Molecular Epidemiological Study on Prevalence of Human Papillomaviruses in Patients with Common Warts in Beijing Area

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Objective To study the circulation, distribution, and genomic diversity of HPVs in common warts in Beijing area of China. Methods Forty eight patients with pathologically diagnosed common warts were screened for the presence of HPV with HPV type-specific PCR and direct sequencing analysis. The genomic diversity of HPVs prevalent in Chinese patients was analyzed based on LCR. Results Forty one (85.5%) samples were positive for HPV DNA, 13(31.7%)-HPV-57, 12(29.3%)-HPV-1a, 5(17%)-HPV-27 and 5(12.2%)-HPV-2a. Four cases were infected with two different HPV types, two (4.9%) with HPV-1a and HPV-27, one (2.4%) with HPV-1 and HPV-57 and one (2.4%) with HPV-27 and HPV-57. In contrast to the prevalence of single strain of novel HPV-57 variant and HPV-1 prototype, two HPV-2 and three HPV-27 novel variants were found to circulate in Beijing. Conclusion HPV-1, -2, -27 and -57 are predominantly prevalent in patients with common warts in Beijing.

Key words: Human papillomavirus; Genotype; Common warts; Variants

REFERENCES


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