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Prevalence and age-related trends of high-risk Human Papillomavirus genomes in Ecuadorian women: a comprehensive cross-sectional study

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Abstract

Background Human Papillomavirus (HPV) is a leading cause of cervical cancer worldwide. Previous studies on HPV prevalence in Ecuador have presented inconsistent findings due to limited sample sizes and regional foci. This study aims to estimate the prevalence and characteristics of HPV infection in Ecuadorian women, identifying high-risk HPV genomes and age-related trends, using data from the Cervical Cancer Screening and Prevention Program.

Methods Data were collected from multiple health centers across Ecuador, particularly focusing on the province of Pichincha, utilizing GeneXpert technology and the Xpert® HPV kit between January 1 and May 31, 2023 were included. The assay reports HPV16, HPV18/45, and pooled channels for 11 HPV types (P3: 31/33/35/52/58; P4: 51/59; P5: 39/56/66/68).

Results Of 16,197 valid tests, 1,776 were HPV-positive, yielding a prevalence of 11.0%. Women aged 30–39 were the most affected demographic, accounting for 39.7% of positive cases. The most common HPV genomes identified were 31/33/35/52/58, constituting 42.3% of HPV-positive women (P3 pooled). The prevalence of multiple HPV genome infections was 13.8%.

Conclusions The study provides a more nuanced understanding of HPV prevalence in Ecuador, indicating that HPV rates are lower than previous national studies but higher than global estimates. The results lay essential groundwork for targeted public health interventions and suggest the need for future research to address methodological limitations.

Keywords HPV infection, High-risk genomes, GeneXpert technology, Women's health, Low- and middle-income countries (LMICs), Prevalence

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Background

Cervical cancer ranks as the fourth most common cancer among women worldwide [1]. The World Health Organization (WHO) estimates that of the 342,000 cervical cancer-related deaths in 2020, over 90% occurred in low- and middle-income countries. There are several factors that increase the risk of cervical cancer; however, the presence of certain strains of Human Papillomavirus (HPV) has been positively associated with a higher risk of developing not only cervical cancer, but also vulvar, penile, and anal cancers in both men and women worldwide [2].

Human papillomavirus (HPV) is the most prevalent sexually transmitted infection globally, affecting approximately 80% of sexually active individuals and leading to over 14 million new infections each year [3, 4]. The virus is implicated in virtually all cases of cervical cancer, as well as a significant portion of anogenital and oropharyngeal cancers, contributing to 630,000 new cancer cases worldwide annually [5, 6].

The worldwide incidence of genital Human Papillomavirus (HPV) infection has shown significant geographical variations, based on data gathered from 1995 to 2022 [7]. Globally, the pooled prevalence stands at 31% for any type of HPV and 21% for high-risk strains. Sub-Saharan Africa leads with a prevalence rate of 37%, closely followed by Europe and Northern America at 36%. In stark contrast, Eastern and South-Eastern Asia show the lowest prevalence rates at 15%, a figure significantly different from other regional estimates [7]. Likewise, the high-risk HPV prevalence in this Asian region is only 10%, below the global average. Turning our attention to Latin America, the prevalence of HPV infection is notably higher than the global average, leading to an estimated 68,220 new cases of cervical cancer and approximately 31,712 fatalities annually [8, 9]. Specific to Ecuador, cervical cancer ranks as the second most common cancer among women, accounting for approximately 1,500 new cases and around 800 deaths each year [10].

The Human Papillomavirus (HPV) is a virus characterized by its double-stranded, circular DNA structure, which has an approximate genome size of 7,900 base pairs. Among the 448 HPV types that have been identified to date, only a subset of 12 types are classified as high-risk or carcinogenic, according to current medical understanding [11]. It is particularly noteworthy that HPV types 16 and 18 are disproportionately impactful, as they are responsible for approximately 71% of all malignant cervical cancer cases [12]. Oncogenesis by high-risk HPV involves infection of basal epithelial cells, capsid-mediated entry, and early gene expression (E1/E2) that supports episomal replication. E5 enhances proliferative signaling via receptor tyrosine kinases, while sustained expression of E6/E7 disrupts p53/Rb pathways, enabling genomic instability and progression from persistent infection to intraepithelial neoplasia and invasive carcinoma [4, 13] (Fig. 1).

Although the immune system can often clear the virus, the persistence of a high-risk HPV infection elevates the risk of developing cervical and other types of cancer [14]. This risk is further amplified when combined with additional risk factors, such as early sexual initiation, smoking, multiple sexual partners, numerous pregnancies, prolonged use of hormonal contraceptives, inadequate hygiene, coexisting sexually transmitted infections, and exposure to tar derivatives and biomass smoke [15–17].

Despite its preventability, widespread implementation of effective and cost-efficient measures to eradicate cervical cancer remains unachieved, particularly in regions where the disease burden is high [18]. While Ecuador has implemented prevention strategies, including immunization and early detection, there remains a lack of comprehensive data on the prevalence and distribution of the most common HPV genotypes, which are crucial for evaluating these strategies [3]. Existing studies on HPV infection in Ecuador suffer from limited representativeness, hindering the development of control and management measures tailored to the local population [16, 19]. Therefore, this study aims to investigate the prevalence of HPV infection and the distribution of HPV genotypes among women in Ecuador. We seek to understand the demographic or clinical characteristics that may influence HPV infection rates among Ecuadorian women.

Materials and methods

Study design

We carried out a cross-sectional observational investigation, scrutinizing the medical records from a secondary-level public healthcare facility situated in Quito, Ecuador. This hospital provides medical services to residents hailing from a minimum of 12 distinct provinces and spans four geographical zones within Ecuador.

Setting and population

Ecuador, located on the equator, adorns the west coast of South America. With an area of approximately 283,560 km^2, it is geographically segmented into four different regions: the Coast, the Andean Mountains, the Amazon, and the Galapagos Islands. From a governance perspective, Ecuador is administratively divided into 24 provinces. As of 2021, Ecuador has a population of 17,757,000, with 50.07% of the population being female. Within this group, approximately 5,535,277 women are of childbearing age (between 10 and 50 years) [20].

This research incorporated data from clinical reports stored at Calderón General Teaching Hospital, focusing on female patients who underwent HPV testing as part of the Cervical Cancer Screening and Prevention

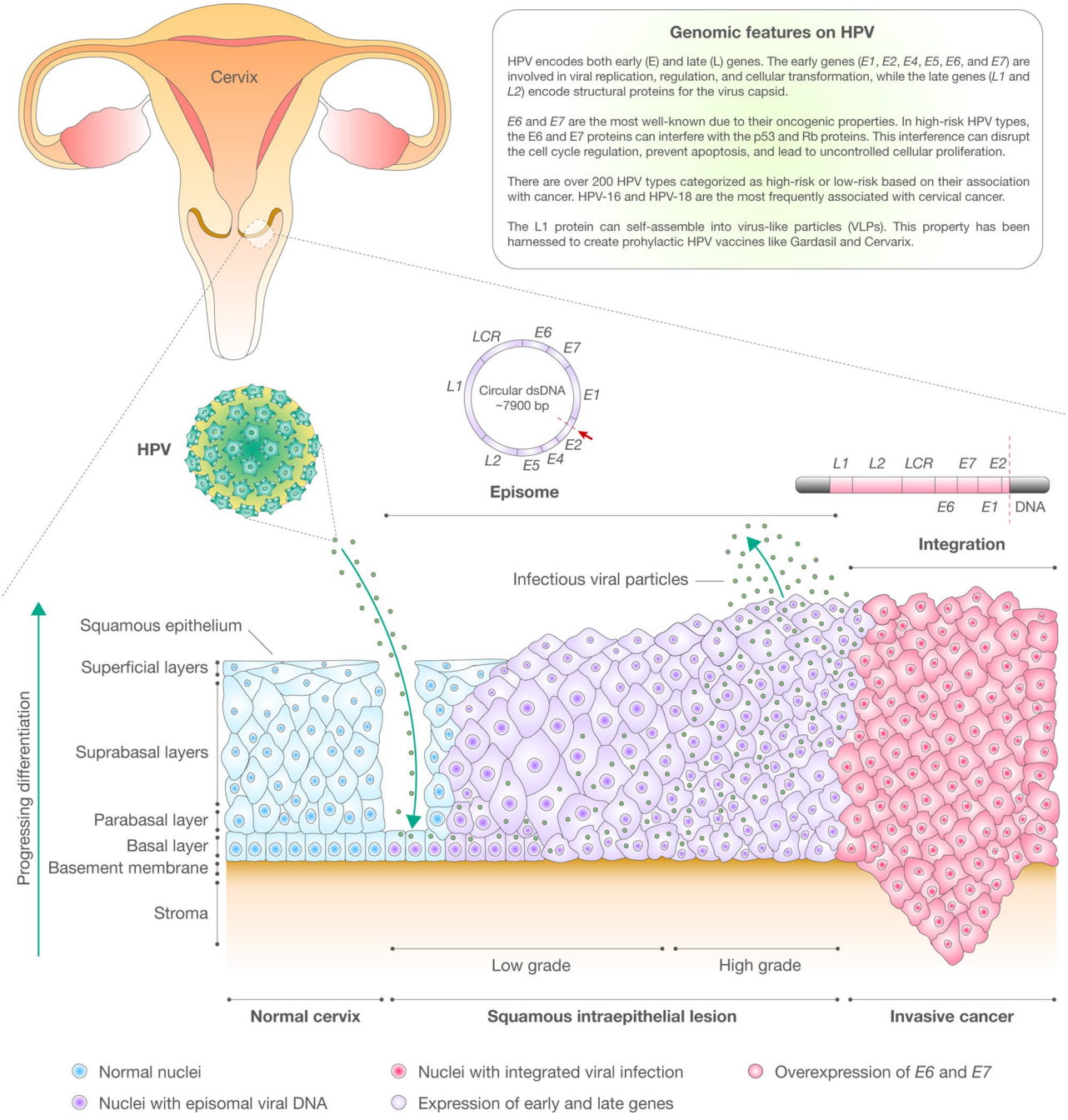

Fig. 1 Schematic representation illustrating the progression of HPV infection in the epithelial tissue. The diagram clearly shows different stages—Grade I, Grade II, and Grade III—indicating the severity of cellular changes. The figure elucidates how persistent HPV infection progressively transforms the epithelium, eventually leading to invasive cancer

Program in Ecuador [21]. The data included were recorded between January and May 2023.

Sample

In this study, we employed a non-probabilistic sampling technique to obtain patient data from consecutive entries in the existing database records. These records encompass patients who had undergone diagnostic tests at diverse healthcare centers throughout Ecuador. The collected data were cataloged within the Pathological Anatomy Service databases of Hospital General Docente de Calderon. Only entries that fell within our predetermined time frame and satisfied our pre-established selection criteria were included in the study.

Inclusion and exclusion criteria

We included medical records of females of any age tested for high-risk HPV using the Xpert® HPV assay (Ref: GXHPV-CE-10) between January 1 and May 31, 2023 at public facilities contributing to the Calderón General Teaching Hospital database in Quito (serving ≥ 12 provinces). We excluded records using non-Xpert assays, tests outside the time window, duplicate entries, and records missing essential variables (HPV result, age, or province).

Collection of samples and data

For data collection, we secured the requisite authorization and accessed the Pathological Anatomy Service databases at Calderón General Teaching Hospital. An initial query revealed 17,914 patient records containing HPV test results. Following the application of pre-established selection criteria and the elimination of structural or systematic errors, 1,717 records were excluded, yielding a final dataset of 16,197 valid records for analysis.

To calculate the prevalence of HPV infection, we subdivided the pool of valid tests into two categories: 14,421 records indicated negative HPV infection outcomes, while 1,776 records confirmed positive results.

Subsequently, we extracted diverse demographic information from the positively-tested records, encompassing variables such as gender, age, province of residence, and the specific health center where testing occurred, as well as patient nationality. Clinical characteristics were also collected, including the type of contraception used, age at sexual debut, interval since the last cervical cytological examination, and the diagnosis derived from the most recent cervical cytological examination, classified according to the Bethesda 2015 system [22].

HPV detection relied on the Xpert® HPV kit (Ref: GXHPV-CE-10), which identifies HPV-16 and HPV-18/45 and reports pooled positivity for an additional 11 high-risk types grouped as P3 (31/33/35/52/58), P4 (51/59), and P5 (39/56/66/68) in under one hour [23]. Because Xpert® reports pooled results for P3, P4, and P5 and combines HPV-18/45, within-pool type-specific prevalence (e.g., HPV-58 within P3) cannot be directly estimated from this dataset.

For genotype-group distributions (HPV-16, HPV-18/45, P3, P4, P5), percentages were computed per individual among HPV-positive women (denominator = 1,776), counting a woman as positive for a group if that group was detected, regardless of co-detection with other groups.

Statistical analysis

Categorical variables were subjected to descriptive analysis, quantified through frequencies and percentages to provide an overview of the distribution patterns within the dataset. To assess the associations between these categorical variables, the Chi-Square test was utilized. The level of statistical significance was set at a p-value threshold of less than 0.05; variables meeting or exceeding this criterion were deemed to exhibit a statistically meaningful relationship.

All statistical computations and analyses were executed using IBM SPSS Statistics for Windows, version 24.0.

Results

Demographic characteristics

Among the 16,197 valid records, high-risk HPV genotypes positivity was 11.0% (n = 1,776) in women. A noteworthy regional distribution was evident, with nearly half (45.9%, n = 814) of the HPV-positive individuals residing in the province of Pichincha. The age group most affected by high-risk HPV infections was 30 to 39 years, comprising 39.7% (n = 704) of the infected cohort. Additionally, an overwhelming majority of the participants, 99.0%, were of Ecuadorian nationality, as detailed in Table 1.

Past medical history and clinical characteristics

The largest subset of participants, accounting for 37.3% (n = 662), reported not using any form of contraception, while tubal ligation emerged as the most prevalent contraceptive method, utilized by 27.7% (n = 491) of the study population. In terms of age at onset of sexual activity, the 18–20 year age group was most frequently represented, encompassing 34.6% (n = 612) of the participants, as depicted in Table 1.

For HPV genotype groups detected by the Xpert® assay, the HPV-P3 pooled channel—which aggregates types 31/33/35/52/58—showed the highest positivity, present in 42.3% (n = 752) of HPV-positive women. This was followed by HPV-P5 (pooled 39/56/66/68) at 23.5% (n = 417) and HPV16 at 20.8% (n = 370); HPV18/45 was the least frequent at 13.7% (n = 243). It is worth noting that 13.8% (n = 245) of women were positive for ≥ 2 HPV categories, as detailed in Table 1. About the most recent cytological assessments, a significant proportion of the participants, 43.4% (n = 771), had undergone testing within the last 1 to 3 years. Of these, the majority received a 'Negative for Intraepithelial Lesion or Malignancy' (NILM) diagnosis, constituting 79.0% of the cytological outcomes, as shown in Table 1.

Geographic distribution according to the test

In all test categories (HPV-16; HPV-18/45; HPV-P3; HPV-P4; HPV-P5), the majority of cases were concentrated in the province of Pichincha. This was followed by the province of Imbabura for the HPV-16, HPV-18/45, and HPV-P3 tests. In the HPV-P4 and HPV-P5 tests, the province of Santo Domingo was the second most frequent (Fig. 2).

Table 1 Demographic and clinical characteristics of study Participants. The table displays the distribution of various characteristics among the 1,776 study participants, including the Province of residence, age group, nationality, HPV test positivity, number of positive HPV tests, type of contraception used, age at onset of sexual activity, time elapsed since the last cervical cytological examination, and diagnosis based on the last cytological examination according to the Bethesda 2015 classification. Data are presented as both Raw counts (n) and percentages (%)

		n	%
Province of residence	Bolivar	28	1.6%
	Chimborazo	96	5.4%
	Cotopaxi	66	3.7%
	Esmeraldas	125	7.0%
	Imbabura	225	12.7%
	Napo	42	2.4%
	Orellana	35	2.0%
	Pichincha	814	45.9%
	Santo Domingo	212	11.9%
	Sucumbios	43	2.4%
	Tungurahua	89	5.0%
Age (years)	Less than 20	9	0.5%
	20–29	161	9.1%
	30–39	704	39.7%
	40–49	434	24.5%
	50–59	360	20.3%
	More than 60	107	6.0%
Nationality	Colombian	5	0.3%
	Ecuadorian	1758	99.0%
	Peruvian	1	0.1%
	Venezuelan	11	0.6%
Positive test	HPV-16 test	370	20.8
	HPV-18/45 test	243	13.7
	HPV-P3 test	752	42.3
	HPV-P4 test	279	15.7
	HPV-P5 test	417	23.5
Number of positive tests	1	1530	86.2%
	2	209	11.8%
	3	31	1.7%
	4	5	0.3%
Contraception	Barrier	74	4.2%
	Hormonal	401	22.6%
	Ligature	491	27.7%
	None	662	37.3%
	Other	147	8.3%
Onset of sexual activity (years)	Less than 18	910	51.4%
	18–20	612	34.6%
	More than 21	247	14.0%
Time since the last cytology performed (years)	Less than 1	318	17.9%
	1 to 3	771	43.4%
	3 to 5	277	15.6%
	More than 5	252	14.2%
	Unknown	8	0.5%
	Never	149	8.4%
Diagnosis of the Last Cytology	NILM	1402	79.0%
	ASC-US	32	1.8%
	ASC-H	1	0.1%
	LSIL	30	1.7%
	HSIL	12	0.7%

Table 1 (continued)

		n	%
	Cancer (SSC)	1	0.1%
	Unknown	297	16.7%

NILM: negative for intraepithelial lesion or malignancy, ASC-US: atypical squamous cell of undetermined significance; ASC-H: high-grade squamous intraepithelial lesion; LSIL: low-grade squamous intraepithelial lesion; HSIL: high grade squamous intraepithelial lesion; SSC: squamous cell

Carcinoma. Note: Percentages for genotype groups are calculated per individual among HPV-positive women (denominator = 1,776); multiple positivity is possible, so percentages do not sum to 100%

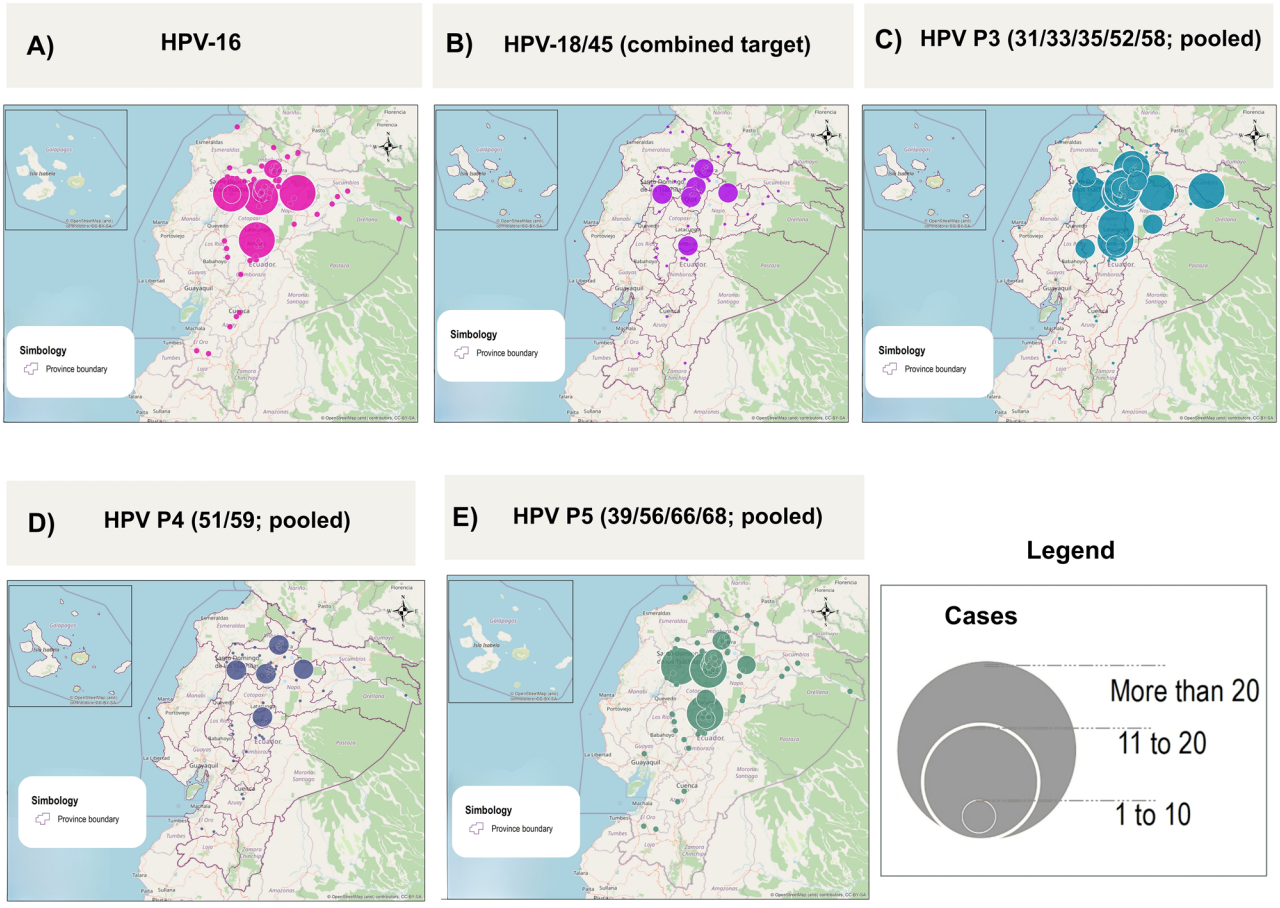

Fig. 2 Geographic distribution of HPV-positive results by genotype group (Xpert® HPV), Ecuador, January–May 2023. Panels show counts of HPV-positive women by province for each assay group: **A**) HPV16; **B**) HPV18/45 (combined target); **C**) HPV P3 (31/33/35/52/58; pooled); **D**) HPV P4 (51/59; pooled); **E**) HPV P5 (39/56/66/68; pooled). Circle size is proportional to the number of positive tests in that province (see legend classes: 1–10, 11–20, > 20 cases). Province boundaries are displayed. Across groups, the highest counts occur in Pichincha. For HPV-16, HPV-18/45, and HPV-P3 tests, the province of Imbabura registers as the second most frequent location of cases. In contrast, for HPV-P4 and HPV-P5 tests, the province of Santo Domingo emerges as the second most common location for cases

Variability in HPV subtypes across patient characteristics

In this study, 13.8% of the study subjects were positive for multiple categories of HPV, with statistical significance ($p < 0.001$), as delineated in Supplementary File 1. When stratified by age, patients between the ages of 30 and 39 exhibited the highest frequency of HPV-16 positivity ($p < 0.001$).

Turning our attention to sexual onset, it was noted that the majority of HPV-P3 positive patients initiated sexual activity before the age of 18 ($p = 0.002$), as depicted in Table 2. Interestingly, a similar pattern was observed for HPV-P4 positive patients, with statistical significance noted ($p = 0.023$) (Supplementary File 1).

Regarding the latest cytological diagnosis, the most sizable cohorts for low-grade squamous intraepithelial lesions (LSIL) and high-grade squamous intraepithelial lesions (HSIL) were again clustered within the 30–39 age range ($p < 0.001$). Notably, the type of contraception did not appear to influence the occurrence of LSIL; there was no statistically significant difference between users of hormonal contraception and those not using any form of contraception ($p > 0.05$).

Table 2 Cross-tabulation of the most recent cytological diagnosis against various factors such as age, number of positive HPV tests, nationality, contraception methods, onset of sexual activity, and time since the last cytological test was performed. Percentages are calculated based on the number of individuals within each category

		Diagnosis of the Last Cytology														
		Unknown		**NILM**		**ASC-US**		**ASCH**		**LSIL**		**HSIL**		**Cancer**		***P* value**
		n	**%**	***n***	**%**	***n***	**%**	***n***	**%**	***n***	**%**	***n***	**%**	***n***	**%**	
Age (years)	Less than 20	1	11.1	6	66.7	2	22.2	0	0.0	0	0.0	0	0.0	0	0.0	**< 0.001**
	20–29	42	26.1	105	65.2	6	3.7	0	0.0	7	4.3	1	0.6	0	0.0	
	30–39	127	18.0	552	78.4	8	1.1	1	0.1	10	1.4	5	0.7	1	0.1	
	40–49	56	12.9	361	83.2	9	2.1	0	0.0	4	0.9	4	0.9	0	0.0	
	50–59	47	13.1	297	82.5	5	1.4	0	0.0	9	2.5	2	0.6	0	0.0	
	More than 60	24	22.4	81	75.7	2	1.9	0	0.0	0	0.0	0	0.0	0	0.0	
Number of positive tests	1	260	17.0	1205	78.8	29	1.9	1	0.1	26	1.7	9	0.6	0	0.0	0.689
	2	30	14.4	169	80.9	2	1.0	0	0.0	4	1.9	3	1.4	1	0.5	
	3	5	16.1	25	80.6	1	3.2	0	0.0	0	0.0	0	0.0	0	0.0	
	4	2	40.0	3	60.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	
Nationality	Colombian	0	0.0	5	100.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0.999
	Ecuadorian	297	16.9	1385	78.8	32	1.8	1	0.1	30	1.7	12	0.7	1	0.1	
	Peruvian	0	0.0	1	100.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	
	Venezuelan	0	0.0	11	100.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	
Contraception	Barrier	12	16.2	57	77.0	3	4.1	0	0.0	1	1.4	1	1.4	0	0.0	**< 0.001**
	Hormonal	62	15.5	318	79.3	8	2.0	0	0.0	11	2.7	2	0.5	0	0.0	
	Ligature	65	13.2	412	83.9	3	0.6	0	0.0	6	1.2	4	0.8	1	0.2	
	None	150	22.7	487	73.6	8	1.2	0	0.0	12	1.8	5	0.8	0	0.0	
	Other	8	5.4	128	87.1	10	6.8	1	0.7	0	0.0	0	0.0	0	0.0	
Onset of sexual life (years)	less than 18	158	17.4	704	77.4	20	2.2	0	0.0	19	2.1	8	0.9	1	0.1	0.463
	18–20	91	14.9	501	81.9	9	1.5	1	0.2	8	1.3	2	0.3	0	0.0	
	More than 21	46	18.6	194	78.5	2	0.8	0	0.0	3	1.2	2	0.8	0	0.0	
Time since the last cytology performed (years)	Less than 1	34	10.7	240	75.5	23	7.2	1	0.3	13	4.1	6	1.9	1	0.3	**< 0.001**
	1 to 3	59	7.7	691	89.6	7	0.9	0	0.0	11	1.4	3	0.4	0	0.0	
	3 to 5	16	5.8	254	91.7	1	0.4	0	0.0	5	1.8	1	0.4	0	0.0	
	More than 5	34	13.5	214	84.9	1	0.4	0	0.0	1	0.4	2	0.8	0	0.0	
	Unknown	6	75.0	2	25.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	
	Never	148	99.3	1	0.7	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	

Moreover, temporal analysis of the cytological findings revealed that the highest frequencies of LSIL and HSIL occurred among subjects who had undergone cytological evaluations within less than one year and between one to three years preceding the study ($p < 0.001$), as corroborated by Table 2.

Furthermore, when exploring the potential impact of HPV genome infection on cytological diagnostic patterns, no statistically significant association was discovered (Supplementary file 2).

Discussion

This study serves as a pioneering comprehensive investigation into the prevalence and characteristics of human papillomavirus (HPV) infection among Ecuadorian women. Utilizing advanced GeneXpert technology and the Xpert® HPV kit, the research was conducted under the aegis of the Cervical Cancer Screening and Prevention Program in Ecuador.

Our findings revealed an estimated HPV prevalence of 11.0%, corresponding to 1,776 cases of infection by various high-risk HPV genomes. Notably, this is a significant departure from earlier studies on limited Ecuadorian populations, which reported prevalence rates oscillating between 24% and 86% for both low and high-risk HPV genomes [24]. While our prevalence rate surpasses the global average of 9.9% in 2019 [3], it falls short of recent figures from populous countries like China (19.97%) and the Republic of Congo (24.8%) [25, 26].

The demographic most impacted by HPV in our study comprised women between 30 and 39 years of age, constituting 39.7% of all cases. This finding diverges from international literature, where the most vulnerable age group is often reported as 25–29 years, such as in the Republic of Congo [26] and Uganda [27]. Although existing epidemiological models propose an inverse relationship between age and HPV infection [28, 29], we hypothesize that cultural factors—particularly early sexual debut, observed in our study to frequently occur before 18—may modulate this trend in the Ecuadorian context.

Regarding genome specifics, the HPV-P3 group (31/33/35/52/58) was most frequent, accounting for 42.3% of HPV-positive women. The predominance of the P3 group (31/33/35/52/58) in our screening cohort (42.3%) is consistent with Ecuador-specific reports of high HPV-58 frequencies in cervical lesions, although our assay could not disaggregate within P3 [30]. This high prevalence can likely be attributed to the broad spectrum of HPV genomes detected by this test, corroborating similar findings from studies in Uganda and Swaziland using the same diagnostic kit [27, 29]. Interestingly, our data points to HPV-18/45 as the least prevalent high-risk genomes in Ecuador, aligning partially with prior studies on Ecuadorian women [30].

Our analysis also revealed that 13.8% of cases demonstrated multiple positive test results for HPV genomes. This data is inconsistent with other studies reporting a varied range of 3.24% to 35.9% for poly-infections [27, 31]. The discrepancy, we argue, may be attributed to the inherent limitations of the test kits used, making it challenging to compare multi-genome infections across different studies.

The study's geographic focus, albeit expansive, was not all-encompassing. Most of the data was collected from Pichincha province, a potential bias introduced by the initial roll-out of the Cervical Cancer Screening and Prevention Program in that region. Despite this limitation, the large sample size affords valuable epidemiological insights that could guide future public health interventions.

It is essential to note the pivotal role of HPV genome characterization in shaping global health policies, especially in resource-constrained settings like Ecuador, Uganda, and Swaziland. Although our study faced challenges in pinpointing the most prevalent high-risk HPV genomes, the identification of unexpected trends, such as the low frequency of HPV-18/45 genomes, presents new avenues for targeted interventions and lays the groundwork for further specialized research.

Programmatic implications in Ecuador include prioritizing HPV primary screening with reflex triage from age 30; reinforcing catch-up vaccination with 9-valent formulations (covering 31/33/45/52/58) given the high P3 burden; targeted outreach in provinces with higher positivity (notably Pichincha, Imbabura, Santo Domingo); and shorter rescreening intervals for women aged 30–39. These actions, integrated into routine monitoring, may reduce lesion progression and optimize resource allocation.

Limitations

While our study has made significant strides in HPV epidemiology, it is not without limitations. The data's geographic scope was largely centered on the Pichincha province, which may affect the national representativeness of our findings. Moreover, the challenges in accurately discerning multiple HPV genome infections due to test kit limitations necessitate cautious interpretation. Because the assay pools genotypes in P3/P4/P5, we could not estimate within-pool type-specific prevalence (e.g., HPV-58). Additionally, several potentially relevant clinical variables (parity, abortions, civil status, ethnicity, family history) were not consistently captured and thus were not analyzed.

Future studies should aim to include a more nationally representative sample and employ multiple diagnostic

methods to overcome the limitations inherent in current test kits. A deeper exploration of sociocultural factors influencing HPV prevalence in different age groups would also be invaluable.

Despite these limitations, our study has far-reaching implications for both national and global health policy, especially concerning cervical cancer prevention. Our findings lay the foundation for the formulation of targeted public health strategies and pave the way for more in-depth, specialized research to combat one of the most common cancers affecting women today.

Conclusions

In conclusion, this study represents a pioneering effort to comprehensively understand the prevalence and characteristics of HPV infection among Ecuadorian women. Utilizing state-of-the-art GeneXpert technology within the framework of the Cervical Cancer Screening and Prevention Program, we estimated an HPV prevalence rate of 11.0%. This rate not only deviates significantly from prior studies on smaller Ecuadorian cohorts but also situates itself between global and regional prevalence estimates.

Our research indicates that women between the ages of 30 and 39 are disproportionately affected by HPV in Ecuador, a finding that diverges from prevalent age-related trends noted in other countries. Moreover, we identified specific high-risk HPV genomes that are unusually common or rare within the Ecuadorian context, offering critical insights for targeted interventions, including vaccination programs.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12879-025-12333-z.

Supplementary Material 1

Supplementary Material 2

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None.

Author contributions
The conceptualization of the study was led by MOG, BNK, MA, AG, and PN-L. Clinical data collection and the process of obtaining informed consent from participants were carried out by the hospital team led by MOG. The study's methodology was developed collaboratively by JSIC and EOP. Resources necessary for the research were provided by JSIC, PLT, MOG, KAS, DG, BNK, MA, AG, MAC, and PN-L. JSIC, ALC, and EOP were responsible for the development and application of software tools. Validation of data and findings was conducted by JSIC, PLT, MOG, KAS, DG, BNK, MA, AG, and PN-L. Data analysis was performed by JSIC, GDR, ALC, and EOP. Importantly, EOP, JSIC, and ALC did not have access to any identifiable patient data and worked exclusively with anonymized datasets during the analysis phase. The original draft of the manuscript was written by JSIC, PLT, MOG, KAS, DG, BNK, MA, AG, MAC, and PN-L, while JSIC, PLT, MOG, GDR, ALC, and EOP contributed to reviewing and editing the manuscript. Visualization of the data and results was handled by JSIC, EOP, ALC and GBR.

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None to declare.

Data availability
All data generated or analyzed during this study are included in this published article and its supplementary information files.

Declarations

Ethical approval
This study was reviewed and approved by the Bioethics Committee of the University of the Americas. Approval was granted for the research protocol titled "*Epidemiological, Cytological, Histopathological, and/or Molecular Characterization of Cervical Samples and Diagnostic Quality in the Pathology Laboratory of the Calderón General Teaching Hospital from 2019 to 2024*" (CEISH-HGDC-2025-002). The approval process involved a thorough review of all ethical, methodological, and legal requirements in accordance with the institution's regulations.

Consent to participate
All patients provided written informed consent prior to participation in this study, in accordance with institutional, local, and regional ethical standards. The study was reviewed and approved by the local Institutional Review Board (IRB) under protocol CEISH-HGDC-2025-002. No risks to participants were identified by the IRB. The approval process included a thorough review of all ethical, methodological, and legal requirements in line with institutional regulations.

Competing interests
The authors declare no competing interests.

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