



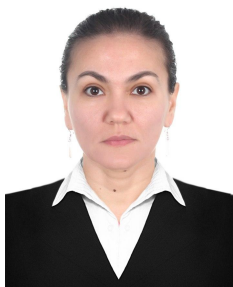
# URGANCH DAVLAT TIBBIYOT INSTITUTI JANUBIY OROLBO'YI TIBBIYOT JURNALI

2 - TOM, 3/1 - SON. 2026

14.00.00 - TIBBIYOT FANLARI ISSN: 3093-8740

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## EPIDEMIOLOGICAL PATTERNS OF HUMAN PAPILLOMAVIRUS INFECTION IN TASHKENT



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**Abstract.** Persistent infection with human papillomavirus (HPV) is a well-established risk factor for the development of malignant epithelial tumors. Despite extensive research in women, the role of men in HPV transmission remains insufficiently studied. To investigate epidemiological patterns, genotype distribution, and risk factors associated with HPV infection in Tashkent.

A total of 183 couples were examined in Tashkent. Urethral and cervical samples (n=366) were analyzed using polymerase chain reaction (PCR) for 14 high-risk HPV genotypes. Viral load was quantified and categorized as low, moderate, or high. Epidemiological data were obtained through structured interviews.

HPV DNA was detected in 56.3% of participants and in 57.4% of couples. Concordant infection between partners was observed in 85.9% of cases. Men with urogenital symptoms demonstrated a significantly higher infection rate (83.5%) compared to asymptomatic men (18.9%) ( $p < 0.001$ ). Genotypes 16 and 18 were predominant. Multiple infections (2–4 genotypes) were frequently observed. Viral load was higher in women, while genotype diversity showed a strong positive correlation with the number of sexual partners in men ( $r = 0.79$ ).

The study demonstrates a high prevalence of HPV infection, significant genotype diversity, and substantial viral load in the population of Tashkent. Men play a key role in HPV transmission, highlighting their importance in prevention strategies.

**Keywords:** human papillomavirus, HPV infection, epidemiology, high-risk HPV genotypes, risk factors

## TOSHKENT SHAHRIDA ODAM PAPILOMAVIRUSI TARQISHINING EPIDEMIOLOGIK XUSUSIYATLARI.

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Respublika ixtisoslashtirilgan epidemiologiya, mikrobiologiya, yuqumli va parazitlar kasalliklar  
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**Annotatsiya.** Toshkent shahrida 183 juftlik tekshirildi. Uretra va bachadon bo'yni namunalari (n=366) yuqori xavfli HPVning 14 genotipi mavjudligini aniqlash uchun polimeraza zanjir reaksiyasi (PZR) yordamida tahlil. Urogenital simptomlari bo'lgan erkaklarda asimptomatik erkaklarga (18,9%) ( $p < 0,001$ ) nisbatan infeksiya darajasi sezilarli darajada yuqori (83,5%) kuzatilgan. 16 va 18 genotiplari ustunlik qilgan. Ko'pincha ko'p sonli infeksiyalar (2-4 genotip) kuzatilgan. Kalit so'zlar: inson papilloma virusi, HPV-infeksiyasi, epidemiologiya, yuqori xavfli



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HPV genotiplari, xavf omillariqori xavfli HPVning 14 genotipi mavjudligini aniqlash uchun polimeraza zanjir reaksiyasi (PZR) yordamida tahlil qilindi. Virus yuklamasi miqdoriy jihatdan aniqlanib, past, o'rtacha yoki yuqori deb tasniflandi. Epidemiologik ma'lumotlar tuzilgan suhbatlar orqali olindi.

HPV DNKsi ishtirokchilarning 56,3 foizida va juftliklarning 57,4 foizida aniqlandi. Hamkorlar o'rtasida muvofiqlashgan infeksiya 85,9 foiz hollarda kuzatildi. Urogenital simptomlari bo'lgan erkaklarda asemptomatik erkaklarga (18,9%) ( $p < 0,001$ ) nisbatan infeksiya darajasi sezilarli darajada yuqori (83,5%) kuzatilgan. 16 va 18 genotiplari ustunlik qilgan. Ko'pincha ko'p sonli infeksiyalar (2-4 genotip) kuzatilgan. Virus yuklamasi ayollarda yuqori bo'lgan, genotipik xilma-xillik esa erkaklarda jinsiy sheriklar soni bilan kuchli ijobiy bog'liqlikni ko'rsatgan ( $r=0,79$ ).

Tadqiqot Toshkent aholisida HPV infeksiyasining yuqori tarqalishi, sezilarli genotipik xilma-xilligi va virus yuklamasini ko'rsatmoqda. Erkaklar HPV yuqishida asosiy rol o'ynaydi, bu ularning profilaktika strategiyalaridagi ahamiyatini ta'kidlaydi.

**Kalit so'zlar:** inson papilloma virusi, HPV-infeksiyasi, epidemiologiya, yuqori xavfli HPV genotiplari, xavf omillari.

## ЭПИДЕМИОЛОГИЧЕСКИЕ ОСОБЕННОСТИ РАСПРОСТРАНЕНИЯ ВИРУСА ПАПИЛЛОМЫ ЧЕЛОВЕКА В г ТАШКЕНТ.

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**Аннотация.** Персистирующая инфекция вирусом папилломы человека (ВПЧ) является хорошо известным фактором риска развития злокачественных эпителиальных опухолей. Несмотря на обширные исследования среди женщин, роль мужчин в передаче ВПЧ остается недостаточно изученной. Целью данного исследования было изучение эпидемиологических закономерностей, распределения генотипов и факторов риска, связанных с инфекцией ВПЧ в Ташкенте.

В Ташкенте было обследовано 183 пары. Образцы уретры и шейки матки ( $n=366$ ) были проанализированы с использованием полимеразной цепной реакции (ПЦР) на наличие 14 генотипов ВПЧ высокого риска. Вирусная нагрузка была количественно определена и классифицирована как низкая, умеренная или высокая. Эпидемиологические данные были получены посредством структурированных интервью.

ДНК ВПЧ была обнаружена у 56,3% участников и у 57,4% пар. Согласованная инфекция между партнерами наблюдалась в 85,9% случаев. У мужчин с урогенитальными симптомами наблюдался значительно более высокий уровень инфицирования (83,5%) по сравнению с бессимптомными мужчинами (18,9%) ( $p < 0,001$ ). Преобладали генотипы 16 и 18. Часто наблюдались множественные инфекции (2-4 генотипа). Вирусная нагрузка была выше у женщин, в то время как генотипическое разнообразие показало сильную положительную корреляцию с количеством половых партнеров у мужчин ( $r=0,79$ ).



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Исследование демонстрирует высокую распространенность ВПЧ-инфекции, значительное генотипическое разнообразие и существенную вирусную нагрузку в популяции Ташкента. Мужчины играют ключевую роль в передаче ВПЧ, что подчеркивает их важность в стратегиях профилактики.

**Ключевые слова:** вирус папилломы человека, ВПЧ-инфекция, эпидемиология, генотипы ВПЧ высокого риска, факторы риска

## Introduction

Human papillomavirus (HPV) infection is one of the most prevalent viral sexually transmitted infections worldwide and represents a major global public health concern. HPV is a DNA virus with epithelial tropism, and persistent infection with high-risk genotypes is a well-established etiological factor in the development of malignant neoplasms, particularly cervical cancer, as well as cancers of the anogenital region and oropharynx.

According to global estimates, a significant proportion of sexually active individuals will acquire HPV infection at some point in their lifetime. Although most infections are transient and asymptomatic, persistent infection with oncogenic HPV types, especially genotypes 16 and 18, is responsible for the majority of HPV-associated cancers worldwide.

In recent decades, substantial progress has been made in HPV prevention through the introduction of vaccination programs and molecular screening strategies. However, the effectiveness of these interventions depends not only on coverage among women but also on a comprehensive understanding of transmission dynamics in both sexes.

Despite this, epidemiological research has predominantly focused on female populations due to the direct link between HPV and cervical cancer. As a result, the role of men in HPV transmission has been relatively under-investigated, even though sexual contact is the primary route of virus spread. Emerging evidence suggests that men may act as asymptomatic carriers, contributing to sustained transmission cycles within stable partnerships.

Furthermore, limited data exist on HPV genotype distribution, viral load dynamics, and associated behavioral risk factors in Central Asian populations, including Uzbekistan. Regional differences in sexual behavior patterns, healthcare access, and screening practices may influence the epidemiology of HPV infection, making localized studies particularly important.

Another important aspect is the role of viral load and multiple genotype infections in disease progression and transmission efficiency. High-risk HPV persistence, combined with multiple genotype infections, may significantly increase oncogenic potential and complicate infection clearance.

Therefore, a detailed understanding of HPV epidemiology in both partners, including genotype diversity, viral load distribution, and behavioral risk factors, is essential for developing effective prevention strategies. This study aims to investigate epidemiological patterns, genotype diversity, viral load distribution, and associated risk factors of HPV infection in Tashkent.

**The purpose of the study** was to investigate the epidemiological patterns of human papillomavirus infection in Tashkent, including viral load characteristics, and associated risk factors of infection.



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Human papillomavirus comprises a large group of DNA viruses with more than 200 identified genotypes, of which at least 14 are classified as high-risk oncogenic types. Genotypes 16 and 18 are responsible for the majority of HPV-associated cancers globally.

Previous studies have demonstrated significant regional variation in HPV prevalence and genotype distribution. Molecular epidemiological studies have also highlighted the importance of viral load as a predictor of disease progression and persistence.

However, most existing research has focused on female populations, while the role of male infection in sustaining transmission chains remains insufficiently explored. Several studies indicate that men may act as asymptomatic carriers, contributing to reinfection cycles within couples.

## Materials and Methods

A cross-sectional study was conducted involving 183 heterosexual couples residing in Tashkent. Participation was voluntary.

The study population included: 109 couples attending medical consultation due to urogenital symptoms in men (dysuria, itching). 74 asymptomatic couples undergoing routine or preventive examinations

Samples were collected from: urethral swabs (men), cervical swabs (women)

A total of 366 biological samples were analyzed.

HPV DNA detection and genotyping were performed using polymerase chain reaction (PCR) with the AmpliSens diagnostic system, targeting 14 high-risk HPV genotypes (16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, 68).

Viral load was quantified as the number of DNA copies per milliliter and classified as:

Low (<3 log copies). Moderate (3–5 log copies). High (>5 log copies)

Epidemiological data were collected through structured interviews assessing sexual behavior and potential risk factors.

Statistical analysis included comparative and correlation methods, with significance set at  $p < 0.05$ .

## Results

HPV DNA was detected in 56.3% of all participants and in 57.4% of couples. Concordant infection (both partners positive) was observed in 85.9% of cases.

Among symptomatic men, HPV prevalence was significantly higher (83.5%) compared to asymptomatic men (18.9%) ( $p < 0.001$ ). Their female partners also demonstrated increased infection rates.

All 14 high-risk HPV genotypes were identified. Genotypes 16 and 18 were predominant, accounting for nearly half of all detected infections. No significant differences in genotype distribution were observed between men and women.

Multiple infections with 2–4 HPV genotypes were frequently observed. On average, infected individuals carried 1.6–1.7 different genotypes.

Viral load analysis showed:

- High load: 7.2%
- Moderate load: 56.7%
- Low load: 36.1%



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Women demonstrated higher viral loads compared to men (approximately 1.3–1.4 times higher).

A strong positive correlation ( $r = 0.79$ ) was identified between the number of sexual partners and HPV genotype diversity in men, whereas no such correlation was observed in women.

## Discussion

The findings of this study confirm the high prevalence of HPV infection among the studied population and demonstrate significant genotype diversity and viral load variability.

A key observation is the high rate of concordant infection between partners, supporting the dominant role of sexual transmission in HPV epidemiology. The presence of multiple high-risk genotypes further increases the potential oncogenic risk.

The significantly higher infection rates observed in symptomatic men suggest that urogenital inflammation may be associated with increased viral susceptibility or shedding. Importantly, men exhibited greater genotype diversity, which was strongly correlated with sexual behavior patterns, highlighting their role in sustaining transmission chains.

Although women showed higher viral loads, men demonstrated broader genotype distribution, suggesting that both sexes contribute differently to the epidemiological dynamics of HPV.

These findings support the hypothesis that men play a significant role in HPV circulation within stable partnerships and may act as important reservoirs of infection.

## Conclusion

This study demonstrates a high prevalence of high-risk HPV infection in the population of Tashkent, characterized by significant genotype diversity, multiple infections, and substantial viral load.

Men with urogenital symptoms exhibited significantly higher infection rates, and male sexual behavior was strongly associated with HPV genotype diversity.

The results indicate that men play a key role in HPV transmission dynamics and may contribute substantially to the persistence and spread of infection.

Detection of HPV in one partner indicates a high probability of infection in the other, emphasizing the importance of couple-based preventive strategies.

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