

A Wider Screening of High-Risk Oncogenic Human Papillomaviruses in Cameroon Calls for An Optimized Generation of Vaccine-Clade Coverage

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Short Report

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Abstract

Background: High-risk oncogenic human papillomaviruses (HR-HPV) are unevenly distributed worldwide, which may affect the effectiveness of current prophylactic vaccines. We assessed the molecular epidemiology of HR-HPV among Cameroonian women and its adequacy with existing vaccine valence.

Methods: Sexually active, unvaccinated women aged 18 years or older were enrolled between June 2020 and May 2022 in two reference hospitals in Yaoundé and Douala, Cameroon. Cervical samples were screened for HR-HPV by real-time PCR, genotyped using a second real-time PCR platform, and discordant or uninterpretable results were confirmed with a third multiplex real-time PCR assay. Logistic regression identified factors associated with HR-HPV positivity.

Results: Of 413 women enrolled (median age 40 years, interquartile range 33 to 49), 96 (23.2%, 95% confidence interval 17.2 to 25.6) tested positive for HR-HPV. Thirteen genotypes were identified, most frequently HPV18 (19.8%), HPV16 (16.7%), HPV58 (16.7%), HPV39 (15.6%), HPV66 (13.5%), and HPV59 (12.5%). Multiple-genotype infections were detected in 37.5% of positive samples, ranging from two to five genotypes per specimen. Cytological abnormalities were observed in 70 women (17%), mostly low-grade lesions. First sexual intercourse before age 15, more than three lifetime sexual partners, and the presence of cervical lesions were significantly associated with HR-HPV positivity.

Conclusion: HR-HPV infection is common among Cameroonian women, with wide genotypic diversity and frequent multiple infections. Non-vaccine genotypes such as HPV39, HPV59 and HPV66 were among the most frequent, a pattern that may warrant consideration of broader-valence HPV vaccines in this setting, alongside continued investment in cervical cancer screening programmes.

Background

Human papillomavirus (HPV) infection remains a major global health issue, largely because of its central role in cervical cancer, the second leading cause of cancer-related death among women worldwide [1]. HPV is one of the most common sexually transmitted infections, with a 60–70% lifetime risk of acquisition among sexually active women, although more than 90% of immunocompetent women clear the infection within 12 to 24 months [2, 3]. Persistent infection with high-risk HPV (HR-HPV) genotypes is the main driver of precancerous lesions and their progression to cervical cancer, which caused an estimated 604,000 new cases and 342,000 deaths in 2020 [4, 5]. Of the more than 200 HPV genotypes described, at least 14 are classified as high-risk – HPV16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66 and 68 – with HPV16 and HPV18 together responsible for around 70% of invasive cervical cancers worldwide [6, 7].

Persistent HR-HPV infection and cervical carcinogenesis are influenced by co-factors such as high parity, prolonged use of hormonal contraceptives, tobacco smoking, coinfection with other sexually transmitted infections, early age at first intercourse, and a higher number of lifetime sexual partners [3, 8, 9]. In a context of limited vaccination coverage, primary prevention of HR-HPV in sub-Saharan Africa must

therefore rely on evidence generated locally on circulating genotypes [3, 8, 9]. Vaccination substantially reduces the risk of HPV-related cancers [10, 11], yet cervical cancer remains the second most common cancer among women worldwide, and HPV infection also raises the risk of anal, vaginal, vulvar, oropharyngeal, lung and bladder tumours, reinforcing the need for early diagnosis and screening in high-risk populations [12–14]. In Cameroon, the quadrivalent vaccine (Gardasil 4) has been introduced, but safety concerns, misconceptions about its effects on sexual behaviour, and limited awareness continue to hamper vaccination coverage among the target population of sexually naïve adolescent girls [15–17]. The overall success of these campaigns could be undermined if the vaccine valence does not match locally circulating genotypes. We therefore assessed the molecular epidemiology of HR-HPV among Cameroonian women.

Main text

Study design, sites and period

A cross-sectional analytic study was conducted between June 2020 and May 2022 at two reference hospitals for cervical cancer management: the Gynaecological-Obstetric and Paediatric Hospital of Yaoundé (GOPHY) and the Laquintinie Hospital of Douala (LHD), Cameroon.

Study population

Eligible participants were sexually active, unvaccinated women aged ≥ 18 years, recruited by convenience sampling; pregnant women and those with a prior total hysterectomy were excluded. A standardised questionnaire captured socio-demographic, gyneco-obstetric and reproductive history data, and whole blood and cervical samples were collected from all consenting women. The minimum sample size, calculated at 313 using an expected cervical cancer prevalence of 23.6% ($Z\alpha = 1.96$, $d = 0.05$), was exceeded, with 413 women enrolled.

Sample processing and cytology

Cervical brush samples (Rovers Medical Devices) were rinsed into PreservCyt solution and processed on a ThinPrep processor for DNA extraction, following a previously described protocol. Cervico-vaginal smears were prepared using the standard Papanicolaou stain and interpreted by experienced pathologists according to the 2001 Bethesda system, as normal, inflammatory, low-grade (LSIL) or high-grade (HSIL) squamous intraepithelial lesions [18, 19].

Genotyping algorithm

All samples were first screened using the Abbott RealTime High-Risk HPV assay, which simultaneously detects HPV16, HPV18, and pools 12 other HR-HPV genotypes (31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66,

68). Positive samples were genotyped using the Sacace HPV Genotypes 14 Real-TM Quant platform [9, 20]. Samples with discordant or uninterpretable results between the two platforms were confirmed using the Anyplex™ II HPV28 assay (Seegene), performed at the Virology Laboratory of CHU Bichat-Claude Bernard, Paris [21]. HIV testing, CD4 count and HPV genotyping were performed at the Chantal BIYA International Reference Centre (CIRCB), Yaoundé.

Data analysis

Data were entered in Excel 2016 and analysed using Epi Info version 7 and GraphPad Prism version 6. Odds ratios (OR) with 95% confidence intervals (CI) were calculated, and variables with $p \leq 0.2$ in univariate analysis were entered into a multivariable logistic regression model to identify factors independently associated with HR-HPV positivity; statistical significance was set at $p < 0.05$.

Ethical considerations

Ethical approval was obtained from the National Ethics Committee (ref. 2020/06/1249/CE/CNERSH/SP), in accordance with the Declaration of Helsinki, with administrative authorisation from both study sites. Written informed consent (in both national languages) was obtained from all participants, and laboratory results were provided free of charge for their clinical benefit.

Results

Study population. Of 413 women enrolled, the median age was 40 years (IQR 33–49). Most participants had secondary or university education (85.98% versus 14.02% with primary education or less); 61.26% were married, divorced or widowed; 53.57% identified as Christian; 52.74% reported a personal source of income; and 77.47% had more than four children. Regarding sexual history, 74% reported more than three lifetime sexual partners and 81.04% had their sexual debut before age 20. Clinically, 3.02% smoked, 3.6% were HIV-positive, 53.02% used contraceptives, and 7.41% had an abnormal Pap smear.

HR-HPV positivity and associated factors. Overall, 96 of 413 women (23.2%, 95% CI 17.2–25.6) tested positive for HR-HPV. Positivity was higher among women under 40 years, among those with sexual debut before age 15 (67.0% versus 24.2% for debut after age 20; $p < 0.01$), and among those reporting three or more lifetime sexual partners (37.5% versus 25.2%; $p < 0.01$) (Table 1). Cervical lesions were also significantly associated with HR-HPV positivity ($p < 0.01$; Table 1).

Table 1

Distribution of HR-HPV positivity and associated factors in the study population (bivariate analysis).

Characteristic		Positive	Negative	Total	OR (95% CI)	p
Coitarche	> 20 years	22 (24.2)	77 (23.9)	99 (24.0)	1	
	15–20 years	8 (8.8)	220 (68.3)	228 (55.2)	7.8 (3.3–18.4)	< 0.01
	≤ 15 years	61 (67.0)	25 (7.8)	86 (20.8)	0.1 (0.1–0.2)	< 0.01
Sexual partners	< 3	60 (62.5)	237 (74.8)	297 (71.9)	1	
	≥ 3	36 (37.5)	80 (25.2)	116 (28.1)	0.7 (0.4–1.2)	< 0.01
Cervical smear	Normal	50 (54.9)	126 (39.1)	176 (42.6)	1	
	NIL/M	26 (28.6)	136 (42.2)	162 (39.2)	2.1 (1.2–3.5)	< 0.01
	LSIL	2 (2.2)	37 (11.5)	39 (9.4)	7.3 (1.7–31.6)	< 0.01
	HSIL	8 (8.8)	9 (2.8)	17 (4.1)	0.4 (0.2–1.2)	0.11

Molecular epidemiology. Thirteen HR-HPV genotypes were identified among the 96 positive samples: HPV18 (19.8%), HPV16 (16.7%), HPV58 (16.7%), HPV39 (15.6%), HPV66 (13.5%), HPV59 (12.5%), HPV35 (9.3%), HPV68 (8.3%), HPV45 (8.3%), HPV52 (7.3%), HPV51 (6.3%), HPV56 (5.2%), and HPV33 (2.1%) (Fig. 1). Multiple-genotype infections were detected in 37.5% (36/96) of positive women, with 2 to 5 genotypes identified per specimen.

Discussion

This study assessed the molecular epidemiology of HR-HPV among Cameroonian women attending two reference hospitals. The overall positivity rate of 23.2% is consistent with prevalence figures reported across sub-Saharan Africa, though higher than the global average of 11–12%, and lower than the 32% reported in Ghana [22], 26% in Tanzania [23], 21% in South Africa [24], and 25% in Burkina Faso [25] – studies conducted in younger populations (median age < 30 years) compared with our cohort (median age 40 years). HPV prevalence is known to peak in young women shortly after sexual debut and to decline with age as immunity develops and infections clear [26, 27].

We identified 13 circulating HR-HPV genotypes, confirming the substantial heterogeneity of genotype distribution previously reported across sub-Saharan Africa [28, 29]. More than a third of positive women (37.5%) carried multiple genotypes (2 to 5 per specimen), a range comparable to that reported by Traoré et al. [30] and Ouedraogo et al. [31] in Burkina Faso. While HPV16 and HPV18 remained prominent, consistent with global epidemiology [32, 33], several other genotypes – notably HPV39 and HPV58 – were also frequent, a pattern also observed by Jary et al. in Mali and Ferré et al. in Togo [12, 21], and elsewhere in the region [8, 34]. Taken together, these findings suggest that the genotype profile circulating in Cameroon only partly overlaps with the valence of currently available vaccines, which

target HPV16 and HPV18. This observation may warrant consideration, in future studies and policy discussions, of broader-valence vaccines such as the nonavalent formulation, alongside efforts to improve vaccination coverage among girls aged 9 to 14 before sexual debut, in line with WHO recommendations.

Consistent with the literature [35–39], women reporting more than three lifetime sexual partners had higher odds of HR-HPV positivity, and those with a sexual debut at or before age 15 had the highest positivity rate (67%), likely reflecting the greater vulnerability of the immature adolescent cervix to infection [8, 40–42]. Contrary to the pattern generally described, in which HR-HPV is more frequently identified in women with cervical lesions, our data showed the opposite trend, with fewer HR-HPV genotypes detected among women with lesions than among those without [12, 16]; this unexpected finding warrants further investigation, including assessment of lesion chronicity and prior treatment history.

Limitations

This study has several limitations. Participants were recruited by convenience sampling at two urban reference hospitals, which limits the generalisability of prevalence estimates to the wider Cameroonian population, particularly rural settings. The cross-sectional design precludes any causal interpretation of the associations identified. The relatively small number of HR-HPV-positive women ($n = 96$) limited the statistical power of the multivariable analysis, particularly for genotype-specific comparisons.

Conclusion

This study confirms a substantial burden of HR-HPV infection among Cameroonian women, marked by wide genotypic diversity and frequent multiple infections. Non-vaccine genotypes such as HPV39, HPV59 and HPV66 were among the most frequently detected, alongside HPV16 and HPV18. These findings support continued molecular surveillance of circulating HR-HPV genotypes in Cameroon and the surrounding sub-region, to inform discussions on optimising vaccine valence and strengthening cervical cancer screening programmes in tropical, resource-limited settings.

Abbreviations

CD4

Cluster of differentiation 4

CI

Confidence interval

CIRCB

“Chantal BIYA” International Reference Centre for research on HIV/AIDS prevention and management

DNA

Deoxyribonucleic acid

GOPHY

Gynaecological-Obstetric and Paediatric Hospital of Yaoundé

HIV

Human immunodeficiency virus

HPV

Human papillomavirus

HR-HPV

High-risk oncogenic human papillomavirus

HSIL

High-grade squamous intraepithelial lesion

IQR

Interquartile range

LHD

Laquintinie Hospital of Douala

LSIL

Low-grade squamous intraepithelial lesion

OR

Odds ratio

PCR

Polymerase chain reaction

WHO

World Health Organization.

Declarations

Ethics approval and consent to participate

Ethical approval was obtained from the Cameroon National Ethics Committee for Research on Human Health (ref. 2020/06/1249/CE/CNERSH/SP), in accordance with the Declaration of Helsinki, with administrative authorisation from the Gynaecological-Obstetric and Paediatric Hospital of Yaoundé and the Laquintinie Hospital of Douala. Written informed consent (in both national languages) was obtained from all participants prior to enrolment.

Consent for publication

Not applicable.

Availability of data and materials

The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

Competing interests

The authors declare that they have no competing interests.

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Authors' contributions

Initiated the manuscript: MCTT, JF, LGMF, VMF, BFB, DTY, DKKK, JEG. **Revised substantially the manuscript:** MCTT, JF, SMS, ENJS, BY, RKS, AN, ADN, NF, JEG, CC(Chenwi), DKKK, ACK, DTY, CFP, VC and VMF. **Contributed to data acquisition and analysis:** MCTT, LGMF, JEG, CC(Charpentier), JF, SMS, ENJS, BY, NF, DTY, CC(Chenwi), ACK, DKKK, VMF. **Contributed to data interpretation:** MCTT, ENJS, BY, CFP, CC(Charpentier), VC, JF and AN. **Approved the final version for publication:** all authors.

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Figures

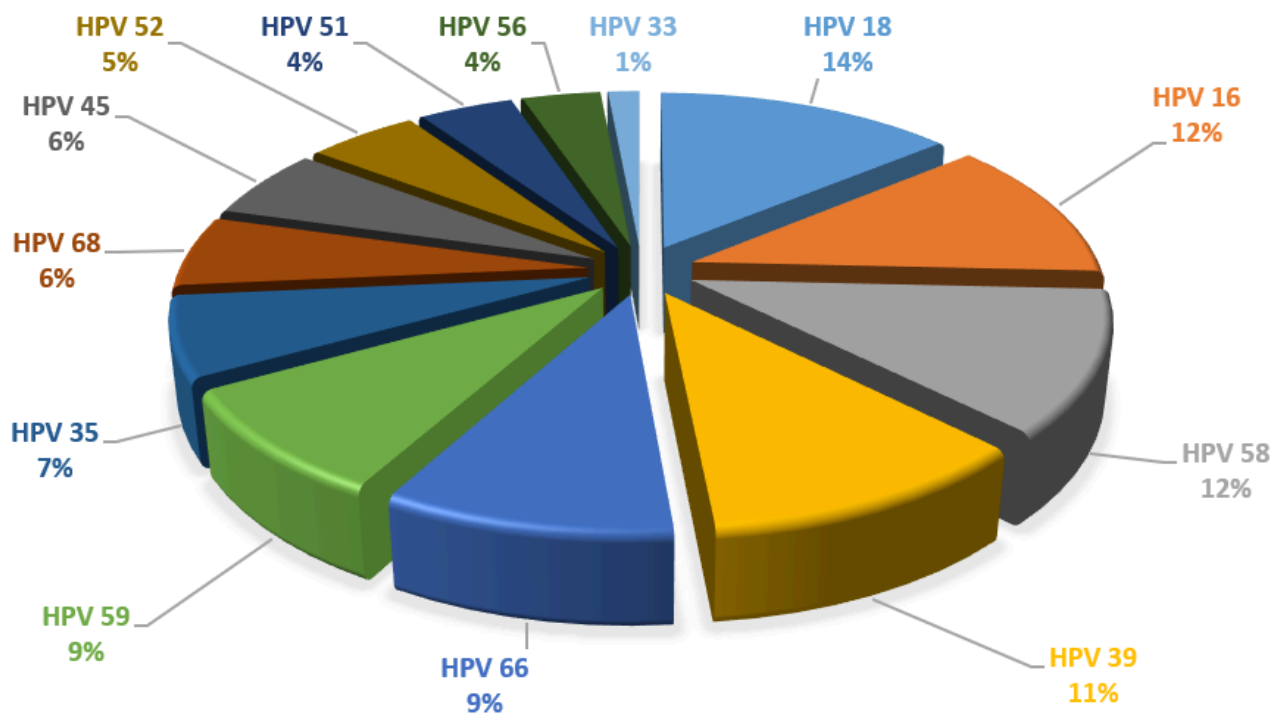


Figure 1

Distribution of participants according to HR-HPV genotype.