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HPV infection incidence and genotype distribution among male patients visiting outpatient departments in Huizhou from 2014 to 2023

Caiyi Wen^{1,2}, Xiaohan Yang³ and Xianjin Wu^{4*}

Abstract

Background There have been no previous studies on male HPV infection in the Huizhou region. This research aims to investigate the HPV infection rate and genotype distribution among male patients in this area, offering valuable insights for developing targeted preventive strategies against HPV infection in male population.

Methods This study included 1009 male patients from Huizhou Central People's Hospital who underwent HPV genotype testing between 2014 and 2023. We analyzed the distribution of HPV genotypes by year, age group, and diagnosis. Additionally, clinical data from 308 HPV-positive patients were retrospectively collected, and differences in high-risk vs. low-risk types, single vs. multiple infections, and genotype correlations were analyzed.

Results The overall HPV positivity rate was 30.53%, with the positive rate(40.56%) in the 2014–2019 group being significantly higher than that in 2021 (25.56%) and 2022 (24.29%)(p<0.05). The most common genotypes were HPV6, HPV52, HPV11, and HPV16. HPV infection was most prevalent in the 41–50 age group, while males aged \leq 30 were predominantly infected with low-risk types (41.73%). The 31–40 age group had a higher prevalence of high-risk types (52.07%), with males under 50 primarily infected with low-risk HPV6, while those aged 51 and above mostly had high-risk HPV52 infections. The highest HPV positivity rate was found in the viral wart group (79.01%). Single infections were more common (64.29%), with co-infection of HPV6 and HPV16 being the most prevalent type.

Conclusion The overall HPV infection rate was relatively high among outpatient male patients in Huizhou, with single infections being predominant. Additionally, HPV infection rates exhibited significant differences across various years, age groups, and diagnostic types, suggesting that these factors should be considered when formulating HPV prevention and control strategies.

Keywords Male, Human papillomavirus, Genotype, Huizhou region

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Introduction

Human papillomavirus (HPV) infection is one of the most common sexually transmitted pathogens worldwide and is closely associated with various diseases, particularly cervical cancer. Studies have shown that [1], assuming individuals have had at least one opposite-sex partner in their lifetime, the lifetime probability of women contracting HPV is approximately 84.6% (range 53.6-95.0%), while the infection rate for men is approximately 91.3% (range 69.5-97.7%). This data underscores that both men and women face a very high risk of HPV infection. Despite this, most infected individuals remain asymptomatic and are often unaware of their infection, leading to unintentional transmission of the virus. HPV can be transmitted asymptomatically for years, even decades, but the human immune system typically clears the virus within one to two years [2], and some individuals can clear the infection within six months [3]. Therefore, despite the high infection risk, the majority of people can effectively resist potential health threats. However, persistent infection with certain high-risk HPV strains can lead to malignant transformations, particularly cervical cancer, with almost all cases of cervical cancer being linked to prior HPV infection [4]. This highlights the significant role HPV plays in global cancer incidence and underscores that HPV-related diseases have become a major public health challenge.

Currently, research on HPV infection mainly focuses on women. However, in recent years, there has been a significant increase in the risk of men becoming infected with HPV, which can lead to malignant tumors such as anal cancer, penile cancer, and even oral cancer. HPV can also be transmitted to sexual partners, thereby increasing their risk of infection [5]. Even with strict condom use, HPV transmission cannot be fully avoided [6], as the skin around the male genital and anal areas is not completely covered. In the past thirty years, the global incidence of anal cancer has increased by an average of 2% per year [7], with HPV being the main cause in most cases. The carcinogenic mechanism of HPV involves the viral oncogenes E6 and E7, which disrupt normal cell cycle regulation, leading to genomic instability and uncontrolled cell growth. According to research [8], HPV16 and HPV18 are closely linked to oral cancer and anal cancer. Moreover, epidemiological data demonstrate significant anatomical site differences in the association between HPV infection and head and neck squamous cell carcinoma. The overall prevalence of HPV infection in head and neck squamous cell carcinoma is 15%, with the highest prevalence in the oropharynx at 30.7%, followed by the oral cavity (11.8%) and larynx (10.1%), and the hypopharynx at a relatively low 2.5% [9]. Notably, patients with HPVrelated head and neck squamous cell carcinoma often have a history of heavy smoking and alcohol use [9],

habits which may further increase the risk of HPV-associated cancers. Therefore, in recent years, research on male HPV infection has gradually increased worldwide.

HPV infection rates exhibit significant regional differences worldwide, influenced by factors such as cultural customs, sexual behavior patterns, medical resources, and sanitary conditions. Research on HPV infection in Chinese men began relatively late, with most studies focusing on major cities and often targeting specific highrisk groups, such as HIV-infected men, men who have sex with men (MSM), men attending sexual health clinics, and men with female partners who have HPV infection or cervical abnormalities [10]. Currently, studies on male HPV infection in China remain limited, particularly in the Huizhou area. As an important economic city in Guangdong Province, Huizhou has no published literature on the epidemiology and genotype distribution of male HPV infections. Thus, there is an urgent need for relevant epidemiological research in this region.

This study aims to analyze the prevalence and genotype distribution of male HPV infections in Huizhou, providing a scientific basis for the development of regional disease control strategies, vaccination plans, and screening measures. Ultimately, these efforts aim to enhance public health prevention and control.

Materials and methods

Study subjects

The subjects of this study were all male outpatients who underwent HPV DNA genotyping at Huizhou Central People's Hospital in Huizhou, Guangdong Province, China, between January 1, 2014, and December 31, 2023. The exclusion criteria included: (i) cases with significant missing or incorrect information; (ii) cases diagnosed with autoimmune diseases; (iii) cases with other malignant cancers. In total, 1009 male patients met the inclusion criteria. As diagnostic data from 2014 to 2019 were not available, and the number of visits during these years was small, the data from this period were grouped together. Thus, the diagnostic data presented in the following charts only include those from 2020 to 2023. This study received ethical approval from the Clinical Research Ethics Committee of Huizhou Central People's Hospital (approval number kyll2024038). Since this is a retrospective study with no direct impact on patients, the Ethics Committee granted an exemption from written informed consent. This study strictly adhered to the Declaration of Helsinki and other relevant ethical guidelines.

Sample collection

The sampling is performed by clinically trained doctors to ensure the standardization and accuracy of the procedure. To maintain consistency throughout the process, suitable areas (e.g. genital region, perianal area, and oral

cavity) are selected based on the patient's specific condition, ensuring the representativeness and completeness of the samples. For the genital region, which includes the glans penis, corona, penile shaft, and scrotum [11], a sterile disposable swab moistened with saline is used to perform repeated 360° swabbing on the glans and corona. This helps to ensure both comprehensive and thorough sampling. Similarly, for the penile shaft, scrotum, and perianal regions, the doctor gently and repeatedly rubs the skin surface at least 3 to 5 times to guarantee sufficient contact between the swab and the skin, allowing the collection of exfoliated cell samples. In addition, when collecting oral samples, the doctor uses a sterile swab to repeatedly scrape the oral cavity (including the tongue surface, under the tongue, lateral tongue, and internal oral mucosa) to obtain secretion samples. For wart sample collection, the doctor chooses the appropriate method according to the characteristics of the warts: small and loose wart particles are gently scraped with a swab, while larger or harder warts are cut into small fragments using laser cutting for further analysis. All collected samples are promptly placed in 2 ml storage tubes containing a cell preservation solution (purchased from Kaipu Biochemical Co., Ltd., Chaozhou, Guangdong, China). The excess brush handle is broken off at the tube opening, leaving the brush head in the sample tube. The tube is tightly sealed, labeled with the sample number and date, and sent to the testing center for analysis as soon as possible. If immediate testing is not possible, the samples can be stored at 4 °C for up to two weeks, or frozen at -20 °C, and must be tested within six months.

Reagents and instruments

The HPV genotyping detection kit (PCR+membrane hybridization method) was obtained from Capu Biochemical Co., Ltd., Chaozhou, Guangdong, China. This kit utilizes gene amplification and flow-through hybridization technology, employing reverse dot hybridization to detect the hybridization signals between the amplified products and type-specific probe membranes. The kit also uses an alkaline phosphatase system for qualitative analysis, allowing precise HPV genotyping. Its high sensitivity enables the accurate detection and differentiation of 21 HPV types, including HPV6, 11, 16, 18, 31, 33, 35, 39, 42, 43, 44, 45, 51, 52, 53, 56, 58, 59, 66, 68, and CP8304, effectively identifying both single and mixed infections. The primary testing instruments include the Veriti Dx96 PCR amplifier (serial number: 299120908), purchased from Applied Biosystems; the fully automatic nucleic acid molecular hybridization instrument HBHM-9000 A (serial number: YYD2303003) and the backup medical nucleic acid molecular hybridization instrument HB-2012 A (serial number: YYC1807029), both purchased from Capu Biochemical Co., Ltd. in Chaozhou, Guangdong, China. All of the above procedures are strictly followed in accordance with the manual provided by the supplier [12].

HPV genotyping classification standards and case diagnostic criteria

According to the 2021 WHO [13], the high-risk carcinogenic HPV genotypes specifically include the following 14 types: HPV16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, and 68. All other types are classified as low-risk. Case diagnosis was categorized based on the consultation department, clinical symptoms, and HPV test results.

Statistical analysis

Data collection and initial processing were performed in Excel, with all statistical analyses conducted using SPSS software version 25.0. For normally distributed quantitative data, the distribution range is expressed as the mean $(\mu) \pm$ standard deviation (σ), while for non-normally distributed quantitative data, the median (Median) and interquartile range (IQR) are used. Differences between groups were assessed using the Kruskal-Wallis test, followed by post-hoc multiple comparisons with the Bonferroni method. The infection positivity rates of human papillomavirus (HPV) and its various genotypes were expressed as the percentage of positive samples among the total samples or as the percentage of positive samples among all positive samples. Some positivity rates were estimated using the 95% confidence interval (CI) of the binomial distribution to assess the infection status. Categorical data were presented as percentages, and intergroup comparisons were made using the Chi-square test or Fisher's exact test, with Bonferroni correction or α -splitting applied for multiple comparisons when necessary. The significance level for this study was set at p < 0.05. The charts were created using the DyCharts website (https://dycharts.com/) and Adobe Illustrator CS5 software.

Results

Basic analysis of HPV infection status

Age distribution of the patient population and HPV infection situation

The 1009 male patients included in this study ranged in age from 1 to 69 years, with a mean age of 32 years (IQR:27–38 years). The participants were divided into four age groups: \leq 30 years, 31–40 years, 41–50 years, and \geq 51 years. The largest proportion was in the under-40 group, with the \leq 30 years group comprising 42.91% (433/1009), the 31–40 years group comprising 40.54% (409/1009), the 41–50 years group comprising 10.90% (110/1009), and the \geq 51 years group comprising 5.65% (57/1009). The highest HPV infection positivity rate was found in the 41–50 years group at 37.27% (41/110,95%

Age Group	Total	Positive	Prevalence	95% CI	Genotype Ranking	Low-Risk Types	High-Risk Types	Mixed Infection
≤30	433	127(41.23 ^c)	29.33	25.00-33.60	HPV6, HPV11	53 ^a (41.73)	42 ^a (33.07)	32 ^a (25.20)
31–40	409	121 (39.29 ^c)	29.58	25.10-34.00	HPV6, HPV52	37 ^a (30.58)	63 ^b (52.07)	21 ^a (17.36)
41-50	110	41 (13.31 ^c)	37.27	28.10-46.50	HPV6, HPV52	14 ^a (34.15)	20 ^{a,b} (48.78)	7 ^a (17.07)
≥51	57	19 (6.17 ^c)	33.33	20.70-46.00	HPV52, HPV6	4 ^a (21.05)	8 ^{a,b} (42.11)	7 ^a (36.84)
Diagnosis								
Viral Warts	81	64 (25.60c)	79.01	70.00-88.10	HPV6, HPV11	40 ^a (62.50)	11 ^a (17.19)	13 ^a (20.31)
Genital papules / Genitouri- nary inflammation	72	14 (5.60 ^c)	19.44	10.10–28.80	HPV16, HPV51	3 ^b (21.43)	6 ^{a,b} (42.86)	5 ^a (35.71)
Fertility Maternity Related	186	46 (18.40 ^c)	24.73	18.50-31.00	HPV52, HPV51	5 ^b (10.87)	31 ^b (67.39)	10 ^a (21.74)
Check-ups/Other	527	126 (50.40 ^c)	23.91	20.30-27.60	HPV52, HPV6	32 ^b (25.40)	72 ^b (57.14)	22 ^a (17.46)

Table 1 Characteristics of HPV infection by age group and diagnosis [n(%)]

Notes:

• The data analysis in this study covers diagnostic data from 2020 to 2023 only, due to unavailability of data from 2014 to 2019

• In this table, "c" represents the proportion of positive samples within each category relative to the total number of positive samples

• Letters "a" and "b" denote different "Age Group" and "Diagnosis" categories, respectively. Comparisons of row proportions between these categories at the 0.05 significance level showed no statistically significant differences



• Viral Warts • Genital papules • Genitourinary inflammation • Fertility Maternity Related • Check-ups/Other

Fig. 1 Age distribution boxplot for different diagnoses in men from Huizhou area

CI:28.10–46.50%). However, there was no statistically significant difference in positivity rates between age groups (χ^2 =3.036, *p* > 0.05) (Table 1).

There were significant differences in age distribution between different diagnostic categories (H = 15.715, p = 0.003). The median age in the viral warts group was 30 (26–36, 95% CI: 29.37–32.90%) years, in the genital papilloma group it was 28(24–34.25, 95% CI: 26.82–32.62%) years, in the urogenital inflammation group the average age was 34.50 (29.25–39.75, 95% CI: 32.62–37.38%) years, in the fertility/pregnancy-related group the median age was 33 (28–38, 95% CI: 32.53–34.81%) years, and in the physical examination/other group the median age was 32 (27–39, 95% CI: 32.93–34.58%) years. The median age in the genital papilloma group was significantly lower than that in the fertility/pregnancy-related group (p = 0.045) and the urogenital inflammation group (p = 0.019), with no significant difference between other groups (p > 0.05) (Fig. 1).

HPV distribution and infection status in different diagnostic types

As shown in Fig. 2, from 2020 to 2023, the number of patients in each diagnostic category increased year by year. The largest group was the physical examination/ other diseases group, comprising 60.85% (527/866), followed by the fertility/pregnancy-related group, comprising 21.48% (186/866). Viral warts patients accounted for 9.35% (81/866), while genital papules and urogenital



Fig. 2 Radial heat map of diagnostic distribution among 866 male patients from 2020 to 2023. The layers, from inner to outer, represent the following diagnoses: viral warts, genital herpes, genitourinary inflammation, fertility and pregnancy-related issues, and routine check-ups or other diseases

inflammation patients comprised 3.70% (32/866) and 4.62% (40/866), respectively.

According to Table 1, there was a statistically significant difference in HPV infection positivity rates between different diagnostic categories ($\chi^2 = 110.160$, p < 0.001). Although the physical exam/other diseases group had the largest number of patients, its HPV positivity rate was not the highest. The viral warts group had the highest HPV positivity rate, at 79.01% (64/81, 95% CI: 70.00–88.10%), significantly higher than that of other diagnostic categories (p < 0.05). No significant differences in positivity rates were observed between the remaining diagnostic categories (p > 0.05).

Variation in positivity rate distribution of different HPV types across years

Changes in the overall HPV positivity rate distribution over the years

As shown in Table 2, among the 1009 patients, 308 were infected with at least one HPV genotype, resulting in an overall positivity rate of 30.53% (95% CI: 27.7–33.4%). The positivity rate during 2014–2019 was 40.56% (58/143), 43.14% (22/51) in 2020, 25.56% (46/180) in 2021, 24.29% (68/280) in 2022, and 32.11% (114/355) in 2023. Overall, the differences in positivity rates across these years were statistically significant (χ^2 = 18.273, *p*<0.05). The HPV positivity rate in the 2014–2019 period (40.56%)

Fable 2 Prevalence of humar	n papillomavirus types amoi	ng men in Huizhou, China by	/ year [n(%)]
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HPV Types	Total	95%Cl	2014-2019	2020	2021	2022	2023	χ²	р
Number of Patients	1009		143	51	180	280	355		
Positive Cases	308(30.53)	27.7-33.4	58(40.56) ^a	22(43.14)	46(25.56) ^a	68(24.29) ^{a, b}	114(32.11)	18.273	0.001
Low-Risk HPV	108(10.70)	8.8-12.6	28(19.58)	8(15.69)	14(7.78) ^a	20(7.14) ^a	38(10.70)	18.440	0.001
High-Risk HPV	133(13.18)	11.1-15.3	13(9.09)	8(15.69)	24(13.33)	32(11.43)	56(15.77)	5.212	0.266
Mixed HPV	67(6.64)	5.1-8.2	17(11.89)	6(11.76)	8(4.44)	16(5.71)	20(5.63)	10.880	0.028
LR-HPV									
HPV6	84(8.33)	6.6-10.0	32(22.38)	6(11.76)	9(5.00) ^a	15(5.36) ^a	22(6.20) ^a	45.736	0.001
HPV11	41(4.06)	2.8-5.3	10(6.99)	3(5.88)	6(3.33)	8(2.86)	14(3.94)	4.885	0.299
HPV42	23(2.28)	1.4-3.2	2(1.40)	3(5.88)	2(1.11)	5(1.79)	11(3.10)	5.355	0.219
HPV43	16(1.59)	0.8-2.4	1(0.70)	1(1.96)	3(1.67)	4(1.43)	7(1.97)	1.314	0.863
HPV44	6(0.59)	0.1-1.1	1(0.70)	0(0.00)	1(0.56)	1(0.36)	3(0.85)	1.093	0.956
CP8304	19(1.88)	1.0-2.7	3(2.10)	2(3.92)	2(1.11)	5(1.79)	7(1.97)	2.182	0.692
HPV53	16(1.59)	0.8-2.4	3(2.10)	2(3.92)	3(1.67)	3(1.07)	5(1.41)	3.076	0.504
HR-HPV									
HPV16	36(3.57)	2.4-4.7	7(4.90)	4(7.84)	8(4.44)	7(2.50)	10(2.82)	5.353	0.253
HPV18	16(1.59)	0.8-2.4	2(1.40)	1(1.96)	2(1.11)	5(1.79)	6(1.69)	0.751	0.973
HPV31	10(0.99)	0.4-1.6	2(1.40)	1(1.96)	2(1.11)	3(1.07)	2(0.56)	2.514	0.620
HPV33	7(0.69)	0.2-1.2	0(0.00)	2(3.92)	2(1.11)	0(0.00)	3(0.85)	8.316	0.033
HPV35	3(0.30))	0.0-0.6	1(0.70)	0(0.00)	0(0.00)	1(0.36)	1(0.28)	2.226	0.792
HPV39	21(2.08)	1.2-3.0	2(1.40)	1(1.96)	3(1.67)	8(2.86)	7(1.97)	1.225	0.885
HPV45	4(0.40)	0.0-0.8	1(0.70)	0(0.00)	0(0.00)	0(0.00)	3(0.85)	3.516	0.462
HPV51	28(2.78)	1.8-3.8	5(3.50)	2(3.92)	5(2.78)	6(2.14)	10(2.82)	1.437	0.846
HPV52	56(5.55)	4.1-7.0	7(4.90)	4(7.84)	9(5.00)	13(4.64)	23(6.48)	1.756	0.780
HPV56	9(0.89)	0.3-1.5	2(1.40)	0(0.00)	0(0.00)	3(1.07)	4(1.13)	2.468	0.632

was significantly higher than in 2021 (25.56%) ($\chi^2 = 8.218$, p = 0.004) and 2022 (24.29%) ($\chi^2 = 11.986$, p = 0.001). Additionally, the positivity rate in 2020 (43.14%) was also higher than in 2022 (24.29%) ($\chi^2 = 7.744$, p = 0.005). There were no significant differences between the remaining years (p > 0.05).

Changes in the distribution of high-risk and low-risk HPV genotypes over the years

As shown in Table 2, among the 308 infected individuals, the highest infection rate was for high-risk HPV alone, at 13.18% (133/1009, 95% CI: 11.1–15.3%). Both pure low-risk HPV infection ($\chi^2 = 18.440$, p < 0.05) and mixed high- and low-risk HPV infections ($\chi^2 = 10.880$, p < 0.05) demonstrated statistically significant differences in overall positivity across different years. Among individuals with pure low-risk HPV infection, the HPV positivity rate in the 2014–2019 group (19.58%) was significantly higher than that in 2021 (7.78%) ($\chi^2 = 9.813$, p = 0.002) and 2022 (7.14%) ($\chi^2 = 14.556$, p = 0.001). In mixed high-risk and low-risk HPV infections, although the overall positivity rates across different years showed statistical differences, no significant differences were found in pairwise comparisons (p > 0.05).

Variation in the infection rates of 21 HPV types over the years

As shown in Table 2, the most common HPV genotype is HPV6, accounting for 8.33% (84/1009, 95% CI: 6.6–10.0%), followed by HPV52 (5.55%, 56/1009, 95% CI: 4.1–7.0%), HPV11 (4.06%, 41/1009, 95% CI: 2.8–5.3%), and HPV16 (3.57%, 36/1009, 95% CI: 2.4–4.7%). In the 2014–2019 group, the most prevalent genotypes were

HPV6 (22.38%, 32/143) and HPV11 (6.99%, 10/143). In 2020, HPV6 (11.76%, 6/51) remained the most common. In 2021, HPV6 (5.00%, 9/180) and HPV52 (5.00%, 9/180) were the most common. In 2022, HPV6 (5.36%, 15/280) and HPV52 (4.64%, 13/280) remained the most prevalent. In 2023, HPV52 (6.48%, 23/355) was the most common, followed by HPV6 (6.20%, 22/355). This indicates that the highest infection rate among high-risk HPV genotypes is HPV52, while the highest infection rate among low-risk HPV genotypes is HPV6.

Among the 21 HPV types, HPV6 ($\chi^2 = 45.736$, p < 0.05), HPV33 ($\chi^2 = 8.316$, p < 0.05), and HPV66 ($\chi^2 = 9.412$, p < 0.05) showed statistically significant differences in the overall positivity rates over the years, but only the infection rate of HPV6 exhibited differences in pairwise comparisons. The positivity rate in the 2014–2019 group (22.38%) was significantly higher than that in 2021 (5.00%) ($\chi^2 = 21.715$, p < 0.005), 2022 (5.36%) ($\chi^2 = 27.765$, p < 0.005), and 2023 (6.20%) ($\chi^2 = 27.606$, p < 0.005). The infection rates of the other types did not show statistically significant differences over the years (p > 0.05).

Comparative analysis of single and multiple HPV infections As shown in Fig. 3, among the 308 HPV-positive patients, single infections accounted for 64.29% (198/308, 95% CI: 58.90–69.70%), making it the most common infection type. Double infections represented 25.65% (79/308, 95% CI: 20.70–30.60%), while triple or higher multiple infections accounted for 10.06% (31/308, 95% CI: 6.70– 13.40%). In all years, the proportion of single infections was the highest, followed by double infections, with triple or higher multiple infections being the least common.



• 2020 • 2021 • 2022 • 2023 • 2014-2019

Fig. 3 Comparison of single and multiple infection cases by year during pre-pandemic, pandemic, and post-pandemic periods

With the increase in patient visits from 2020 to 2023, the proportions of all infection types also increased. However, there were no significant differences in infection types across years ($\chi^2 = 3.721$, p > 0.05).

Analysis of the distribution of High-risk and Low-risk HPV genotypes by age and diagnostic type

The proportion of HPV genotypes and High-risk/Low-risk genotypes by different age groups

As shown in Table 1, patients younger than 50 years predominantly had infections with the low-risk HPV type HPV6, while in patients aged 51 and older, the infection rate of the high-risk HPV type HPV52 was the highest, followed by HPV6. In the \leq 30 years group, low-risk infections accounted for 41.73% (53/127), whereas in the 31–40 years group, high-risk infections were most common, comprising 52.07% (63/121). The differences in infection types among different age groups were statistically significant ($\chi^2 = 13.069$, p < 0.05), with the 31–40 years group showing significantly higher rates of high-risk infections compared to the \leq 30 years group (p < 0.05). No significant differences were observed among age groups for mixed high-risk and low-risk infections (p > 0.05).

The distribution of HPV genotypes and high/low-risk types by different diagnostic categories

As shown in Table 1, viral warts are primarily caused by low-risk HPV types, specifically HPV6 and HPV11, while the health check/other disease group is primarily infected by high-risk HPV52 and low-risk HPV6. In other diagnostic groups, high-risk HPV infections are more common, such as in the fertility and pregnancy-related group, which is predominantly infected with high-risk HPV52. There are significant differences in infection types between different diagnostic categories ($\chi^2 = 47.971$, p < 0.05). The viral warts group has the highest proportion of low-risk HPV infections, accounting for 62.50% (40/64), significantly higher than in other diagnostic groups (p < 0.05). The fertility and pregnancy-related group has the highest proportion of high-risk HPV infections, at 67.39% (31/46), which is significantly higher than in the viral warts group (p < 0.05). There were no significant differences in the distribution of mixed high/low-risk infections between diagnostic groups (p > 0.05).

Genotype correlation analysis of HPV infection

As shown in Fig. 4, a total of 110 patients exhibited dual or higher HPV infections. The co-infection patterns of different HPV genotypes are clearly illustrated through a chord diagram. The most common co-infection was between HPV6 and HPV16, which occurred 7 times, followed by the combinations of HPV52 and CP8304, as well as HPV6 and CP8304, each occurring 6 times. In the physical examination/other diseases group, HPV52 was the most frequently detected genotype, occurring 31 times. In the viral warts group, HPV6 was the most prevalent, occurring 30 times, followed by HPV11, which was detected 17 times. In the pregnancy-related group, HPV52 was also the most commonly detected infection, occurring 12 times. Finally, to visually present the overall research plan for better understanding, we created a distribution diagram of the study subjects, as shown in Fig. 5.



Fig. 4 HPV-related chord diagram in males from the Huizhou region. (A) Between different genotypes. (B) Between different diagnoses and genotypes



≥51 (n=57)

2022 (n=280)

2023 (n=355)

Statistical analysis and plotting

Single infectio (n=198)

Double infection (n=79)

Multiple infection (n=31)

Fig. 5 Flowchart of study subject distribution

Discussion

According to WHO standards

Low-risk type (n=108)

High-risk type (n=133)

Mixed HPV (n=67)

This study is the first to systematically analyze the epidemiological characteristics of male HPV infections in Huizhou, China, from 2014 to 2023, with an overall HPV positivity rate of 30.53% (308/1009). This finding aligns closely with the 31% male HPV infection rate reported in a 2023 study across 35 countries globally, further validating the rationale of our research results

21 genotype results

were obtained

[10]. When comparing the HPV infection rate in Huizhou to other regions in China during the same period, it was found that Huizhou's rate is higher than Beijing's 25.19% (1288/5114) [14],but lower than Shandong Liaocheng's 64.87%(2388/3681) [15] and Guangdong Guangzhou's 42.15%(1575/3737) [16]. These data indicate significant regional differences in HPV positivity rates across China, reflecting varying effects of regional transmission and prevention measures, which provide a basis for the development of region-specific public health strategies.

In the period analysis, the overall HPV positivity rate in the 2014–2019 group (40.56%) was significantly higher than that in 2021 (25.56%) and 2022 (24.29%), and the positivity rate in 2020 (43.14%) was also higher than in 2022 (24.29%). This change may be attributed to multiple factors. First, between 2014 and 2019, the HPV genotyping tests in this medical institution were still in the early stages. During this period, the tests were mainly focused on high-risk populations or individuals with qualitative or quantitative positive virus results. Genotyping tests were typically performed to further understand specific virus genotypes, leading to a smaller sample size but a higher proportion of positives. Furthermore, 2020 marked the first year of the COVID-19 outbreak in Huizhou, which significantly reduced the sample size, potentially causing a representativeness bias in the samples. As the pandemic alleviated in 2021, the number of male patients seeking medical care increased annually, making the sample more diverse and representative. This shift likely contributed to the gradual decrease in the positivity rate. In the early stages of the pandemic, many patients delayed seeking medical care due to concerns about infection, resulting in a significant decrease in the number of visits, particularly among low-risk populations. This behavior likely led to an increase in the proportion of higher-risk populations, which in turn may have contributed to a higher HPV positivity rate. Therefore, the higher positivity rate in 2020 may represent an abnormal medical trend, influenced by the visit patterns of specific groups and biases in sample selection.

Fertility Maternity Related (n=186)

Check-ups/Other (n=527)

We also found that single HPV infection dominated among the 308 positive patients, accounting for 64.29% (198/308), which was significantly higher than the rates of dual infections (25.65%) and triple or higher multiple infections (10.06%). This result aligns with findings from other regions [14–16], suggesting that HPV infection in Huizhou males predominantly manifests as a single-type infection. Further analysis revealed that the rate of single high-risk HPV infection was 13.18% (133/1009), which was slightly higher than the rate of low-risk HPV infection (10.70%, 108/1009). This suggests that the male population in Huizhou faces a higher risk of high-risk HPV infection, highlighting the importance of strengthening the prevention and screening of high-risk HPV in this region.

Regarding age factors, although males under 40 years old are the main patient group, reflecting their higher health awareness and willingness to seek medical care, the HPV positivity rate is highest in males aged 41–50, which differs from the findings in other regions. For example, in Turkey, the highest positivity rate was found in the under-31 group (37.6%) [17]; in Shandong, the highest positivity rate appeared in the 30–39 age group (34.09%) [15]; while in Guangzhou, the highest positivity rates were observed in the under-25 group (47.6%) and the 40-44 age group (44.51%) [16]. The high infection rate in middle-aged males in Huizhou may be related to factors such as an increase in the number of sexual partners, frequent sexual activity, and decreased immunity. Therefore, special attention should be given to HPV prevention strategies targeting this group. Moreover, males under 50 years old are primarily infected with low-risk HPV type 6, whereas males aged 51 and older are more frequently infected with high-risk HPV type 52. This suggests the need for tailored prevention strategies for different age groups. For older males, persistent HPV infection increases their risk of genital cancers, such as penile and anal cancers. Therefore, comprehensive HPV screening is crucial for early detection and risk reduction.

Studies [18] have shown that children and adolescents may also acquire HPV through non-sexual transmission routes, such as mother-to-child transmission or skin contact. In this study, 16 cases of HPV infection were identified among males under 18 years old, including one case in a 1-year-old child (HPV positive), seven cases in adolescents aged 13–17 (two HPV positive), and eight cases in young adults aged 18 (three HPV positive). Although the source of infection in the 1-year-old child could not be determined, considering the child's age, it is suspected that the infection may have occurred through vertical mother-to-child transmission. A study in Chile reported [19] that the HPV infection rate in children and adolescents is 30.9%. Among this group of adolescents, most had sexual contact and were infected with high-risk HPV; in children, some had a history of sexual abuse, but most were infected with low-risk HPV, indicating that children and adolescents who experience sexual abuse or early sexual activity have a significantly increased risk of HPV infection. Therefore, early screening and prevention strategies are essential for this group.

In terms of HPV genotype distribution, low-risk HPV type 6 is the most common among males in Huizhou, accounting for 8.33% (84/1009). Although HPV type 6 typically does not cause serious health problems, its high transmissibility in sexually active populations warrants attention. In addition, HPV52 (5.55%) is the most prevalent high-risk genotype, underscoring the necessity of monitoring and preventing this type of HPV. The four most common genotypes with the highest infection rates are HPV6, HPV52, HPV11, and HPV16, a finding consistent with research from certain regions in China and abroad [15, 16, 20, 21]. Furthermore, HPV types 16, 6, 52, and 58 are considered the most common genotypes among homosexual men [22]. This study reveals that the high-risk HPV types with the highest positivity rates are HPV52, HPV16, HPV51, and HPV58, while the three low-risk types with the highest positivity rates are HPV6, HPV11, and HPV42. However, a study in Shanghai showed [23] that the most common high-risk HPV types in that area are HPV16, HPV59, HPV52, and HPV51. These data reveal the diversity and complexity of HPV epidemic patterns across different regions and populations, reflecting the potential impact of different environments on HPV infection types. Moreover, co-infection with HPV types 6 and 16 was most common in this study, but the mechanisms behind co-infection and genotype conversion remain unclear, requiring further research.

Diagnostic analysis reveals that the largest number of patients are from the health checkup/other diseases group, with a positivity rate of 23.91% (126/527), suggesting that many men may carry HPV asymptomatically, consistent with findings from other studies [16]. High-risk HPV type 52 infection is prominent, indicating a potential risk of precancerous lesions, which necessitates enhanced monitoring. The viral warts group has the highest HPV positivity rate, with the main pathogenic types being HPV6 and HPV11. This is consistent with findings from the United States [24], South Korea [25], and Qingyuan [26], Guangdong, further supporting the crucial role of low-risk HPV in genital warts. Research indicates that sperm motility is significantly reduced in semen samples from men with HPV infection [27], and infected men can transmit the virus to their female partners, potentially affecting pregnancy and childbirth [28], highlighting a possible link between HPV infection and fertility-related problems. In this study, 21.48% (186/866) of men visited the clinic for fertility problems, with an HPV positivity rate of 24.73% (46/186), predominantly HPV type 52, further suggesting a strong association between high-risk HPV and male infertility. For these patients, incorporating fertility evaluation into clinical treatment is recommended.

The routine vaccine covers HPV16 and HPV18, which are closely related to 92% of anal cancer, 89% of oropharyngeal cancer, and 63% of penile cancer [29]. HPV16 is also associated with bladder cancer, breast cancer, and colorectal cancer, while HPV18 is considered a risk factor for prostate cancer, lung cancer, ovarian cancer, and breast cancer. Furthermore, HPV16 might provide protection against prostate cancer, lung cancer, anal cancer, and oropharyngeal cancer, while HPV18 might serve as a protective factor for vaginal cancer [30]. However, this study did not include data from patients with HPVrelated cancers, likely due to the focus on outpatient cases. Future studies could explore the epidemiology of HPV-related cancers in hospitalized patients in the Huizhou region.

Research indicates that widespread HPV vaccination can significantly lower HPV infection rates and the incidence of related cancers [31]. Our study found that men across different age groups are infected with HPV, highlighting the importance of early vaccination for men in Huizhou. Previously, China only provided bivalent, quadrivalent, and nonavalent HPV vaccines for females. However, on January 8, 2025, Merck (known as Merck & Co., based in Rahway, New Jersey, USA) announced that its quadrivalent HPV vaccine (brand name: Gardasil) was approved for use in men in China. This development brings new hope for the widespread adoption and prevention of HPV vaccination, with several domestic vaccine companies also launching HPV vaccines for men, which is expected to lead to a gradual increase in supply.

Merck's quadrivalent HPV vaccine is now available for male vaccination, with the same components as the quadrivalent vaccine for females, preventing infections with HPV types 6, 11, 16, and 18. It is suitable for males aged 9 to 26, and the vaccination cost is the same as for females. This is the first and currently the only approved male HPV vaccine in China. Persistent infections with high-risk HPV types 18 and 52 are closely linked to anal cancer, penile cancer, and oropharyngeal cancer in men. This study found that the high-risk HPV infection rate in men in Huizhou is higher for HPV 52 rather than HPV 18, and since HPV 52 is not covered by this vaccine, it limits its protection. Nevertheless, this vaccine can still cover some of the high-infection-rate HPV genotypes in the Huizhou region, effectively preventing genital warts and related cancers, making it a valuable option for male vaccination in the region. We also anticipate the release of future male HPV vaccines that will cover more genotypes and a broader age range. Although women aged 9 to 45 in China already have the opportunity to receive the HPV vaccine for many years, the actual vaccination coverage remains low, standing at only 6.21% by the end of 2022 [32]. This vaccination rate is far from the target set by the World Health Organization to eliminate cervical cancer by 2030. The male population in China has only recently started to have access to the HPV vaccine, and the challenge of eliminating the threat of HPV to male health remains significant.

Although this study provides valuable epidemiological data on male HPV in the Huizhou region, it has several limitations. First, as a single-center, retrospective analysis covering a ten-year period, the sample size remains relatively small, which may limit its ability to comprehensively reflect the HPV epidemic in this region's male population. Second, the study data are sourced from medical system records, which may introduce biases that could affect the generalizability of the results. Third, the HPV testing kit used in this study detects only 21 genotypes, which, while covering the most common types in the Asian population, does not include all subtypes, thus limiting a more complete understanding of HPV infections. Fourth, the absence of diagnostic data from 2014 to 2019 results in an incomplete analysis of diagnostic trends during that period. Fifth, the study did not investigate persistent high-risk HPV infections and their potential progression to related diseases. Lastly, the lack of data on factors such as smoking, number of sexual partners, condom use frequency, sexual health check-ups, and vaccination history hinders a deeper analysis of the relationship between these factors and HPV infections.

In summary, this study provides insights into the characteristics of HPV infection in males in Huizhou, highlighting the importance of increasing awareness about vaccination. It also underscores the need for implementing effective prevention and control measures to reduce the risk of high-risk HPV infections and associated diseases. Future studies should incorporate sociodemographic and lifestyle data, adopt long-term tracking designs, and further explore HPV infection dynamics particularly the mechanisms and progression of persistent high-risk HPV infections. These efforts will provide critical evidence to inform the development of public health policies and interventions, ultimately improving population health.

Conclusion

This study reports that the HPV infection positivity rate among male outpatients in Huizhou is 30.53%, with the most common HPV genotypes being HPV6, HPV52, HPV11, and HPV16. Single-type infections are predominant, and the highest positivity rates are observed in the 41–50 age group. Additionally, the distribution of HPV subtypes varies with age, highlighting the need for agespecific prevention strategies. These findings provide essential evidence for improving the clinical diagnosis, treatment, and prevention of male HPV infections in Huizhou, and offer valuable insights for the development of future public health policies. Future research should investigate the relationship between HPV infection and other potential risk factors, including lifestyle and immune status, to further enhance the prevention and control of high-risk HPV infections and mitigate the burden of related diseases.

Abbreviations

CI	Confidence interval
HIV	Human immunodeficiency virus
HPV	Human papillomavirus
HR-HPV	High risk human pailloma virus
IQR	Interquartile Range
LR-HPV	Low risk human pailloma virus
MSM	Men who have sex with men
PCR	Polymerase chain reaction
WHO	World Health Organization

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Author contributions

All authors contributed to the study design, data collection, data curation, data analysis, and interpretation. First author Caiyi Wen participated in drawing figures, drafting the article, and revising it for important intellectual content. Corresponding author Xianjin Wu reviewed and edited the manuscript. All authors read and approved the final version of the manuscript.

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Data availability

No datasets were generated or analysed during the current study.

Declarations

Ethical approval and informed consent

This study has been approved by the Clinical Research Ethics Committee of Huizhou Central People's Hospital (approval number: kyll2024038). Given that this is a retrospective study with no direct impact on patients, the ethics committee waived the requirement for written informed consent. This study strictly adheres to the principles of the Declaration of Helsinki and other relevant ethical guidelines.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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References

- Chesson HW, Dunne EF, Hariri S, Markowitz LE. The estimated lifetime probability of acquiring human papillomavirus in the United States. Sex Transm Dis. 2014;41(11):660–4. https://doi.org/10.1097/OLQ.000000000000193
- Zhang C, Yang Z, Luo P, et al. Association of TLR4 and TLR9 gene polymorphisms with cervical HR-HPV infection status in Chinese Han population. BMC Infect Dis. 2023;23(1):152. https://doi.org/10.1186/s12879-023-08116-z

- Zeng M, Li X, Jiao X, et al. Roles of vaginal flora in human papillomavirus infection, virus persistence and clearance. Front Cell Infect Microbiol. 2023;12:1036869. https://doi.org/10.3389/fcimb.2022.1036869
- Schiffman M, Castle PE, Jeronimo J, Rodriguez AC, Wacholder S. Human papillomavirus and cervical cancer. Lancet. 2007;370:890–907.
- Kalinganire N, Uwineza A, Kyokunda L, Banura C. Oral-genital HPV infection transmission, concordance of HPV genotypes and genital lesions among spouses/ partners of patients diagnosed with HPV-related head and neck squamous cell carcinoma (HNSCC): a scoping review. Infect Agents Cancer. 2023;18(1):63. https://doi.org/10.1186/s13027-023-00539-2
- Stewart J, Calderon M, Hathaway A, Winer RL, Zunt J. Human papillomavirus infection among male clients of female sex workers soliciting sex in brothels in Peru. Int J STD AIDS. 2018;29(2):178–84. https://doi.org/10.1177/095646241 7721563
- Lekoane KMB, Kuupiel D, Mashamba-Thompson TP, Ginindza TG. Evidence on the prevalence, incidence, mortality and trends of human papilloma virusassociated cancers in sub-Saharan Africa: systematic scoping review. BMC Cancer. 2019;19(1):563. https://doi.org/10.1186/s12885-019-5781-3
- De Sanjosé S, Serrano B, Tous S, et al. Burden of human papillomavirus (HPV)related cancers attributable to HPVs 6/11/16/18/31/33/45/52 and 58. JNCI Cancer Spectr. 2018;2(4):pky045. https://doi.org/10.1093/jincics/pky045
- Du M, Lin Q, Yan S, Gao X, Yang C, Li Z, et al. Clinicopathologic characteristics of HPV-associated head and neck squamous cell carcinoma in Southern China: long-term retrospective study of 400 cases. Med Oncol. 2024;16:17588359241242962.
- Bruni L, Albero G, Rowley J, et al. Global and regional estimates of genital human papillomavirus prevalence among men: a systematic review and meta-analysis. Lancet Global Health. 2023;11(9):e1345–62. https://doi.org/10. 1016/S2214-109X(23)00305-4
- Giuliano AR, Nielson CM, Flores R, et al. The optimal anatomic sites for sampling heterosexual men for human papillomavirus (HPV) detection: the HPV detection in men study. J INFECT DIS. 2007;196(8):1146–52. https://doi.org/10 .1086/521629
- Wang X, Ji Y, Li J, et al. Prevalence of human papillomavirus infection in women in the autonomous region of inner Mongolia: a population-based study of a Chinese ethnic minority. J Med Virol. 2018;90(1):148–56. https://doi. org/10.1002/jmv.24888
- WHO. Guideline for screening and treatment of cervical pre-cancer lesions for cervical cancer prevention: use of mRNA tests for human papillomavirus (HPV). Second edition. World Health Organization; 2021.
- Wang S, Ma QY, Du J, et al. Detecting and genotyping high-risk human papillomavirus among male patients during 2015–2023 in Beijing, China. Emerg Microbes Infections. 2024;13(1):2313848. https://doi.org/10.1080/22221751.2 024.2313848
- Zheng L, Zheng L, Chen S, Liu W, Qi J, Li K. Human papillomavirus prevalence and genotype distribution in Liaocheng men between 2016 and 2022. J Med Virol. 2024;96(1):e29360. https://doi.org/10.1002/jmv.29360
- Liu P, Yang X, Zhao H, Liang L, Chen M, Yin A. High burden of human papillomavirus infection among men in Guangzhou, South China: implications for HPV vaccination strategies. Hum Vaccines Immunotherapeutics. 2024;20(1):2337161. https://doi.org/10.1080/21645515.2024.2337161
- Tekkesin N, Goktas S, Alkis V, Tekkesin E, Goktas P. Male human papillomavirus infection and genotyping in Turkey. Asian Pac J Cancer Prev. 2023;24(12):4187–93. https://doi.org/10.31557/APJCP.2023.24.12.4187
- Loenenbach A, Pawlita M, Waterboer T, et al. Seroprevalence of mucosal and cutaneous human papillomavirus (HPV) types among children and adolescents in the general population in Germany. BMC Infect Dis. 2022;22(1):44. htt ps://doi.org/10.1186/s12879-022-07028-8
- Romero FP, Ramírez VE, Muñoz OM, et al. Lesiones anogenitales Por virus papiloma Humano. Estudio de prevalencia En Niños, Niñas y adolescentes no vacunados. Andes Pediatr. 2023;94(1):29. https://doi.org/10.32641/andespedi atr.v94i1.3534
- Salehi-Vaziri M, Sadeghi F, Bokharaei-Salim F, et al. The prevalence and genotype distribution of human papillomavirus in the genital tract of males in Iran. Jundishapur J Microbiol. 2015;8(12). https://doi.org/10.5812/jjm.21912
- Hu J, Ji L, Li P et al. Genital HPV prevalence, follow-up and persistence in males and HPV concordance between heterosexual couples in Wenzhou, China. IDR. 2022;15:7053–7066. https://doi.org/10.2147/IDR.S387226
- Zhou Y, Lin YF, Meng X, et al. Anal human papillomavirus among men who have sex with men in three metropolitan cities in Southern China: implications for HPV vaccination. Vaccine. 2020;38(13):2849–58. https://doi.org/10.10 16/j.vaccine.2020.02.009

- Li X, Xiang F, Chen Z, et al. Genital human papillomavirus prevalence and genotyping among males in Putuo district of Shanghai, China 2015–2019. Med Sci Monit. 2021;27. https://doi.org/10.12659/MSM.932093
- 24. Arima Y, Winer RL, Feng Q, et al. Development of genital warts after incident detection of human papillomavirus infection in young men. J INFECT DIS. 2010;202(8):1181–4. https://doi.org/10.1086/656368
- Kim YT, Serrano B, Lee JK, et al. Burden of human papillomavirus (HPV)related disease and potential impact of HPV vaccines in the Republic of Korea. Papillomavirus Res. 2019;7:26–42. https://doi.org/10.1016/j.pvr.2018.12. 002
- Yin WG, Yang M, Peng L, et al. Male papillomavirus infection and genotyping in the Qingyuan area. Virol J. 2020;17(1):155. https://doi.org/10.1186/s12985-0 20-01423-w
- 27. Cao X. Impact of human papillomavirus infection in semen on sperm progressive motility in infertile men: a systematic review and meta-analysis. Published Online. 2020. https://doi.org/10.1186/s12958-020-00604-0
- Wei S, Wang K, Cheng F, et al. Prevalence of human papillomavirus infection in the female partner of infertile couples undergoing IVF/ICSI-ET and subsequent reproductive outcomes. JCM. 2022;11(23):7185. https://doi.org/10.339 0/jcm11237185
- Kamolratanakul S, Pitisuttithum P. Human papillomavirus vaccine efficacy and effectiveness against cancer. Vaccines. 2021;9(12):1413. https://doi.org/10.339 0/vaccines9121413
- Sun J, Xiang J, An Y, et al. Unveiling the association between HPV and pancancers: a bidirectional two-sample Mendelian randomization study. Cancers. 2023;15(21):5147. https://doi.org/10.3390/cancers15215147

- Fappani C, Bianchi S, Panatto D, et al. HPV type-specific prevalence a decade after the implementation of the vaccination program: results from a pilot study. Vaccines. 2021;9(4):336. https://doi.org/10.3390/vaccines9040336
- Hu JP, Wang JL, Li Y, et al. Prevalence and genotype distribution of human papillomavirus infection among 66000 women from 2014 to 2023 in the plateau region of Southwest China. Virol J. 2024;21(1):176. https://doi.org/10. 1186/s12985-024-02447-2

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