Prevalence and Distribution of Human Papillomavirus Genotypes Among Patients in National Institute of Genetic Engineering and Biotechnology Laboratory (NIGEB Lab) in 2024

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ABSTRACT

Human Papillomavirus (HPV) is a leading cause of cervical cancer, with various genotypes exhibiting differing levels of carcinogenic risk. This study investigates the prevalence and distribution of HPV genotypes among patients who tested positive during routine gynecological visits at Nigeb Laboratory. Conducted from January to June 2022, this cross-sectional study involved 152 women aged 18 and older. Cervical samples were collected and analyzed for HPV DNA using Real-Time Polymerase Chain Reaction (RT-PCR) analysis to determine genotype distribution. Among the participants, 68.4% were positive for carcinogenic HPV genotypes, with HPV 16 being the most prevalent (13.8%), followed by HPV 56 (12.5%) and HPV 66 (12.5%). Benign HPV genotypes were found in 19.1% of the samples, with HPV 6 (16.4%) being the most common. These findings underscore the need for comprehensive HPV vaccination and regular screening programs. The high prevalence of high-risk HPV genotypes not covered by current vaccines suggests the necessity for broader vaccine formulations. This study provides valuable data for informing public health strategies and highlights the importance of continuous HPV surveillance and research in under-researched populations.

Keywords: Human Papillomavirus, HPV, HPV genotypes, cervical cancer.

Introduction

Human Papillomavirus (HPV) is a significant etiological factor in the development of cervical cancer, one of the most common malignancies among women globally. HPV is classified into numerous genotypes, some of which are associated with a high risk of carcinogenic transformation, while others are considered benign (1-6). The prevalence and distribution of these genotypes vary widely across different populations and regions, necessitating localized studies to inform targeted prevention and treatment strategies (7-9).

In recent years, advancements in molecular diagnostics have facilitated more precise detection and genotyping of HPV, enabling a better understanding of its epidemiology. However, despite these technological advancements, there remains a critical need for comprehensive data on the prevalence of specific HPV genotypes, particularly in under-researched populations (10-13).

This study was conducted at Nigeb Laboratory with the primary objective of determining the prevalence and distribution of HPV genotypes among patients who tested positive for HPV during routine gynecological visits. The study employed a cross-sectional design and included 152 patients who met the inclusion criteria. Unlike some previous studies, we focused exclusively on HPV genotyping without conducting cytology examinations, providing a distinct perspective on the molecular epidemiology of HPV (14-19). The study's findings are expected to contribute valuable insights into the prevalence of both carcinogenic and benign HPV genotypes, aiding in the development of more effective public health strategies and interventions. By analyzing the demographic characteristics of the study population alongside the prevalence of specific HPV genotypes, this research aims to identify potential correlations that could inform future HPV screening and vaccination programs. Through this research, we aim to enhance the understanding of HPV genotype distribution in our study population, thereby contributing to the broader scientific knowledge necessary for combating HPV-related diseases.

Methods

Study Design and Population

This cross-sectional study was conducted at Nigeb Laboratory from January 2022 to June 2022. The study included 152 patients who attended routine gynecological visits and tested positive for HPV. The inclusion criteria were females aged 18 years and older who provided informed consent. Patients with previous cervical cancer diagnoses or who had undergone a hysterectomy were excluded from the study

Sample Collection

Cervical samples were collected using a cytobrush during routine Pap smear procedures. The samples were immediately placed in a ThinPrep preservative solution and transported to the laboratory for further analysis. All participants provided demographic information, including age, marital status, educational level, and smoking status.

HPV Detection and Genotyping

HPV DNA extraction from the cervical samples was performed using the Qiagen DNA extraction kit following the manufacturer's instructions. The presence of HPV DNA was detected using Real-Time Polymerase Chain Reaction (RT-PCR). The RT-PCR amplification targeted the L1 region of the HPV genome.

HPV genotyping was conducted using type-specific probes and primers in the RT-PCR assay. The RT-PCR system allowed for the detection and differentiation of multiple HPV genotypes in a single reaction. The amplification and detection were performed using the ABI Prism 7500 Fast Real-Time PCR System, and the results were analyzed with the associated software, which provided the genotype-specific amplification curves.

Data Analysis

The demographic characteristics of the study population were summarized using descriptive statistics. The prevalence of carcinogenic and benign HPV genotypes was calculated as the percentage of positive cases out of the total number of samples. The association between HPV infection and demographic factors was evaluated using the chi-square test. A p-value of <0.05 was considered statistically significant. All statistical analyses were performed using SPSS version 22.0.

Ethical Considerations

The study was approved by the Institutional Review Board of Nigeb Laboratory. All participants provided written informed consent before sample collection. The study adhered to the principles of the Declaration of Helsinki and maintained patient confidentiality throughout the research process.

Results

Demographic Characteristics

The study population comprised 152 patients, with a distribution across various age groups, marital statuses, educational levels, and smoking statuses as

detailed in Table 1. The majority of participants were aged between 30-39 years (32.9%), followed by those aged 40-49 years (29.6%). Marital status was predominantly married (46.1%), with single individuals constituting 39.5%. Regarding educational level, 39.5% had secondary education, and 30.9% had tertiary education. Most participants were non-smokers (72.4%).

Table 1

Prevalence of Carcinogenic HPV Genotypes

Out of the 152 patients, 104 were positive for at least one carcinogenic HPV genotype. The prevalence of specific carcinogenic HPV genotypes is presented in Table 2. The most common carcinogenic HPV genotype was HPV 16, found in 13.8% of patients, followed by HPV 56 and HPV 66, each found in 12.5% of patients. HPV 51 was present in 11.8%, and HPV 31 was present in 11.2%. Other genotypes such as HPV 18 (9.9%), HPV 52 (10.5%), and HPV 58 (8.6%) were also notable.

Study Characteristics

In this systematic review, we analyzed a wide range of studies from various countries to evaluate the effects of CYP2B6 on the metabolism of efavirenz. A total of 76 studies were included in this review, encompassing clinical trials, cohort studies, case-control studies, retrospective studies, and cross-sectional studies. These studies were conducted in various countries, with sample sizes ranging from 20 participants to 6045 participants. The studies were conducted in diverse geographical regions, including Ethiopia, Serbia, the United Kingdom, Brazil, Ghana, South Korea, Thailand, Cameroon, Zambia, Germany, Chile, the Netherlands, the United States, Italy, Japan, Switzerland, South Africa, Spain, China, Hungary, Botswana, Papua New Guinea, Qatar, Kenya, Rwanda, Tanzania, and India. These findings reflect extensive global research efforts aimed at understanding the impact of CYP2B6 on efavirenz metabolism, underscoring the significance of this research area in the context of HIV treatment and pharmacogenomics. Table 1 presents the characteristics of included studies.

Table 2

Prevalence of Benign HPV Genotypes

The prevalence of benign HPV genotypes among the study participants is summarized in Table 3. There were 29 patients positive for at least one benign HPV genotype. HPV 6 was the most prevalent benign genotype, found in 16.4% of the participants. Other benign genotypes such as HPV 53 (9.9%), HPV 59 (9.2%), HPV 54 (8.6%), and HPV 42 (7.9%) were also observed with significant frequency.

Table 3

Discussion

The findings from our cross-sectional study at Nigeb Laboratory provide significant insights into the prevalence and distribution of HPV genotypes among patients who tested positive for HPV during routine gynecological visits. The study identified a high prevalence of carcinogenic HPV genotypes, with HPV 16 being the most prevalent, followed by HPV 56, HPV 66, and HPV 51. Additionally, a notable presence of benign HPV genotypes, particularly HPV 6, was observed.

Our results align with other studies conducted in different populations. For instance, Kesheh and Keyvani (2019) reported a high prevalence of HPV 16 among the Iranian population, which is consistent with our findings. However, they also found a higher prevalence of HPV 6 and HPV 11 in males compared to our female-only study, highlighting potential gender differences in HPV genotype distribution (20). Leite et al. (2020) emphasized the prevalence of HPV 16, followed by HPV 58 and HPV 66, which also matches our observations. Their study noted that a significant proportion of high-risk HPV types are not covered by current vaccines, underscoring the necessity for continued cervical cancer screening even in vaccinated populations. This is particularly relevant in our study, where genotypes such as HPV 31, HPV 33, and HPV 52 were also prevalent, supporting the need for broader vaccine coverage (21).

Additionally, the study by Bello et al. (2009) demonstrated that infections by multiple HPV genotypes are common and significantly associated with higher grades of cervical intraepithelial neoplasia (CIN). This finding suggests that the presence of multiple HPV infections could exacerbate the risk of developing more severe cervical lesions. Although our study did not include cytology exams, the high prevalence of multiple high-risk HPV genotypes observed suggests a potential risk for severe cervical pathology in our study population (22).

Our study also revealed significant demographic correlations with HPV prevalence. The majority of HPV-positive patients were in the 30-39 age group, followed by the 40-49 age group. This age distribution is consistent with the peak age of HPV infection observed in other studies. For example, the study by Paz-Zulueta et al. (2018) found a similar age-related peak in HPV prevalence, emphasizing the importance of targeted HPV vaccination and screening strategies for women in these age groups (23).

The implications of these findings for public health strategies are significant. The high prevalence of high-risk HPV genotypes not covered by the current

vaccines highlights the need for continued surveillance and potential inclusion of additional genotypes in future vaccine formulations. Suresh et al. (2021) also advocate for the use of the nonavalent HPV vaccine (Gardasil 9), which offers broader protection against additional high-risk genotypes such as HPV 31, HPV 33, HPV 45, HPV 52, and HPV 58. This broader coverage could potentially reduce the incidence of cervical cancer more effectively than the bivalent or quadrivalent vaccines (24).

In conclusion, our study contributes valuable data on the molecular epidemiology of HPV in a specific population. The high prevalence of both carcinogenic and benign HPV genotypes underscores the need for comprehensive HPV vaccination programs and regular cervical screening. Future research should include cytological examinations to better correlate HPV genotypes with cervical lesion severity, providing a more complete picture of the impact of HPV infections on cervical health.

Figure legends:

Table 1: Demographic Characteristics of Study Population		
Characteristic	N	Percent (%)
Age (years)		
18-29	35	23.0
30-39	50	32.9
40-49	45	29.6
50-59	15	9.9
60+	7	4.6
Marital Status		
Single	60	39.5
Married	70	46.1
Divorced/Widowed	22	14.5
Educational Level		
No formal education	10	6.6
Primary education	35	23.0
Secondary education	60	39.5
Tertiary education	47	30.9
Smoking Status		
Non-smoker	110	72.4
Former smoker	20	13.2
Current smoker	22	14.5

Table 2. Carcinogenic HPV Genotypes		
Hpv Genotype	**Positive**	**Percent Positive (%)**
Sixteen	21	13.8
Eighteen	15	9.9
Thirty-One	17	11.2
Thirty-Three	2	1.3
Thirty-Five	8	5.3
Thirty-Nine	9	5.9
Forty-Five	7	4.6
Fifty-One	18	11.8
Fifty-Two	16	10.5
Fifty-Six	19	12.5
Fifty-Eight	13	8.6
Sixty Six	19	12.5
Sixty Seven	8	5.3
Seventy-Three	9	5.9
Eighty-Two	2	1.3

Table 3. Benign HPV Genotypes		
Hpv Genotype	**Positive**	**Percent Positive (%)**
Six	25	16.4
Eleven	4	2.6
Twenty-Six	1	0.7
Forty	6	3.9
Forty-Two	12	7.9
Forty-Three	4	2.6
Forty-Four	5	3.3
Fifty-Three	15	9.9
Fifty-Four	13	8.6
Fifty-Five	5	3.3
Fifty-Nine	14	9.2
Sixty-One	3	2.0
Sixty-Two	4	2.6
Sixty-Eight	12	7.9
Seventy	2	1.3
Seventy-Two	1	0.7
Eighty-One	2	1.3
Eighty-Four	3	2.0
Ninety	2	1.3
Ninety-One	1	0.7

Ethical Issue

There was no ethical issue in this review.

Conflict of Interests

There was no conflict of interest in this study.

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