Prevalence and genotype distribution of human papillomavirus in outpatients and healthy female subjects in Wenzhou, Zhejiang Province, China

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Abstract

The present study examined the prevalence of human papillomavirus (HPV) and its genotype distribution in outpatients and healthy female subjects in Wenzhou so as to develop local HPV vaccination strategies and contribute to the prevention of this disease. The present retrospective study enrolled 164,137 women, including 118,484 outpatients and 45,653 healthy female subjects from 2015 to 2020. Cervical exfoliated cells were collected from these women for DNA extraction. The DNA samples were detected with a fluorescence in situ hybridization method and 27 HPV genotypes were analyzed. The overall prevalence of HPV was 17.35%; this corresponded to a prevalence of 19.10% in the outpatient group and 12.82% in the healthy female group. HPVs 52, 58, 16, 53, and 61 were the five most prevalent HPV genotypes in the outpatient group. The five most common genotypes were HPV 52, 53, 58, 61, and 81 in the healthy female group. The HPV infection peak was estimated to be 44.65% in the 10–19 age group and 27.35% in the 60–69 age group. The burden of HPV infection in this area was high; therefore, a scientific and reasonable vaccination strategy should be adopted. The universal use of multivalent vaccines is recommended and considerable attention should be paid to HPV types that are not targeted by the vaccines. Cervical screening should be performed routinely in patients with gynecological clinical symptoms to avoid cervical intraepithelial neoplasia following persistent infection of high-risk HPV, notably in women over 60 years of age.

Background

Human papillomavirus (HPV) is one of the most common sexually transmitted infections, which infects the human epithelium (1). More than 200 genotypes of HPV have been identified and categorized as low-risk HPVs (LR-HPVs) or high-risk HPVs (HR-HPVs) (2). Infections with the LR-HPV types, such as HPV 6 and 11, cause genital warts, which are, to their majority, clinically visible benign lesions. Persistent HR-HPV infection causes the development of cervical cancer (CC), which is the second most common cancer in women worldwide (3). Based on epidemiological data, the International Agency for Research on Cancer (IARC) categorized HPVs 16, 18, 26, 31, 33, 35, 39, 45, 51, 52, 53, 56, 58, 59, 66, 68, and 82 as carcinogenic or probably carcinogenic (4). The total direct medical costs related to CC prevention and treatment have been estimated at ~$6 billion in the United States of America (5). As a country with a large population, GLOBOCAN reported that China had 109,741 new CC cases and 59,060 CC-related deaths in 2020 (6).

The prevalence of HPV is high in countries where the burden of CC is high. HPV screening and the use of vaccines are considered the most effective measures for preventing HPV infection (7). HPV screening allows early intervention in these cases, thereby reducing the healthcare burden (8). HPV vaccination is the most effective means of providing protection to subjects without HPV infection (9). In China, >16 million HPV vaccines were issued from 2016 to 2019; however, the market gap has been estimated to be >1 billion vaccine doses (10). The first domestic bivalent vaccine from Xiamen Wantai Canghai Biotechnology was approved for women aged 9 to 45, and the cost of the three injections was <$200. Certain regional governments have offered free HPV vaccinations. As a result, all women at an appropriate age would be vaccinated for HPV in China. And the data on HPV prevalence and genotype distribution can provide a
baseline estimation of the burden of HPV infection and can aid the guidance of programs on HPV-based CC screening and the development of strategies for vaccine-based HPV prevention.

Recent studies in China have shown that the infection rate of HPV varies significantly in different regions and populations, ranging from 15.5–28.95%; the top three subtypes with the highest infection rates were the following: HPV52, HPV16, and HPV58 (11–17). However, the majority of these studies are based on single, healthy, or hospital-visiting females. The present study compared for the first time the HPV infection rate and type distribution in gynecological disease carriers and healthy females, so as to provide useful data for the systematic and epidemiological assessment of HPV and its vaccination in this region.

Methods

Study population. From January 2015 to December 2020, 164,137 females (age range 12–89 years) were enrolled in this retrospective study, including 118,484 outpatients from the outpatient services of the departments of gynecology and 45,653 healthy female subjects from the physical examination center of The Second Affiliated Hospital and Yuying Children's Hospital of Wenzhou Medical University.

The patients from the department of gynecology performed HPV tests for various reasons, including vaginitis, urethritis, irregular vaginal bleeding, cervicitis, undiagnosed abdominal pain, and genital warts. These patients were divided into the outpatient group (OG). The female subjects who had no complaints of gynecological symptoms from the physical examination center were classified into the healthy female group (HFG).

Sample collection and HPV genotyping. Repeated samples from the same women were excluded from the study. Cervical exfoliated cells were obtained from women using a cytobrush (Shanghai Tellgen Life Technologies Inc.) for genomic DNA extraction. DNA was extracted and purified using a commercial kit (Shanghai Tellgen Life Technologies Inc.) by the exchange resin adsorption method. The method was performed according to the manufacturer's instructions. Subsequently, HPV DNA was detected and genotyped by flow-through hybridization and gene chip of Tellgenplex®HPV 27 genotyping Assay (CFDA20173404697, Shanghai Tellgen Life Technologies Inc.), following the manufacturer's instructions. This method uses multiplex PCR amplification with universal primers and flow fluorescence hybridization to simultaneously detect 27 types of HPV DNA, including 10 LR-HPV genotypes (6, 11, 40, 42, 43, 44, 55, 61, 81, and 83), and 17 HR-HPV genotypes (16, 18, 26, 31, 33, 35, 39, 45, 51, 52, 53, 56, 58, 59, 66, 68, and 82). The advantages of the flow fluorescence hybridization method used in the present study have been confirmed in previous studies (18).

Positive and negative controls were used during testing to verify the reliability of the results. The β-globin gene was used as the internal reference sequence and the signal value < 1000 was considered to be an unqualified detection. The manufacturer's verification report indicated that by using the Sanger sequencing method as the reference method, the sensitivity, specificity, and total coincidence rate of the assay would be 100%, 76.33%, and 96.08%.
Statistical analysis was performed using WPS Office and GraphPad Prism 5 (GraphPad Software, Inc.). The differences in the HPV positive rates and proportions of the multiple-type HPV infections between the OG and the HFG were assessed by the unpaired Student's t-test. \( P < 0.01 \) was considered to indicate a statistically significant difference.

Results

**Overall and type-specific HPV prevalence.** A total of 164,137 women were involved in the present study, including 118,484 females in the OG and 45,653 females in the HFG. Of the 164,137 cases, 28,480 women were positive for HPV, with an overall HPV infection rate of 17.35%. The positive cases accounted for 19.10\% (22,626/118,484) of the OG and 12.82\% (5,854/45,653) of the HFG, respectively. The HPV infection rate of the OG was significantly higher than that of the HFG (\( P < 0.01 \)).

A total of 27 HPV genotypes were identified in the present study (Table 1). The total number of positive HPV genotypes was 37,106, among which 29,703 were from the OG, with a per capita carrying rate of 0.25 (29,703/118,484). A total of 7,403 positive HPV genotypes were noted in the HFG, with a per capita carrying rate of 0.16 (7,403/45,653).

In total, HPVs 52 (3.29\%), 58 (1.96\%), 53 (1.87\%), 16 (1.67\%), and 61 (1.34\%) were the five most prevalent HPV genotypes. The five most common genotypes were HPV 52, 58, 16, 53, and 61 in the OG, and the five most common genotypes were HPV 52, 53, 58, 61, and 81 in the HFG (Fig. 1). The percentage of positive detection for each HPV type was analyzed over a total period of 5 years (Fig. 2). The six most common genotypes, namely HPV 52 (14.54\%), 58 (8.68\%), 53 (8.27\%), 16 (7.40\%), 61 (5.94\%), and 81 (5.76\%), accounted for ~50\% of all infection types (Fig. S1).

**Genotype-specific prevalence of HR-HPV.** HR-HPV was detected in 26,568 individuals, with a total infection rate of 16.19\% (26,568/164,137). The HR-HPV infection rate of the OG and the HFG was 18.08\% (21,424/118,484) and 11.27\% (5,144/45,653), respectively. The HR-HPV infection rate of the OG was significantly higher than that of the HFG (\( P < 0.01 \)).

The most prevalent HR-HPV genotypes were HPV 52 (3.29\%, 5,397/164,137), followed by HPV 58 (1.96\%, 3,220/164,137), HPV 53 (1.87\%, 3,070/164,137), HPV 16 (1.67\%, 2,746/164,137), and HPV 39 (1.19\%, 1,947/164,137).

**Distribution characteristics of single and multiple HPV infections.** The frequency and number of HPV infections are shown in Table 2. Among women with a single HPV infection, HR-HPV infection accounted for 74.33\% (12,867/17,286) in the OG and for 70.33\% (3,273/4,654) in the HFG (\( P > 0.01 \)). Among women with multiple HPV infections, the multiple infections with the HR-HPV rate accounted for 93.39\% (4,987/5,340) of the population in the OG and for 92\% (1,104/1,200) of the population in the HFG (\( P > 0.01 \)).

Multiple and single HPV genotypes accounted for 40.87\% (15,166/37,106) and 59.13\% (21,940/37,106) of all positive types, respectively. Single infections and multiple infections were identified across all
genotypes (Fig. 2). The prevalence of HPV 16, 39, 52, and 58 in the single infection group was higher than that of the multiple infection group (P<0.01).

**Time trends of prevalence and genotype of HPV.** The prevalence of HPV in Wenzhou from 2015 to 2020 was analyzed; the infection rate of the OG and the HFG indicated almost the same trend (Fig. 3A). The total prevalence of HPV indicated a significant decrease from 23.35% in 2015 to 13.71% in 2017. Subsequently, the infection rate slowly increased to 18.35% in 2020. The number of HPV genotyping tests increased every year during the period 2015-2019. However, the percentage of HPV testing decreased in 2020 due to the COVID-19 lockdown (Fig. 3B).

The majority of the viral infection types were consistent with the general trend of HPV-positive infection; however, certain genotypes exhibited an increasing or decreasing trend change every year (Fig. 4).

**Age-specific prevalence and genotype of HPV.** All the participants were stratified into 8 groups based on their age. The age-specific prevalence of HPV was calculated (Table 3). The overall age-specific prevalence of HPV exhibited two peaks. The following infection rates were noted for the specific age groups: 44.65%, 19.79%, 15.14%, 15.90%, 19.76%, 27.35%, 23.04%, and 15.87% (Fig. 5). The first peak corresponded to 44.65% in the 10-19 age group. The prevalence of the infection decreased to 19.79% in the 20-29 age group and continuously increased to 27.35% in the 60-69 age group. The lowest prevalence (under 16%) was found in the 30-49 age group and the majority of the samples were obtained from women corresponding to that age stage range. Two infection peaks corresponding to subjects under 20 and between 60 and 69 years of age were noted in the OG, while only one infection peak was noted in the 60-79 age group in the HFG.

The age-specific percentage of the HPV genotype in the positive cases was analyzed (Table S1). The data indicated that young subjects under the age of 20 infected with HPVs 6, 11, 16, 18, and 52 were the main subjects infected, accounting for nearly 50% of the total infection cases. The infection rates of HPVs 6 and 11 were significantly higher in the aforementioned age group (<20 years of age) than those of the other age groups, while HPV 53 infected a significantly lower number of subjects in the <20-year group compared with that of the other age groups.

The overall risk of the six most common HR-HPV genotypes (HPV 52, 58, 53, 16, 39, and 18) was increased with age. However, the individual genotypes indicated different trends in relation to age (Fig. 6).

**Discussion**

The current retrospective study presents the prevalence and distribution of HPV among 164,137 women including outpatients and healthy females between 2015 and 2020 in Wenzhou which is a coastal city of 9 million people located in southeast China. The present study adopted the same detection method in the same area for five years, providing solid evidence of HPV epidemiology in the region. The data revealed that the overall prevalence of HPV was 17.35%, whereas the HPV prevalence of the OG was ~ 6% higher.
than that of the HFG. The damage to the vaginal microecological environment caused by gynecological
diseases may lead to susceptibility to HPV (19). Different study target populations can lead to a significant
deviation in the HPV infection rate.

According to previous reports, HPV prevalence ranges from 6.70 to 44.50% in China, which features a vast
territory and different levels of economic development (20–21). The variation may be due to cultural
diversity, the sampling strategy, identification techniques, as well as the sensitivity and specificity of the
HPV detection assays. In the present study, the trend of HPV infection decreased from 23.35% in 2015 to
13.71% in 2017; subsequently, it increased to 18.35% in 2020. The HPV prevalence data in China were
compared and analyzed. The data corresponded to the time period between 2010 and 2021. The
prevalence of HPV may change with the socioeconomic development of a city, and the majority of the
cities in China have developed rapidly in the past ten years. The HPV infection rates are generally > 20%
across China before 2016, including studies in the middle economic income area, such as Harbin, Henan,
Fujian, Jiangxi, Zhejiang, and Chongqing, with corresponding infection rates of 36.45%, 23.98%, 22.5%,
22.49%, 20.54%, and 26.2%, respectively (22–28). Huzhou, Chongqing, and Chenzhou, which have the
same financial income as that of previous regions, have shown HPV prevalence of < 20% following 2016.
The exact prevalence percentages for these three regions were 15.5%, 19.9%, and 18.7%, respectively (7, 16,
27). In addition, all studies in developed areas, such as Shanghai, Guangdong, and Shenzhen have shown
HPV infection rates < 20% (11, 29–33). Therefore, it was considered that the financial and social
development affect HPV prevalence since economically developed areas provide improved living
conditions, medical standards, and HPV vaccination coverage. However, HPV maintains a high level of
infection in China that requires additional medical solutions.

Certain countries have an even higher HPV prevalence, including Malaysia (24.7%), Iran (38.68%), and
Turkey (36.3%) (34–36). A previous study including 157,879 women with normal cervical cytology indicated
that HPV prevalence in Africa was 22.1%, while 20.4% was noted in Central America and Mexico, 11.3% in
northern America, 8.1% in Europe, and 8.0% in Asia (37). In addition to socioeconomic differences,
geographic, religious, ethnic, and other factors may influence the prevalence of HPV. This requires cross-
national and regional cooperation so as to carry out further studies to confirm this finding.

Worldwide meta-analysis studies indicate that the five most common infection types are HPV16, HPV18,
HPV52, HPV31, and HPV58 (37–38). However, the current study identified HPV 52, 58, 53, 16, and 39 as the
five most common HR-HPV genotypes. Recent studies in China indicate that the proportion of the major
common HPV genotypes is similar to that reported in the current study (11–15). Compared with the
previous studies, HPVs 16 and 18 indicated a decreased infection trend in the present study. As 70% of CCs
are caused due to persistent HPV16 and 18 infections, the two types are the most widely studied and
remain the primary targets of detection (39). The decline of HPV 16 and 18 infections may be due to a
number of factors. Firstly, the detection sensitivity has been improved over the years and the number of
participants has increased. Secondly, the approval and mass vaccination of the bivalent HPV vaccine has
significantly reduced the number of new cases of HPV 16 and 18 infections. Lastly, the use of
circumferential electrosurgical procedures and advanced medical techniques has decreased the number of
positive patients. The present study indicated an increased trend of HPV 53 and 59 infections, which were
not covered by the nine-valent HPV vaccine. The IARC designates HPV 53 as group 2B (possibly carcinogenic), which may be associated with an infrequent incidence of CC (4). However, due to the high infection rate of HPV 53 in China, this viral strain requires considerable attention.

A previous study has shown that young women exhibit the highest HPV prevalence in southeast China (40), which is consistent with the findings of the present study. The high infection rate in young women may result from higher sexual activity prior to their immune systems becoming less sensitive to HPV. The infection rate of HPV 6 was particularly high. The infection of HPV 6 manifests clinically as papilloma and patients typically seek medical treatment. Although young women are known to have high risks for HPV infection, this effect may be temporary and may disappear within a year or two; therefore, their prevalence declined gradually with regard to their age. It was predicted that the prevalence of HPV was slightly lower in the 20–39 age group, whereas it was significantly increased in the 50–69 age group, which was consistent with the data in most developed countries reported by Laia et al (38). The data indicated that women over 40 years exhibited an increased HPV prevalence, whereas those that had an age range of 60–69 years reached the peak. Women over 40 years of age were still sexually active; however, their immune response was reduced. Therefore, it is recommended that cervical screening should be performed every six months or a year for women over 40 years of age.

The present study contains certain limitations. Certain factors affecting the HPV infection rate, including medical history, financial situation, and educational level, were not collected and analyzed. The number of females < 20 years and > 80 years was too small, which may lead to inaccurate results in these age stages. The findings failed to identify and elucidate the rule of multiple infection combinations, and to point out possible interactions between various HPV types. Although the results indicated that HPV 16 had a decreasing trend with age, the data on post-infection deaths were not available. The reasons why HPV 52 exhibited an “M” curve type with peaks at 30–39 and 60–69 years old could not be explained. These questions need to be further addressed in future studies.

Conclusions

The present study revealed the prevalence and genotype distribution of HPV in Wenzhou in terms of time trends and age distribution. The most common infection types were from HPVs 52, 58, 53, 16, and 61. HPVs 53 and 59 which were not covered by the nine-valent HPV vaccine indicated an increasing trend. This study suggested that cervical screening should be performed routinely in patients with gynecological clinical symptoms, notably in women over 60 years of age, so as to avoid cervical intraepithelial neoplasia following persistent infection of HR-HPV.

Declarations

Acknowledgements

Not applicable.
Funding sources and support

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Availability of data and materials

The data generated in the present study may be requested from the corresponding author.

Authors’ contributions

XC and QC were involved in the conception of the study and the study design. XC provided assistance in the methodology of the study. QC, WQ, YZ, LS, and YW were involved in the data acquisition. QC, XC, and WQ participated in writing the manuscript draft and revising it for important intellectual content. QC, WQ, YZ, LS, YW, and XC gave the final approval for the publication of the manuscript.

Ethics approval and consent to participate

The present study was performed in accordance with the ethical guidelines under the protocols approved by the Institutional Medical Ethics Review Board of The Second Affiliated Hospital and Yuying Children's Hospital of Wenzhou Medical University, Zhejiang, P.R. China (2018305824).

Competing interests

The authors declare that they have no competing interests.

References


Tables

Table 1. HPV genotype distribution in the total population, the OG, and the HPG. HPV, human papillomavirus; OG, outpatient group; HPG, healthy female group.
<table>
<thead>
<tr>
<th>Genotype</th>
<th>Total (n = 164,137)</th>
<th>OG (n = 118,484)</th>
<th>HPG (n = 45,653)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n</td>
<td>P%</td>
<td>n</td>
</tr>
<tr>
<td>HR-HPV</td>
<td>26568</td>
<td>16.19%</td>
<td>21424</td>
</tr>
<tr>
<td>HPV 16</td>
<td>2746</td>
<td>1.67%</td>
<td>2371</td>
</tr>
<tr>
<td>HPV 18</td>
<td>1473</td>
<td>0.90%</td>
<td>1215</td>
</tr>
<tr>
<td>HPV 26</td>
<td>41</td>
<td>0.02%</td>
<td>36</td>
</tr>
<tr>
<td>HPV 31</td>
<td>467</td>
<td>0.28%</td>
<td>394</td>
</tr>
<tr>
<td>HPV 33</td>
<td>853</td>
<td>0.52%</td>
<td>693</td>
</tr>
<tr>
<td>HPV 35</td>
<td>612</td>
<td>0.37%</td>
<td>483</td>
</tr>
<tr>
<td>HPV 39</td>
<td>1947</td>
<td>1.19%</td>
<td>1546</td>
</tr>
<tr>
<td>HPV 45</td>
<td>372</td>
<td>0.23%</td>
<td>301</td>
</tr>
<tr>
<td>HPV 51</td>
<td>1442</td>
<td>0.88%</td>
<td>1158</td>
</tr>
<tr>
<td>HPV 52</td>
<td>5397</td>
<td>3.29%</td>
<td>4259</td>
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<tr>
<td>HPV 53</td>
<td>3070</td>
<td>1.87%</td>
<td>2363</td>
</tr>
<tr>
<td>HPV 56</td>
<td>1425</td>
<td>0.87%</td>
<td>1134</td>
</tr>
<tr>
<td>HPV 58</td>
<td>3220</td>
<td>1.96%</td>
<td>2663</td>
</tr>
<tr>
<td>HPV 59</td>
<td>1227</td>
<td>0.75%</td>
<td>986</td>
</tr>
<tr>
<td>HPV 66</td>
<td>1211</td>
<td>0.74%</td>
<td>997</td>
</tr>
<tr>
<td>HPV 68</td>
<td>629</td>
<td>0.38%</td>
<td>469</td>
</tr>
<tr>
<td>HPV 82</td>
<td>436</td>
<td>0.27%</td>
<td>356</td>
</tr>
<tr>
<td>LR-HPV</td>
<td>10538</td>
<td>6.42%</td>
<td>8279</td>
</tr>
<tr>
<td>HPV 06</td>
<td>862</td>
<td>0.53%</td>
<td>725</td>
</tr>
<tr>
<td>HPV 11</td>
<td>484</td>
<td>0.29%</td>
<td>436</td>
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<tr>
<td>HPV 40</td>
<td>169</td>
<td>0.10%</td>
<td>132</td>
</tr>
<tr>
<td>HPV 42</td>
<td>603</td>
<td>0.37%</td>
<td>465</td>
</tr>
<tr>
<td>HPV 43</td>
<td>1302</td>
<td>0.79%</td>
<td>1044</td>
</tr>
<tr>
<td>HPV 44</td>
<td>1379</td>
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</tr>
<tr>
<td>HPV 55</td>
<td>1170</td>
<td>0.71%</td>
<td>891</td>
</tr>
<tr>
<td>HPV 61</td>
<td>2204</td>
<td>1.34%</td>
<td>1686</td>
</tr>
<tr>
<td>HPV 81</td>
<td>2137</td>
<td>1.30%</td>
<td>1648</td>
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</table>
Table 2. Frequency and prevalence of single and multiple HPV infection. HPV, human papillomavirus.

<table>
<thead>
<tr>
<th>Variables</th>
<th>Total (n = 164,137)</th>
<th>OG (n = 118,484)</th>
<th>HPG (n = 45,653)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n</td>
<td>P%</td>
<td>n</td>
</tr>
<tr>
<td>Single</td>
<td>21,940</td>
<td>13.37%</td>
<td>17,286</td>
</tr>
<tr>
<td>Double</td>
<td>4,989</td>
<td>3.04%</td>
<td>4,056</td>
</tr>
<tr>
<td>Triple</td>
<td>1,156</td>
<td>0.70%</td>
<td>954</td>
</tr>
<tr>
<td>Quadruple</td>
<td>294</td>
<td>0.18%</td>
<td>244</td>
</tr>
<tr>
<td>Quintet</td>
<td>72</td>
<td>0.04%</td>
<td>59</td>
</tr>
<tr>
<td>Sextuple</td>
<td>29</td>
<td>0.02%</td>
<td>27</td>
</tr>
</tbody>
</table>

n, number of cases; P%, prevalence rate.

Table 3. Summary of HPV infection in the OG and HPG at each age group. HPV, human papillomavirus; OG, outpatient group; HPG, healthy female group.
<table>
<thead>
<tr>
<th>Age group</th>
<th>Cases</th>
<th>Positive cases</th>
<th>Positive rate</th>
<th>Multiple infection cases</th>
<th>Multiple infection rate</th>
<th>HR-HPV infection Cases</th>
<th>HR-HPV infection rate</th>
<th>Percentage of HR-HPV in positive cases</th>
</tr>
</thead>
<tbody>
<tr>
<td>OG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>10-19</td>
<td>301</td>
<td>140</td>
<td>46.51%</td>
<td>61</td>
<td>20.27%</td>
<td>113</td>
<td>37.54%</td>
<td>80.71%</td>
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<tr>
<td>20-29</td>
<td>16,940</td>
<td>3,559</td>
<td>21.01%</td>
<td>1035</td>
<td>6.11%</td>
<td>2,888</td>
<td>17.05%</td>
<td>81.15%</td>
</tr>
<tr>
<td>30-39</td>
<td>40,785</td>
<td>6,868</td>
<td>16.84%</td>
<td>1445</td>
<td>3.54%</td>
<td>5,580</td>
<td>13.68%</td>
<td>81.25%</td>
</tr>
<tr>
<td>40-49</td>
<td>38,732</td>
<td>6,747</td>
<td>17.42%</td>
<td>1328</td>
<td>3.43%</td>
<td>5,147</td>
<td>13.29%</td>
<td>76.29%</td>
</tr>
<tr>
<td>50-59</td>
<td>16,452</td>
<td>3,655</td>
<td>22.22%</td>
<td>950</td>
<td>5.77%</td>
<td>2,800</td>
<td>17.02%</td>
<td>76.61%</td>
</tr>
<tr>
<td>60-69</td>
<td>4,403</td>
<td>1,440</td>
<td>32.70%</td>
<td>455</td>
<td>10.33%</td>
<td>1,148</td>
<td>26.07%</td>
<td>79.72%</td>
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<tr>
<td>70-79</td>
<td>758</td>
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<td>95.00%</td>
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<td>22,626</td>
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<td>5,854</td>
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<td>1,200</td>
<td>2.63%</td>
<td>3274</td>
<td>7.17%</td>
<td>55.93%</td>
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Figures
**Figure 1**

The prevalence of HPV genotypes ranked from highest to lowest. The abscissa was sorted by HPV prevalence in total from high to low. HPV, human papillomavirus.
**Figure 2**

Comparison of the number of multiple infections and single infections.

**Figure 3**

Summary of HPV testing volume and infection rate from 2015 to 2020. (A) Trend of HPV infection rate in each group. (B) The number of HPV genotyping tests during the period 2015-2020. HPV, human
papillomavirus.

Figure 4

Time trends of specific genotypes of HPV. (A) HPVs 16, 18, and 33 indicated a downward trend. (B) HPVs 52, 53, 59 and 61 indicated an upward trend. HPV, human papillomavirus.

Figure 5

The overall age-specific prevalence of HPV. HPV, human papillomavirus.
Figure 6

Age-specific prevalence of the six most common HR-HPV genotypes. (A) The overall infection rates of HPVs 52, 58, 53, 16, 39, and 18 was gradually increased with age. (B) HPV 52 indicated an apparent bimodal pattern, while HPV 18 hardly changed with age. HPVs 53 and 58 increased with age, while HPV 16 decreased with age until 70. HR-HPV, high-risk HPV; HPV, human papillomavirus.

Supplementary Files

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- Supplementary.docx