

Prevalence and Risk Factors of Human Papillomavirus infection and Cervical Cytological lesions Among Women in Shanxi, China: A Cross-Sectional Study

Shanshan Ge

First Hospital of Shanxi Medical University

Haining Gao

Shanxi Medical University

Jing Wang

First Hospital of Shanxi Medical University

Siyao Guo

Shanxi Medical University

Yunqi Chang

Shanxi Medical University

Yueyue Qi

Shanxi Medical University

Jingrui Han

Shanxi Medical University

You Jia

Shanxi Medical University

Jianyu Dong

First Hospital of Shanxi Medical University

Feixue Wei

weifeixue@sxmu.edu.cn

Shanxi Medical University

Research Article

Keywords: Human papillomavirus, prevalence, type distribution, cervical cytology diagnosis

Posted Date: February 18th, 2026

DOI: <https://doi.org/10.21203/rs.3.rs-8667686/v1>

License: © ⓘ This work is licensed under a Creative Commons Attribution 4.0 International License.
[Read Full License](#)

Additional Declarations: No competing interests reported.

Version of Record: A version of this preprint was published at Virology Journal on September 9th, 2026.
See the published version at <https://doi.org/10.1186/s12985-026-03300-4>.

Abstract

Background.

China incorporated the Human papillomavirus (HPV) vaccine into the national immunization programme in October 2025. Population-level data on HPV prevalence and genotype distribution are essential for guiding local prevention strategies and establishing a baseline to evaluate vaccine effectiveness as coverage expands.

Methods.

We conducted a retrospective cross-sectional study including women who underwent routine health examinations with both HPV DNA testing and cervical cytology diagnosis at our hospital from January 2021 to December 2024 in Shanxi, China. We estimated type-specific and grouped HPV prevalence, assessed patterns of single and multiple HPV infections, and compared genotype distribution across cytological categories. Logistic regression was used to identify factors associated with high-risk HPV (HR-HPV) infection and cytological abnormalities.

Results.

A total of 19,384 women aged ≥ 18 years were included (median age 42 years, IQR 36–51). HR-HPV prevalence was 10.7%, with HPV52 (2.3%), HPV16 (1.7%), and HPV58 (1.7%) as the most common HR-HPV genotypes. The prevalence of HPV16/18 and HPV6/11/16/18/31/33/45/52/58 was 2.3% and 5.1%, respectively. Women aged > 65 years had higher odds of HR-HPV infection (adjusted odds ratio [AOR] = 2.1, 95% CI 1.5–2.8), while married women had lower odds compared with unmarried women (0.5, 95% CI 0.4–0.7). Two percent of women had abnormal cytology. Among HPV-positive women, HPV16/18 prevalence increased substantially from low-grade squamous intraepithelial lesion (LSIL) to atypical squamous cells cannot exclude HSIL (ASC-H)/high-grade squamous intraepithelial lesion (HSIL) (OR = 3.4, 95% CI 1.0–11.5), HPV31/33/45/52/58 prevalence showed only a mild and non-significant rise (1.8, 95% CI 0.6–5.6), whereas non-16/18/31/33/45/52/58 HR-HPV prevalence declined (0.6, 95% CI 0.1–2.2).

Conclusions.

HR-HPV prevalence in Shanxi was moderate, dominated by genotypes 52, 16, and 58, and increased with age. These findings provide essential local baseline data for evaluating China's newly implemented national HPV vaccination programme and highlight the need to expand vaccination coverage and enhance age-appropriate, genotype-informed screening strategies—particularly for older women who are unlikely to benefit from vaccination alone.

Background

Human papillomavirus (HPV) is the most common sexually transmitted infection among women worldwide and the necessary cause of cervical cancer (CC)(1). Both the prevalence and genotype distribution of HPV show substantial geographic variation, with markedly higher burdens in Africa and Asia than in Europe or the Americas(2). Within Asia, Eastern and Southeastern regions demonstrate distinct genotype profiles—particularly the predominance of HPV16, 18, 52, 58, and 33—which have important implications for vaccine performance and screening strategies(3). China similarly exhibits pronounced regional heterogeneity, with high-risk HPV (HR-HPV) prevalence varying from 9.6% to 23.6% across provinces(4) and HPV52 and HPV58 consistently ranking among the most common carcinogenic types except for HPV16 and 18(3).

In October 2025, China incorporated HPV vaccination into the national immunization programme, marking a major milestone in cervical cancer prevention(5). Establishing robust baseline data on HPV prevalence and genotype distribution before large-scale vaccine rollout is essential for evaluating vaccine effectiveness, monitoring potential type replacement, and guiding region-specific vaccination and screening policies. Although large national datasets exist, population-based genotype data from high-risk provinces remain limited and uneven, restricting the ability to tailor prevention strategies to local epidemiology. Shanxi Province has one of the highest cervical cancer burdens in China, yet evidence on HPV genotype distribution in the general female population remains scarce(6). HPV vaccination coverage in Shanxi also remains low(7), underscoring the need for high-quality baseline epidemiological data to support implementation of the national immunization programme and to inform cervical cancer screening policies.

To address these gaps, we conducted a large retrospective study among women in Shanxi, China, who underwent routine health examinations, to estimate type-specific and grouped HPV prevalence, identify demographic factors associated with HR-HPV infection, and examine genotype distribution across cytological diagnoses.

Methods

Study population

This retrospectively cross-sectional study included women who underwent routine health check-ups at the Department of Physical Examination, First Hospital of Shanxi Medical University, between January 2021 and December 2024. A total of 19,384 women aged 18 years or older who completed both HPV DNA testing and ThinPrep Cytologic Test (TCT) cytology during the study period were eligible. For individuals with multiple records, only the first HPV and TCT results was analyzed.

Sociodemographic and lifestyle information was collected using standardized questionnaires at the time of examination, including age, marital status (married or unmarried), body mass index (BMI, categorized as underweight < 18.5, normal weight 18.5–23.9, overweight 24.0–27.9, or obesity ≥ 28.0 kg/m²), and

exercise frequency (none, occasional, or regular). The study was approved by the Ethics Committee of the First Hospital of Shanxi Medical University (Approval No. KYLL-2024-300).

HPV DNA testing

Cervical exfoliated cell samples were collected by trained gynecologists following standardized procedures. Women were instructed to avoid menstruation, vaginal medication, and sexual intercourse within 24 hours before sampling. Cervical exfoliated cells were obtained using a cervical brush inserted into the squamocolumnar junction, rotated 3–5 times, and placed into 3 ml of cell preservative solution. Samples were stored at 4°C and tested within 48 hours.

DNA extraction was performed using the Bioperfectus extraction kit (Jiangsu Shuoshi, China), targeting the L1 region of the HPV genome(8). HPV genotyping was performed using real-time fluorescent polymerase chain reaction (PCR) on the SLAN-96S platform (Shanghai Hongshi, China), detecting 21 HPV genotypes, including 16 high-risk types (HR-HPV: 16, 18, 26, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68, 73, 82) and 5 low-risk types (LR-HPV: 6, 11, 53, 66, 81)(3).

Cervical cytology

Cytological evaluation was performed by experienced cytopathologists according to the 2014 Bethesda System. Results were classified as: negative for intraepithelial lesion or malignancy (NILM), atypical squamous cells of undetermined significance (ASC-US), low-grade squamous intraepithelial lesion (LSIL), atypical squamous cells cannot exclude HSIL (ASC-H), high-grade squamous intraepithelial lesion (HSIL), and CC(9).

Data analysis

Type-specific and grouped HPV prevalence and corresponding 95% confidence intervals (CIs) were estimated. Grouped categories included HPV16/18, HPV6/11/16/18, HPV6/11/16/18/31/33/45/52/58, HR-HPV, and any HPV. A participant was considered positive for a group if at least one included genotype was detected. Among HPV-positive women, we analyzed the distribution of single and multiple infections and explored co-infection patterns.

Grouped and type-specific HPV prevalence were compared across cytological categories using chi-square tests for trend to assess associations with lesion severity. To further explore potential causal associations between HPV infections and high-grade cytological abnormalities, odds ratios (ORs) with 95% CIs were calculated, comparing the prevalence of HPV16/18, HPV31/33/45/52/58, and other HR-HPV types (26, 35, 39, 56, 59, 68, 73, 82) between HPV-positive women with ASC-H/HSIL and those with LSIL.

Risk factors associated with HR-HPV infection and abnormal cytology (ASC-US, LSIL, ASC-H, HSIL) were identified using logistic regression models. Variables with $p < 0.20$ in univariate analyses were included in multivariate models to control for potential confounding. All analyses were performed using R software (version 4.4.3).

Results

Study population

A total of 19,384 women aged ≥ 18 years (median 42 years, IQR 36–51) were included (**Appendix Table 1**). Most were married (97.9%). Overall, 26.0% were overweight and 11.6% were obese. Nearly half of women were examined in 2024 (44.8%). Occasional physical activity was reported by 68.4% of participants.

HPV prevalence and genotype distribution Overall, 13.7% ($n = 2,650$) of women were HPV-positive, including 10.9% ($n = 2,106$) infected with HR-HPV (Table 1). The prevalence of HPV16/18, HPV 6/11/16/18, and HPV6/11/16/18/31/33/45/52/58 was 2.3% (95% CI: 2.1–2.5), 2.6% (95% CI: 2.3–2.8), and 5.1% (95% CI: 4.8–5.5), respectively. Among individual genotypes, HPV52 was the most prevalent (2.3%, 95% CI: 2.1–2.5), followed by HPV16 (1.7%, 95% CI: 1.5–1.9), HPV58 (1.7%, 95% CI: 1.5–1.9), and HPV53 (1.7%, 95% CI: 1.5–1.8). HPV6 and HPV11 was detected in 0.2% (95% CI: 0.2–0.3) and 0.1% (95% CI: 0.1–0.2) of women, respectively.

Among HPV-positive women, 15.7% had multiple infections. Co-infections most frequently involved HPV53, HPV52, HPV16, HPV58 and HPV39 (Fig. 1A). The most common infection pairs were HPV16 + HPV52 (3.8%) and HPV52 + HPV53 (2.9%) (Fig. 1B). HPV16 most often co-occurred with HPV52 or HPV 53, whereas HPV53 commonly co-infected with HPV52, HPV58, HPV39, or HPV16.

Age-specific patterns showed a clear rise in HR-HPV prevalence with age (Fig. 2A). Prevalence remained stable before age 55, increased sharply at 56–65 years (15.6%, 95%CI: 14.1–17.1), and peaked in women > 65 years (17.0%, 95%CI: 13.7–20.3). Similar patterns were observed for any HPV, HPV6/11/16/18/31/33/45/52/58, HPV6/11/16/18, and HPV16/18.

Factors associated with HR-HPV infection

Compared with women aged 20–35 years, those aged 56–65 years (AOR = 2.0, 95% CI 1.6–2.3) and > 65 years (AOR = 2.1, 95% CI 1.5–2.8) had significantly higher risk of HR-HPV infection (Table 2). Married women had lower risk of HR-HPV infection than unmarried women (AOR = 0.5, 95% CI 0.4–0.7). No other demographic or lifestyle factors were independently associated with infection.

HPV Infection and cytological abnormalities

Among all participants, 97.7% (n = 18,968) had NILM cytology, 1.8% had ASC-US (n = 403), 0.4% LSIL (n = 96), 0.1% ASC-H (n = 15), and < 0.1% HSIL (n = 9) (**Appendix Table 1**). The prevalence of grouped and type-specific HR-HPV increased markedly with lesion severity (Table 3). HR-HPV prevalence rose from 9.9% in NILM to 100.0% in ASC-H and HSIL (p for trend < 0.001). HPV16 and HPV18 showed the strongest enrichment in high-grade cytology, with HPV16 rising from 1.5% in NILM to 40.0% in HSIL, and HPV18 from 0.5% to 20.0% (both p for trend < 0.001).

Multivariate models showed the strong association between HPV infection and cytological abnormalities (Table 2). Compared with HPV-negative women, the odds of abnormal cytology were substantially higher in those infected with HPV16/18 (AOR 19.9, 95% CI 13.0–29.9), HPV31/33/45/52/58 (AOR 21.1, 95% CI 15.4–28.9), and other HR-HPV types (AOR 16.5, 95% CI 11.5–23.5). No other factors were associated with cytological abnormalities.

When restricting the analysis to HPV-positive women, subtype-specific patterns were observed (Fig. 2B). HPV16/18 prevalence increased progressively from LSIL to ASC-H/HSIL, with an OR of 3.4 (95% CI 1.0–11.5). A milder but non-significant increase was observed for HPV31/33/45/52/58 (OR = 1.8, 95% CI 0.6–5.6). In contrast, non-16/18/31/33/45/52/58 HR-HPV types declined from LSIL to ASC-H/HSIL (OR = 0.6, 95% CI 0.1–2.2).

Discussion

This large cross-sectional study in Shanxi Province provides a refined baseline of HPV epidemiology before large-scale vaccine implementation. Although the overall prevalence of HR-HPV was relatively moderate (10.9%), the type of distribution was dominated by HPV52, HPV16, HPV58, and HPV53. The age-specific curve showed a marked late-age resurgence, indicating a substantial burden among older women who are both under screened and outside the routine vaccination target age. A clear risk hierarchy was evident among HPV-positive women. HPV16/18 were the primary drivers of high-grade lesions, showing a significant rise from LSIL to ASC-H/HSIL, whereas HPV31/33/45/52/58 increased only non-significantly, and non-16/18/31/33/45/52/58 HR-HPV types declined.

The overall HR-HPV prevalence was 10.9%, which is consistent with the reported globally. A systematic review of 2,755,734 people with normal cervical cytology worldwide revealed marked geographic variation in HR-HPV prevalence(3). The highest prevalence was observed in Latin America and the Caribbean (22%), whereas Eastern/Southeastern Asia and Africa showed generally lower levels (< 15%), and the lowest prevalence occurred in North America (9%). In addition to differences in age structure, sampling methods, and HPV detection assays, the variation in HPV prevalence across continents can also be largely attributed to region-specific sexual behavior patterns, particularly given that HPV is primarily sexually transmitted(10). Among Asian populations, particularly in China, cultural and societal factors often delay the age of sexual debut, reduce the number of lifetime sexual partners, and promote stable marital relationships, thereby limiting opportunities for the transmission of sexually transmitted infections(11). A study in China indicates that the average age of sexual debut among the younger

generation is 17 years(11), whereas a study in Latin America and the Caribbean reports an average age of sexual debut of 15.8 years in that region(12).

The 10.9% HR-HPV prevalence observed in this study is consistent with previously reported rates for Northern China(4). The observed prevalence in this study is higher than rates documented in southern China (e.g., 6.6%–6.8% in Guangdong)(13), yet remains markedly lower than figures reported for East China (18.4% in Xiamen)(14) and Northeast China (16.95%)(15). These findings align with large-scale epidemiological surveys, which indicate significant regional disparities in HR-HPV positivity across China, with reported ranges such as 15.3%–24.4% (16), highlighting pronounced geographic heterogeneity in the distribution of infection burden.

Beyond the factors previously mentioned, the regional disparities in HR-HPV prevalence observed in this study can also be attributed to two additional aspects. First, variations in sexual behavior patterns—including age at first sexual intercourse and number of sexual partners—directly influence exposure risk and transmission dynamics(17). Second, disparities in HPV vaccination coverage play a significant role. In Guangdong province, the first-dose vaccination rate has reached 15.65%, supported by higher socioeconomic status and health literacy(7). In contrast, Northeast China exhibits markedly lower coverage rates (ranging from 3.97% to 7.99%). There are also significant disparities in HPV vaccine coverage between the eastern and western regions of China. In September 2022, Guangdong Province launched a free HPV16/18 vaccination program for eligible females(18). Jiangsu Province followed closely, implementing free HPV vaccination for female students in the first grade of junior high school with local school enrollment status starting from 2023. In contrast, the Northeast China had not introduced any provincial-level free HPV vaccination policies prior to the national inclusion of HPV vaccines in the Expanded Program on Immunization in 2025(19). From the perspective of national overall vaccination coverage, by 2022, the first-dose HPV vaccination coverage rate in China was only 10.2%, and the full three-dose coverage rate was even lower at 6.2%. Notably, these figures are significantly below the global average coverage rates for females in 2019, which stood at 20% for the first dose and 15% for the full vaccination series. Given that national current overall HPV vaccination coverage remains low and far from the threshold required to achieve herd immunity (previous studies have indicated that a coverage rate exceeding 50% is necessary), it is essential to not only prioritize the promotion of vaccination among age-eligible females but also attach importance to improving the HPV vaccination rate among females of other age groups. This measure aims to further expand the scope of vaccine protection and enhance the overall effectiveness of cervical cancer prevention and control.

Our study found that HPV52, 16, and 58 were the most prevalent in Shanxi Province, which differs from the results of a 2022 nationwide meta-analysis. This meta-analysis showed that HPV genotype 16 was predominant in northern, northeastern, and central China, while HPV genotype 52 was more common in southern and eastern regions of the country(20). Although HPV16 has historically been the major genotype in northern China, inter-provincial heterogeneity has been observed across studies. Recent regional and multicenter investigations reported increasing prevalence of HPV52 and HPV58 in eastern and parts of northern China (21–23), suggesting a gradual shift in genotype distribution. A population-

based study in Beijing also identified HPV52 as the predominant genotype, consistent with our findings, indicating that the predominance of HPV52 in Shanxi may reflect a new regional trend in northern China rather than a deviation from the national epidemiological pattern(24). Although overall HPV vaccination coverage in China remains relatively low (25), early evidence has shown a decline in HPV16 infection in some urban areas and among younger women. With the continued expansion of vaccination programs, further reductions in HPV16 infection could lead to a relative increase in the prominence of HPV52, which was already common at baseline. This potential shift underscores the importance of ongoing surveillance of HPV genotype dynamics and highlights the need to evaluate vaccine effectiveness against non-16/18 high-risk genotypes such as HPV52 and HPV58 (26). It is important to note that currently widely used bivalent HPV vaccines only protect against HPV types 16 and 18, and do not cover high-risk genotypes such as HPV 52 and 58—which are gradually emerging as prevalent types. Therefore, when personal financial conditions permit and age eligibility criteria for vaccination are met, choosing a nonavalent HPV vaccine can provide broader genotype coverage to address potential changes in the epidemiological trends of HPV genotypes.

The prevalence of multiple-type HPV infections among the study participants was 15.7%, with HPV53, HPV52, HPV16, and HPV58 identified as the most prevalent co-infecting genotypes. This multiple-type prevalence is broadly consistent with findings from recent large-scale epidemiological studies conducted in China and other countries (27, 28). Recent studies have revealed regional variations in dominant co-infecting genotypes, with HPV52 and HPV58 emerging as the primary types in multiple parts of China, frequently co-infection with HPV16 and HPV53, which is highly consistent with our findings(29, 30).

Women aged ≥ 56 years had the highest HR-HPV prevalence (16.2%), indicating a late-age peak in HR-HPV infection. There was a significant difference between this finding and the bimodal distribution of HR-HPV infection (age < 25 years and 55–59 years) reported in previous studies(31, 32). Women aged ≥ 56 years have a relatively high HR-HPV prevalence. However, this population falls outside the recommended age range (9–45 years) for HPV vaccination, making them inaccessible to primary prevention. Therefore, secondary prevention (cervical cancer screening) is essential to mitigate their risk of developing cervical cancer. Data from a 2025 Chinese study revealed that the screening rate among women aged ≥ 55 years was merely 38%, which is significantly lower than the 57% observed in women aged 35–54 years(33). This finding indicates that women aged ≥ 55 years have weak awareness of cervical cancer screening and low participation rates, highlighting an urgent need to enhance the promotion of screening programs for this demographic. In the 20–30-year age group, unmarried women accounted for only 18.0% of the population, whereas married women comprised 82.0%. Because unmarried women generally exhibit higher HR-HPV prevalence(14), with 11.6% in this study compared with 7.6% among married women, the small proportion of unmarried women substantially diluted the overall infection estimate for this age stratum, resulting in an underestimation of the true HR-HPV prevalence among women aged 20–35 years. This markedly skewed marital composition may also help explain why the age-specific pattern in our study did not display the characteristic “dual-peak” distribution frequently reported in previous research. In many populations, the early peak is largely driven

by young unmarried women or those at the onset of sexual activity; however, their low representation in our dataset reduced the magnitude of this early-age increase and thereby obscured the bimodal pattern. Additionally, because HR-HPV infections in young women are often transient, the limited representation of newly sexually active women further contributed to the absence of an early-age rise in prevalence (34). Marital status was significantly associated with HR-HPV prevalence. In the present study, married women had a lower prevalence (9.9%) than unmarried women (16.3%), and this significant difference may be attributed to the stable sexual behavior and partner fidelity among married women. Consistent with this finding, a study proposed that marriage may help reduce sexual risk behaviors, which in turn lowers the risk of HR-HPV infection (35).

HPV infection is closely associated with cervical cytological abnormalities, with its prevalence increasing alongside the severity of lesions. A clear risk stratification was observed among HPV-positive women. HPV16/18 emerged as the primary drivers of high-grade lesions (ASC-H/HSIL), demonstrating a significant increase in prevalence from LSIL to ASC-H/HSIL, consistent with previous studies in Chinese and Macedonian populations (31, 36–38). In contrast, HPV31/33/45/52/58 showed only a mild and non-significant increase across cytological grades, while non-16/18/31/33/45/52/58 HR-HPV prevalence declined, suggesting their relatively limited contribution to disease progression(3). These findings highlight the importance of integrating type-specific HR-HPV testing with cytology in cervical cancer screening programs, while also suggesting the potential role of other HR-HPV types in disease development in certain populations.

The strength of this study lies in collecting data from a health examination population and analyzing the relationship between HPV infection and TCT cytological diagnosis using rigorous statistical methods, but this study has several limitations. First, the participants were recruited from individuals undergoing routine health check-ups at a tertiary hospital, which generally serves people with higher socioeconomic status due to its relatively higher service costs and the greater health awareness of its patient population. As a result, the observed prevalence of HR-HPV may be underestimated, especially for women aged 20–30 years. Second, because this study was retrospective and the questionnaire was not specifically designed for this project, it did not systematically collect potential risk factors associated with HPV infection, such as sexual behavior, number of sexual partners, contraceptive methods, and history of sexually transmitted infections. This limitation may affect the comprehensive assessment of risk factors for HPV infection and restrict the in-depth analysis of causal relationships. Third, we did not collect information on participants' HPV vaccination status, which could have led to underestimation of prevalence for vaccine-targeted genotypes.

Conclusions

HR-HPV prevalence in Shanxi was moderate, dominated by genotypes 52, 16, and 58. These findings provide essential baseline data for evaluating China's newly implemented national HPV vaccination programme. The high oncogenicity and greater prevalence of HPV16/18 among older adults necessitate

both expanded vaccination and targeted, genotype-specific screening—essential for older women who benefit little from vaccination.

Abbreviations

Abbreviation	Full term
HPV	Human papillomavirus
HR-HPV	High-risk human papillomavirus
LR-HPV	Low-risk human papillomavirus
CC	Cervical cancer
TCT	ThinPrep Cytologic Test
NILM	Negative for intraepithelial lesion or malignancy
ASC-US	Atypical squamous cells of undetermined significance
LSIL	Low-grade squamous intraepithelial lesion
ASC-H	Atypical squamous cells cannot exclude HSIL
HSIL	High-grade squamous intraepithelial lesion
PCR	Polymerase chain reaction
DNA	Deoxyribonucleic acid
OR	Odds ratio
CI	Confidence interval

Declarations

Ethics approval and consent to participate. The study protocol was reviewed and approved by the Ethics Committee of the First Hospital of Shanxi Medical University (Approval No.: KYLL-2024-300).

Consent for publication. All participants provided written informed consent for participation in the study. No individual personal data (such as images, videos, or identifiable clinical details) are included in this article.

Availability of data and materials. The data supporting the findings of this study are available from the corresponding author upon reasonable request. However, the data are not publicly accessible due to privacy and ethical restrictions.

Competing interests. All authors declare that they have no competing interests.

Funding. Noncommunicable Chronic Diseases-National Science and Technology Major Project (2023ZD0518700), the National Natural Science Foundation of China (82404330) and Research Project Supported by Shanxi Scholarship Council of China (2024-080).

Authors' contributions. SG and FW designed the study. SG and JW collected the data. HG performed the data analysis and drafted the first version of the manuscript. HG wrote the first draft of the manuscript. FW acted as the second reviewer and revised the manuscript. All authors provided input, approved the final manuscript, and had final responsibility for the decision to submit for publication.

Acknowledgements. We extend our gratitude to all participants.

References

1. Organization WH. Human papillomavirus and cancer. 2024 Mar 5 [Available from: <https://www.who.int/zh/news-room/fact-sheets/detail/human-papilloma-virus-and-cancer>.
2. Osmani V, Hörner L, Nkurunziza T, Rank S, Tanaka LF, Klug SJ. Global prevalence of cervical human papillomavirus in women aged 50 years and older with normal cytology: a systematic review and meta-analysis. *The Lancet Microbe*. 2025;6(1).
3. Wei F, Georges D, Man I, Baussano I, Clifford GM. Causal attribution of human papillomavirus genotypes to invasive cervical cancer worldwide: a systematic analysis of the global literature. *The Lancet*. 2024;404(10451):435–44.
4. Zhao C, Zhao Y, Li J, Li M, Shi Y, Wei L. Opportunities and challenges for human papillomavirus vaccination in China. *Human Vaccines & Immunotherapeutics*. 2024;20(1).
5. China TSCotPsRo. China plans to add HPV vaccine to national immunization program, expanding coverage for females. [updated September 11, 2025. Available from: https://english.www.gov.cn/news/202509/11/content_WS68c27731c6d00fa19f7a25cf.html.
6. Song L, Lyu Y, Ding L, Li X, Gao W, Wang M, et al. Prevalence and Genotype Distribution of High-Risk Human Papillomavirus Infection in Women with Abnormal Cervical Cytology: A Population-Based Study in Shanxi Province, China. *Cancer Management and Research*. 2020;Volume 12:12583–91.
7. Chen J, Zhang Z, Pan W, Song Y, Zheng L, Li L, et al. Estimated Human Papillomavirus Vaccine Coverage Among Females 9-45 Years of Age - China, 2017-2022. *China CDC Wkly*. 2024;6(19):413–7.
8. Wang Q, Zhang B, Yin Z, Zhang J, Li Y. Predictive value of quantitative HPV genotyping in cervical lesions. *Progress in Modern Obstetrics and Gynecology*. 2018;27(05):351–4+8.
9. Nayar R WD, editors. *The Bethesda System for Reporting Cervical Cytology: Definitions, Criteria, and Explanatory Notes*. 3rd ed: Springer; 2015.
10. Yang YM SY, Li SY, Yan H. Occurrence of sexual behavior among college students in mainland China: a meta-analysis. *Chinese Journal of Public Health*. 2018;34(1):142–7.

11. Zhao FH, Tiggelaar SM, Hu SY, Xu LN, Hong Y, Niyazi M, et al. A multi-center survey of age of sexual debut and sexual behavior in Chinese women: suggestions for optimal age of human papillomavirus vaccination in China. *Cancer Epidemiol.* 2012;36(4):384–90.
12. Aguirre Rivera JC, Restrepo Soto JA. Conducta sexual en jóvenes universitarios: Estudio de revisión. *Psicogente.* 2022;25(48):1–25.
13. Zhong H, Pan W, Chen B, Gu J, Liang Y, Sun G, et al. A real-world, cross-sectional, and longitudinal study on high-risk human papillomavirus genotype distribution in 31,942 women in Dongguan, China. *Frontiers in Public Health.* 2024;12.
14. Yao X, Li Q, Chen Y, Du Z, Huang Y, Zhou Y, et al. Epidemiology of human papillomavirus infection in women from Xiamen, China, 2013 to 2023. *Frontiers in Public Health.* 2024;12.
15. Zhang H, Zhang S. Prevalence and genotype distribution of human papillomavirus infection among female outpatients in Northeast China: a population-based survey of 110,927 women. *Archives of Gynecology and Obstetrics.* 2022;308(1):35–41.
16. Zeng Z, Austin RM, Wang L, Guo X, Zeng Q, Zheng B, et al. Nationwide Prevalence and Genotype Distribution of High-Risk Human Papillomavirus Infection in China. *American Journal of Clinical Pathology.* 2022;157(5):718–23.
17. Cervical Carcinoma and Sexual Behavior: Collaborative Reanalysis of Individual Data on 15,461 Women with Cervical Carcinoma and 29,164 Women without Cervical Carcinoma from 21 Epidemiological Studies. *Cancer Epidemiology, Biomarkers & Prevention.* 2009;18(4):1060–9.
18. Commission GPH. Policy Interpretation of "Work Plan for Free HPV Vaccine Vaccination for Eligible Girls in Guangdong Province (2022-2024)" 2021 [Available from: https://wsjkw.gd.gov.cn/hdjl_zcjd/content/post_3659022.html].
19. National Health Commission of the People's Republic of China ea. Notice on Issuing the Action Plan for Accelerating the Elimination of Cervical Cancer (2023–2030) 2023 [Available from: https://www.gov.cn/zhengce/zhengceku/2023-01/21/content_5738364.htm].
20. Yu Y-Q, Hao J-Q, Mendez MJG, Mohamed SB, Fu S-L, Zhao F-H, et al. The Prevalence of Cervical HPV Infection and Genotype Distribution in 856,535 Chinese Women with Normal and Abnormal Cervical Lesions. *Journal of Cytology.* 2022;39(4):137–47.
21. Shu Z, Zhao W, Zhan X, Zeng J, Li J. Epidemiology and genotypes analysis of human papillomavirus infection in Huizhou, China. *Front Public Health.* 2024;12:1440480.
22. Liu S, Mei B, Ouyang Y, Li C. Prevalence and genotype distribution of human papillomavirus infection among women in Jingzhou, China: a population-based study of 51,720 women. *Virol J.* 2023;20(1):297.
23. Jin R, Qian H, Zhang Y, Yuan D, Bao J, Zhou H, et al. The prevalence and genotype distribution of human papillomaviruses among women in Taizhou, China. *Medicine (Baltimore).* 2019;98(39):e17293.
24. Zhang W, Guo N, Li B, Shang E, Wang J, Zhang M, et al. Prevalence and genotype distribution of human papillomavirus infections in Beijing, China between 2016 and 2020. *Virol J.* 2023;20(1):11.

25. Junlei Chen, Zhaonan Zhang, Jiakai Ye, Weiyi Pan, Yifan Song, Lu Zheng, et al. Estimated Human Papillomavirus Vaccine Coverage Among Females 9–45 Years of Age – China, 2017–2022. *China CDC Weekly*. 2025;6(19):413–7.
26. Chen Q, Wang S, Lin Q, Zhang G. Temporal changes in prevalence and geographical distribution of human papillomavirus infection in mainland China: a systematic review and analysis of 1.07 million females from 2010 to 2021. *BMC Public Health*. 2025;25(1):3083.
27. Gong P, Shi B, Cong X, Yang L, Gong C, Zhou Y, et al. Multiple infections containing the top five prevalent HPV genotypes and their impact on cervical lesions in Changzhou, China. *Hum Vaccin Immunother*. 2023;19(2):2245723.
28. Kim JM, Song HS, Hwang J, Kim JK. The Prevalence of Multi-Type Infections Among Human Papillomavirus Types in Korean Women. *Pathogens*. 2025;14(4).
29. Hou J, Zeng M, Liu C, Xie B, Li Y, Wu L, et al. Cervical HPV infection in Yueyang, China: a cross-sectional study of 125,604 women from 2019 to 2022. *Front Public Health*. 2023;11:1210253.
30. Silvia de Sanjosé MD, Xavier Castellsagué, Gary Clifford, Laia Bruni, Nubia Muñoz, F Xavier Bo. Worldwide prevalence and genotype distribution of cervical human papillomavirus DNA in women with normal cytology: a meta-analysis. *Lancet Infect Dis*. 2007;7(7):453–9.
31. Wang J, Li H, Zhang J, Wang H, Li Y, Liu Z, et al. Epidemiology and genotypes analysis of human papillomavirus infection in Beijing, China. *Virology Journal*. 2024;21(1).
32. Lin X, Chen L, Zheng Y, Yan F, Li J, Zhang J, et al. Age-specific prevalence and genotype distribution of human papillomavirus in women from Northwest China. *Cancer Medicine*. 2022;11(22):4366–73.
33. Mei Zhang LW, Xiao Zhang, Chun Li, Zhenping Zhao, Mengting Yu, Maigeng Zhou, Jing Wu, Linhong Wang. Cervical Cancer Screening Rates Among Chinese Women – China, 2023–2024. *China CDC Weekly*. 2025;7(10):321–6.
34. Feng T, Cheng B, Sun W, Yang Y. Outcome and associated factors of high-risk human papillomavirus infection without cervical lesions. *BMC Womens Health*. 2023;23(1):599.
35. Onwuamah CK, Feng N, Momoh AE, Uwandu M, Ahmed RA, Idigbe I, et al. Prevalence and risk factors for high-risk human papillomavirus infection among women from three southern geopolitical zones of Nigeria. *Front Oncol*. 2023;13:1254304.
36. Zhou Y, Liu J, Chen S, Xin X, Xiao M, Qiang X, et al. Correlation of different HPV genotype viral loads and cervical lesions: A retrospective analysis of 1585 cases. *Cancer Cytopathol*. 2025;133(1):e22920.
37. Aleksioska-Papestiev I, Chibisheva V, Micevska M, Dimitrov G. Prevalence of Specific Types of Human Papilloma Virus in Cervical Intraepithelial Lesions and Cervical Cancer in Macedonian Women. *Med Arch*. 2018;72(1):26–30.
38. Li S, He X, Li S, Su Y, Wang X, Li C. The prevalence of HPV in Chongqing, China from 2017 to 2022: a retrospective cohort study. *Sci Rep*. 2024;14(1):23973.

Tables

Table 1
Prevalence of grouped and type-specific human papillomavirus (HPV) infection
among 19,384 women in Shanxi, China, 2021–2024

HPV types	Number of women	Prevalence (%; 95%CI)
Any HPV positive	2650	13.7 (13.2–14.2)
HR-HPV positive	2106	10.9 (10.4–11.3)
16	336	1.7 (1.5–1.9)
18	105	0.5 (0.4–0.7)
26	4	0.0 (0.0–0.0)
31	123	0.6 (0.5–0.8)
33	96	0.5 (0.4–0.6)
35	50	0.3 (0.2–0.3)
39	224	1.2 (1.0–1.3)
45	35	0.2 (0.1–0.3)
51	133	0.7 (0.6–0.8)
52	437	2.3 (2.1–2.5)
56	177	0.9 (0.8–1.1)
58	336	1.7 (1.5–1.9)
59	113	0.6 (0.5–0.7)
68	167	0.9 (0.7–1.0)
73	18	0.1 (0.1–0.1)
82	32	0.2 (0.1–0.2)
LR-HPV positive	746	3.8 (3.6–4.1)
6	42	0.2 (0.2–0.3)
11	20	0.1 (0.1–0.2)
53	321	1.7 (1.5–1.8)
66	178	0.9 (0.8–1.1)
81	211	1.1 (0.9–1.2)
HPV16/18	438	2.3 (2.1–2.5)

HPV types	Number of women	Prevalence (%; 95%CI)
HPV6/11/16/18	496	2.6 (2.3–2.8)
HPV6/11/16/18/31/33/45/52/58	996	5.1 (4.8–5.5)

HR-HPV=high-risk HPV; LR-HPV=low-risk HPV.

Table 2

Risk factors for high-risk human papillomavirus (HR-HPV) infection and cytological abnormalities among 19,384 women in Shanxi, China, 2021–2024

Factors	HR-HPV positive			Cytological abnormalities		
	Prevalence (%, 95% CI)	OR (95% CI)	AOR (95% CI) *	Prevalence (%, 95% CI)	OR (95% CI)	AOR (95% CI) *
Age						
36–45	9.7 (9.0–10.3)	1.0 (0.9–1.1)	1.1 (0.9–1.2)	2.2 (1.9–2.6)	1.0 (0.7–1.2)	...
46–55	10.3 (9.5–11.1)	1.1 (0.9–1.2)	1.1 (1.0–1.3)	2.0 (1.7–2.5)	0.9 (0.7–1.1)	...
56–65	14.9 (13.5–16.3)	1.6 (1.4–1.9)	2.0 (1.6–2.3)	1.7 (1.2–2.3)	0.7 (0.5–1.1)	...
> 65	16.2 (13.2–19.6)	1.8 (1.4–2.3)	2.1 (1.5–2.8)	2.0 (1.0–3.7)	0.9 (0.5–1.7)	...
Body Mass Index						
Normal weight (18.5–23.9)	10.9 (9.0–13.0)	1.0 (0.8–1.3)	1.2 (0.9–1.5)	2.6 (1.6–4.0)	1.2 (0.8–2.0)	1.3 (0.7–2.1)
Overweight (24.0–27.9)	9.9 (9.1–10.7)	0.9 (0.8–1.0)	0.9 (0.8–1.0)	1.8 (1.5–2.2)	0.9 (0.7–1.1)	0.8 (0.6–1.1)
Obesity (≥ 28.0)	11.9 (10.7–13.2)	1.2 (1.0–1.3)	0.9 (0.7–1.1)	2.7 (2.1–3.4)	1.3 (1.0–1.7)	0.9 (0.6–1.5)
Marital status						
Married	9.9 (9.4–10.3)	0.6 (0.4–0.7)	0.5 (0.4–0.7)	2.1 (1.9–2.4)	0.7 (0.4–1.4)	1.1 (0.6–2.5)
Frequency of exercise						
Occasionally	10.1 (9.5–10.6)	1.0 (0.8–1.2)	1.0 (0.8–1.2)	2.3 (2.0–2.6)	2.1 (1.1–3.8)	2.6 (1.4–5.5)

Factors	HR-HPV positive			Cytological abnormalities		
	Prevalence (%, 95% CI)	OR (95% CI)	AOR (95% CI) *	Prevalence (%, 95% CI)	OR (95% CI)	AOR (95% CI) *
Age						
Often	11.2 (10.3– 12.2)	1.1 (0.8– 1.4)	1.0 (0.8– 1.2)	1.9 (1.5–2.3)	1.7 (0.9– 3.2)	1.8 (0.9– 3.9)
HPV status						
Positive for HPV16/18	...	...	...	12.8 (9.8– 16.3)	19.5 (14.0– 27.1)	19.9 (13.0– 29.9)
Positive for HPV31/33/45/52/58 only	...	...	...	11.7 (9.7– 13.9)	17.6 (13.5– 22.9)	21.1 (15.4– 28.9)
Positive for other HR- HPV only	...	...	...	9.4 (7.3– 11.7)	13.7(10.1– 18.6)	16.5 (11.5– 23.5)
Positive for LR-HPV only	...	...	...	10.5 (8.0– 13.4)	15.6 (11.2– 21.5)	15.4 (10.1– 22.8)

CI: confidence intervals; OR: odds ratio; AOR: adjusted OR.

*Variables with a *P*-value <0.2 in the univariate analysis were included in the multivariate regression model to adjust for potential confounding factor.

Table 3

Prevalence of grouped and type-specific HPV infection by cytological diagnosis among 19,384 women in Shanxi, China, 2021–2024 footnote

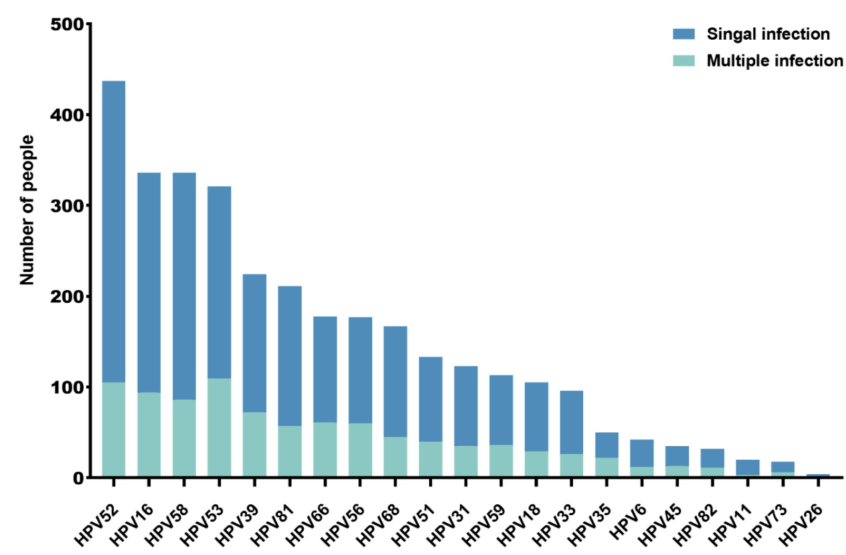
HPV type	NILM (n, %)	ASC- US (n, %)	LSIL (n, %)	ASC-H (n, %)	HSIL (n, %)	χ^2 trend (P)
Any HPV positive	2,359 (12.4)	211 (64.3)	66 (89.2)	9 (100.0)	5 (100.0)	1114.985 (< 0.001)
Any HR-HPV	1,872 (9.9)	168 (51.2)	52 (70.3)	9 (100.0)	5 (100.0)	920.737 (< 0.001)
16	291 (1.5)	29 (8.8)	12 (16.2)	2 (22.2)	2 (40.0)	255.611 (< 0.001)
18	94 (0.5)	9 (2.7)	3 (4.1)	1 (11.1)	1 (20.0)	41.744 (< 0.001)
31	111 (0.6)	9 (2.7)	2 (3.1)	0 (0.0)	0 (0.0)	28.074 (< 0.001)
33	83 (0.4)	11 (3.4)	1 (1.4)	1 (11.1)	0 (0.0)	47.335 (< 0.001)
35	47 (0.2)	1 (0.3)	1 (1.4)	0 (0.0)	1 (20.0)	16.101 (< 0.001)
39	209 (1.1)	11 (3.4)	4 (5.4)	0 (0.0)	0 (0.0)	19.064 (< 0.001)
45	27 (0.1)	4 (1.2)	1 (1.4)	2 (22.2)	1 (20.0)	163.143 (< 0.001)
51	116 (0.6)	10 (3.0)	7 (9.5)	0 (0.0)	0 (0.0)	79.312 (< 0.001)
52	388 (2.0)	39 (11.9)	9 (12.2)	1 (11.1.)	0 (0.0)	136.815 (< 0.001)
56	154 (0.8)	15 (4.6)	8 (10.8)	0 (0.0)	0 (0.0)	98.599 (< 0.001)
58	289 (1.5)	35 (10.7)	10 (13.5)	2 (22.2)	0 (0.0)	205.408 (< 0.001)
59	102 (0.5)	10 (3.0)	1 (1.4)	0 (0.0)	0 (0.0)	17.934 (< 0.001)
68	150 (0.8)	12 (3.7)	4 (5.4)	1 (11.1)	0 (0.0)	51.947 (< 0.001)
HPV16/18	382 (2.0)	38 (11.6)	12 (16.2)	3 (33.3)	3 (60.0)	297.610 (< 0.001)

HPV type	NILM (n, %)	ASC- US (n, %)	LSIL (n, %)	ASC-H (n, %)	HSIL (n, %)	χ^2 trend (P)
HPV6/11/16/18	431 (2.3)	44 (13.4)	15 (20.3)	3 (33.3)	3 (60.0)	346.572 (< 0.001)
HPV6/11/16/18/31/33/45/52/58	1,256 (6.6)	126 (38.4)	35 (47.3)	9 (100.0)	4 (80.0)	762.549 (< 0.001)

NILM: negative for intraepithelial lesion or malignancy; ASC-US: atypical squamous cells of undetermined significance; LSIL: low-grade squamous intraepithelial lesion; ASC-H: atypical squamous cells cannot exclude HSIL; HSIL: high-grade squamous intraepithelial lesion.

Figures

A) Single and multiple HPV infections



B) Patterns of HPV co-infection



Figure 1
Distribution of type-specific HPV infections among 19,384 women in Shanxi, China (2021-2024)

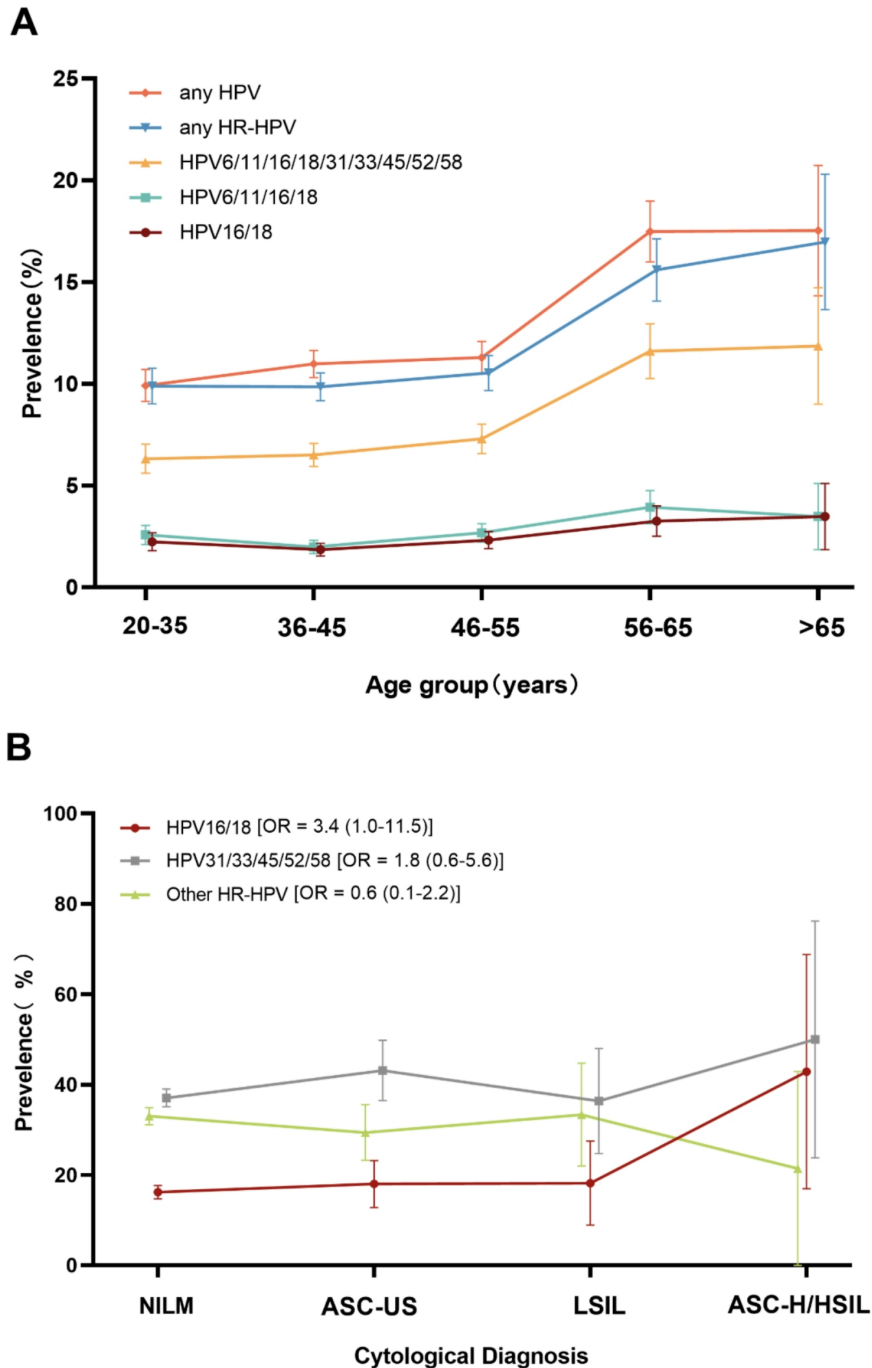


Figure 2

HPV prevalence by age group among all women (A) and by cytological diagnosis among HPV-positive women (B) in Shanxi, China, 2021–2024.

*OR value represents ASC-H/HSIL-to-LSIL ratio of the relative HPV prevalence. NILM: negative for intraepithelial lesion or malignancy; ASC-US: atypical squamous cells of undetermined significance; LSIL:

low-grade squamous intraepithelial lesion; ASC-H: atypical squamous cells cannot exclude HSIL; HSIL: high-grade squamous intraepithelial lesion.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [AppendixTable1Characteristicsof19.docx](#)