

Assessment of Human Papillomavirus in Lung Tumor Tissue

Jill Koshiol, Melissa Rotunno, Maura L. Gillison, Leen-Jan Van Doorn, Anil K. Chaturvedi, Letizia Tarantini, Hebin Song, Wim G. V. Quint, Linda Struijk, Alisa M. Goldstein, Allan Hildesheim, Philip R. Taylor, Sholom Wacholder, Pietro Alberto Bertazzi, Maria Teresa Landi, Neil E. Caporaso

Manuscript received July 6, 2010; revised December 13, 2010; accepted December 30, 2010.

Correspondence to: Jill Koshiol, PhD, Infections and Immunoepidemiology Branch, Division of Cancer Epidemiology and Genetics, National Cancer Institute, 6120 Executive Blvd, Rm 7070, Bethesda, MD 20892-7248 (e-mail: koshiolj@mail.nih.gov).

Background Lung cancer kills more than 1 million people worldwide each year. Whereas several human papillomavirus (HPV)-associated cancers have been identified, the role of HPV in lung carcinogenesis remains controversial.

Methods We selected 450 lung cancer patients from an Italian population-based case-control study, the Environment and Genetics in Lung Cancer Etiology. These patients were selected from those with an adequate number of unstained tissue sections and included all those who had never smoked and a random sample of the remaining patients. We used real-time polymerase chain reaction (PCR) to test specimens from these patients for HPV DNA, specifically for E6 gene sequences from HPV16 and E7 gene sequences from HPV18. We also tested a subset of 92 specimens from all never-smokers and a random selection of smokers for additional HPV types by a PCR-based test for at least 54 mucosal HPV genotypes. DNA was extracted from ethanol- or formalin-fixed paraffin-embedded tumor tissue under strict PCR clean conditions. The prevalence of HPV in tumor tissue was investigated.

Results Specimens from 399 of 450 patients had adequate DNA for analysis. Most patients were current (220 patients or 48.9%) smokers, and 92 patients (20.4%) were women. When HPV16 and HPV18 type-specific primers were used, two specimens were positive for HPV16 at low copy number but were negative on additional type-specific HPV16 testing. Neither these specimens nor the others examined for a broad range of HPV types were positive for any HPV type.

Conclusions When DNA contamination was avoided and state-of-the-art highly sensitive HPV DNA detection assays were used, we found no evidence that HPV was associated with lung cancer in a representative Western population. Our results provide the strongest evidence to date to rule out a role for HPV in lung carcinogenesis in Western populations.

J Natl Cancer Inst 2011;103:501-507

More than 1 million people die of lung cancer each year (1). Although smoking is the major etiologic factor, most smokers will not develop lung cancer (2), indicating that additional cofactors are needed for lung carcinogenesis. Lung cancer is also a major cause of cancer deaths even among never-smokers (3).

Certain types of human papillomavirus (HPV) are firmly established as human carcinogens. These HPV types cause essentially all human cervical cancers (4,5) and are strongly implicated in the etiology of a substantial proportion of other anogenital cancers (6) and oropharyngeal cancers (7,8). HPV has been hypothesized to play a role in lung cancer pathogenesis, largely on the basis of more than 50 studies (9,10) in which HPV genomic DNA was detected in 0%–100% (median = 16.7%) of lung tumor tissues. However, these studies are not definitive because of power constraints, restricted study populations, use of nonspecific and/or insensitive laboratory approaches, and use of HPV detection techniques that are limited to regions of the viral genome that may be lost with viral

integration into the cellular host DNA. Although geographic differences in the prevalence of HPV could potentially explain some variability in study results, interlaboratory variability and inadequate sample collection and handling leading to contamination may also contribute to the variability in reported results (10). Therefore, the role of HPV in lung carcinogenesis remains unclear.

Part of the reason why HPV is hypothesized to be associated with lung carcinogenesis is because the respiratory tract is in close proximity to the oropharynx, where HPV is known to cause a substantial proportion of cancers (7,8). HPV has been detected in respiratory papillomas, which are sometimes found in the bronchi and occasionally progress to malignancy, and also has been detected in respiratory tumors, as noted above (9,10). In addition, HPV can transform bronchial cells *in vitro* (11).

Furthermore, cervical cancer survivors and immunosuppressed populations are at increased risk for lung cancer and established HPV-related malignancies (12–14). Although smoking is an

CONTEXT AND CAVEATS

Prior knowledge

Human papillomavirus (HPV) is associated with cervical and oropharyngeal cancers. A role for HPV in lung cancer has been proposed, although previous reports of HPV in lung tumor tissue have been inconclusive.

Study design

Paraffin-embedded tissue specimens from 450 lung cancer patients who were smokers or never-smokers enrolled in the Environment and Genetics in Lung Cancer Etiology study were evaluated for HPV DNA by real-time polymerase chain reaction to determine the HPV prevalence in tissues from lung cancer patients in a representative Western population.

Contribution

Two specimens were found to be HPV positive at low copy number but were negative on additional genotype-specific testing and on testing for a broad spectrum of HPV types. The study found no evidence to support an association between HPV and lung cancer.

Implications

HPV is not associated with lung carcinogenesis in lung cancer patients from a representative Western population.

Limitations

Multiple tissue specimens were used from each patient for analysis and were not necessarily adjacent to or from the same paraffin block. Also, the possible contamination of specimens during collection could not be determined. Because of geographic variances in the prevalence of HPV reported in lung tumors, further studies in non-Western populations should be completed.

From the Editors

established cofactor for cervical squamous cell carcinoma, it is not associated with an increased risk of cervical adenocarcinoma (15). However, cervical adenocarcinoma survivors have approximately twofold increased risk of lung cancer (16). In addition, HIV–AIDS patients, who have an increased risk of HPV and HPV-related malignancies (17), also have an increased risk of lung cancer that has not been completely accounted for by increased smoking (13). These epidemiological data are consistent with a hypothesis that HPV contributes to respiratory carcinogenesis in a smoking-independent manner.

A difficulty with the hypothesis that HPV is a lung carcinogen is the fact that HPV is not generally transmitted as an aerosol, making transmission to the lung difficult (18). However, the existence of rare recurrent respiratory papillomatosis demonstrates that HPV can reach the respiratory tract. In addition, recurrent respiratory papillomatosis shows a second peak in young adults aged approximately 20 years (19) that is associated with oral sex and number of lifetime sex partners (20), consistent with sexual transmission. The oral cavity, in which HPV infections are established largely through sexual transmission (21), may act as a reservoir for transmission of HPV to the respiratory tract, possibly through aspiration or mucosal transfer. The probability of such transmission may be exceedingly low, however, considering the rarity of recurrent respiratory papillomatosis.

The goal of our study was to complete a more definitive evaluation of HPV in lung cancer. We tested for the presence of HPV DNA with highly sensitive polymerase chain reaction (PCR) and took rigorous precautions against PCR contamination in tumor tissues from 450 lung cancer patients from the well-characterized population-based case–control study, Environment and Genetics in Lung Cancer Etiology (EAGLE).

Materials and Methods

Study Population

EAGLE is a large population-based case–control study with 2100 lung cancer patients that was designed to investigate the genetic and environmental determinants of lung cancer and smoking persistence (22). As previously described (22), individuals with newly diagnosed lung cancer were recruited from April 22, 2002, to February 28, 2005, from 13 hospitals in the Lombardy region of Italy (see Notes). Each participant provided written informed consent. The study was approved by the institutional review board of each participating hospital and university in Italy and by the National Cancer Institute, Bethesda, MD. Lung cancer was diagnosed by standard clinical criteria and confirmed by pathology reports from surgery, biopsy, or cytology samples (approximately 95% of patients) or through clinical history and imaging (approximately 5% of patients) (22). Tumor histology was classified by the 1999 World Health Organization Histological Typing of Lung and Pleural Tumors (23). The 13 Italian hospitals treat approximately 80% of all patients with newly diagnosed lung cancer in the area, which includes more than 1.3 million people aged 35–79 years from five cities and surrounding towns and villages. EAGLE had a participation rate of 86.6% among lung cancer patients. Thus, participants in the EAGLE study should be broadly representative of lung cancer patients in Western populations.

We decided to test 450 adult male and female lung cancer patients, including all 30 never-smokers and a random sample of 420 smokers who had an adequate number of unstained tissue slides and at least one slide available that was stained with hematoxylin and eosin. These stained slides were reviewed by H. Song to establish the presence and estimate proportion of tumor tissue in the sample, but these slides were not necessarily adjacent to the tissue that was tested for HPV DNA. The samples were formalin fixed for 399 patients and ethanol fixed for 51 patients.

HPV DNA Testing

All 450 patients were tested for HPV16 and HPV18 DNA because these are the most common types found in cervical cancer (24) and account for the overwhelming majority of noncervical HPV-associated cancers (25). Type-specific PCR for HPV16 and HPV18 was conducted in a laboratory at the Ohio State University, as described below. For a subset of 100 patients including all never-smokers and a random selection of smokers, a second tissue specimen was sent to DDL Diagnostic Laboratory (Voorburg, the Netherlands) for broad-spectrum HPV typing.

Type-Specific PCR for HPV16 and HPV18. All specimen receipt, processing, and pre-amplification analysis procedures were performed in ultraviolet light–irradiated laminar flow hoods in a

Ohio State University were taken. All pre-amplification procedures were performed in ultraviolet light-irradiated laminar flow hoods that were separate from a postamplification analysis laboratory. During DNA isolation, PCR amplification, and post-PCR analyses, specific negative (water blank) and positive (HPV DNA extracted from the HPV18-positive HeLa cell line) controls were included. We monitored potential contamination of samples with negative controls and the sensitivity of the procedure with low-concentration positive controls. All reagents had been prepared in a separate reagent laboratory and subjected to strict quality control to confirm efficacy and the absence of contaminants.

DNA amplification by PCR with SPF₁₀ primers was followed by a reverse hybridization line-probe assay (LiPA₂₅, version 1; Labo Bio-Medical Products, Rijswijk, the Netherlands) for genotyping of 25 HPV types in SPF₁₀- and DEIA-positive samples. These primers produce very short PCR fragments of approximately 65 bp, making them ideal for amplification in formalin-fixed specimens (29–31). Eight specimens did not appear to have tumors in the tissue specimen received for testing. DNA was extracted for 92 specimens (from 65 ever-smokers and 27 never-smokers) with identifiable tumor in the tissue specimen. For each specimen, half of the tissue section was removed from the slide with a swab after confirming the presence of tumor cells in that part of the section. This part of the tissue was transferred to a microtube (Sarstedt, Etten-Leur, the Netherlands) and digested with proteinase K buffer (45 mM Tris-HCl at pH 8, 0.9 mM EDTA, 0.45% Tween 20, and proteinase K at 1 mg/mL). Proteinase K solution (100 µL) was added to each microtube and incubated for 16–24 hours at 56°C. Proteinase K solution was inactivated by incubating the tubes at 95°C for 10 minutes. Resulting DNA preparations were stored at –20°C. During this process, negative and positive DNA isolation controls were included. In these samples, DNA quality and quantity were adequate as measured by real-time PCR for the human β-actin gene in the same DNA specimens as used for the SPF₁₀ PCR. For one patient (a current smoker) where additional investigation was warranted due to weak HPV16 positivity in the sample tested at the Ohio State University, type-specific PCR for HPV16 was performed with a 92-bp amplicon as previously described (32).

Statistical Analysis

Our goal in determining sample size was to be able to rule out a true HPV prevalence greater than 1.0%. Using *cii* in Stata (StataCorp LP, College Station, TX), we determined that zero HPV positives among 450 lung cancer patients would generate a one-sided 97.5% confidence interval (CI) of 0% to 0.82% and that one observed HPV-positive patient among 450 lung cancer patients would provide a two-sided 95% confidence interval of 0.0056% to 1.2%; zero positives among 400 lung cancer patients would provide a one-sided 97.5% confidence interval of 0% to 0.92%, and one observed HPV-positive patient would provide a two-sided 95% confidence interval of 0.0063% to 1.4%. The chance of finding at least one positive when the true prevalence is 1.0% or more was 98.9% with a sample size of 450 patients; thus, finding no positives with a sensitive assay rules out even a low prevalence of infection with high confidence.

In addition to the sample size calculations described above, we used the *cii* command in Stata (StataCorp LP), version 9.0, to estimate HPV prevalence and corresponding confidence intervals.

Results

Among the 450 lung cancer patients, 246 (54.7%) had adenocarcinoma and 137 (30.4%) had squamous cell carcinoma (Table 1). Most patients had a history of tobacco smoking: 220 patients (48.9%) were current smokers, 198 patients (44.0%) were former smokers, and 30 patients (6.7%) were never-smokers. The median age at diagnosis of lung cancer was 67.6 years (range = 35.4–79.9 years), and the median body mass index was 25.3 kg/m² (range = 15.9–60.8 kg/m²). Among smokers, the median duration of smoking was 45 years (range = 1–70 years), the median average smoking intensity was one pack per day (range = 0–3 packs per day), the median pack-years was 43.8 (range = 0.1–192 pack-years), and the median age at initiation of smoking was 16 years of age (range = 6–45 years). Ninety-two patients (20.4%) were women. The majority of patients had less than a high school education (72.5% or 319 patients), drank alcohol (84.3% or 365 patients), were married or cohabitating (82.2% or 356 patients), had abnormal respiratory

Table 1. Characteristics of 450 lung cancer patients from the population-based case-control Environment and Genetics in Lung cancer Etiology study, including histology, smoking status, and human papillomavirus (HPV) status

Lung cancer histology	Smoking status, No. (%)				HPV DNA status by PCR* testing, No. (% HPV positive)	
	Never	Former	Current	Unknown	Type-specific HPV16 and HPV18†	Broad-spectrum HPV typing‡
Adenocarcinoma (n = 246)	25 (83.3)	103 (52.0)	117 (53.2)	1 (50.0)	221 (0.0)	63 (0.0)
Squamous cell (n = 137)	2 (6.7)	68 (34.3)	66 (30.0)	1 (50.0)	123 (0.0)	27 (0.0)
Large cell (n = 30)	1 (3.3)	10 (5.1)	19 (8.6)	0 (0.0)	24 (0.0)	0 (0.0)
Small cell (n = 13)	0 (0.0)	5 (2.5)	8 (3.6)	0 (0.0)	11 (0.0)	0 (0.0)
Other (n = 24)§	2 (6.7)	12 (6.1)	10 (4.5)	0 (0.0)	20 (0.0)	2 (0.0)

* PCR = polymerase chain reaction.

† Results from 399 specimens with adequate DNA of 450 selected for testing.

‡ Results from 92 specimens with tumor present in the sample of 100 selected for testing.

§ Includes mixed type (adenosquamous, n = 10), synchronous (two different lung cancers, n = 6), non-small cells (n = 2), and other (including poorly differentiated, epithelial, neuroendocrine, mucoepidermoid, non-small cell, pleomorphic, sarcomatoid, n = 6).

function (51.7% or 186 patients), and had stage IIB disease or less (71.3% or 321 patients) (Table 2).

The median number of cells evaluable for the HPV16 and HPV18 PCR as measured by ERV3 real-time PCR was 3680 cells (range = 1.9–399750 cells). One specimen was negative for ERV3. The median 260/280 ratio was 1.63 (range = 1.23–1.94). Combining these data, 399 (88.7%) of 450 specimens had adequate DNA quantity and quality for analysis (ie, 100 or more cell equivalents and a 260/280 ratio between 1.5 and 2.2). On review of the 450 slides that were stained with hematoxylin and eosin, 412 specimens contained tumor cells. Of those tumor-positive specimens, 73.8% (n = 304 specimens) contained greater than 60% tumor. We included all specimens with adequate DNA (n = 399 specimens) in the prevalence estimate.

Table 2. Descriptive characteristics of 450 lung cancer patients from the population-based case-control Environment and Genetics in Lung cancer Etiology study*

Characteristic	No. of patients (% of total)
Age, y	
<60	93 (20.7)
60–69	181 (40.2)
≥70	176 (39.1)
Sex	
Male	358 (79.6)
Female	92 (20.4)
Area of Italy	
Brescia	72 (16.0)
Milano	268 (59.6)
Monza	54 (12.0)
Pavia	22 (4.9)
Varese	34 (7.6)
Education†	
None	27 (6.1)
Elementary school	161 (36.6)
Middle school	131 (29.8)
High school (teaching training, job training, college training)	105 (23.9)
University degree (bachelor, master, PhD)	16 (3.6)
Alcohol consumption†	
No	68 (15.7)
Yes	365 (84.3)
Marital status†	
Married or cohabitating	356 (82.2)
Neither married nor cohabitating	77 (17.8)
Spirometry-based respiratory function†	
Normal	174 (48.3)
Mild COPD	51 (14.2)
Moderate COPD	68 (18.9)
Severe and very severe COPD	17 (4.7)
Potentially restrictive disease	50 (13.9)
Stage	
IA	84 (18.7)
IB	126 (28.0)
IIA	14 (3.1)
IIB	97 (21.6)
IIIA	58 (12.9)
IIIB	43 (9.6)
IV	28 (6.2)

* COPD = chronic obstructive pulmonary disease.

† Numbers do not sum to total because of missing values.

Among the 399 specimens with adequate DNA, one female former smoker with adenocarcinoma was positive for HPV16 on initial testing. Given the very low viral load in this tumor (average = 0.4 per 1000 cell equivalents across three tests of the same sample), we tested another tumor tissue specimen from this patient. We found no evidence of HPV16 or HPV18 DNA in this second specimen. The hematoxylin–eosin slide from this specimen consisted of greater than 80% cancer cells, indicating there was adequate tumor available to detect any HPV DNA if it were present. This patient was diagnosed with stage IB lung cancer at 72 years of age and had smoked for 48 years at an average intensity of 0.75 packs per day (36 pack-years).

PCR analysis targeting an 81-bp amplicon in the HPV16 E6 region confirmed the prior positive test (average of two viral copies per 1000 cell equivalents) in the first sample, and the second tumor tissue specimen from this patient was again negative. Another patient who was initially negative for HPV16 tested positive with this assay but at low copy number (131 per 1000 cell equivalents). This second patient was a male with squamous cell carcinoma diagnosed at 64 years of age who had smoked for 43 years at an average intensity of one pack per day (43 pack-years). The hematoxylin–eosin slide from this patient also contained greater than 80% cancer cells.

In the subset of 92 specimens tested with the broad-spectrum assay SPF₁₀-DEIA-LiPA₂₅ (including those from the two patients who tested positive with low viral load, as described above), no specimens were positive for HPV16 DNA or for any HPV type. DDL Diagnostic Laboratory conducted type-specific testing for HPV16 as a follow-up test for the male patient identified as being HPV positive by PCR analysis targeting an 81-bp amplicon in the HPV16 E6 region. The specimen tested negative for HPV DNA with this type-specific test. These results indicate that the prevalence of HPV DNA is 0.0% (Table 1) with an upper 97.5% confidence interval of 0.92% for the 399 specimens with adequate DNA, including 370 ever-smokers (upper 97.5% confidence bound = 0.99%) and 27 never-smokers (upper 97.5% confidence bound = 12.8%).

Discussion

In this study, which is to our knowledge the largest study of HPV in lung tumor tissue from a Western country, we found no evidence that HPV is associated with lung carcinogenesis. Extensive laboratory efforts to avoid DNA contamination and state-of-the-art, highly sensitive HPV DNA detection assays were performed. The two tumors that tested positive had a very low viral load of less than one copy of HPV16 per cell, despite being composed of greater than 80% tumor cells. One of these patients tested negative in a separate tissue specimen, and the other was negative on additional type-specific HPV16 testing in a separate sample. None of the subset of 92 patients was positive for any other HPV type by the very sensitive SPF₁₀-DEIA-LiPA₂₅ testing method. HPV-related carcinogenesis at other anatomical sites indicates that HPV should be present in every tumor cell if it truly contributed to the development of that tumor (25). Thus, whereas low-level HPV positivity in one tissue sample and complete lack of HPV in a separate sample may be possible, such tumor heterogeneity is unlikely

to reflect a truly causal association. On the basis of these results, the prevalence of HPV in lung tumor tissue from this population was essentially 0%.

A limitation of this study was that the tissue specimens were not necessarily adjacent or from the same block, although as described above, lack of uniform HPV results throughout the tumor would suggest that HPV was not associated with tumorigenesis. Because tissue was collected for diverse purposes, it was not possible to address contamination in specimen collection. However, all laboratory assays were performed under stringent precautions to avoid contamination. We also used viral load to assess whether detected HPV DNA was present at a meaningful level, as described above. Although DNA degradation may occur in paraffin-embedded tissues, DNA quality was confirmed by satisfactory 260/280 ratio and real-time PCR for the human β -actin gene and/or ERV-3 in 399 of the 450 specimens. These results indicate that the contamination precautions used during PCR analysis were largely sufficient to avoid contamination and that the DNA from the paraffin-embedded tissues was adequate for HPV DNA detection.

A particular strength of this study was that two independent laboratories extracted DNA (at the Ohio State University using phenol-chloroform extraction and at DDL Diagnostic Laboratories using crude extraction methods, as described in "Materials and Methods") from different tissue specimens from the same patient and conducted separate PCR assays for HPV DNA. All 450 specimens were tested for the E6 and E7 oncogenes of HPV16 and HPV18, the two types most strongly associated with cancer outside the cervix (25), which circumvented concerns about false-negative results because of loss of the L1 gene through integration. A substantial proportion (92 specimens from 450 lung cancer patients) was tested for a broad range of HPV types with the L1-based SPF₁₀-DEIA-LiPA₂₅ system. The SPF₁₀-DEIA-LiPA₂₅ system is the gold standard for HPV DNA testing in paraffin-embedded tissue because of its short PCR product (31) and ensured that specimens were tested for all carcinogenic and many noncarcinogenic HPV types.

Geographic differences in the prevalence of HPV in lung tumor tissue may be associated with variation in smoking habits, sexual behaviors, or other factors related to environmental exposures, culture, topography, or genetics (10). Asian studies typically report higher PCR-based HPV prevalences of HPV in lung tumors than European studies, with a summary meta-estimate of 11.6% (95% CI = 9.5% to 14.2%) for HPV16 and 8.8% (95% CI = 6.0% to 12.8%) for HPV18 in lung tumor tissues from Asia compared with 3.5% (95% CI = 2.3% to 5.3%) for HPV16 and 3.6% (95% CI = 2.3% to 5.7%) for HPV18 in lung tumor tissues from Europe (10). The largest PCR-based Asian studies found HPV DNA in 42.0% (n = 92 specimens, 95% CI = 35.6% to 48.6%) of 219 paraffin-embedded lung tumor tissues (33,34) and 44.1% (n = 138 specimens, 95% CI = 38.5% to 49.8%) of 313 fresh-frozen lung tumor tissues (10,35). Similar to our study, the largest previous European PCR-based study from France found a very low prevalence of HPV DNA in 218 fresh-frozen lung tumor tissues (1.8% prevalence, 95% CI = 0.7% to 4.8%, n = 4 positive samples) (10,36). Part of this geographic discrepancy may be because of differences in smoking habits. For example, Asian women typically do not smoke. A study of lung cancer in Taiwan

found that nonsmoking female lung cancer patients were more likely to have HPV-positive lung tumor tissue than male lung cancer patients, who were more likely to smoke (37). Environmental tobacco exposure is unlikely to account entirely for the increased risk in never-smokers. Non-smoking-related factors must therefore contribute to lung cancer among never-smokers. Given the high upper confidence limit of our prevalence estimate in never-smokers (12.8%), further study of HPV in lung tumor tissue from never-smokers may be warranted.

Nevertheless, the prevalence of HPV can vary markedly within the same country. For example, the PCR-based prevalence of HPV in lung tumor tissues from Japan ranges from 0.0% to 78.3% (10). Although we found essentially no HPV in lung tumor tissues from Italy, others have reported 12.8%–21.1% HPV DNA positivity in Italian lung cancer patients (10). Such disparities within the same geographic region emphasize the importance of taking precautions to avoid PCR contamination and prevent false-positive results (38) when using sensitive HPV DNA detection assays to avoid false-negative results. Our study used such precautions in two independent laboratories, verified DNA quality before HPV detection, and used multiple sensitive methods for HPV DNA detection. Although a few previous Asian and European studies have found 0% prevalence of HPV in lung tumor tissues, these studies included less than 100 patients. With nearly 400 patients evaluated, we had a sufficient sample size to detect any true prevalence of HPV greater than 1%. Our study was twice as large as the next largest study in Europe (n = 218 specimens).

In conclusion, using multiple state-of-the-art methods to evaluate the presence of HPV DNA in resected lung cancer tumors from a representative Western study population, we found no evidence that HPV is associated with the development of lung cancer. Although we detected essentially no HPV in specimens from the EAGLE study, evaluation in a larger population of never-smokers, in which the attributable risk of non-smoking-related risk factors is necessarily higher, may be informative. Differences in smoking habits could potentially account for the higher prevalence of HPV DNA detected in lung tumor tissue from Asian countries. For Western populations, however, this study found no data to support that HPV is associated with lung carcinogenesis.

References

1. Parkin DM, Bray F, Ferlay J, Pisani P. Global cancer statistics, 2002. *CA Cancer J Clin*. 2005;55(2):74–108.
2. Thun MJ, Henley SJ, Calle EE. Tobacco use and cancer: an epidemiologic perspective for geneticists. *Oncogene*. 2002;21(48):7307–7325.
3. Sun S, Schiller JH, Gazdar AF. Lung cancer in never smokers—a different disease. *Nat Rev Cancer*. 2007;7(10):778–790.
4. Bosch FX, de Sanjose S. The epidemiology of human papillomavirus infection and cervical cancer. *Dis Markers*. 2007;23(4):213–227.
5. Walboomers JM, Jacobs MV, Manos MM, et al. Human papillomavirus is a necessary cause of invasive cervical cancer worldwide. *J Pathol*. 1999;189(1):12–19.
6. Munoz N, Castellsague X, de Gonzalez AB, Gissmann L. Chapter 1: HPV in the etiology of human cancer. *Vaccine*. 2006;24S3(23):S1–S10.
7. Kreimer AR, Clifford GM, Boyle P, Franceschi S. Human papillomavirus types in head and neck squamous cell carcinomas worldwide: a systematic review. *Cancer Epidemiol Biomarkers Prev*. 2005;14(2):467–475.
8. Marur S, D'Souza G, Westra WH, Forastiere AA. HPV-associated head and neck cancer: a virus-related cancer epidemic. *Lancet Oncol*. 2010;11(8):781–789.

9. Giuliani L, Favalli C, Syrjanen K, Ciotti M. Human papillomavirus infections in lung cancer. Detection of E6 and E7 transcripts and review of the literature. *Anticancer Res*. 2007;27(4C):2697–2704.
10. Srinivasan M, Taioli E, Ragin CC. Human papillomavirus type 16 and 18 in primary lung cancers—a meta-analysis. *Carcinogenesis*. 2009;30(10):1722–1728.
11. Willey JC, Broussoud A, Sleemi A, et al. Immortalization of normal human bronchial epithelial cells by human papillomaviruses 16 or 18. *Cancer Res*. 1991;51(19):5370–5377.
12. Caporaso NE, Dodd KW, Tucker MA, et al. Chapter 6: new malignancies following cancer of the respiratory tract. In: Curtis RE, Freedman DM, Ron E, eds. *New Malignancies Among Cancer Survivors: SEER Cancer Registries, 1973–2000*. Bethesda, MD: National Cancer Institute; 2006:145–179. NIH Publication 05–5302.
13. Chaturvedi AK, Pfeiffer RM, Chang L, et al. Elevated risk of lung cancer among people with AIDS. *AIDS*. 2007;21(2):207–213.
14. Kalliala I, Dyba T, Nieminen P, Hakulinen T, Anttila A. Mortality in a long-term follow-up after treatment of CIN. *Int J Cancer*. 2010;126(1):224–231.
15. International Collaboration of Epidemiological Studies of Cervical Cancer. Comparison of risk factors for invasive squamous cell carcinoma and adenocarcinoma of the cervix: collaborative reanalysis of individual data on 8,097 women with squamous cell carcinoma and 1,374 women with adenocarcinoma from 12 epidemiological studies. *Int J Cancer*. 2007;120(4):885–891.
16. Chaturvedi AK, Kleinerman RA, Hildesheim A, et al. Second cancers after squamous cell carcinoma and adenocarcinoma of the cervix. *J Clin Oncol*. 2009;27(6):967–973.
17. Heard I. Prevention of cervical cancer in women with HIV. *Curr Opin HIV AIDS*. 2009;4(1):68–73.
18. Gillison ML, Shah KV. Chapter 9: role of mucosal human papillomavirus in nongenital cancers. *J Natl Cancer Inst Monogr*. 2003;31:57–65.
19. Shykhon M, Kuo M, Pearman K. Recurrent respiratory papillomatosis. *Clin Otolaryngol Allied Sci*. 2002;27(4):237–243.
20. Kashima HK, Shah F, Lyles A, et al. A comparison of risk factors in juvenile-onset and adult-onset recurrent respiratory papillomatosis. *Laryngoscope*. 1992;102(1):9–13.
21. Gillison ML. Current topics in the epidemiology of oral cavity and oropharyngeal cancers. *Head Neck*. 2007;29(8):779–792.
22. Landi MT, Consonni D, Rotunno M, et al. Environment And Genetics in Lung cancer Etiology (EAGLE) study: an integrative population-based case-control study of lung cancer. *BMC Public Health*. 2008;8:203–213.
23. Travis WD, Colby TV, Corrin B, Shimosato Y, Brambilla E. *Histological Typing of Lung and Pleural Tumors*. 3rd ed. Berlin, Germany: Springer; 1999.
24. Smith JS, Lindsay L, Hoots B, et al. Human papillomavirus type distribution in invasive cervical cancer and high-grade cervical lesions: a meta-analysis update. *Int J Cancer*. 2007;121(3):621–632.
25. Gillison ML, Chaturvedi AK, Lowy DR. HPV prophylactic vaccines and the potential prevention of noncervical cancers in both men and women. *Cancer*. 2008;113(10 suppl):3036–3046.
26. Yuan CC, Miley W, Waters D. A quantification of human cells using an ERV-3 real time PCR assay. *J Virol Methods*. 2001;91(2):109–117.
27. Baay MF, Verhoeven V, Lambrechts HA, et al. Feasibility of collecting self-sampled vaginal swabs by mail: quantity and quality of genomic DNA. *Eur J Clin Microbiol Infect Dis*. 2009;28(11):1285–1289.
28. Gravitt PE, Peyton C, Wheeler C, et al. Reproducibility of HPV 16 and HPV 18 viral load quantitation using TaqMan real-time PCR assays. *J Virol Methods*. 2003;112(1–2):23–33.
29. Kleter B, van Doorn LJ, ter Schegget J, et al. Novel short-fragment PCR assay for highly sensitive broad-spectrum detection of anogenital human papillomaviruses. *Am J Pathol*. 1998;153(6):1731–1739.
30. Kleter B, van Doorn LJ, Schrauwen L, et al. Development and clinical evaluation of a highly sensitive PCR-reverse hybridization line probe assay for detection and identification of anogenital human papillomavirus. *J Clin Microbiol*. 1999;37(8):2508–2517.
31. Gravitt PE, Viscidi R. Chapter 5: measurement of exposure to human papillomaviruses. In: Rohan TE, Shah KV, eds. *Cervical Cancer: From Etiology to Prevention (Cancer Prevention-Cancer Causes)*. Boston, MA: Kluwer Academic Publishers; 2004:119–141.
32. van Doorn LJ, Molijn A, Kleter B, Quint W, Colau B. Highly effective detection of human papillomavirus 16 and 18 DNA by a testing algorithm combining broad-spectrum and type-specific PCR. *J Clin Microbiol*. 2006;44(9):3292–3298.
33. Miyagi J, Kinjo T, Tshako K, et al. Extremely high Langerhans cell infiltration contributes to the favourable prognosis of HPV-infected squamous cell carcinoma and adenocarcinoma of the lung. *Histopathology*. 2001;38(4):355–367.
34. Miyagi J, Tshako K, Kinjo T, Iwamasa T, Hirayasu T. Recent striking changes in histological differentiation and rate of human papillomavirus infection in squamous cell carcinoma of the lung in Okinawa, a subtropical island in southern Japan. *J Clin Pathol*. 2000;53(9):676–684.
35. Wang Y, Wang A, Jiang R, et al. Human papillomavirus type 16 and 18 infection is associated with lung cancer patients from the central part of China. *Oncol Rep*. 2008;20(2):333–339.
36. Coissard CJ, Besson G, Polette MC, et al. Prevalence of human papillomaviruses in lung carcinomas: a study of 218 cases. *Mod Pathol*. 2005;18(12):1606–1609.
37. Cheng YW, Chiou HL, Sheu GT, et al. The association of human papillomavirus 16/18 infection with lung cancer among nonsmoking Taiwanese women. *Cancer Res*. 2001;61(7):2799–2803.
38. Koshiol J, Kreimer AR. Lessons from Australia: HPV is not a major risk factor for esophageal squamous cell carcinoma. *Cancer Epidemiol Biomarkers Prev*. 2010;19(8):1889–1892.

Funding

This work was supported by an Intramural Research Award from the Division of Cancer Epidemiology and Genetics, National Cancer Institute at the National Institutes of Health, and a National Cancer Institute Director’s Innovation Award, National Cancer Institute at the National Institutes of Health to J.K.; General Funds from the Intramural Research Program of the National Cancer Institute at the National Institutes of Health; and the Cancer Prevention Fellowship Program, Office of Preventive Oncology, National Cancer Institute at the National Institutes of Health, Bethesda, MD. The Division of Cancer Epidemiology and Genetics reviewed and approved the EAGLE case-control study and cleared the article for publication but had no role in the analysis, decision to publish, or preparation of the article.

Notes

We thank the 13 hospitals that contributed to this study: A.O. Ospedale Niguarda Cà Granda, Milano; A.O. Spedali Civili, Brescia; Istituto Clinico Humanitas, Rozzano (Milano); Ospedale di Circolo e Fondazione Macchi, Varese; Fondazione IRCCS Ospedale Maggiore Policlinico, Mangiagalli e Regina Elena, Milano; Istituto Scientifico Universitario Ospedale San Raffaele, Milano; A.O. Ospedale Luigi Sacco, Milano; A.O. San Paolo, Milano; A.O. Ospedale San Carlo Borromeo, Milano; IRCCS Policlinico San Matteo, Pavia; A.O. San Gerardo, Monza; A.O. Ospedale Fatebenefratelli e Oftalmico, Milano; Ospedale San Giuseppe, Milano as listed on the EAGLE Web site (<http://eagle.cancer.gov/>, accessed January 14, 2011).

Affiliations of authors: Division of Cancer Epidemiology and Genetics, NCI/NIH/DHHS, Bethesda, MD (JK, MR, AKC, AMG, AH, PRT, SW, MTL, NEC); Department of Internal Medicine, Ohio State University Comprehensive Cancer Center—James Cancer Hospital and Solove Research Institute, The Ohio State University, Columbus, OH (MLG, HS); DDL Diagnostic Laboratory, Voorburg, the Netherlands (L-JVD, WGVQ, LS); EPOCA Research Center, Department of Occupational and Environmental Health, Università degli Studi di Milano, Milan, Italy (LT, PAB); Epidemiology Unit, Fondazione IRCCS Ospedale Maggiore Policlinico, Mangiagalli e Regina Elena, Milan, Italy (LT, PAB).