EPH231

HPV genotyping in invasive cervical cancer samples from women attended at an oncological hospital between 2017 and 2021 in Ecuador

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Background and rationale

Persistent infection by human papillomavirus (HPV) is the primary etiologic factor for developing cervical cancer, and other types of cancer including vaginal, anal, penile, and head and neck cancers[1,2]

Currently, more than 230 HPV genotypes have been identified; from those, the International Agency for Research on Cancer (IARC) has recognized 12 genotypes as carcinogenic to humans: HPV 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, and 59.[3] From these carcinogenic genotypes, HPV 16 and 18 are the most prevalent, causing about 70% of all invasive cervical cancers.[4]

Globally, cervical cancer ranks fourth in incidence among women, and it is commonly diagnosed in low- and middle-income countries in Africa and Latin America, settings with serious limitations in accessing early cancer detection and health services in general.[5]

In Ecuador, cervical cancer is the second leading cause of female cancer, with an age standardized incidence rate of 17.5 per 100,000 women and a mortality rate of 8.2 per 100,000 women[6]

However, there is a lack of research on HPV genotypes distribution in advanced cervical cancer samples in Ecuador. Understanding the local prevalence of HPV genotypes in cervical cancer samples is crucial for effective prevention and control strategies, as it can have implications for screening, diagnosis, and treatment strategies. Thus, there is a need for accurate and up-to-date information on HPV genotype distribution in Ecuador.

Objective

To determine the distribution of HPV genotypes in invasive cervical cancer samples from Ecuadorian women who attended the Cancer Institute (Sociedad de Lucha Contra el Cáncer – SOLCA), between 2017 and 2021

Methods

This retrospective cross-sectional study utilized archival formalin-fixed paraffin-embedded (FFPE) invasive cervical cancer tissue samples. The samples were obtained from the Pathology department of SOLCA between 2017 and 2021.

Cases were identified according to the ICD-10 (C53), including patients with histopathological diagnosis of cervical cancer of any type. The corresponding FFPE samples were retrieved from the archives of the Department of Pathology and processed at the Laboratory of Molecular Biology for HPV detection. Only samples obtained as pre-treatment biopsies or resection tissue samples were included, following SOLCA's routine protocols for diagnostics and handling.

The study included patients aged 18 or older diagnosed with confirmed invasive cervical cancer at SOLCA between 2017 and 2021; low-quality or non-confirmatory tissue samples were excluded.

Results

A total of 200 samples from the study period were identified, and after removing duplicates and applying the inclusion/exclusion criteria, 190 FFPE samples were included in the study.

From the included samples, 190 women were diagnosed with invasive cervical cancer with a mean age of 52.5 years. Of these, 150 (78.94%) had squamous cell carcinomas, while 40 (21.05%) had adenocarcinoma (**Table 1**).

Regarding socio-demographic and clinical characteristics, most women included in the study had a low socioeconomic status – 155 (81.6%), with elementary-level education being the most common – 102 (53.7%), followed by high school – 49 (25.8%). The most prevalent occupation was domestic chores – 160 (84.2%) (**Table 1**).

The frequency of HPV detection was higher in patients with a lower level of education, with 117 testing positive for HPV (61.6%), compared to patients with higher education, where 36 tested positive (18.9%) (*P*<0.05 by X2 Chi-square test). No statistically significant associations were observed between HPV presence and other characteristics such as age, socioeconomic status, occupation, and histopathology. (**Table 1**)

Table 1. Frequency analysis according to sample characteristics

Variables	HPV+	HPV-	Total	*P*-value X² test
Level of education				0.036
Elementary	117	22	139	
High school/tertiary	36	15	51	
Total	153	37	190	
Socioeconomic status				
Low	123	32	155	0.391
Middle	30	5	35	
Total	153	37	190	
Occupation				
Domestic chores	132	29	161	0.231
Other	21	8	29	
	153	37		
Age				
18-39	29	12	41	
40-59	79	16	95	0.27
60-79	40	7	47	
≥80	5	2	7	
Total	153	37	190	
Histopathology				
AD	28	12	40	0.058
SCC	125	25	150	
Total	153	37	190	

A total of 146 cases (76.8%) had unavailable or lack of screening information before cervical cancer diagnosis. Among the remaining patients, a Pap smear was performed less than 3 years before diagnosis in 30 cases (5.8%), more than 3 years prior in 11 cases (5.8%), and more than 10 years prior in one patient (0.55%). The most common clinical manifestations reported were bloody discharge in 98 patients (51.6%) and pelvic pain in 63 cases (33.2%).

Data on the FIGO stage was available for 148 cases (77.9%), while 42 patients (22.1%) had no recoverable data. Among the cases with available information, 24 (12.63%) were classified as FIGO stage I (tumor confined to the cervix), 82 (43.16%) as FIGO stage II (tumor invades beyond the uterus but has not extended to the lower third of the vagina or pelvic wall), 36 (18.95%) as FIGO stage III (tumor involves the lower third of the vagina, extends to the pelvic wall, or causes hydronephrosis), and 6 (3.16%) as FIGO stage IV (carcinoma has spread beyond the pelvis, to the bladder or rectum).

Regarding HPV distribution, 153 samples (80.53%) tested positive for HPV DNA, while 37 (19.47%) were negative. High-risk carcinogenic genotypes, including HPV 16, 18, and 58, as recognized by the IARC, showed the highest relative frequencies (**Figure 1**). HPV genotypes 16 and 18 were the most frequent in squamous and adenocarcinoma histological types.

Among the samples, 127 (66.8%) tested positive for a single HPV genotype. From the 153 positive samples, the most prevalent genotypes were HPV 16, found in 98 samples (64.05%); HPV 18 in 26 samples (16.99%); HPV 58 in 10 samples (6.54%); and HPV 45 in 7 samples (4.58%).

In 26 cases (13.7%), multiple genotypes were detected. The most frequent combinations included HPV 16/HPV 58 in 6 samples (23.08%), HPV 16/HPV 18 in 3 samples (11.54%), and HPV 16/HPV 33 in 2 samples (7.69%). All combinations involved at least one high-risk genotype (**Figure 2**).

Figure 1. Relative frequency of different human papillomavirus genotypes (%)

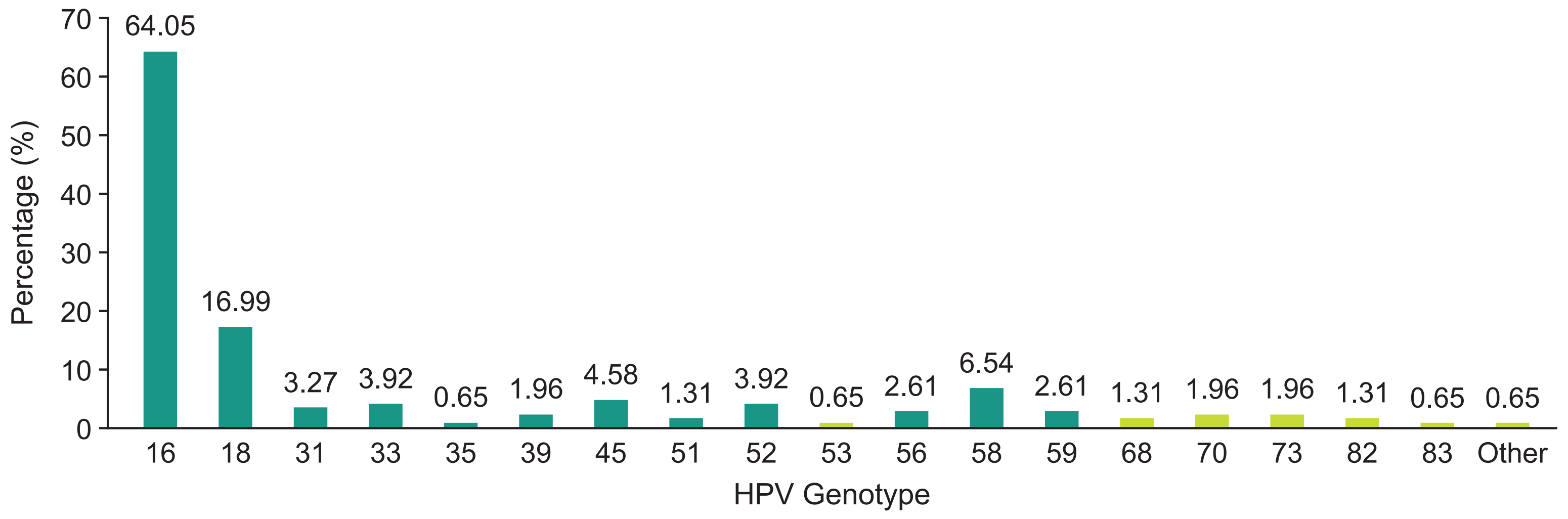
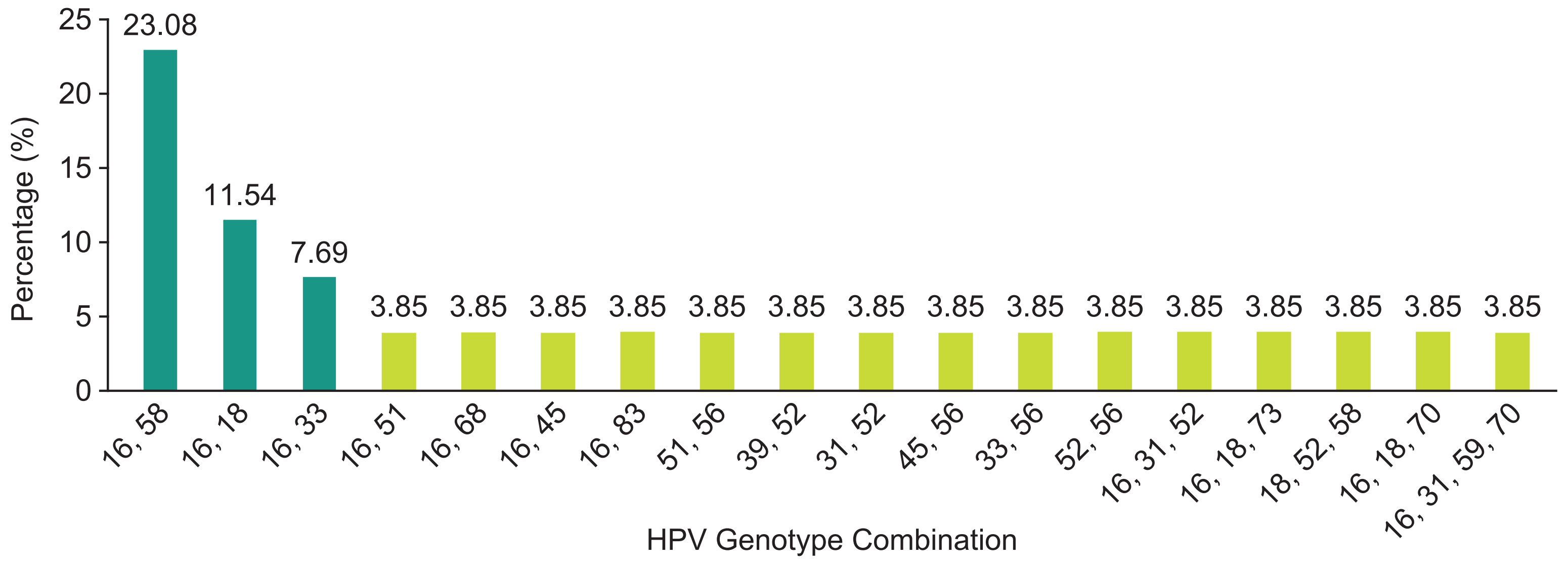


Figure 2. Frequency of multiple genotype combinations (%)



Conclusions

This study provides valuable insights into the distribution of HPV genotypes in cervical invasive cancer samples from Ecuadorian women. The results indicate an elevated presence of HPV 16, HPV 18, and HPV 58, these types being vaccine-preventable.

Further studies are needed in order to provide more insights in HPV prevalence in women and men, and to understand the impact of HPV-related disease on Ecuador health system.

References

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Disclosure

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