The prevalence and distribution of human papillomavirus among 10,910 Chinese Han women

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Research Article

Keywords: Human papillomavirus, Type-specific prevalence, Distribution, risk, Chinese Han

Posted Date: December 4th, 2020

DOI: https://doi.org/10.21203/rs.3.rs-120310/v1

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Version of Record: A version of this preprint was published on March 25th, 2021. See the published version at https://doi.org/10.1186/s13027-021-00360-9.
Abstract

Objective

To assess the prevalence and distribution of HPV genotypes among Chinese Han women, and to explore the risk of high-grade cervical lesions associated with individual hr-HPV genotypes.

Methods

Genotyping and histopathology data from the Chinese Multi-Center Screening Trial (CHIMUST) and its pilot screening trial, from 6 regions across mainland China, were re-analyzed. The data from physician (direct) collected samples from 10910 Chinese Han women (ages 30-69) were used to determine the prevalence and distribution of hr-HPV and to explore the risk association between hr-HPV genotypes and precancerous lesions.

Results

9.1% of the study population tested hr-HPV positive. The prevalence varied regionally rom the lowest in Guangdong (6.3%) to the highest in Inner Mongolia (12.9%). The most prevalent genotypes found were HPV-52 (21.5%), HPV-16 (19.2%), HPV-58 (15.0%), HPV-39 (8.9%), and HPV-51 (8.2%). The overall odds ratios for CIN2+ and CIN3+ for the presence of HPV-16 was 59.7 (95% CI 39.9-89.3) and, 92.0 (95%CI 54.5-155.3), respectively and remained the highest odds ratio for CIN3+ in all 6 regions.

Conclusion

Geographical variation exists in the prevalence and distribution of hr-HPV in mainland China. HPV-16/52/58 were the most prevalent genotypes, and HPV-16 had the highest risk for high-grade cervical lesions.

Full Text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the manuscript can be downloaded and accessed as a PDF.

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Risk of CIN2+/CIN3+ according to high-risk Human Papillomavirus (hr-HPV) genotyping, overall

Figure 3
Risk of CIN2+/CIN3+ according to high-risk Human Papillomavirus (hr-HPV) genotyping, Inner Mongolia

![Graph showing risk of CIN2+/CIN3+ for Inner Mongolia]

**Figure 4**

Risk of CIN2+/CIN3+ according to high-risk Human Papillomavirus (hr-HPV) genotyping, Hebei Province

![Graph showing risk of CIN2+/CIN3+ for Hebei Province]

**Figure 5**
Risk of CIN2+/CIN3+ according to high-risk Human Papillomavirus (hr-HPV) genotyping, Hubei Province

Figure 6

Risk of CIN2+/CIN3+ according to high-risk Human Papillomavirus (hr-HPV) genotyping, Jiangxi Province

Figure 7
Risk of CIN2+/CIN3+ according to high-risk Human Papillomavirus (hr-HPV) genotyping, Guangdong Province

Figure 8

Risk of CIN2+/CIN3+ according to high-risk Human Papillomavirus (hr-HPV) genotyping, Shenzhen City