A Study on the Association between Human Papillomavirus Infection, Vaginal Microecological Imbalance, and Cervical Lesions in Women from Xinjiang, China

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Abstract

This study analyzes the relationship between Human Papillomavirus (HPV) infection, vaginal microecological, and cervical lesions to provide a basis for the prevention and treatment of cervical cancer (CC) in the Xinjiang region. qRT-PCR was used for HPV genotyping and viral load.The Gram staining and dry biochemical enzyme kit were utilized to diagnose vaginal secretions.The positive rate of HPV infection and vaginal microecological indicators was compare by χ^2 test. Logistic regression analysis was used to analyze the correlation between vaginal microecological evaluation indicators and HPV infection with the grade of cervical lesions. The HPV infection rate among women in the Xinjiang region is 30.29%, of which single HPV infection accounts for 77%. HPV16 and HPV52 are the main infection types. There are significant differences in the HPV infection rate and infection types among the Han, Uighur, Hui, and Kazakh ethnic groups. The viral load of HPV16 and HPV52 increases with the upgrade of cervical lesions. There are significant differences in vaginal microecological evaluation indicators H_2O_2, SNA, LE, GUS, trichomonas, clue cells, and lactobacilli among different ethnic groups. HPV negative patients with varying grades of cervical lesions exhibit a notable variance in H_2O_2 and LE, which is statistically significant. single HPV infection and high viral load HPV significantly increase the risk of CC. This study indicate that the HPV infection and vaginal microecological are differences among ethnic groups, Which have a strong correlation with the progression of CC, Offering guidance on CC screening and interventions in the Xinjiang area.

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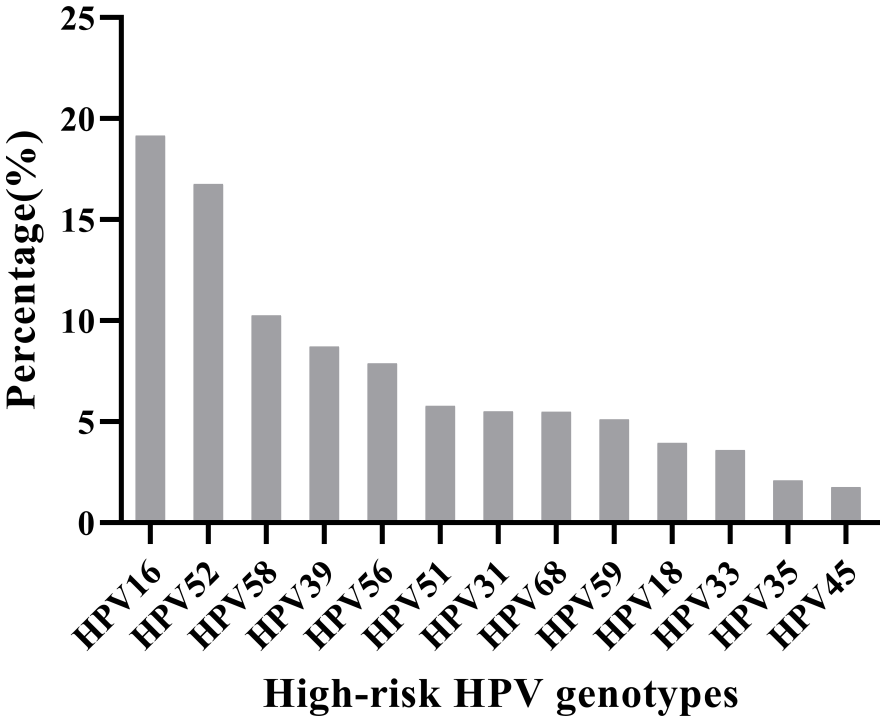

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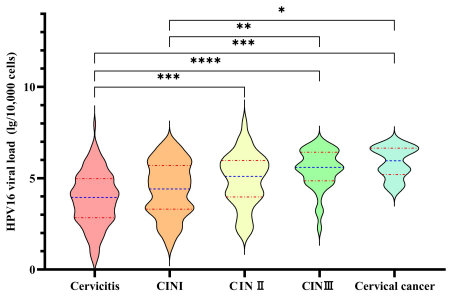

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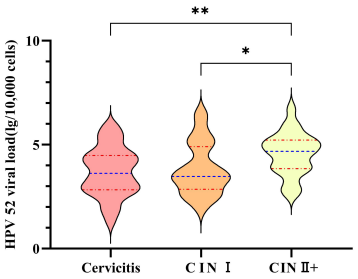
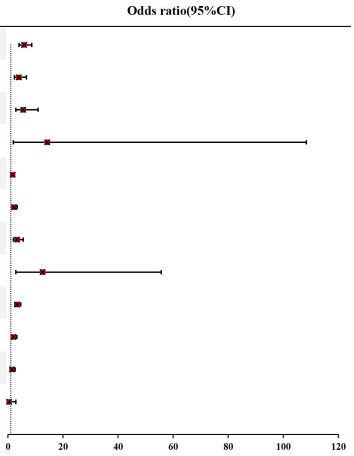
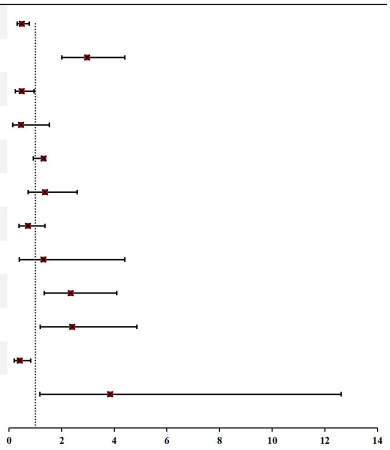


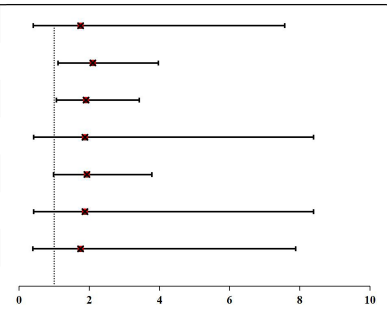
Study type	Number	Cervical lesions	N(%)	*P* value	OR(95%CI)
HPV +	350	CINI	203（58.00%）	<0.001	5.839（3.942 to 8.650）
		CINII	74（21.14%）	<0.001	3.903（2.290 to 6.652）
		CINIII	58（16.57%）	<0.001	5.506（2.775 to 10.924）
		Cervical cancer	15（4.29%）	0.01	14.239（1.872 to 108.303）
Single infection	222	CINI	114（51.35%）	0.001	1.675(1.249 to 2.245)
		CINII	50（22.52%）	0.001	2.134(1.381 to 3.296)
		CINIII	44（19.82%）	<0.001	3.286(1.958 to 5.515)
		Cervical cancer	14（6.31%）	0.001	12.547(2.832 to 55.591)
Multiple infection	128	CINI	89（69.53%）	<0.001	3.303(2.387 to 4.572)
		CINII	24（18.75%）	0.011	1.926(1.165 to 3.184)
		CINIII	14（10.94%）	0.271	1.415(0.762 to 2.624)
		Cervical cancer	1（0.78%）	0.33	0.364(0.048 to 2.778)



Study type	Number	Cervical lesions	N(%)	*P* value	OR(95%CI)
Low viral load	86	CINI	43（50.00%）	0.002	0.487（0.308~0.772）
		CINII	24（27.91%）	<0.001	2.970（2.002~4.406）
		CINIII	15（17.44%）	0.035	0.484（0.246~0.950）
		Cervical cancer	4（4.65%）	0.207	0.458（0.137~1.539）
Medium viral load	96	CINI	54（56.25%）	0.13	1.315（0.923~1.873）
		CINII	17（17.71%）	0.335	1.369（0.723~2.593）
		CINIII	21（21.88%）	0.319	0.721（0.378~1.374）
		Cervical cancer	4（4.17%）	0.663	1.309（0.389~4.407）
High viral load	69	CINI	37（53.62%）	0.003	2.345（1.345~4.088）
		CINII	16（23.19%）	0.015	2.399（1.184~4.863）
		CINIII	11（15.94%）	0.012	0.407（0.202~0.821）
		Cervical cancer	5（7.25%）	0.026	3.843（1.170~12.619）



Indicator	*B*	*SE*	*Wald* χ^2	*P* value	OR(95%CI)
SNA	0.561	0.746	0.566	0.452	1.753（0.406 to 7.565）
LE	0.743	0.324	5.272	0.022	2.102（1.115 to 3.965）
H_2O_2	0.646	0.299	4.672	0.031	1.909（1.062 to 3.430）
GADP	0.63	0.764	0.679	0.41	1.877（0.420 to 8.394）
Lactobacillus	0.659	0.344	3.679	0.055	1.933（0.986 to 3.789）
Clue cell	0.63	0.764	0.679	0.41	1.877（0.420 to 8.394）
Fungi	0.561	0.767	0.536	0.464	1.753（0.390 to 7.878）



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