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Multicenter study on the prevalence of human papillomavirus infection, genotype distribution, and cytological findings in public hospitals in the city of buenos Aires

Abstract

Introduction: Cervical cancer (CC) is a public health problem of global significance, with persistent human papillomavirus (HPV) infection being its primary etiological factor. People living with HIV constitute a high-risk population.

Objective: To characterize the prevalence and genotypic distribution of HPV and its association with high-grade cytology (HG) findings in women treated at public hospitals in Buenos Aires, while exploratorily assessing the impact of HIV serostatus on these parameters.

Materials and methods: A descriptive, retrospective, multicenter, cross-sectional study conducted at four public hospitals in the GCABA (Fernández, Argerich, Durand, and Penna). Study period: March 2022–December 2025. Patients aged ≥30 years who were not pregnant and screened with the Abbott HPV test were included. Patients with a history of conization, hysterectomy, lack of follow-up, or incomplete data were excluded. Genotype categories were defined as mutually exclusive, with "single infection" defined as the presence of a single high-risk genotype and "multiple" defined as coinfection with two or more. For the exploratory analysis by serological status, two groups were formed: confirmed HIV-positive patients and HIV-negative patients or those with no serology record (reference group).

Results: Of the 8,444 patients screened, 7,888 were included. The overall prevalence of HPV was 15.8% (n=1,246). In the HPV-positive population, the "other" category predominated as a single infection (72%, n=892), followed by genotype 16 alone (16%, n=205), genotype 18 alone (4%, n=54), and multiple infections (8%, n=95). The prevalence of HG results in the HPV-positive population was 17% (n=209). HIV-positive patients had a higher prevalence of HPV than the rest of the population (28.3% vs. 14.7%; p<0.00001) and a higher frequency of multiple infections (13% vs. 7%; p=0.002), with no significant differences in HG results (21% vs. 16%; p=0.09). Among HIV-positive patients with HG (n=38), a CD4 count <200 cells/mm³ (p<0.001), detectable viral load (p<0.001), and lack of antiretroviral therapy (ART) (p=0.01) were associated with a higher frequency of HG lesions.

Conclusion: The findings confirm the predominance of high-risk genotypes other than 16/18, reinforcing the importance of extended genotyping over strategies based solely on HPV 16/18 for risk stratification. The higher prevalence of HPV and multiple co-infections in HIV-positive individuals supports the need for differentiated screening algorithms. Immunosuppression without ART was associated with a higher risk of HG lesions in this subgroup

Keywords: human papillomavirus, human immunodeficiency virus, cervical cancer, women, cytologic lesions, genotypes

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Introduction

Cervical cancer (CC) represents a major public health problem, particularly in low-and middle-income countries. In 2022, there were an estimated 662,000 new cases and 348,000 deaths from CC.[1] In Argentina, approximately 4,600 new cases are diagnosed each year, and there are about 2,200 deaths; it is the leading cause of death from gynecologic cancer and the fourth leading cause of cancer-related death among women.[2,3]

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Persistent infection with the human papillomavirus (HPV), particularly with high-risk oncogenic genotypes, is the primary etiological factor for CCU.[4–6] About 80% of sexually active people will acquire some type of HPV during their lifetime; in most cases, these are transient infections that resolve within two to three years—a common occurrence in women under 30 years of age, which justifies the established age range for HPV testing.[2,4] Among the more than 200 identified genotypes, at least 14 are high-risk, with HPV 16 and 18 being the most prevalent and accounting for approximately 70% of cervical cancer cases.[7]

In people living with HIV, immunosuppression promotes the persistence of HPV infection, the development of precancerous lesions, and coinfection with multiple genotypes simultaneously, making this population a high-risk group that requires tailored screening strategies.[8] HPV testing, implemented as a primary strategy in Argentina since 2011, has proven to be superior to conventional cytology in detecting precancerous lesions.[9] Genotyping using real-time PCR (Abbott test) detects DNA from 14 high-risk genotypes, including 16 and 18 separately, and groups the other 12 (31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, and 68) into an "other" category.[10,11]

Since 2022, some institutions in the GCABA public hospital network have implemented HPV PCR testing as the primary screening method, increasing the detection of precancerous lesions and improving patient follow-up. In this context, we set out to analyze the characteristics of HPV infection, with a particular focus on genotype distribution, multiple infections, and the frequency of high-grade cytological lesions according to patients' immune status, thereby contributing local evidence to an issue of global significance.

Objetives

Primary Objectives:

a) Describe the prevalence of HPV infection; to characterize the distribution of HPV genotypes;

b) Determine the prevalence of high-grade or high-grade-suspected (AG) cytology results in the HPV-positive population.

Secondary Objectives:

a) Compare the prevalence of HPV infection and the distribution of genotypes in patients with and without HIV infection;

b) Compare the prevalence of AG cytology results in the HPV-positive population according to HIV status;

c) Analyze its relationship with immune status in HIV-positive patients.

d) The comparative analysis based on HIV serostatus was not pre-specified in the original protocol but emerged as an exploratory finding during data processing; therefore, these secondary objectives are exploratory and hypothesis-generating in nature, without implying confirmatory inferences (*see Materials and Methods*).

Method

A descriptive, retrospective, multicenter, cross-sectional study based on an analysis of medical records and databases from the Cervical Pathology and Lower Gential Tract (TGI for Spanish "Tracto Genital Inferior") clinics at four public hospitals in the City of Buenos Aires (CABA): "Carlos G. Durand," "José M. Penna," "Cosme Argerich," and "Juan A. Fernández," where the Abbott HPV test was available (March 2022–December 2025).

Patients aged 30 years or older who were not pregnant and who had been screened with the Abbott HPV test were included. Patients with a history of conization (scalpel, LEEP, or laser), total hysterectomy, lack of follow-up, or incomplete information were excluded (Figure 1).

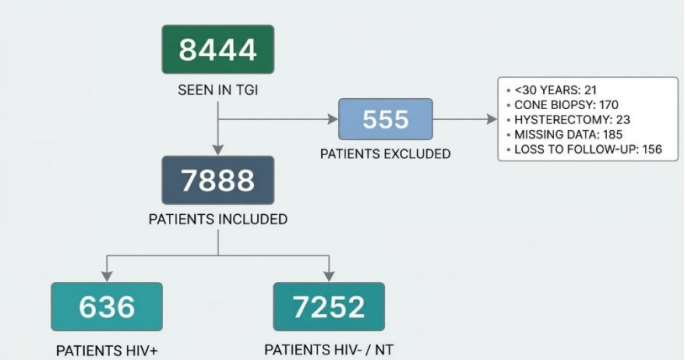


Figure 1 Study population. TGI: LGT: lower genital tract. HIV: human immunodeficiency virus. HPV: human papillomavirus.

The following variables were collected: smoking status, STIs other than HIV, HIV diagnosis, place of origin (CABA/PBA), parity, and health insurance coverage. Screening was performed using the Abbott® test beginning in 2022; in positive cases, procedures were carried out according to the SAPTGIyC 202212 guidelines, with triage based on cytology. In HIV-positive patients, co-testing was performed during the screening visit, unlike in the HIV-negative population.

The detected high-risk genotypes were categorized as "16," "18," "others" (genotypes 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, and 68) or "multiple" (two or more genotypes in the same patient), which are mutually exclusive categories. Cytological findings were categorized as "negative/L-SIL," "ASC-US," "H-SIL/ASC-H/ACG," and "no results," according to the Bethesda criteria,13 with the presence of high-grade cytology (H-SIL, ASC-H, or ACG) noted in the HPV-positive population.

The variable "HIV diagnosis" was prospectively included in the protocol approved by the ethics committee; however, the HIV+/HIV– comparative analysis was a post-hoc, non-prespecified, exploratory, and hypothesis-generating subgroup analysis. In HIV+ patients, cytological findings were associated with CD4 count (<200/≥200 cells/mm³), viral load (<40/≥40 copies/mL), and adherence to ART.

The data were entered into Excel; descriptive analysis was performed using absolute and relative frequencies. To compare genotype prevalences between groups, the chi-square test with Bonferroni correction was used; for the overall comparison between HIV+ and HIV- groups, the chi-square test was also applied, with $p < 0.05$ considered statistically significant.

Result

From March 2022 through December 2025, 8,444 patients were screened; of these, 555 were excluded (21 because they were under 30 years of age, 23 because they had undergone a total hysterectomy, 170 because they had undergone conization, 156 because of lack of follow-up, and 185 because of incomplete information), leaving 7,888 patients included in the study.

The median age was 46 years (range 30–65). Fifteen percent (n = 1,177) were smokers, and 5% (n = 413) had at least one concomitant STI. Thirty-one percent (n=2,420) resided in the PBA, and 75%

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(n=5,933) lacked health insurance; 86% (n=6,816) were multiparous. The prevalence of HIV-positive cases was 8% (n=636) (Table 1).

Table 1 Sociodemographic characteristics of the population (n=7,888)

Genotype	HIV+ n (%)	HIV-/NT n (%)	p
16	28 (16%)	177 (17%)	0.72
18	3 (2%)	51 (5%)	0.057
"Others"	125 (69%)	767 (72%)	0.49
Multiple	24 (13%)	71 (7%)	0.002
Total	180 (100%)	1066 (100%)	

The overall prevalence of HPV was 15.8% (n=1,246) (Figure 2). Among HIV-negative/untested women, it was 14.7% (n=1,066), and among HIV-positive women, it was 28.3% (n=180), a statistically significant difference (p<0.00001; RR=1.86 [95% CI: 1.68–2.20]) (Figure 3).

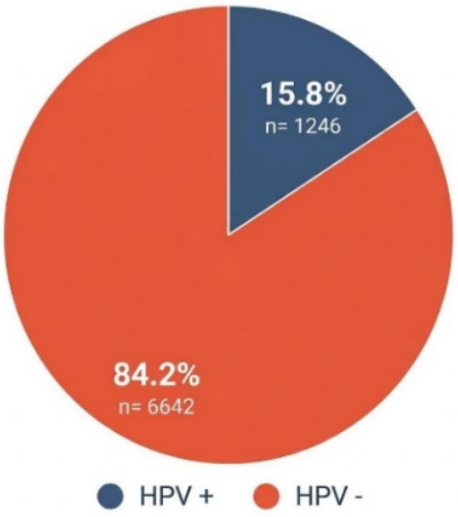


Figure 2 Test positivity rate in the general population (n=7888).

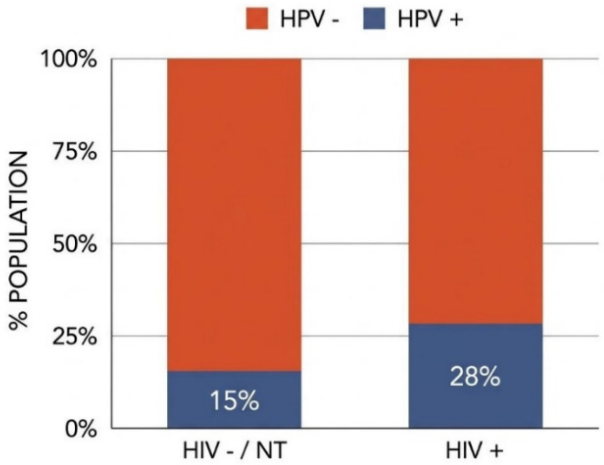


Figure 3 Test positivity rate in HIV - / NT (n=7252) / HIV+ (n=636).

In the HPV-positive population (n=1,246), the "other" category as a single infection was the most prevalent (72%, n=892), followed by genotype 16 alone (16%, n=205), multiple infections (8%, n=95), and genotype 18 alone (4%, n=54), with a statistically significant overall difference by chi-square test (p<0.005) (Figure 4).

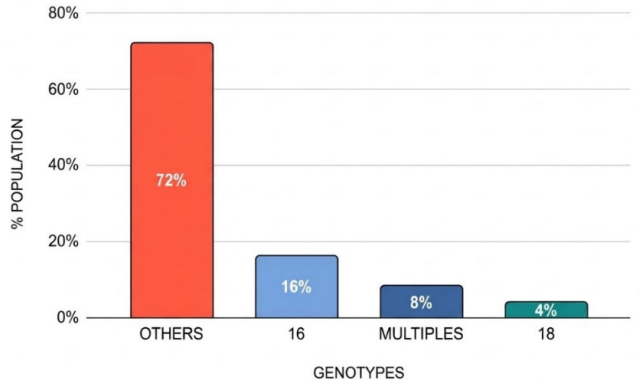


Figure 4 Distribution of genotypes in HPV+ population (n=1246).

By HIV serostatus, the pattern was similar: "others" was the most prevalent category (69% in HIV-positive vs. 72% in HIV-negative/NT; p=0.49), genotype 16 was similar (16% vs. 17%; p=0.72), and genotype 18 was less frequent in HIV+ individuals, though not significantly so (2% vs. 5%; p=0.057). The most relevant finding was the higher frequency of multiple infections in HIV+ individuals (13% vs. 7%; p=0.002) (Table 2).

Table 2 Distribution of genotypes by HIV serostatus: HIV+ (n=180) and HIV-/NT (n=1,066)

Genotype	HIV+ n (%)	HIV-/NT n (%)	p
16	28 (16%)	177 (17%)	0.72
18	3 (2%)	51 (5%)	0.057
"Others"	125 (69%)	767 (72%)	0.49
Multiple	24 (13%)	71 (7%)	0.002
Total	180 (100%)	1066 (100%)	

In the HPV-positive population, 83% (n=1,037) had a negative cytology result, and 17% (n=209) had an abnormal cytology result (H-SIL, ASC-H, or ACG) (Figure 5). No significant differences were found between HIV+ and HIV-/NT groups (21% vs. 16%; p=0.09; RR=1.32 [95% CI: 0.96–1.80]) (Table 3).

Table 3 Cytological findings in HPV-positive patients, by HIV status (HIV-positive vs. HIV-negative or untested)

Cytology	HIV+ n (%)	HIV- n (%)	p
Negative	142 (79%)	895 (84%)	0.09
High-grade (HSIL-ASC-H-AGC)	38 (21%)	171 (16%)	
Total	180 (100%)	1066 (100%)	

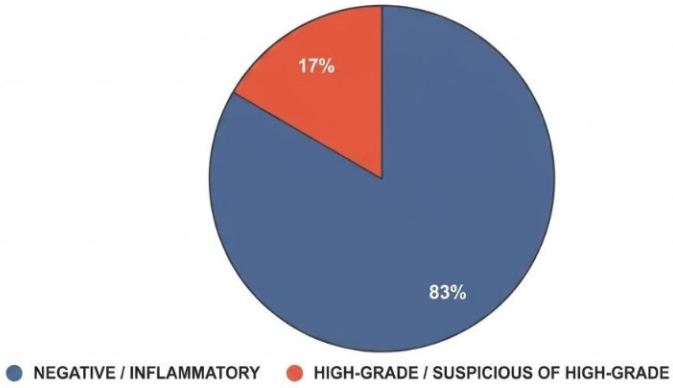


Figure 5 Cytological findings in HPV-positive population (n=1246).

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Among HIV-positive individuals with AG cytology (n=38): a CD4 count <200 cells/mm³ was associated with a higher prevalence of AG compared with a CD4 count ≥200 (71% vs. 14%; p<0.001; RR=4.92 [95% CI: 3.10–7.86]); viral load ≥40 copies/mL vs. <40 (77% vs. 13%; p<0.001; RR=5.81 [95% CI: 3.68–9.19]); no ART vs. ART (50% vs. 19%; p=0.01; RR = 2.62 [95% CI: 1.38–5.01]) (Table 4).

Table 4 Relationship between cytology and immune status in HIV-positive patients (n=180; AG=38, NEG=142)

Immune status	HSIL Cytologies	NEG Cytologies	Total	p	RR (95% CI)
CD4 <200 cells/mm³	15 (71%)	6 (29%)	21	<0.001	4.92 (3.10–7.86)
CD4 ≥200 cells/mm³	23 (14%)	136 (86%)	159		
VL ≥40 copies/ml	17 (77%)	5 (23%)	22	<0.001	5.81 (3.68–9.19)
VL <40 copies/ml	21 (13%)	137 (87%)	158		
ART NO	6 (50%)	6 (50%)	12	0.01	2.62 (1.38–5.01)
ART YES	32 (19%)	136 (81%)	168		

Discussion

This study analyzes the prevalence of HPV infection in four public hospitals in the City of Buenos Aires (GCABA), characterizing the distribution of genotypes to establish a local epidemiological and screening framework, and comparing the findings with the literature.[12,13]

The HPV positivity rate (15.8%) is comparable to that reported by the Ministry of Health (16.6% in adult women),[14] and higher than that reported in Spain (12.4%).[15] Among HIV-positive individuals, the prevalence (28.3%) was significantly higher than in our HIV-negative cohort (14.7%; p<0.00001; RR=1.86 [95% CI: 1.68–2.20]), consistent with international evidence.[16]

The "other" category—twelve genotypes other than 16 and 18—was the most prevalent in both groups (69% HIV-positive vs. 72% HIV-negative/NT), consistent with studies on genotype distribution in other regions where, in addition to 16 and 18, other genotypes are among the most common17. Genotype 16 was distributed similarly (16% vs. 17%; p=0.72); genotype 18 showed a trend toward lower frequency in HIV-positive individuals, though not statistically significant (2% vs. 5%; p=0.057), likely due to the sample size. The most relevant finding was the higher frequency of multiple infections in HIV-positive individuals (13% vs. 7%; p=0.002), consistent with the fact that this frequency increases with immunosuppression, exceeding 40% when CD4 <200 cells/mm.[3,18,19]

The prevalence of AG cytology (17% among HPV-positive patients) is similar to that reported in an Australian study of more than 157,000 patients (15.3%).[20,21] The absence of significant differences in AG between HIV+ and HIV-/NT patients (21% vs. 16%; p=0.09; RR=1.32 [95% CI: 0.96–1.80]) could be explained by good viral suppression on ART21 and by routine co-testing in HIV+ patients. In the HIV-positive subgroup with AG, a CD4 count <200 was associated with nearly five times the risk (RR=4.92; p<0.001), a detectable viral load was associated with nearly six times the risk (RR=5.81; p<0.001), and the absence of ART doubled the risk (RR=2.62; p=0.01), consistent with the inverse correlation between HPV and CD4 count (42.9% with CD4 ≤200 vs. 23.2% with CD4 >500)[22] and with the persistence of AG lesions under ART with a CD4 count <350 cells/µL.[23]

Limitations: retrospective design; grouping of twelve genotypes under "others," limiting comparison with complete genotyping; the HIV+/HIV– analysis was post hoc and exploratory, to be confirmed with a larger sample of HIV+ participants (636 vs.7,252). The serostatus of untested individuals could not be determined; given the prevalence of HIV among adult women in Argentina (0.4%), the impact would be negligible (636→639 HIV+; 180→181 HPV+ among HIV+ individuals).

An additional strength is the consistent use of the same genotyping platform across all four institutions, which provides, for the first time, local epidemiological data on HPV prevalence in the City of Buenos Aires and opens the door to prospective longitudinal studies on persistence, genotype evolution, and progression to cytological and histological lesions.

Conclusion

The prevalence of HPV infection was 15.8%, with a predominance in the "other" category (72%) and an AG cytology rate of 17% among HPV-positive patients. In the exploratory analysis, HIV-positive patients had a higher prevalence of HPV and multiple co-infections; severe immunosuppression and the absence of antiretroviral therapy (ART) were significantly associated with AG cytology in this group.

The completion of this multicenter study—which brought together four public hospitals in the GCABA network and enabled the collection of data from 7,888 patients—is in itself a significant achievement for the public health system of the City of Buenos Aires and sets a precedent for collaborative efforts in future research on gynecologic and reproductive health.

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Conflicts of interest

The authors declare no potential conflicts of interest.

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