

Human papillomavirus genotypes in 108 patients with anogenital warts in a sexually transmitted disease clinic in Tehran

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Background and Objective: Genital warts, the most common sexually transmitted disease (STD), are caused by human papillomavirus (HPV). Few studies have been performed on Iranian women with genital warts or cervix cancer but there is no documented data about genital warts and HPV genotyping in Iranian men. In this study, we determined HPV genotypes in 108 male and females with anogenital warts in an STD clinic in Tehran.

Methods: In this cross sectional study, HPV genotypes were determined by the PCR method in 108 males and females with anogenital warts who were visited at an STD clinic in Tehran within January–June 2012. Age, sex, number of sexual partners, education level, and marital status were recorded in the questionnaires.

Results: We determined HPV genotypes in 108 patients including 36 men and 72 women. The mean age of the patients was 31.5 ± 12.3 years. The most common type was type 6 (62%). Other common genotypes were 11 (28.7%), 18 (15.7%), 16 (14.8%), 31 (4.6%), 33 (0.9%), 51 (0.9%), 56 (0.9%), and 66 (0.09%). We found that genotypes 16 ($P=0.003$) and 31 ($P=0.013$) were more prevalent in the patients with a higher number of sexual partners. In addition, there was a statistically significant association between the number of sexual partners and multi type HPV infection ($P=0.045$). Genotypes 16 ($P=0.036$) and 11 ($P=0.039$) were significantly associated with the female gender.

Conclusion: Our results showed that HPV 6 was the most prevalent HPV type followed by HPV 11, 18, and 16.

Keywords: wart, human papiloma virus, genotype, condyloma acuminata, cervical cancer

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INTRODUCTION

Genital warts are among the most prevalent sexually transmitted infections all over the world¹. About 40 genotypes of Human papillomavirus (HPV) can cause anogenital warts²⁻³. The association of some HPV genotypes with cancers such as anogenital, cervix, breast, head and neck,

and lung cancer has been evaluated in numerous investigations⁴⁻¹³. Studies show that more than 90% of genital warts are due to low risk 11 and 6 genotypes whereas high risk genotypes such as genotypes 16 and 18 contribute to about 70% of cervical cancers^{2,14}. Various studies have evaluated the distribution of HPV genotypes in different regions worldwide. These studies have shown

that genotype distribution may be somewhat different in various countries^{11,15-19}. HPV genotype distribution and high risk populations may help us to plan for preventive policies such as education and vaccination.

Although few studies have been performed on Iranian women with genital warts or cervix cancers²⁰⁻²³, there is no documented data about genital warts and HPV genotyping in Iranian men. Therefore, in this study, we determined HPV genotypes in 108 patients with anogenital warts in an STD in Tehran.

PARTICIPANTS AND METHODS

In this cross sectional study, we evaluated 108 patients who were visited at a sexually transmitted disease (STD) clinic in Razi Hospital, Tehran with a diagnosis of genital warts within January –June 2012. The diagnosis of warts was first made clinically by an infectious diseases specialist and a dermatologist in Razi Hospital; then, biopsy and PCR were performed for confirming the diagnosis.

Data such as sex, age, number of sexual partners, education level, marital status, and age at the first intercourse was recorded in questionnaires. All patients signed informed consent forms before participating in this study. All of the questionnaires were collected and handled confidentially. No additional expenses were paid by the patients.

HPV genotypes were identified based on the multiplex real-time PCR assay utilizing specific sets of amplification primers and probes with fluorescent signals to obtain detection results. HPV detection and genotyping was performed using the ABI StepOnePlus thermocycler (Applied Biosystems, USA). HPV genotypes were classified as 13 high risk HPV types (16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59 and 68) and 5 low risk HPV types (6, 11, 42, 43, and 44) from a wart sample. Moreover, reaction of each sample contained a cellular Internal control (IC) which could fully monitor the whole testing process starting from DNA extraction to signal detection.

Data was analyzed using SPSS (SPSS Inc., Chicago, IL, USA) software version 16. Continuous quantitative variables were reported as mean \pm standard deviation and nominal variable were reported as frequency and percentage. Chi-2 was used for the comparison of rates and ANOVA was

used for comparing the means. *P*-values less than 0.05 were considered significant.

RESULTS

In this study, 108 patients with genital warts were enrolled. The mean age of the patients was 31.5 ± 12.3 years (range: 4.5-75 years). Approximately one third of the patients were male. General information such as marital status, educational level, number of sexual partners, and various types of HPV and the number of genotypes in each patient is summarized in Table 1.

HPV genotypes are compared between male and female participants in Table 2. According to the data, genotypes 16 and 11 were significantly more prevalent in female patients. Less frequent genotypes including 51, 56, and 66 are not presented in Table 2. Our study showed that more than one

Table 1. Demographic, number of partners, and HPV genotyping results in 108 patients with anogenital warts.

Variables	Frequency (%)
Sex	
Male	36 (33.3%)
Female	72 (66.7%)
Marital status	
Single	50 (46.3%)
Married	53 (49.1%)
Divorced	5 (4.6%)
Educational level	
Not finishing high school	33 (30.6%)
High school diploma	50 (46.3%)
University education	25 (23.1%)
Number of sexual partners (including spouse in married patients)	
1	15 (13.9%)
2	74 (68.6%)
>3	19 (17.5%)
HPV genotypes	
6	67 (62%)
11	31 (28.7%)
18	17 (15.7%)
16	16 (14.8%)
31	5 (4.6%)
33	1 (0.9%)
51	1 (0.9%)
56	1 (0.9%)
66	1 (0.9%)
Number of HPV genotypes in patients	
1 type	85 (78.7%)
2 types	16 (14.8%)
3 types	6 (5.6%)
4 types	1 (0.9%)

Table 2. Distribution of HPV genotypes in males and females.

HPV types	Gender	Frequency(%t)	P value	Odds ratio (95% CI)
6	Male	23 (63.9%)	0.779	1.126 (0.49-2.6)
	Female	44 (61.1%)		
11	Male	6 (16.7%)	0.039	2.1 (1.1-4.6)
	Female	25 (34.7%)		
18	Male	6 (16.7)	0.852	1.11 (0.38-3.3)
	Female	11 (15.3%)		
16	Male	2 (5.6%)	0.046	3.5 (1.8-14.5)
	Female	14 (19.4%)		
31	Male	0 (0%)	0.105	0.93 (0.87-1.9)
	Female	5 (6.9%)		

HPV genotype was detected in the 22 females (30.6%) and 1 male (2.8%). This difference was statistically significant ($P=0.001$, odds ratio=11; CI 95%: 1.5-78.5).

According to our results, the distribution of HPV genotypes was not significantly different between high educated and low educated patients as well as married, single, and divorced men and women. In addition, there was no significant association between multi type infection with marital status and educational level.

In the current study, we compared the mean age of the patients with different HPV genotypes and found no significant association between age and infection with a specific HPV genotype ($P=0.424$). The mean age of the patients in the first intercourse was relatively similar in each HPV genotype ($P=0.671$).

Our study showed that type 16 was more frequent in divorced patients in comparison with single and married patients ($P=0.013$).

We evaluated the association between the number of sexual partners and various types of HPV and found that genotypes 16 ($P=0.003$) and 31 ($P=0.013$) were more prevalent in the patients with a higher number of sexual partners. In addition, there was statistically significant association between the number of sexual partners and multi type HPV infection ($P=0.045$); more than one HPV genotype was detected in 7 patients (82.1%) with more than 3 partners and 14 (18.9%) patients with 1-2 sexual partners.

DISCUSSION

According to our research, most of our patients were females and also the majority of our participants were in the age group 20-45 years

that is the age of sexual activity. Since the genital wart is a sexually transmitted disease, this age predominance was expectable. The frequency of single and married patients was rather similar in our study. In addition, patients were in a wide spectrum regarding to the educational level; more than two-thirds of them had high school and university education. Therefore, all adults, even educated ones, are at risk for genital warts.

HPV genotyping has been done in various countries worldwide. Although most of these studies have reported relatively similar results, the prevalence of HPV genotypes may have some differences in different regions. For example, in a study in Arizona, type 6 and 16 were the most prevalent HPV types whereas in another study in Seattle on college students, type 16 was the most frequent HPV type. In our study, genotypes 6 and 11 were the most prevalent types²⁴⁻²⁵. Chan and colleagues reported that types 6 and 11 were the most common types of genital samples. In a study in the southwest of Iran²², types 6 and 18 were the most prevalent genotypes.

In our study, genotypes 16 and 11 were significantly more prevalent in female patients. Our study showed that more than one HPV genotype was detected in 22 females (30.6%) and 1 male (2.8%). This difference is statistically significant ($P=0.001$, odds ratio=11; CI 95%: 1.5-78.5).

Although several studies have been performed on the distribution of HPV genotypes in Iranian women, we could not find a study on HPV genotyping in Iranian men. According to our results, the most common HPV genotype in men with genital warts was type 6. In addition, the frequency of types 18 and 11 was equal and less than type 6. In a multinational cohort study on 2487 men with genital warts, HPV 6 (43.8%) was

the most common followed by HPV 11 (10.7%) and HPV 16 (9.8%)²⁶. In another multi-centric survey in France 15, among 256 women and 260 men with external acuminata condylomata with a median age of 30 years (range: 18-72 years), the most prevalent genotypes were 6 (69%) and 11 (16%) followed by 16 (9%), 51 (8%), 52 (7%), 66 (6%), 53 (5%), 31 (3%), and 18 (3%).

We evaluated the association between the number of sexual partners and various types of HPV. We found that genotypes 16 ($P=0.003$) and 31 ($P=0.013$) were more prevalent in the patient with a higher number of sexual partners. In addition, there was a statistically significant association between the number of sexual partners and multi type HPV infection ($P=0.045$); more than one HPV genotype was detected in 7 patients (82.1%) with more than 3 partners and 14 (18.9%) patients with 1 or 2 sexual partners. In a study on men with multiple type HPV infection, the number of female sexual partners, condom use, and smoking were reported as modifiable factors associated with multiple HPV infection²⁷.

In conclusion, to the best of our knowledge, this study for the first time determined HPV genotypes in an Iranian population including men and women. Our results showed that the most prevalent HPV type was HPV 6 followed by HPV 11, 18, and 16. Further multi-centric studies with more participants are needed to obtain more accurate results on the distribution of HPV genotypes.

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