



Sinonasal Squamous Cell Carcinoma: Etiology, Pathogenesis, and the Role of Human Papilloma Virus

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Abstract

Purpose of Review Sinonasal squamous cell carcinoma (SNSCC) is a rare disease with considerable histologic diversity. Currently, there is a poor understanding of the etiology and pathogenesis of SNSCC. Here, we review recent literature to summarize what is known regarding (1) the etiology of SNSCC, (2) the role of Human Papilloma Virus (HPV) in SNSCC, and (2) the molecular underpinnings of SNSCC.

Recent Findings 1. High risk HPV appears to play a role in the pathogenesis of a subset of SNSCCs. SNSCCs with high risk HPV have improved survival compared with those without HPV and occur in patients who are younger, similar to HPV mediated oropharyngeal cancer. 2. A subset of inverted papillomas have transcriptionally active low-risk HPV and have a higher risk of transformation, while low risk HPV negative inverted papillomas frequently have EGFR mutations.

Summary SNSCC is a diverse disease with likely multiple etiologies including carcinogen, irritant exposure, and HPV. While not definitively proven, evidence supports a role for high-risk HPV in a subset of SNSCC, and low-risk HPV in a subset of inverted papillomas which transform to SNSCC. In-depth molecular and genomic studies are needed in SNSCC to better understand the genomic underpinnings and oncogenic drivers.

Keywords Sinonasal squamous cell carcinoma · HPV

Introduction

Squamous cell carcinoma (SCC) of the nasal and paranasal sinuses (SNSCC) is the most common histologic subtype of all sinonasal tumors, making up more than 50% of cases [1, 2]. SNSCCs arise from mucosal sites throughout the paranasal sinuses with contemporary literature supporting the most common originating site to be the nasal cavity, followed by maxillary sinus [3] (Table 1). The incidence of SNSCC in males is 0.52 cases per 100,000 patients, and females 0.23 cases per 100,000 patients, with a male to female incidence ratio of 1.85–2.26:1 [1, 2, 4–6]. While the incidence of

SNSCC is decreasing, 5-year overall survival (OS) rates have not changed appreciably over the last three decades, hovering around 50% [1–4]. This is in part due to the advanced stage of disease at diagnosis and high rate of local recurrence [7, 8]. When outcomes are sub-stratified by tumor site, patients with nasal cavity SCC have improved 5-year relative survival (RS) (74.5%) compared with patients with maxillary sinus SCC (35%) and ethmoid sinus SCC (33%) (Table 1). Frontal and sphenoid sinus SCC carry the worst prognosis with 5 year survival of ~30% [3, 9]. Worsened survival in these subsites, compared with nasal SCC, may be related to stage of presentation, difficulty accessing the tumors due to proximity to vital structures or, as discussed below, etiologic variability. Across all tumors, increased age, T and N classification is associated with worse overall survival (OS) [2, 9]. Smoking status is associated with worse outcomes in SNSCC, with current smokers having a decreased 5-year OS compared with reformed smokers [10]. Worse outcomes are also seen in patients with poor performance status and African American patients, similar to the HNSCC overall [9]. The incidence of SNSCC arising as a second primary in head and neck cancer patients is low (0.2%) [11]. Below, we will review current

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Table 1 SNSCC incidence and 5-year relative survival by site

Common sites of SNSCC	Incidence	Relative survival 5 years
Nasal cavity	46.5%	74.5%
Maxillary sinus	40.2%	35.0%
Ethmoid sinus	5.6%	33.0%
Not otherwise specified and accessory sinus	2.5%	31.2%
Sphenoid sinus	2.3%	30.0%
Overlapping lesions	1.6%	41.0%
Frontal sinus	1.1%	31.8%

Based on SEER data between 1973 and 2011 (5567 SNSCC patients) [3]

opinions on the etiology and pathogenesis of SNSCC, with an emphasis on emerging data assessing the role of human papilloma virus (HPV) in SNSCC.

Etiology

Carcinogen Exposure

Occupational hazards can explain some of the etiologic risk for SNSCC, as well as the male predominance [1, 4, 12]. For example, professionals with multi-year histories of working with wood, which is a designated human carcinogen, and more specifically softwood dust, have up to 20-times increased risk of developing SNSCC compared with the general population and compared with other sinonasal tumors [13–19]. Occupational exposure to several industrial compounds and chemical substances, such as leather dust, glues, formaldehyde, chrome, nickel, arsenic and welding fumes, and various compounds used in the textile industry, have been attributed to tumorigenesis in up to 30% of SNSCC [4, 15–17, 20–22]. Limited reports have also been published of SNSCC in hairdressers and rubber workers [23].

Historic case-control studies have analyzed the role of smoking in the development of SNSCC [24–28]. All suggest that smoking poses an increased risk for the development of SNSCC. Presence of a dose–response relationship in most studies and the decrease in risk associated with time since quitting, support the existence of a causal association [17]. Importantly, evidence suggests that smoking tobacco can increase the risk of SNSCC two to threefold which is significantly less than for many other tobacco-associated cancers [24, 29]. There is further evidence to support secondhand tobacco smoke exposure as a risk factor [18].

Viral Oncogenesis

HPV is well established as a causative etiology in a HNSCC [30]. Up to 80% of oropharyngeal SCC (OPSCC) are HPV mediated and ~5% of other upper aerodigestive tract subsites

as well [31, 32]. When evaluating tonsillar tissue subsites (lingual and palatine tonsils), up to 92% of cases are HPV mediated [32]. Importantly, HPV mediated OPSCC (HPVmOPSCC) is not only etiologically distinct from non-HPVmOPSCC but also epidemiologically and molecularly. For example, HPVmOPSCC is increasing in incidence, carries a significantly improved prognosis and lacks many of the driver mutations seen in non-HPVmOPSCC, such a TP53 [33]. The role of HPV in SNSCC is not established; however, emerging epidemiologic and molecular literature supports a potential role for HPV in a subset of SNSCC [34, 35].

HPV Prevalence in SNSCC

Recent retrospective studies and meta-analyses suggest that ~30% of SNSCC have HPV present, regardless of detection method [36, 37]. Firstly, it is important to recognize that different HPV detection methods (for example, In Situ Hybridization (ISH), DNA PCR, RNA PCR) have different analytic sensitivities. Briefly, HPV detection methods can be divided to:

- (i) Nucleic acids hybridization assays such as Southern blot, Dot Blot hybridization, and ISH. These techniques use labeled nuclei acid hybridization assays to detect HPV in samples. Although the specificity of this method is high, sensitivity can be lower, and less than that seen in PCR analysis [38]. However, ISH is more specific for HPV infection than p16 immunohistochemical staining (IHC) [39].
- (ii) Immunohistochemical staining (IHC). p16 protein is a surrogate marker of transcriptionally active HPV infection has been found to be highly sensitive yet less specific [40].
- (iii) Nucleic acids amplification assays such as Polymerase chain reaction (PCR). These assays commonly have primers designed to amplify a region of HPV DNA or mRNA and have high sensitivity [41, 42].
- (iv) Signal-amplification assays such as Hybrid Capture 2 (hc2) and the Cervista HPV. These assays use a non-

radioactive signal-amplification method based on the hybridization of the target HPV-DNA to labeled RNA probes in solution [41, 42].

HPV DNA is detected across many head and neck subsites by PCR; however, the detection of HPV DNA does not indicate causation as an oncogenic driver. Methods to assess transcriptional activity are assumed to more accurately assess if HPV may potentially be driving tumorigenesis, as opposed to a bystander infection, for example, the detection of HR-HPV E6 or E7 mRNA by RT-PCR, among other techniques. Combined detection techniques are also advocated for determining a potentially causative viral infection, such as detection of both 70% nuclear and cytoplasmic p16 expression and HR-HPV DNA by PCR or ISH (or RNA by RT-PCR or ISH) [43, 44].

Prevalence of HPV Genotypes in SNSCC

Fifteen oncogenic HPV genotypes are associated with mucosal tumors and include 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68, 73, and 82 [45]. Several studies have assessed HPV genotypes in SNSCC and found HPV-16 to be the most common, similar to other HPVmHNSCCs [34, 37, 45–49]. Less commonly identified genotypes are HPV-18, 31, and 33, again paralleling HPVmOPSCC [34, 37, 45, 50]. Rare cases of HPV 35, 39, 45, and 82 have also been reported [45]. Table 2 summarizes recent literature examining the prevalence of HPV in SNSCC, as well as the detection methodology. HPV prevalence also appears to vary by anatomic subsite within the sinonasal cavity with the nasal cavity having the highest prevalence (Table 3) [36].

Epidemiology and Demographics of HPV-Associated SNSCC

Numerous studies have examined of the epidemiology of SNSCC with and without HPV present in the tissue. These studies lack standardization for how HPV presence is detected making interpretation challenging. Overall, HPV-positive cases are associated with younger age patients (58.0 vs 63.7 years) similar to HPVmOPSCC [56]. However, unlike HPVmOPSCC, HPV positive SNSCC is more often found in patients who smoke, or are reformed smokers [49]. HPV positive SNSCC are less likely to be well-differentiated compared with SNSCC without HPV present [36]. Importantly, HPV positive SNSCC patients appear to have higher 5 years OS compared with HPV negative SNSCCs (68.1–80% vs 31–51.5%) [36, 46]. In a meta-analysis, Syrjänen et al. stratified the prevalence of HPV in SNSCC by the geographic origin and found the highest summary effect size (64.8%) is derived from studies reported in China, followed by those conducted in Europe 39.4%, and USA/Canada 32.9%, and Asia 22.7%

(Table 3)[37]. These results suggest SNSCC may differ in etiology by geography, similar to nasopharyngeal carcinoma [36, 37]. In a study published this year, Oliver et al reviewed the NCDB for SNSCC cases with HPV testing, finding again, that HPV is associated with younger age and improved OS [57].

HPV and SNSCC Histologic Subtypes

A portion of the heterogeneity reported in HPV prevalence in SNSCC may be explained by evaluation of different SNSCC subtypes. The presence of transcriptionally active HR-HPV varies for the various SCC subtypes in the sinonasal tract and is more frequently detected in nonkeratinizing SCC (NKSCC) compared with keratinizing (KSCC) (35–50% vs 4–25%, respectively) but is lower than in non-keratinizing OPSCC [36, 43, 46, 49, 58, 59]. Other SNSCC variants show even higher transcriptionally active HR-HPV prevalence, such as basaloid 46–56.5%; papillary 42–80% [36, 43] and adenosquamous carcinomas 66–83% [34, 43].

HPV in Sinonasal Papillomas

Sinonasal papillomas (SP) are benign epithelial neoplasms arising in the sinonasal tract and are histopathologically divided into three subtypes: (i) Inverted (ISP) 62%, (ii) exophytic (ESP) 32%, and (iii) oncocytic (OSP) 6% [60].

Inverted Sinonasal Papilloma

While ISPs are fundamentally benign, malignant transformation rates are reported as 1.9–11% [43, 60, 61]. The majority of carcinomas associated with ISP are present at the time of diagnosis (64%) while 36% are identified after initial treatment [61]. Most cases of carcinoma associated with ISP are SCC (75%), but rarely other tumor types such as sinonasal undifferentiated carcinoma or verrucous carcinoma have been described [61]. HPV in ISPs has been detected by different methods (DB—Dot Blot hybridization, SB—Southern Blot hybridization, ISH and PCR) with Low-risk HPV (LR-HPV) (6 and 11) being 2.8 times as frequent as HR-HPV (16 and 18) in ISP and ISP-associated SCC (ISPSCC) [62]. However, HR-HPV is more frequent in cases with high-grade dysplasia and carcinoma [54, 63]. A recent meta-analysis suggests that HPV-18 may be specifically associated with ISPSCC [64]. When examining the literature surrounding HPV and ISPs, there is enormous variability with reports using similar detection approaches reporting vastly different HPV detection rates. For example, HR- HPV mRNA was detected by ISH in 100% of ISPs by Stoddard et al. ($n = 19$) while Rooper et al reported 0% detection [65, 66]. Interestingly, Udager et al. have demonstrated that many ISPs (88%) and SNSCC arising from ISPs (77%), possess EGFR mutations while non ISP related

Table 2 Prevalence of HR-HPV infection in SNSCC by detection method and genotype

Authors and year	SNSCC cases	HPV + cases	HPV + %	Detection methods				HPV genotypes			
				p 16 IHC	HPV DNA ISH	HPV DNA PCR	HPV E6/E7 mRNA ISH	HPV E6/E7 mRNA PCR	HPV 16	HPV 18	HPV others
Laco et al. 2015 [49]	49	17	34%	16/49 (33%)	12/49 (24%)	8/42 (19%)	13/49 (26%)	8/46 (17%)	4/17 (23%)	5/17 (29%)	HPV-35 1/17 (5%); 7/17—Unknown
Yamashita et al. 2015 [47]	16	4	25%	1/4 (25%)	NA	4/16 (25%)	NA	NA	3/4 (75%)	1/4 (25%)	NA
Chung et al. 2015 [51]	26	14	53%	NA	NA	14/26 (53%)	NA	NA	NA	NA	NA
Doescher et al. 2015 [33]	44	3	(3/42) 7%	13/44 (29.5%)	9/44 (20.5%)	NA	NA	NA	NA	NA	NA
Becker 2016 [52]	39	4	10.8%	NA	NA	4/39 (10.8%)	NA	NA	3/4 (75%)	NA	NA
Chowdhury 2017 [45]	26	16	62%	17/19 (89%)	NA	16/26 (62%)	NA	NA	8/16 (50%)	2/16 (12.5%)	HPV-33 1/16 (6.25%); HPV-35 1/16 (6.25%); HPV-39 1/16 (6.25%); HPV-42 1/16 (6.25%); HPV-82 1/16 (6.25%)
Sahmane et al. 2018 [53]	12	1	8%	12/12 (100%)	1/12 (8%)	NA	NA	NA	NA	NA	NA
Ambreen et al. 2018 [50]	10	2	20%	NA	NA	2/10 (20%)	NA	NA	2/2 (100%)	1/2 (50%)	NA
Udager et al. 2018 [54•]	14	5	35.7%	NA	NA	5/14 (35.7%)	NA	NA	2/5 (40%)	1/5 (20%)	HPV-33 1/5 (20%); 1/5—Unknown
Bulane et al. 2019 [55]	25	4	16%	NA	NA	4/25 (16%)	NA	4/4 (100%)	1/4 (25%)	1/4 (25%)	HPV-45 2/4 (50%)

SNSCCs do not harbor EGFR mutations [67]. Further, the same group reported that all ISPs ($n = 58$) and ISPSCCs ($n = 22$) demonstrate either an EGFR mutation or HPV infection, and that HPV and EGFR mutation are mutually exclusive in all cases of ISPSCC. All paired ISP and ISPSCC samples demonstrated concordant HPV status, and EGFR genotypes and ISP progression to SNSCC were significantly associated with the presence of HPV infection and the absence of an EGFR mutation [54•]. In a study published this year, Mehrad et al. extended these findings, demonstrating that a subset of ISPs has transcriptionally active LR-HPV and that these lack EGFR mutations and have a higher risk of transformation. Similarly, LR-HPV negative ISPs frequently have EGFR mutations, further supporting the concept that EGFR mutations and LR-HPV infection are mutually exclusive [68••].

Oncocytic Sinonasal Papilloma

Malignant transformation occurs in 4–17% of OSPs, most of these being SCC [69]; however, mucoepidermoid, small cell, adenocarcinoma, and sinonasal undifferentiated carcinomas have also been described [70, 71]. In WHO 2017, and additional literature, HPV has not been found to be associated with OSP [70, 72, 73]. However, recent studies and meta-analysis found 22.5% of OSPs cases are HPV positive [62, 63]. Interestingly, a recent study identified KRAS alterations in OSP ($n = 51$) and OSP-associated SCC ($n = 5$) suggesting it is indeed a precursor lesion to SCC yet is biologically distinct from other SNSCCs [69].

Exophytic Sinonasal Papilloma

ESPs may also be etiologically related to HPV. In a large meta-analysis, ESPs were associated with HPV in 63.5% of cases, predominantly with low-risk HPV (6 and 11), and rarely with types 16 and 57 [62]. HPV status has not been shown to correlate with carcinoma development [73]. Malignant change in ESP is extremely rare [74]. In summary, while the majority of SNSCCs arise de novo, a subset arises from sinonasal papillomas. HPV DNA has clearly been demonstrated to be present in some papillomas; however, the role of HPV in this transformation process remains unclear.

HPV-Related Multiphenotypic Sinonasal Carcinoma

HPV related multiphenotypic sinonasal carcinoma with adenoid cystic-like features (HMSC) is a newly described entity under the category of NKSCC in the latest WHO classification [75]. HMSC has a high predisposition for local recurrence (–38%), has a female predominance and typically affects the nasal cavity (89%) with or without paranasal sinus involvement [76]. HMSC is associated with strong and diffuse p16 staining in all cases and Ki-67 staining in 40–90% [77, 78]. HMSC is by definition associated with high-risk HPV infection, with HPV-33 and HPV-35 being the most common genotypes [78–82] and less frequently HPV 56, 16 and 82 [78, 82, 83].

Pathogenesis

Unlike the remainder of mucosal HNSCCs (oral, oropharynx, larynx), in which the genomic landscape is well described, in large part, through The Cancer Genome Atlas (TCGA), the pathogenesis and genomic underpinnings of SNSCC remains poorly defined.

SNSCC Genomics

The genomic landscape of SNSCC is poorly defined. Here, we summarize what is known as follows:

- (i) Somatic mutations: TP53 mutations have been described in a significant portion of SNSCCs, particularly in those tumors associated with exposure to wood dust (70%) [14, 33]. Similar to other HNSCCs, patients with TP53 altered SNSCC appears to have worse OS (43.8% vs 84.1% 3-year OS) [33]. Mutations in KRAS and HRAS have been found in a small subset of SNSCCs and as noted above, KRAS alterations are particularly common in OSP associated SCC [69, 84, 85].
- (ii) Copy number alterations: Amplification of FGFR1 has been reported in 20% of SNSCC and in 33% carcinomas associated with ISP [65] while SOX2 amplification has been demonstrated in 37% of SNSCC cases and was

Table 3 SNSCC HPV positive prevalence by site and geographic origin [36, 37].

Prevalence of HPV by site	Percentage	Prevalence of HPV by geographic origin	Percentage
Nasal cavity	49.4%	China/Taiwan	64.8%
Maxillary sinus	18.8%	Europe	39.4%
Ethmoid sinus	18.8%	USA/Canada	32.9%
Frontal sinus	18.2%	Asia	22.7%

associated with significantly higher rate of tumor recurrences [86].

- (iii) Expression changes: p53 expression alterations have been reported in around 50% of SNSCCs [8, 87, 88]. Several studies have demonstrated EGFR overexpression in 40–89% of SNSCCs which was associated with significantly shorter disease-free survival and worse local recurrence rate [33, 88, 89]. Overexpression of HER2 (ErbB2) has also been detected in a subset of SNSCCs [88, 89]. Finally, overexpression of VEGFR-encoding gene has been reported in ~50% of SNSCCs [62, 90].
- (i) Genome instability: A possible factor involved in pathogenesis of SNSCCs is microsatellite instability (MSI). DNA mismatch repair deficiency has been reported to occur in 21% of SNSCC [91].
- (ii) Chromosomal aberrations: SNSCCs appear to have a number of chromosomal alterations [92]. One study identified losses occurring at 9p21, 13q14, 17p13, 17q21, and 18q11 with frequent gains observed on 8q24, 11q13, 17q12, 19p13, and 20q11–q13 [92] and resultant amplification of 7p12(EGFR), 11p13(CD44), 11q13(CCND1 and EMS1), and 17q21 (ERBB2)[92], with some of these common to HNSCC [93, 94].

SNSCC Immune Microenvironment

Immune checkpoint inhibitors (anti-PD-1) have dramatically altered treatment paradigms for advanced HNSCC; however, initial clinical trials leading to their approval did not include SNSCC [95][96]. In HNSCC, tumors expressing PD-L1 have improved response rates compared with non-PD-L1 positive tumors [96]. Riobello et al. evaluated the prevalence of PD-L1 expression in 96 SNSCC tumors, observing that 17%, 30%, and 50% of tumors have >50%, 5%, and 1% membranous PD-L1 staining of tumor cells, respectively [7•]. Our institutional experience ($n = 11$ patients) with advanced SNSCC treated with anti-PD-1 therapy is that response rates are at least equivalent to other HNSCCs (unpublished). Considering the poor survival of patients with recurrent or metastatic SNSCC, studies are needed to evaluate the efficacy of anti-PD-1 treatment.

Conclusions

SNSCC is a complex disease with likely numerous etiologic subtypes and processes driving tumorigenesis. The molecular underpinnings, etiology, and pathogenesis of SNSCC is significantly understudied and remains poorly understood compared with other HNSCCs. Current literature supports a role for HPV in SNSCC, yet the size of this contribution and

effects on outcomes require significantly more dissection. High-quality studies that aim to rigorously interrogate SNSCC molecular etiology and pathogenesis are greatly needed.

Compliance with Ethical Standards

Conflict of Interest Katya Elgart and Daniel L. Faden declare that they have no conflict of interest.

Human and Animal Rights and Informed Consent This article does not contain any studies with human or animal subjects performed by any of the authors.

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