Gynecologic Oncology Reports 56 (2024) 101526

Contents lists available at ScienceDirect

Gynecologic Oncology Reports

journal homepage: www.elsevier.com/locate/gynor

Prevalence and genotype distribution of high-risk *Human Papillomavirus* infection among Vietnamese women in Ho Chi Minh City, Viet Nam: A population-based cross-sectional study

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ARTICLE INFO

Keywords:
Human Papilomavirus
High-risk HPV infection
HPV genotype
Viet Nam

ABSTRACT

Introduction: Persistent infection with high-risk *Human Papillomavirus* (HR-HPV) genotypes are wellknown to increase the risk of cervical cancer significantly. This study aims to determine the prevalence and distribution of high-risk HR-HPV genotypes among women in Ho Chi Minh City (HCMC), Viet Nam.

Methods: A population-based cross-sectional study was conducted between June 2020 and September 2020 in all 24 districts of HCMC, Viet Nam. Socio-demographic and behavioral data were collected from 2478 women aged 25 to 65 who had sexual intercourse using a self-administered questionnaire. Vaginal swab specimens from all participants were collected to identify HR-HPV genotypes using Polymerase Chain Reaction (PCR) protocols.

Results: The prevalence of HR-HPV infection was 3.5 % (87 women, including 20 cases infected with multi-genotypes), 3.1 % in urban and 0.4 % in rural areas. The most detected HR-HPV genotypes among positive cases were 58 (25.3 %), 52 (21.8 %), 16 (21.8 %), 68 (10.3 %), 51 (10.34 %) and 18 (9.2 %). The prevalence of multi-type HR-HPV genotypes was 0.81 %, of which the most common co-infection genotypes were 52 and 58 (20.0 %), 16 and 56 (10.0 %), and 16 and 39 (10.0 %). The percentages of one-, two-, three-, and four-genotypes of HPV among positive cases were 77.0 %, 16.1 %, 4.6 % and 2.3 %, respectively.

Conclusions: Our findings explore a low prevalence of HR-HPV infection in Vietnamese women, of which genotypes 52 and 58 are more popular than 16 and 18. Continuously updated data on the genotype distribution of HPV are helpful for vaccine development and planning preventive activities to prevent HPV-related cancers.

1. Introduction

Globally, in 2020, cervical cancer was the fourth most common diagnosed cancer and cancer-related death in women (Sung et al., 2021). Between 1990 and 2019, there was a decrease in the incidence (from 7.64 to 6.81 per 100.000 population) and mortality rate (from 4.46 to 3.40 per 100.000 population) of cervical cancer due to vaccination, advances in medical treatment and diagnosis, and the improvement of socioeconomic status. However, the absolute number of incident cases (from 335.64 to 565.54 million) and deaths (from 184.53 to 280.48 million) still increased significantly in the recent past three decades (Yang et al., 2022). There was a sharp divergence in the declining burden of cervical cancer when the stable decreasing trend was observed in Human Development Index (HDI) countries in contrast with an unacceptably slow reduction rate in low– and middle-income countries (LMICs) (even increasing in certain countries in eastern Europe and sub-Saharan Africa) (International Agency for Research on Cancer, 2020; Singh et al., 2023). Globally, LMICs contributed to 84.0 % of incidence and from 87.0 % to 95.0 % of cervical cancer mortality (Ebrahimi et al., 2023).

Human Papillomavirus (HPV) was the most common sexually transmitted infection and the second-leading cause of incidence of infection-attributable cancer (de Martel et al., 2020). Although HPV infection was not a sufficient cause of cervical cancer, persistent infection with HR-HPV was a well-established cancer cause (Walboomers et al., 1999). However, cervical cancer was preventable, particularly by vaccination

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https://doi.org/10.1016/j.gore.2024.101526
Received 11 August 2024; Received in revised form 22 September 2024; Accepted 1 October 2024
Available online 9 October 2024

and screening. As an effective solution to prevent the precursors to cervical cancer, HPV vaccines played a crucial role in a global campaign to eliminate cervical cancer called by WHO together with cervical cancer screening and management of detected disease (WHO, 2020; de Sanjose et al., 2019). A modeling study predicted that scaled-up vaccination and HPV-based screening could result in a cumulative effect on averting the number of cervical cancer cases (Simms et al., 2019). Beneficial impact of HPV vaccination on cervical cancer incidence and mortality was shown in high-income countries (Singh et al., 2023; Falcaro et al., 2021). However, there were considerable challenges in LMICs to implement HPV-based screening and vaccination due to limited resources (Tsu et al., 2021). Despite the increased number of LMICs initiating HPV vaccination, only 41 % of LMICs introduced the HPV vaccination program in mid-2020 (Tsu et al., 2021).

In Viet Nam, cervical cancer was the third most common cancer among women aged 15 to 44 years, with 4177 new cases annually (Bruni, 2019). However, published data on HPV infection and the distribution of its genotypes was minimal, particularly in the general women population (Tran et al., 2015; Dung et al., 2017; Van et al., 2017; Tran et al., 2018). This study aims to determine the prevalence and distribution of genotypes of high-risk HPV infection among women in Ho Chi Minh City (HCMC), Viet Nam.

2. Materials and Methods

2.1. Study design and settings

This population-based cross-sectional study was conducted in HCMC, Viet Nam, between June and September 2020. HCMC was the south city in Viet Nam, the second most populous city nationally, with more than 8.6 million inhabitants living in 24 districts (in 2020) (World Population Review, 2023). This study recruited women from all 24 districts participating in the cervical cancer screening program, jointly organized by the HCMC People's Committee, HCMC Department of Health, and Family Health International organization (FHI 360) to screen cervical cancer HCMC residents.

2.2. Participants, sample size, and sampling

A formula to calculate adequate sample size for estimating the proportion in prevalence study was applied, with p of 0.09 being the prevalence of HR-HPV infection among HCMC women reported by Tran et al. (2015) (Tran et al., 2015), d of 0.025, and Z(1-α/2) of 1.96. The minimal sample size was determined to be 2014. The number of participants for each district was identified based on its proportion to the total population of HCMC in 2020. Then, one ward/commune in selected districts was chosen randomly, followed by two of its next wards/communes to form a cluster of three adjacent wards/communes chosen in each district. All women aged 25–65 years in selected wards/communes were invited to participate in the study by community health workers.

Eligible participants included registered women residents aged 25–65 years living in Ho Chi Minh City for at least six months, whoever had sexual intercourse and agreed to participate. Exclusion criteria included (1) women with a uterine cancer diagnosis or treatment, (2) being pregnant, or (3) having a history of hysterectomy. Participants were fully informed of the purpose and procedure of the study, as well as the benefits and risks of participation, before obtaining their written informed consent. Among 4800 eligible women who joined the cervical cancer screening program, 2478 were invited to participate in the study and agreed to have HPV tests (Fig. 1).

2.3. Data collection

Data on participants' demographic and behavioral characteristics and their husbands/partners was collected using a self-administered questionnaire. Trained personnel introduced and consented to the women; those who agreed to participate filled out a designed questionnaire. Data included age (25–35, 36–45, 46–55, 56–65 years), residential area (urban, rural), education level (secondary school or lower, high school, higher high school, unknown/missing), number of children (0, 1, 2, ≥3, unknown/missing), HPV vaccination (yes, no, unknown/missing), history of sexually transmitted diseases (STDs) (no, yes, unknown/missing), tobacco smoking (never, ever), age of first intercourse (<20, 20–26,>26) (Tran et al., 2015), lifetime number of partners (1,

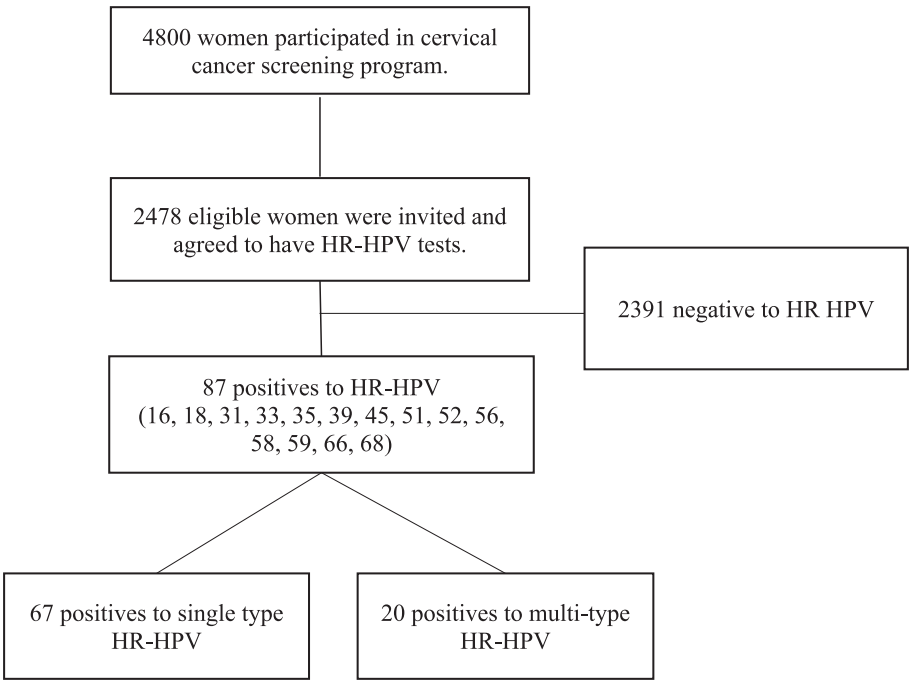

Fig. 1. Flow chart of participant recruitment.

>1), and regular condom use (regular, not regular/not use). Data of the women's husband/partner was also obtained, comprising education level (secondary school/ lower, high school, higher high school, unknown/missing), smoking history (never, ever), history of STDs (no, yes, unknown/missing), and lifetime number of sexual partners (1, >1).

Trained community health workers did a speculum examination and took a cervical swab from each woman. The cervical specimens were placed in storage tubes and transferred daily to a standard HCMC Department of Health accredited laboratory. A two-stage procedure using real-time PCR technology was performed to detect HR-HPV genotypes, including qualitative screening and genotype detection. All positive specimens detected by qualitative screening were genotyped based on real-time PCR technology, with a sensitivity of 1,000 copies/ml and specificity of 100 %. This test procedure could detect 14 high-risk HPV genotypes of 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, and 68 (Sacace Biotechnologies and Genotypes 14 Real-TM Quant, 2020).

2.4. Data analysis

Data were analyzed using Stata version 15.0 (Stata Corp, College Station, Texas). The prevalence of HR HPV infection of single-genotypes and multi-genotypes was calculated. Logistic regression was used to calculate Odds Ratios (ORs) and 95 % confidence intervals (95 % CIs) to estimate the association between demographic and behavioral characteristics of women and their partners with the HR-HPV infection. All variables with a p-value of <0.2 in the bivariate model were chosen to develop a multivariate model of related factors of HR-HPV infection. All p-values were two-sided, and a p-value of $\leq$ 0.05 (alpha value) was considered to indicate statistical significance.

3. Results

Table 1 shows the characteristics of participants and the prevalence of single-genotype and multi-genotype HR-HPV infection. The mean age of women was 45.1 $\pm$ 10.0 years. The mean age of first intercourse was reported at 24.2 $\pm$ 4.4 years (100 unknown/missing data). Most participants lived in urban areas (79.3 %) and were married (86.2 %). Almost all women (90.1 %) had a lifetime of one sexual partner, and 2.5 % had a history of STDs. Most women did not use condoms (90.8 %). Only 4.0 % of participants reported getting HPV vaccination.

The prevalence of HR-HPV infection was 3.5 % (95 %CIs: 2.8–4.3 %). All 14 surveyed HR-HPV genotypes were identified in our study (Fig. 2). Among positive women, the most common HR-HPV genotypes detected were 58 (25.3 %), 16 (21.8 %), 52 (21.8 %), 68 (10.3 %), 51 (10.3 %) and 18 (9.2 %) (Supplementary 1). The percentage of multi-genotype HR-HPV infection was 0.8 % (95 %CIs: 0.5–1.2 %), of which the most common genotypes of HR-HPV co-infections consisted of 52 and 58 (20.0 %), 16 and 56 (10.0 %), and 16 and 39 (10.0 %) (Supplementary 2). Among 87 positive cases, the percentages of one-, two-, three-, and four genotypes of HR-HPV were 77.0 % (67 cases), 16.1 % (14 cases), 4.6 % (4 cases), and 2.3 % (2 cases), respectively (Data not shown).

Table 2 illustrates the analysis of the association between demographic and behavioral characteristics and HR-HPV infection. Univariate analysis suggested the difference in HR-HPV infection by residential area, education level, marital status, and women partner's education level. HR-HPV infection was significantly higher in urban areas (OR=2.06, 95 %CI: 1.06–4.00) than in rural areas; widowed/divorced/never married participants (OR=2.33, 95 %CI: 1.43–3.81) than married ones. However, in multivariate analysis, only marital status remained statistically significant (OR=2.15, 95 %CI: 1.08—4.25). There was no difference in HR-HPV infection by other characteristics of participants (e.g., age group, number of children, a history of HPV vaccination, history of STDs, tobacco smoking, age of first intercourse, the lifetime number of partners, and regular condom use, and participant's partner(s) (e.g., history of STDs). Because of a low frequency of

Table 1
Prevalence of high-risk HPV infection among Vietnamese women in Ho Chi Minh City, Viet Nam, 2020, by characteristics of participants.

Characteristics	n (%)	Any High-risk HPV infection		Multi-type high-risk HPV infection	
		n	Percentage (95 %CI)	n	Percentage (95 %CI)
Total	2478 (100)	87	3.5 (2.8, 4.3)	20	0.8 (0.5, 1.2)
Age groups					
25–35 years	501 (20.2)	16	3.2 (1.8, 5.1)	3	0.6 (0.1, 1.7)
36–45 years	793 (32.0)	32	4.0 (2.8, 5.6)	6	0.8 (0.3, 1.6)
46–55 years	727 (29.3)	31	4.3 (2.9, 6.0)	10	1.4 (0.7, 2.5)
56–65 years	457 (18.4)	8	1.8 (0.8, 3.4)	1	0.2 (0.0, 1.2)
Residual area					
Rural	514 (20.7)	10	1.9 (0.9, 3.5)	3	0.9 (0.5, 1.4)
Urban	1964 (79.3)	77	3.9 (3.1, 4.9)	17	0.6 (0.1, 1.7)
Education level of participant					
Secondary school or lower	1219 (49.2)	35	2.9 (2.0, 4.0)	4	0.3 (0.1, 0.8)
High school	623 (25.1)	31	5.0 (3.4, 7.0)	8	1.3 (0.6, 2.5)
Higher high school	619 (25.0)	20	3.2 (2.0, 4.9)	7	1.1 (0.5, 2.3)
Missing/Unknown	17 (0.7)	1	5.9 (0.1, 28.7)	1	5.9 (0.1, 28.7)
Education level of partner					
Secondary school or lower	1009 (40.7)	27	2.7 (1.8, 3.9)	6	0.6 (0.2, 1.3)
High school	701 (28.3)	25	3.6 (2.3, 5.2)	5	0.7 (0.2, 1.7)
Higher high school	594 (24.0)	21	3.5 (2.2, 5.4)	7	1.2 (0.5, 2.4)
Missing/Unknown	174 (7.0)	14	8.0 (4.5, 13.1)	2	1.1 (0.1, 4.1)
Marital status					
Married	2136 (86.2)	64	3.0 (2.3, 3.8)	13	0.6 (0.3, 1.0)
Widowed/divorced/ never married	342 (13.8)	23	6.7 (4.3, 9.9)	7	2.0 (0.8, 4.2)
Number of children					
0	99 (4)	5	5.1 (1.7, 11.4)	0	0.0
1	321 (13)	10	3.1 (1.5, 5.7)	6	1.9 (0.7, 4.0)
2	893 (36)	32	3.6 (2.5, 5.0)	7	0.8 (0.3, 1.6)
3 and higher	333 (13.4)	4	1.2 (0.3, 3.0)	1	0.3 (0.0, 1.7)
Missing/Unknown	832 (33.6)	36	4.3 (3.0, 5.9)	6	0.7 (0.3, 1.6)
HPV vaccination					
Yes	100 (4.0)	2	2.0 (0.2, 7.0)	0	0.0
No	2128 (85.9)	73	3.4 (2.7, 4.3)	16	0.8 (0.4, 1.2)
Missing/Unknown	250 (10.1)	12	4.8 (2.5, 8.2)	4	1.6 (0.4, 4.0)
Participant's history of STDs					

(continued on next page)

Table 1 (*continued*)

Characteristics	n (%)	Any High-risk HPV infection		Multi-type high-risk HPV infection	
		n	Percentage (95 %CI)	n	Percentage (95 %CI)
No	2232 (90.1)	77	3.4 (2.7, 4.3)	17	0.8 (0.4, 1.2)
Yes	62 (2.5)	3	4.8 (1, 13.5)	1	1.6 (0.0, 8.7)
Missing/Unknown	184 (7.4)	7	3.8 (1.5, 7.7)	2	1.1 (0.1, 3.9)
Partner's History of STDs					
No	2174 (87.7)	74	3.4 (2.7, 4.3)	18	0.8 (0.5, 1.3)
Yes	20 (0.8)	2	10.0 (1.2, 31.7)	1	5.0 (0.1, 24.9)
Missing/Unknown	284 (11.5)	11	3.9 (1.9, 6.8)	1	0.4 (0.0, 1.9)
Tobacco smoking					
Never	2438 (98.4)	87	3.6 (2.9, 4.4)	20	0.8 (0.5, 1.3)
Ever	40 (1.6)	0	0.0	0	0.0
Age of first intercourse					
<20	273 (11)	7	2.6 (1.0, 5.2)	0	0.0
20–26	1517 (61.2)	59	3.9 (3.0, 5.0)	14	0.9 (0.5, 1.5)
>26	588 (23.7)	19	3.2 (2.0, 5.0)	4	0.7 (0.2, 1.7)
Missing/Unknown	100 (4)	2	2.0 (0.2, 7.0)	2	2.0 (0.2, 7.0)
Participant's number of partner					
1	2232 (90.1)	73	3.3 (2.6, 4.1)	16	0.7 (0.4, 1.2)
>1	51 (2.1)	1	2.0 (0.0, 10.4)	1	2.0 (0.0, 10.4)
Missing/Unknown	195 (7.9)	13	6.7 (3.6, 11.1)	3	1.5 (0.3, 4.4)
Condom use (n = 2,225)					
Regular	228 (9.2)	7	3.1 (1.2, 6.2)	2	0.8 (0.5, 1.3)
Not regular/Not use	2250 (90.8)	80	3.6 (2.8, 4.4)	18	0.9 (0.1, 3.1)

multi-genotype HR-HPV infections (n = 20), the study did not explore its associated factors.

4. Discussion

We investigated a broad spectrum of HR-HPV genotypes based on a population-based cross-sectional study in HCMC, Viet Nam. The prevalence of HR-HPV infection among women aged 25–65 was 3.5 % (3.9 % in urban, 1.9 % in rural) and 0.8 % for multi-genotypes (0.9 % in urban, 0.6 % in rural). Our study reported a lower proportion than previous studies in Vietnamese women, ranging from 2 % to 11 % (Tran et al., 2015; Van et al., 2017; Vu et al., 2012; Vu et al., 2013; Vu and Le, 2011). A survey conducted on HCMC women residents in 2008 and 2009 reported a prevalence of 9.0 % for any type and 1.9 % for multi-type HR-HPV infection (Tran et al., 2015). Other research on married women in five large cities (2011) reported the infection of HPV type 16 and/or 18 ranged from 3.1 % (in Hanoi) to 7.4 % (in Can Tho), including HCMC (4.9 %) (Vu et al., 2013). An estimation by the HPV Information Centre for Viet Nam (Bruni, 2019) (updated data in 2017) indicated the prevalences of cervical HPV-16/18 infection in the general population were 2.1 %, 37.4 %, and 82.8 % in individuals with normal cytology, high-grade lesions, and cervical cancer, respectively (Bruni, 2019). Our study suggested a lower prevalence of HR-HPV infection in Vietnamese women compared to previous reports. This finding was consistent with a downtrend in the prevalence and incidence of HPV infection observed globally, either with or without vaccination (Yousefi et al., 2021). In 2016, the Viet Nam Ministry of Health (MOH) and the United Nations Population Fund (UNFPA) jointly launched a national plan to prevent and control cervical cancer (Viet Nam Ministry of Health and UNFPA, 2016). This plan implemented comprehensive intervention to reduce the burden of cervical cancer, including HPV vaccination and education for mature women, as well as screening and treatment of cervical pre-cancer and cancer. These implements might reduce risk factors for HPV infection, leading to a reduction of infection. A report by the Viet Nam MOH and UNFPA estimated a reduction of 300000 cervical cancer by 2100 under different scenarios of HPV vaccination, cervical cancer screening, and treatment (Viet Nam Ministry of Health and UNFPA, 2023).

Regarding the HR-HPV genotypes, the three most common types detected were 58, 16, and 52 (HPV-18 was only in the 6th position). In Viet Nam, there is limited epidemiological data on the distribution of HR-HPV genotypes in the general population. To our best knowledge, the most up-to-date publication was in 2017 (using 2015 data in Da Nang) (Van et al., 2017). This study found that 16, 18, 58, and 59 were the most common types of HR-HPV infections, respectively. Our finding differed from a systematic review, which analyzed seven publications

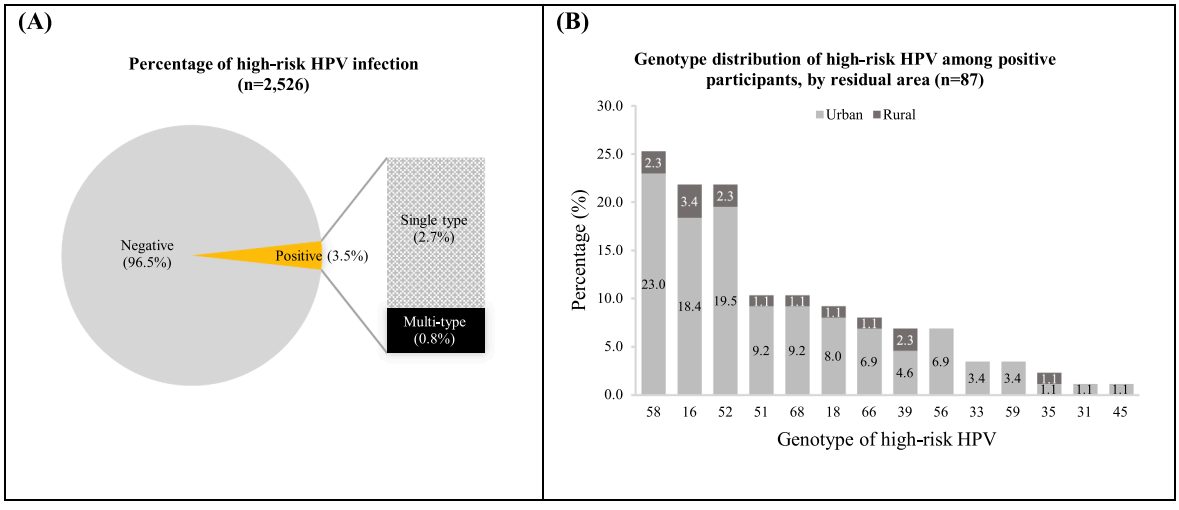

Fig. 2. Percentage of high-risk HPV infection (A) and genotype distribution among positive participants by residual area (B).

Table 2
Risk factors of high-risk HPV infection among Vietnamese women in Ho Chi Minh City, Viet Nam, 2020.

Characteristics	High-risk HPV		Crude OR (95 %CI)	P value	Adjusted OR (95 %CI)[a]	P value
	Positive (n = 87)	Negative (n = 2391)				
Age groups						
25–35 years	16	485	1		1	
36–45 years	32	761	1.27 (0.69, 2.35)	0.436	1.3 (0.67, 2.49)	0.437
46–55 years	31	696	1.35 (0.73, 2.50)	0.338	1.35 (0.67, 2.69)	0.402
56–65 years	8	449	0.54 (0.23, 1.27)	**0.160**	0.5 (0.19, 1.31)	0.161
Residual area						
Rural	10	504	1		1	
Urban	77	1887	2.06 (1.06, 4.00)	**0.034**	1.71 (0.83, 3.49)	0.143
Education level of women						
Secondary school/ lower	35	1184	1		1	
High school	31	592	1.77 (1.08, 2.90)	**0.023**	1.73 (0.95, 3.15)	0.073
Higher high school	20	599	1.13 (0.65, 1.97)	0.669	0.93 (0.41, 2.08)	0.854
Missing/Unknown	1	16	2.11 (0.27, 16.4)	0.474	1.03 (0.1, 10.36)	0.981
Education level of partner						
Secondary school/lower	27	982	1		1	
High school	25	676	1.35 (0.77, 2.34)	0.293	0.99 (0.51, 1.94)	0.986
Higher high school	21	573	1.33 (0.75, 2.38)	0.331	1.19 (0.55, 2.56)	0.654
Missing/Unknown	14	160	3.18 (1.63, 6.20)	**0.001**	1.76 (0.71, 4.34)	0.22
Marital status						
Married	64	2072	1		1	
Widowed/divorced/never married	23	319	2.33 (1.43, 3.81)	**0.001**	2.15 (1.08, 4.25)	**0.029**
Number of children						
0	5	94	1		1	
1	10	311	0.6 (0.20, 1.81)	0.369	0.69 (0.22, 2.18)	0.527
2	32	861	0.70 (0.27, 1.84)	0.467	0.86 (0.31, 2.43)	0.783
3 and higher	4	329	0.23 (0.06, 0.87)	**0.030**	0.31 (0.08, 1.27)	0.104
Missing/Unknown	36	796	0.85 (0.33, 2.22)	0.740	0.91 (0.33, 2.46)	0.845
HPV vaccination						
Yes	2	98	1			
No	73	2055	1.74 (0.42, 7.20)	0.444		
Missing/Unknown	12	238	2.47 (0.54, 11.25)	0.242		
Participant's history of STDs						
No	77	2155	1		1	
Yes	3	59	1.42 (0.44, 4.64)	0.559		
Missing/Unknown	7	177	1.11 (0.50, 2.44)	0.801		
Partner's History of STDs						
No	74	2100	1		1	
Yes	2	18	3.15 (0.72, 13.84)	**0.128**	4.01 (0.79, 20.39)	0.094
Missing/Unknown	11	273	1.14 (0.60, 2.18)	0.684	0.6 (0.26, 1.39)	0.233
Tobacco smoking						
Never	87	2351	–	–		
Ever	0	40	–	–		
Age of first intercourse						
<20	7	266	1			
20–26	59	1458	1.54 (0.69, 3.40)	0.288		
>26	19	569	1.27 (0.53, 3.06)	0.595		
Missing/Unknown	2	98	0.78 (0.16, 3.80)	0.754		
Participant's number of partner						
1	73	2159	1		1	
>1	1	50	0.59 (0.08, 4.34)	0.606	0.46 (0.06, 3.78)	0.471
Missing/Unknown	13	182	2.11 (1.15, 3.88)	**0.016**	1.47 (0.72, 2.99)	0.285
Condom use						
Regular	7	221	1			
Not regular/Not use	80	2170	1.16 (0.53, 2.55)	0.705		

[a] All variables with p value less than 0.2 in the bivariable model were added into the multivariable model.

from 2000 to 2013, indicating a dominance of type 16 and 18 in the Vietnamese population (Dung et al., 2017). Globally, HPV types 16 and 18 were still the most common types, together with 52 and 58 (Bruni et al., 2010). However, a recent study of Vietnamese female university students showed that HPV type 52 was the most common HR-HPV type, followed by 39, 66/68 (Van Trang et al., 2022). HPV type 52 was also the most prevalent high-risk type among women sex workers, followed by 56 and 58 (Hoang et al., 2013; Pham et al., 2022). HPV genotype distributions differed by race, country, region, and geographical environment (Bruni et al., 2010). However, a change in HPV genotype related to HPV vaccination was suggested in several studies (Freire-Salinas et al., 2021; Drolet et al., 2019). A meta-analysis that included studies from 14 high-income countries explored that HPV type 16 and 18 significantly decreased by 83 % among girls aged 13–19 years and 66 % among women aged 20–24 after 5–8 years of vaccination introduction (Drolet et al., 2019). In Viet Nam, three HPV vaccines were approved, including bivalent (Cervarix®, against HPV genotype 16 and 18, in 2008), quadrivalent (Gardasil4® against HPV type 6, 11, 16, and 18, in 2008), and nonvalent (Gardasil9®, against HPV type 6, 11, 16, 18, 31, 33, 45, 52, and 58, in 2021). We found HPV genotype 18 dropped to the 6th position while type 16 remained the second most common genotype. Factors that influence HPV genotype-specific differences are less explored. Although these changes might partly be due to post-vaccination, our findings showed that only 4.0 % of participants received HPV vaccination. Therefore, further research is needed to understand better the contribution of other factors, such as sexual behaviors and lifestyle behaviors (Drolet et al., 2019; Bergqvist et al., 2021), in HPV-type change in the Vietnamese population and other populations with low coverage of HPV vaccination. In addition, differences in the prevalent HPV types in our study compared with previous studies suggest that the development of HPV vaccines, as well as HPV screening tests, should consider the changes in HR-HPV genotype distribution in the community to perform appropriate updates.

The uptake of HPV vaccination remains low among the target population in Viet Nam. Our study found that only 4.0 % of participants reported getting HPV vaccination. The low coverage of HPV vaccination was also reported in previous studies in the young population, including women and girls aged 19.81 ± 1.59 years (7.5 %) (Kamimura et al., 2018) and 15–29 (12 %) (Viet Nam Ministry of Health and UNPFA, 2023). A meta-analysis included low- and middle-income countries showed that the estimated uptake of HPV vaccination in women was 45.48 % and 5.22 % in high-uptake and low-uptake countries, respectively (Dorji et al., 2021). In countries with high uptake in 2006–2014, there was a decline in uptake of HPV vaccination in 2015–2020, while in countries with low uptake in 2006–2014 there was an increase in uptake in 2015–2020 (Dorji et al., 2021). In Viet Nam, the HPV vaccine was not included in the National Expanded Program of Immunization. Therefore, users must pay between 45 and 100 USD for their vaccination. High costs were one of the significant barriers to increasing HPV vaccine coverage in the target population. A study on Vietnamese women of childbearing age showed that the percentage of intention to get HPV vaccination significantly decreased after they were informed of the price of the vaccine (Le et al., 2020). In addition, other challenges of HPV vaccine programs in low- and middle-income countries, including Viet Nam, were logistical challenges, concerns about vaccine safety, and insufficient knowledge and awareness of HPV-related morbidities (Toh et al., 2017).

This study has limitations. Although it uses multi-stage random sampling, women participated on a voluntary basis. Therefore, its generalizability to the country's population should be applied with caution. Second, a low frequency of positive cases limits us from exploring associated factors. Third, the sexual and risk behaviors of women and their partners were self-reported, which might lead to an underestimation (Tran et al., 2015). The potential reason might be our study's considered percentage of "unknown" answers or missing data relating to behavioral variables. Moreover, we used a self-administered questionnaire, as it is a widely used tool to collect data in large population-based studies. However, inherent in its design, our study may suffer from recall bias. A self-reported questionnaire is still a valid tool for collecting data in surveys with big sample sizes and is commonly used. Our limitation suggests further multi-settings research recruiting more provinces to understand the genotype distribution of HR-HPV in Viet Nam and explore factors that influence HPV genotype differences in the community. Despite the limitations, this population-based study has a large sample size and was conducted in the community with a statistically valid design. Our study provides valuable data on the genotype distribution of HR-HPV with a broad spectrum in 25–65 women living in the community. Besides, our findings show a low prevalence of HR-HPV genotype in the community, which suggests the benefits of applied intervention programs. These data are valuable contributions to the public health surveillance system.

5. Conclusion

The prevalence of HR-HPV infection is 3.5 % (95 %CIs: 2.8–4.3 %) among women in HCMC, Viet Nam. Types 58, 16, and 52 are the most common high-risk types, while type 18 is only ranked at the 6th. The prevalence of multi-type HR-HPV infection is 0.8 %. Paired types of 52 & 58, 16 & 56, and 16 & 39 are the most prevalent multi-type of HPV infections. Continued surveillance is warranted to update the prevalence of the disease and to monitor the change of HPV genotype in the community, particularly under the impact of interventions of vaccination and cervical cancer prevention programs.

Funding

The present study partly used the data collected from the program named "Expanding the Abundant Health Project through Activities to Improve Cervical Cancer Screening Capacity for Grassroots Health Care Levels in Ho Chi Minh City" funded by Family Health International (FHI360) with permission.

CRediT authorship contribution statement

Ho Minh Nguyet: Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Phan Thanh Tam:** Writing – review & editing, Validation, Project administration, Methodology, Data curation, Conceptualization. **Quach Kim Ung:** Writing – review & editing, Validation, Supervision, Project administration, Methodology, Data curation, Conceptualization. **To Gia Kien:** Writing – review & editing, Visualization, Validation, Supervision, Conceptualization. **Le Hong Phuoc:** Writing – review & editing, Writing – original draft, Visualization, Validation, Methodology, Investigation, Formal analysis, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

We would like to thank all the participants for their time and support for this study. In addition, we would like to thank all community health workers for their essential contribution to this study. We extend our gratitude to our colleagues at the Department of Nutrition and Non-Communicable Disease , HCDC, and HCMC Department of Health for their contribution

Appendix A. Supplementary material

Supplementary data to this article can be found online at https://doi.org/10.1016/j.gore.2024.101526.

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