positivity of p16^{INK4A} by IHC because very little direct evidence exists for using it as a screening method for HPV detection, and only some authors have suggested algorithms for this purpose (22, 31, 39).

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