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Cross-Sectional Study on the Correlation Between Vaginal Microecology and High-Risk Human Papillomavirus Infection: Establishment of a Clinical Prediction Model

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Purpose: High-risk human papillomavirus (HR-HPV) is a significant risk factor for cervical precancerous lesions and cancer. This study aimed to investigate the relationship between vaginal microecology and HR-HPV infection and to evaluate the clinical applicability of vaginal microecology in predicting HR-HPV infection.

Patients and Methods: Overall, 2000 women with simultaneously detected vaginal discharge and cervical HPV were selected between March 2022 and March 2023, including 241 and 1759 cases in the HR-HPV positive and HPV negative groups, respectively.

Results: No significant differences were found in age, vulvovaginal candidiasis, trichomonas vaginitis, and β-N-acetylglucosaminosidase between the two groups (P>0.05). Significant differences were observed in *Lactobacillus* deficiency, bacterial vaginitis (BV), aerobic vaginitis (AV), glucuronidase (GUS), sialidase (SNA), and leukocyte esterase (LE) between the two groups (P<0.05). In the multivariate logistic regression equation, *Lactobacillus* deficiency, BV, AV, SNA, LE, and GUS were risk factors for HR-HPV infection (P<0.05). Three prediction models, namely, logistic regression, decision tree, and random forest, were established to rank the importance of the predictors. BV ranked first among the three prediction models. The logistic regression model demonstrated the highest accuracy in predicting the risk of HR-HPV infection. The calibration curve of the logistic regression model showed a strong correlation between the predicted and actual probabilities, and decision curve analysis revealed that the prediction model had good clinical applicability.

Conclusion: Overall, vaginal microecology imbalance was closely associated with cervical HR-HPV infection, particularly BV and AV. The logistic regression model for the risk of HR-HPV infection based on six predictive factors (BV, AV, LE, SNA, *Lactobacillus* deficiency, and GUS) had good accuracy and clinical applicability.

Keywords: vaginal microecology, high-risk human papillomavirus, logistic regression, decision tree, random forest

Introduction

Human papillomavirus (HPV) has universal infectivity. High-risk human papillomavirus (HR-HPV) is one of the most common infectious viruses in clinical practice. HR-HPV has been recognized as a significant risk factor for cervical precancerous lesions and cancer. HR-HPV replicates in large numbers in mature epithelial basal cells after infecting the host. When the body's immune system decreases, it randomly integrates into the host genome, inducing cell mutations.[1] An approach to preventing cervical cancer involves averting HPV infection, promptly detecting HPV, and blocking HR-HPV infection.

With the increased understanding of the vaginal microecology, it has received extensive attention as a female-specific microecosystem. Vaginal microbiology focuses on the vaginal microbiota. The vaginal microbiota is the collection of

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microorganisms inhabiting the human vagina. Similar to all microbiota, it includes bacteria, fungi, viruses, archaea, and protists. During the childbearing age, a healthy vagina has long been considered a simple ecosystem dominated by rod-shaped Gram-positive bacteria, currently known as lactobacilli.[2,3] A balance in vaginal microecology plays a crucial role in maintaining female reproductive health, such as participating in human material metabolism, forming mucosal barriers, and regulating immunity. An imbalance of vaginal microecology, including disturbance of the vaginal microbiome, abnormal vaginal pH, and lack of hydrogen peroxide, can lead to a decline in the resistance of the vagina to pathogens, which are prone to reproductive tract infectious diseases.

Recently, several studies have suggested that cervical HR-HPV infection is associated with an imbalance in vaginal microecology. Abnormal vaginal microbiome may result in the persistence of HPV.[4,5] When the vaginal microenvironment is destroyed, it interferes with local immunity and enhances the expression of HR-HPV, thereby inhibiting apoptosis and enabling HPV to escape immune supervision in the body. This causes the cell cycle to lose control and accelerates the evolution of cervical intraepithelial lesions. Without timely intervention, this can lead to cervical cancer. However, the correlation between HR-HPV infection and an imbalance in vaginal microecology remains unknown, and research on predictive models of vaginal microecology and HR-HPV infection risk in China remains limited. Therefore, this study, which was based on the fact that HR-HPV infection is a high-risk factor for cervical cancer, aimed to analyze the correlation between vaginal microecological change and HR-HPV infection and to build a prediction model for the imbalance of vaginal microecology and the risk of HR-HPV infection. Furthermore, this study aimed to provide a theoretical basis for the prevention and intervention of HR-HPV infection.

Materials and Methods

Study Participants

Women who underwent both vaginal microecology and cervical HPV testing admitted to the Department of Gynecology and Obstetrics of Xiangyang Hospital of Integrated Chinese and Western Medicine (Xiangyang, China) from March 2022 to March 2023 were enrolled in this study. The inclusion criteria were as follows: 1) all participants were women of childbearing age; 2) voluntary participation; and 3) no previous history of HPV treatment. The exclusion criteria were as follows: 1) history of sexual activity, vaginal medication, or use of antibiotics within 1 week; 2) history of abortion within 1 month; 3) women experiencing menopause, menstruation, pregnancy, or lactation; 4) concomitant severe diseases or immune dysfunction; 5) patients participating in other studies; and 6) withdrawal or loss of follow-up during the study period.

In total, 2000 patients, for which we obtained complete data according to the inclusion and exclusion criteria, were included in this study. Overall, 241 patients with HR-HPV infection were included in the positive group, and 1759 hPV negative cases were selected as the negative group.

The Ethics Committee of Xiangyang Hospital of Integrated Chinese and Western Medicine approved this study (Xiangyang Traditional Chinese and Western Medicine Ethics Review No. 20220220–001).

Sample Collection

The patient was placed in the lithotomy position, and the cervix was exposed with a vaginal speculum. Subsequently, a small amount of secretion from the lateral wall and posterior fornix of the vagina was obtained with a sterile cotton swab for vaginal microecology testing. Cervical secretions were collected using a cervical brush.

Sample Detection

Gram staining was used to detect the dominant bacteria and various types of vaginitis under a microscope. The RT-F600 vaginal secretion detector manufactured by Shenzhen Ruitu Biotechnology Co., Ltd. was used to detect glucuronidase (GUS), β-N-acetylglucosaminosidase (NAG), sialidase (SNA), and leukocyte esterase (LE). The criteria for the above indicators in normal vaginal microecology were as follows: the dominant bacteria were gram-positive large bacilli (*Lactobacillus*), no pathogenic microorganisms were found, and all enzymes were negative. In this study, severe

reduction or deficiency of *Lactobacillus* and excessive growth of other bacteria were defined as *Lactobacillus* deficiency; cases of mixed vaginal infections were not included in the statistics.

The polymerase chain reaction (PCR)-reverse point-hybrid method was used for cervical HPV detection.

a. Reagents and instruments

Reagent: The HPV genotyping test kit produced by Yaneng Biotechnology (Shenzhen) Co., Ltd. can detect 23 hPV types; the forward and reverse primers were contained within the "HPV genotyping test kit" and kit catalog number: 20193401918. The high-risk types included HPV 16,18, 3, 31, 33, 35, 39, 451, 51, 52, 53, 56, 58, 59, 66, 68, 73, and 82, whereas the low-risk types included HPV types 6,11, 42, 70, 81 and 83.

Instrument: RT-F600 automatic nucleic acid molecular hybridization instrument (produced by Yaneng Biotechnology (Shenzhen) Co., Ltd); SLAN-96P fluorescence quantitative PCR instrument (produced by Shanghai Hongshi Medical Technology Co., Ltd).

b. Methods and steps

① Extraction of DNA: Fully eluting cervical brush, 1.0 mL of the eluate was taken and centrifuged at 13,000 r/min for 10 min, left to precipitate, and added with 100 μL DNA of extract (lysate); it was then shaken and mixed well in a 100 °C boiling water bath for 10 min. After cooling, it was centrifuged at 13,000 r/min for 10 min. Furthermore, 5 μL of the supernatant was added to the PCR reaction tube for machine testing, with one negative and positive control set for each test.

② Amplification of PCR: i) One cycle: 50 °C, 15 min; ii) One cycle: 95 °C 10 min; iii) Forty cycles: 94 °C, 10s→46 °C 60s→72 °C 20s; iv) 72 °C, 5 min; and v) Run the thermal denaturation program.

③ Hybridization: Film washing and color development were performed strictly according to the instructions.

④ HPV positive control: In addition to the color development signal of the IC point, the corresponding position of type HPV16 should also show color.

⑤ The results determine that the IC position appears in blue spots, and the other loci are colored as the corresponding genotypes.

Statistical Methods

Statistical analysis was performed using IBM SPSS Statistics for Windows, version 22.0 (IBM Corp., Armonk, N.Y., USA) and R 4.2.1. Data were expressed as the mean ± standard deviation if the measurement data met normality, or median and upper and lower quartiles M (P25 and P75) if it did not meet normality. Two groups were compared using the *t*-test or Wilcoxon rank-sum test. Count data were expressed as frequency and percentage (n, %), and two groups were compared using the χ^2 test. By incorporating statistically significant single factors into the multivariate logistic regression equation, the backward logistic regression method was used to screen for predictive factors, construct a logistic regression prediction model, and calculate the corresponding odds ratio (OR) and 95% confidence interval (CI). The receiver operating characteristic (ROC), calibration, and clinical decision curves were used to evaluate the discrimination, consistency between the predicted and actual probabilities, and clinical applicability of the prediction model, respectively, as well as the predictive effects of the logistic regression, decision tree, and random forest models on infection status, with alpha=0.05 (bilateral) as the test level. Statistical significance was set at $P<0.05$.

Results

Related Factors and Vaginal Microecological Test Results

In this study, the positive group included 241 patients, with a median age of 35 years and upper and lower quartiles of 31 and 40 years, respectively. Furthermore, 1759 cases were included in the negative group, with a median age of 36 years and upper and lower quartiles of 31 and 40 years, respectively. No significant difference was found in age between the two groups ($P>0.05$). Microecological results showed no significant differences in vulvovaginal candidiasis (VVC), trichomonas vaginitis (TV), and NAG between the two groups ($P>0.05$), whereas significant differences were found in *Lactobacillus* deficiency, bacterial vaginitis (BV), aerobic vaginitis (AV), GUS, SNA, and LE ($P<0.05$) (Table 1).

Table 1 Comparison of Vaginal Microecology Detection Between the Two Groups ((n, %) or M (P_{25}, P_{75}))

Dependent Variable		Positive Group (n=241)	Negative Group (n=1759)	Z/χ^2	*P*
Age (years))		35 (31, 40)	36 (31, 42)	−1.085	0.278
Lactobacillus deficiency	Positive	160 (66.4)	336 (19.1)	254.150	<0.001
	Negative	81 (33.6)	1423 (80.9)		
BV	Positive	132 (54.8)	113 (6.4)	405.350	<0.001
	Negative	109 (45.2)	1646 (93.6)		
AV	positive	102 (42.3)	98 (5.6)	318.112	<0.001
	Negative	199 (57.7)	1161 (94.4)		
VVC	Positive	42 (17.4)	244 (13.9)	2.187	0.139
	Negative	199 (82.6)	1515 (86.1)		
TV	Positive	15 (6.2)	70 (4.0)	2.624	0.105
	Negative	226 (93.8)	1689 (96.0)		
GUS	Positive	82 (34.0)	69 (3.9)	275.167	<0.001
	Negative	159 (66.0)	1690 (96.1)		
SNA	Positive	130 (54.2)	113 (6.4)	450.786	<0.001
	Negative	111 (45.8)	1646 (93.6)		
LE	Positive	180 (74.7)	406 (23.1)	272.516	<0.001
	Negative	61 (25.3)	1353 (76.9)		
NAG	Positive	32 (13.3)	181 (10.3)	1.989	0.158
	Negative	209 (86.7)	1578 (89.7)		

Screening for Risk Factors and Construction of the Logistic Regression Prediction Model

By incorporating statistically significant single factors into the multivariate logistic regression equation, we used the backward logistic regression method to screen for predictive factors and found that BV, AV, SNA, LE, GUS, and *Lactobacillus* deficiency were all risk factors for HR-HPV infection (P<0.05) (Table 2). A nomogram was constructed based on selected predictive factors (Figure 1A).

Table 2 Multivariate Logistic Regression Analysis Results

Dependent Variable	*β*	*Se*	*Wald*/χ^2	*P*	*OR*	95% CI
Lactobacillus deficiency	0.539	0.271	3.955	0.047	1.714	1.008~2.916
BV	1.002	0.311	10.360	0.001	2.724	1.480~5.014
AV	0.958	0.301	10.144	0.001	2.606	1.445~4.699
GUS	0.648	0.324	3.922	0.046	1.912	1.012~3.610
SNA	0.668	0.327	4.161	0.041	1.950	1.026~3.703
LE	0.695	0.290	5.747	0.017	2.003	1.135~3.536

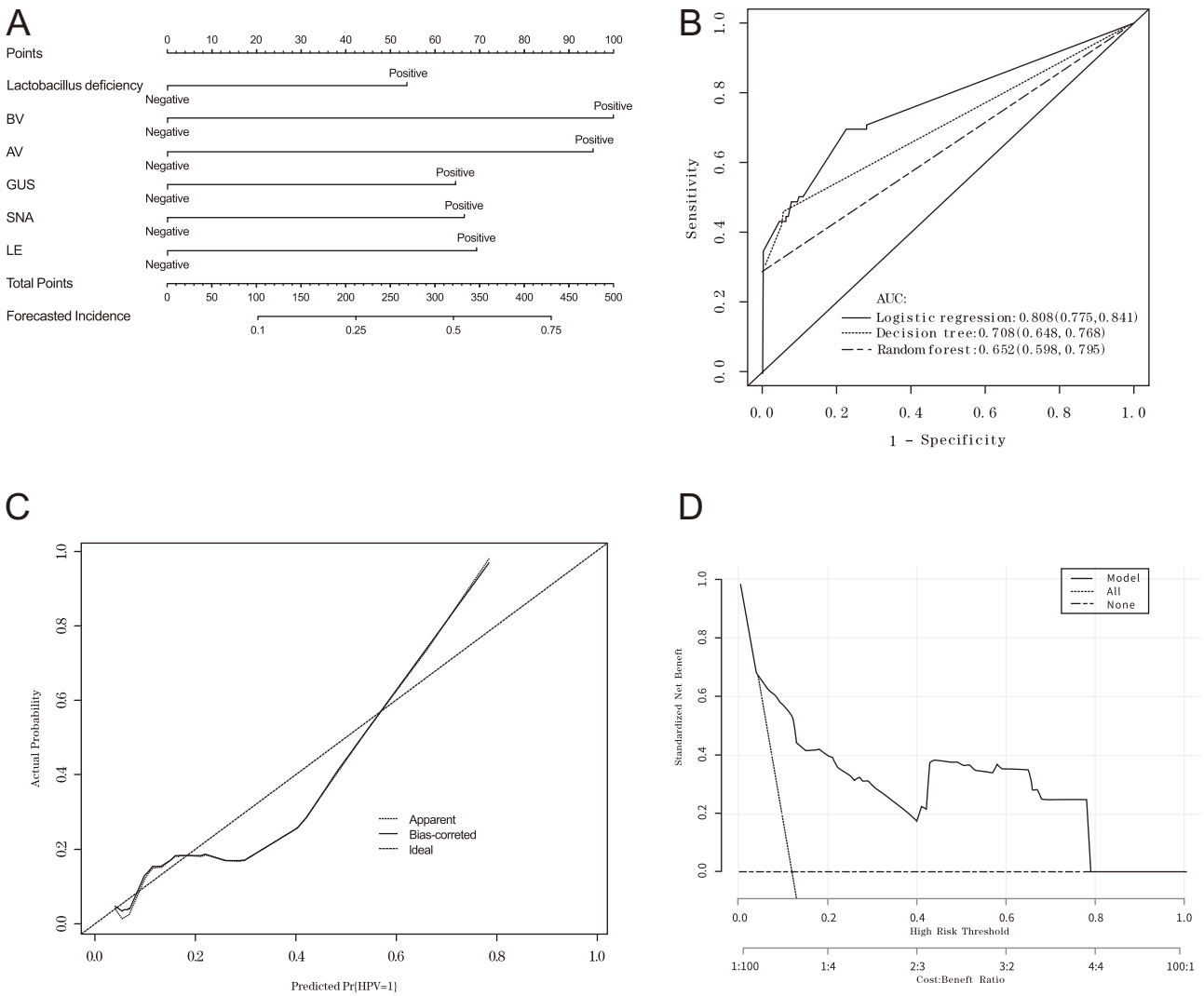

Figure 1 Clinical prediction model for HR-HPV infection caused by abnormal vaginal microecology. (**A**) Nomogram for predicting the risk of HR-HPV infection: This nomogram predicts the incidence of HR-HPV infection caused by deficiencies in *Lactobacillus*, bacterial vaginosis (BV), aerobic vaginitis (AV), sialidase (SNA), leukocyte esterase (LE), and glucuronidase (GUS). (**B**) ROC Curve and AUC for logistic regression, decision tree, and random forest models: Among the three models, the logistic regression model exhibited the highest AUC value (0.808). (**C**) Calibration curve for the logistic regression model: The calibration curve closely approximated a straight line with a slope of 1. (**D**) Decision curve analysis for the logistic regression model: When the prediction rate of the logistic regression model was <0.78, using nomogram A to predict the risk of HR-HPV infection was more beneficial than employing the extreme curve strategy.

Evaluation of the Effectiveness of Different Prediction Models

Three prediction models, namely, logistic regression, decision tree, and random forest, were designed to predict the importance of six variables (BV, AV, SNA, LE, GUS, and *Lactobacillus* deficiency) on HR-HPV infection. Among the three prediction models, BV ranked first for all, and AV ranked second, third, and second, respectively, while the importance of *Lactobacillus* deficiency was ranked fifth, fifth, and sixth, respectively (Table 3).

The area under the ROC curve (AUC; Figure 1B) values of the three prediction models were 0.808 (95% CI: 0.775–0.841), 0.708 (95% CI: 0.648–0.768), and 0.652 (95% CI: 0.598–0.795), respectively. The logistic regression model had the maximum AUC value, indicating that the logistic regression model had superior accuracy in predicting the occurrence of HR-HPV infection. As shown in Figure 1C, the calibration curve of the logistic regression model closely approximated to a straight line, with a slope of 1, indicating a strong correlation between the actual HR-HPV infection and the predicted likelihood.

Table 3 Importance Ranking of Predicted Variables by Different Prediction Model

Sort	Logistic Regression	Decision Tree	Random Forest
1	BV	BV	BV
2	AV	SNA	AV
3	LE	AV	SNA
4	SNA	GUS	LE
5	Lactobacillus deficiency	Lactobacillus deficiency	GUS
6	GUS	LE	Lactobacillus deficiency

Decision Curve Analysis of the Logistic Regression Model

The clinical decision curve was used to evaluate the accuracy of the predictive models. As shown in Figure 1D, when the prediction rate of the logistic regression model was <0.78, using the nomogram from this study to predict the risk of HR-HPV infection was more beneficial than using the extreme curve strategy, indicating that the prediction model had clinical applicability.

Discussion

HPV is highly prevalent. There are more than 200 strains of HPV; however, most cervical neoplasia cases are attributable to persistent sexually transmitted infections caused by oncogenic strains, including HPV-16, HPV-33, HPV-18, HPV-31, HPV-45, HPV-52, and HPV-58. Cervical carcinoma is the third most common cancer regarding incidence and mortality in the female population, with over 600,000 new cases and more than 340,000 deaths annually.[6,7] The vaginal microecosystem is a part of human microecology, and its balance plays an important role in maintaining female reproductive health. Recently, it has been found that HPV infection frequently coexists with abnormal vaginal micro-ecology. An HPV infection can also cause an imbalance in vaginal microecology, which is linked to the development and progression of cervical cancer.[8]

As the dominant bacteria, *Lactobacilli* play a vital role in the vaginal microbiota of women of reproductive age. These bacteria generate lactic acid as the main antimicrobial substance, and this gentle acid can inhibit unwanted pathogens, many of which are sexually transmitted. These pathogens pose a health hazard to a woman, her partner, and her baby during pregnancy and childbirth.[2] Several studies have indicated a strong correlation between a reduced presence of *Lactobacilli* in the female vagina and HPV infection. *Lactobacillus*, the dominant strain in the vagina, can promote the clearance of HPV and reduce the occurrence of cervical lesions.[9,10]*Lactobacillus* could act as similar plasmids to integrate the HPV16 virus and prevent it from binding to host cells.[11] The results of this study showed a significant difference in *Lactobacillus* deficiency between the positive and negative groups. Multivariate logistic regression analysis suggested that *Lactobacillus* is a protective factor against HPV infection. Therefore, vaginal microbes dominated by *Lactobacillus* are key to maintaining the balance of vaginal microecology and are an important line of defense against infection by pathogens, including HPV.

A common feature of BV and AV is the reduction or disappearance of *Lactobacilli*; BV has the same epidemiological characteristics as HPV. Some studies have suggested that BV and AV are most closely related to HR-HPV.[11,12] The results of this study showed that the incidence of BV and AV was higher in the positive group than in the negative group, with a significant difference (P<0.001). The multivariate logistic regression analysis suggested that BV and AV were both risk factors for HR-HPV infection. It is suggested that the decrease or disappearance of *Lactobacilli* in patients with BV and AV increases the susceptibility to HR-HPV infection. Additionally, a large number of aerobic bacteria in AV produce GUS, which further produces high-level inflammatory factors, including interleukin-1 (IL-1) and IL-6, leading to cervical epithelial cell damage and increasing the probability of HR-HPV infection.[13] The coagulase produced by *Staphylococcus aureus* in AV can secrete fibrin, which is deposited on the cell surface; this inhibits the function of phagocytic cells,

thereby reducing the defense effect of the mucosa. SNA and other substances produced by BV can damage the mucus layer of the vaginal epithelium and form a biofilm with bacteria to resist the body's immunity, which is conducive to the persistence of HPV, and is an independent risk factor for HPV infection.[14] Anaerobic bacteria can also produce carcinogens, such as nitrosamines, which increase the susceptibility of viruses. In this study, three prediction models (logistic regression, decision tree, and random forest) were designed to predict the importance of six variables (BV, AV, SNA, LE, GUS, and *Lactobacillus* deficiency) on HR-HPV infection. BV ranked first for all three models, AV ranked second, third, and second, respectively, while the importance of *Lactobacillus* deficiency was ranked fifth, fifth, and sixth, respectively, indicating that the probability of HR-HPV infection in patients with BV and AV was significantly higher than that of *Lactobacillus* deficiency, possibly because the metabolites and the microecological environment caused by BV and AV were more likely to increase the probability of HR-HPV infection.

Currently, the results of the association between HR-HPV infection with VVC and TV are inconsistent. Liu et al[15] suggested that VVC was a high-risk factor for HR-HPV infection, and Wang et al[16] reported that VVC infection was negatively correlated with HPV. *Candida* can resist HPV infection by reducing the vaginal pH and enhancing immune cell responses. Yang et al[17] suggested that TV is associated with HR-HPV infection and increases the risk of cervical intraepithelial neoplasia in patients with HR-HPV infection. In this study, the incidences of VVC and TV were not significantly different between the positive and negative groups ($P>0.05$). It is suggested that VVC does not increase the risk of HR-HPV infection because of the following reasons: *Candida* hosts in the vagina and produces complement chemotactic factors, leading to local vascular dilation, increased permeability, and inflammatory reactions. These factors might be an allergic reaction caused by VVC without significantly damaging the vaginal microecology, and carriers with spores without clinical symptoms and signs might be diagnosed with VVC infection. Although *Candida* was detected, the vaginal microecology of many patients did not change significantly, and these patients might have normal immunity and a lower risk of HPV infection. Vaginal microecology may change only when the body's immunity is weakened and *Candida* multiplies quickly. Therefore, future studies may employ laboratory tests using culture methods and combining patient symptoms and signs to make the final diagnosis of VVC to eliminate bias caused by diagnostic methods.

The TV sample size in this study was relatively small and showed no significant correlation with HR-HPV infection. Currently, several studies have shown that HPV infection is unrelated to TV. However, some studies have concluded that HPV infection is related to TV, perhaps because TV merges with BV in many cases, and the interference of BV may not have been ruled out. In the future, experimental studies with multiple centers, large sample sizes, and the exclusion of other confounding factors, such as BV, will be required to explore the correlation between TV and HPV infection.

This study found that the positive group had significantly higher rates of SNA, LE, and GUS positivity than the negative group, while the difference in the positive rate of NAG was not significant. The multivariate logistic regression analysis suggested that SNA, LE, and GUS were risk factors for HR-HPV infection, which is consistent with previous studies.[18] Recently, enzyme detection has been widely applied in evaluating vaginal microecology. LE is a specific enzyme produced by white blood cells in the body. A positive result indicates damage to the vaginal microecology and is a marker of the inflammatory response in the body. SNA is an effective marker of pathogenic bacteria, such as *Gardnerella*, and is an important indicator for the clinical diagnosis of BV. As early as 2008, Gelber et al[19] found, from the perspective of a pathogenic mechanism, that *Gardnerella vaginalis* could use the complement regulatory molecule CD59 to activate the p38-mitogen-activated protein kinase pathway in cervical epithelial cells, leading to the death of cervical epithelial cells, a decrease in vaginal *Lactobacilli*, and an increase in pH, which created conditions for HPV infection. GUS is secreted by numerous aerobic bacteria in the vagina and is a marker of AV infection. These results confirm the close correlation between BV, AV, and HR-HPV infection.

This study established the following three predictive models based on the correlation between six predictive factors and the risk of HR-HPV infection: logistic regression, decision tree, and random forest models. The AUC values calculated from the ROC curves of the three prediction models were 0.808, 0.708, and 0.652, respectively. The logistic regression model had the largest AUC value, indicating that it had better accuracy in predicting the risk of HR-HPV infection than the other two models. By verifying the calibration and clinical decision curves, the calibration curve of the logistic regression model closely approximated to a straight line, with a slope of 1, indicating that there was a strong correlation between the probability of HR-HPV infection predicted by the model and the actual incidence rate. When the

prediction rate using this model was <0.78, employing the nomogram to predict the risk of HR-HPV infection was more beneficial than the extreme curve strategy at the same probability, indicating that the logistic regression model had good clinical applicability. The above indicated that the logistic regression model established based on the correlation between six predictive factors and the risk of HR-HPV infection had good predictive performance.

Conclusion

The imbalance of vaginal microecology was closely related to HR-HPV infection, and in clinical practice, attention should be paid to the treatment of various types of vaginitis, particularly BV and AV. HPV testing and treatment for vaginal microbiota regulation should be performed to achieve a balance in the vaginal microecology, thereby reducing the risk of HPV infection and cervical lesions. The logistic regression model for the risk of HR-HPV infection based on six predictive factors (BV, AV, LE, SNA, *Lactobacillus* deficiency, and GUS) had good accuracy and clinical applicability.

Since this study relied on cross-sectional data and did not establish a causal relationship between vaginal microecology and HPV infection, our next step will involve conducting a cohort study to uncover the dynamics of disease development. This study did not analyze the patients' general clinical data, such as frequency of sexual activity, age of first sexual activity, education level, and income. However, when constructing a predictive model, incorporating these factors may improve the model's predictive performance. In this study, samples with viral load below 1.0×104 copies/mL could not be detected when using the reagent kit produced by Yaneng Biotechnology (Shenzhen) Co., Ltd. to detect HPV. Because the model was only based on research from one center, the next step will be to expand the sample size for further analysis, as well as external validation from multiple centers to evaluate its stability and place it into clinical practice. Additionally, many studies have found that in the next 2 years, the clearance rate of HR-HPV will be higher than 95%, with most of them being transient infections. In addition to vaginal microecology, other factors, including the immune system, oral contraceptives, exercise, and sleep status,[20] will all affect HPV infection, which require further research. Moreover, anti-HPV vaccinations are also an interesting topic. Many studies believe that the anti-HPV vaccination is highly effective in preventing HPV infection.[21,22] In a multi-center retrospective study, Giorgio et al[23] evaluated the potential effect of vaccination after hysterectomy for high-grade cervical intraepithelial neoplasia and early-stage cervical cancer. Their results highlighted that vaccination could decrease the burden of HPV-related disease. Even after hysterectomy, vaccination could prevent approximately 70% of anal, vulvar, and vaginal HPV-related lesions (any grade). Therefore, popularizing vaccination is crucial for preventing HPV infection.

Abbreviations

Human papillomavirus (HPV), high-risk human papillomavirus (HR-HPV), bacterial vaginitis (BV), aerobic vaginitis (AV), glucuronidase (GUS), sialidase (SNA), leukocyte esterase (LE), β-N-acetylglucosaminosidase (NAG), odds ratio (OR), confidence interval (CI), receiver operating characteristic (ROC), vulvovaginal candidiasis (VVC), trichomonas vaginitis (TV), area under the ROC curve (AUC).

Data Sharing Statement

The datasets used and/or analyzed during the current study are available from the corresponding author upon reasonable request.

Ethics Approval and Consent to Participate

The study protocol was approved by the Ethics Committee of Xiangyang Hospital of Integrated Chinese and Western Medicine (Xiangyang Traditional Chinese and Western Medicine Ethics Review No. 20230220-001). This study was conducted in accordance with The Declaration of Helsinki. Written informed consent was obtained from all participants.

Patient consent for publication

Informed consent was obtained from all patients regarding the publication of the data.

Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising or critically reviewing the article; gave final approval of the version to be published; have agreed on the journal to which the article has been submitted; and agree to be accountable for all aspects of the work.

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Disclosure

The authors declare that they have no competing interests.

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