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Prevalence of infection with high-risk human papillomavirus in women in Colombia

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Abstract

The prevalence of human papillomavirus (HPV) infections in 2109 females inhabiting five cities of Colombia was determined. Of the 49.2% with an HPV infection, 59.8% were infected with more than one viral type. Species 7 (of the the genus *Alphapapillomavirus*) was associated with multiple infections. Analysis of the socio-demographic data revealed a statistically significant protective effect associated with the status of civil union (civil recognition of cohabitation without marriage), and indigenous ethnicity proved to be a risk factor for HPV infection. This is the first study comparing HPV infection among women from geographical regions of Colombia with different socio-cultural structures.

Keywords: Colombia, genotypes, high-risk HPV, human papillomavirus, multiple infections

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Cervical cancer (CC) has been primarily associated with infection with high-risk human papillomavirus (HPV) (HR-HPV) types, mainly with *Alphapapillomavirus* species 7 (HPV-18, HPV-39, HPV-45, HPV-59 and HPV-68) and species 9 (HPV-16, HPV-31, HPV-33, HPV-35, HPV-52, HPV-58 and HPV-67) [1].

Although prior HPV infection is a necessary step for the development of CC, there are several other factors that can increase the risk of developing CC, including age, number of sexual partners, age at first intercourse, pregnancies, smoking habits, contraceptive methods, and co-infection with other pathogens or different HPV types [2]. Co-infection with other pathogens or different HPV types (which ranges in frequency between 30% and 40% around the world [3,4]) especially contributes to the severity of the lesions.

Colombia is one of the countries with the highest incidence of CC in the world, the disease affecting 23–48 individuals per 100 000 females, mainly those aged 30–39 years [5]. The present study involved females from five geographical regions, where CC mortality rates ranged between 3.12 and 5.67 [6]: Leticia (Amazon jungle); Chaparral, mainly inhabited by a mestizo population; Tumaco, where most of the black females enrolled in this study live; Bogota, the country's capital; and Girardot, a tourist destination.

The study involved 2109 women (mean age 38.8 years), attending a local CC prevention programme during 2007, from the different regions as follows: 173 women from the League Against Cancer (Leticia, south-east Colombia); 174 women from the Hospital San Juan Bautista (Chaparral region); 921 women from the Hospital de Engativa (Bogota); 334 women from the Nuevo Hospital San Rafael de Girardot-Cundinamarca (central Colombia); and 508 women from the Hospital San Andres de Tumaco-Nariño (south-west Colombia). Each patient filled out a questionnaire regarding risk factors and gave her signed consent. The study was supervised and approved by each institution's ethics committee.

All cervical epithelium samples were preserved in 95% ethanol [7]. Samples were washed with phosphate-buffered saline and digested in lysis buffer [8]. To assess cervical sample integrity, the human β-globin gene was amplified using the GH20/PC04 primers, as previously described [9].

Samples yielding DNA of adequate quality were amplified following two PCR protocols using consensus primers GP5+/GP6+ and MY09/MY11 [10]. HPV DNA-positive samples, according to one or both generic amplification reactions, were assessed by DNA amplification with HR-HPV-16, HR-HPV-31, HR-HPV-33, HR-HPV-45, HR-HPV-58 and HR-HPV-18 type-specific primers [11–13]. The viral types HPV-16, HPV-31, HPV-33 and HPV-58 were grouped into species 9, and viral types HPV-18 and HPV-45 were grouped into species 7 [14].

Owing to poor DNA quality, 295 samples were excluded. Of the remaining samples, 921 (50.8%) were negative for viral DNA. The 893 positive samples (49.2%) were included in the statistical analysis. As shown in Table 1, the HPV-16 type (species 9) was the most prevalent in single infections but appeared at the lowest rate in multiple infections.

Regarding species 7, HPV-18 was the second most prevalent type in single infections, whereas HPV-45 was found only in multiple infections. These results agree with those of previous reports showing that genotypes belonging to this species are more often present in multiple infections than in single infections [15].

The study revealed a higher viral prevalence and percentage of multiple infections than previous reports [4,16]. This higher prevalence could be explained by the use of both viral DNA amplification primer sets, the MY09/11 system being more efficient in detecting viral DNA (38.8%) than the GP5+/GP6+ set (17.3%) (data not shown). All viral types assessed in this study had a higher prevalence when associated with multiple infections. Within the single-infection group, HPV-16 was the most representative genotype, thus contributing to the highest prevalence of species 9. The high frequency of this type could not be attributed to the infection mechanism, as all HPV genotypes involved in the study have the same transmission mechanism [17]. Nevertheless, the analysis was clearly limited by the cross-sectional study design, as it failed to accurately establish whether infection with HPV-16 conferred a higher risk of concomitant infection with other viral types.

TABLE 1. Distribution of human papillomavirus (HPV) types associated with single and multiple infections

HPV type (%)	Species	Single infection, *n* (%)	Multiple infections, *n* (%)
16 (46.2)	9	321 (38.3)	518 (61.7)
31 (15.9)	9	4 (1.4)	286 (98.6)
33 (10.6)	9	1 (0.52)	193 (99.5)
58 (5.1)	9	3 (3.2)	91 (96.8)
18 (14.7)	7	30 (11.2)	238 (88.8)
45 (9.4)	7	0	172 (100)
Total	–	359 (40.2)	534 (59.8)

Associations between categorical variables (age, age at first intercourse, number of sexual partners, and number of pregnancies) were assessed using ORs and 95% CIs. ORs were adjusted according to a logistic regression model, where the presence or absence of co-infection was the main outcome variable. All statistical procedures were performed using STATA software.

TABLE 2. Behavioural and socio-demographic factors associated with single and multiple infections

Variables	Single infection, *n* (%)	Multiple infections, *n* (%)	Crude ORs (95% CI)	Adjusted ORs[a] (95% CI)
Age (years)				
<25	49 (35.8)	88 (64.2)	–	–
26–40	154 (44.4)	193 (55.6)	0.71 (0.43–1.17)	0.71 (0.42–1.19)
>40	156 (38.1)	253 (61.9)	0.75 (0.42–1.3)	0.69 (0.38–1.26)
Pregnancies				
None	23 (33.8)	45 (66.2)	–	–
1–2	120 (39.6)	183 (60.4)	1.01 (0.52–1.97)	1.05 (0.53–2.09)
3–4	136 (44.2)	172 (55.8)	0.84 (0.41–1.71)	.86 (0.41–1.81)
>4	70	110 (61.1)	1.15 (0.53–2.47)	1.29 (0.58–2.88)
Sexual partners				
1	145 (38.1)	236 (61.9)	–	–
2–3	156 (41.4)	221 (58.6)	0.78 (0.56–1.10)	0.82 (0.57–1.17)
>3	39 (42.9)	52 (57.1)	0.66 (0.381–1.14)	0.74 (0.40–1.23)
Contraceptive method				
None	142 (39.9)	214 (60.1)	–	–
Hormonal	39 (39.8)	59 (60.2)	1.25 (0.61–2.56)	0.9 (0.66–1.46)
Surgery	110 (43.3)	144 (56.7)	1.01 (0.69–1.47)	0.77 (0.35–1.69)
Condom	15 (37.5)	25 (62.5)	0.89 (0.42–1.86)	1.16 (0.69–1.95)
Intrauterine device	41 (40.6)	60 (59.4)	1.01 (0.61–1.67)	0.60 (0.29–1.21)
Status				
Single	43 (29.7)	102 (70.3)	–	–
Married	76 (37.1)	129 (62.9)	0.58 (0.32–1.04)	0.63 (0.34–1.17)
Civil union	204 (46.4)	236 (53.6)	**0.55 (0.33–0.92)**	**0.57 (0.33–0.99)**
Separated	25 (41)	36 (59)	0.52 (0.25–1.06)	0.49 (0.23–1.04)
Widowed	10 (37)	17 (63)	0.85 (0.3–2.41)	0.77 (0.25–2.34)
Ethnicity				
White	37 (24.5)	114 (75.5)	–	–
Indigenous	6 (20)	24 (80)	1.83 (0.63–5.31)	**3.30 (1.03–10.5)**
Mestizo	212 (41.2)	303 (58.8)	**0.57 (0.37–0.88)**	1.44 (0.84–2.46)
Black	99 (54.7)	82 (45.3)	**0.35 (0.20–0.58)**	1.38 (0.65–2.94)
Age at first intercourse (years)				
<15	86 (41.7)	120 (58.3)	–	–
16–19	176 (39.6)	268 (60.4)	1.07 (0.73–1.57)	1.07 (0.73–1.57)
>19	82 (39)	128 (61)	1.00 (0.62–1.62)	1.00 (0.62–1.62)

Values in bold had $p < 0.05$.
[a]OR adjusted for age, number of pregnancies, age at first intercourse, number of sexual partners, ethnicity, geographical region, and contraceptive method.

When ORs were estimated without considering the geographical origin of the sample (Table 2), the status of civil union (frequent in Colombia) and ethnicity (mestizo and black) appeared to be the main significant factors associated with a lower risk of co-infection (taking single status and white ethnicity, respectively, as references). When the ORs were adjusted, the status of civil union remained a protective factor, possibly due to the lower number of sexual partners and the habitual use of oral contraceptive methods associated with this status, as compared to the increased risk of sexual behaviours associated with other statuses (e.g. single) [18].

Conversely, indigenous ethnicity proved to be associated with a higher risk of co-infection once the ORs were adjusted, possibly due to the vulnerability of this population related to the conditions under which they live (poverty, deficient diet, unprotected sexual behaviour, poor access to adequate health services, etc.) [19]. However, the higher risk may also be related to intrinsic biological and cultural characteristics, or to environmental factors associated with this ethnic group; these possibilities were not taken into consideration in this study, but should be analysed in further studies.

Previous studies in Colombian women involved mainly urban populations with better access to health services and a more uniform racial distribution, whereas this study analysed different geographical regions and considered a more ethnically diverse population. The differential geographical distribution seen in this study stresses the importance of applying HPV control measures in accordance with the HPV prevalance observed in each region.

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Transparency Declaration

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