



Prevalence and genotype distribution of human papillomavirus in women in the Henan Province

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ABSTRACT. We studied human papillomavirus (HPV) prevalence and genotype distribution among women in the Henan Province to provide epidemiological data as a means of preventing cervical cancer and developing a vaccine. A total of 14,873 samples were genotyped by using polymerase chain reaction reverse dot-blot. The overall HPV-positive rate in the sample was 23.98% (3566/14873), of which 69.01% (2461/3566) were infected with high-risk HPV types and 17.33% (618/3566) with low-risk types. Eighteen high-risk HPV types were detected; HPV 16 (16.73%) was the most common, followed by 58 (10.17%), 52 (9.11%), 56 (6.48%), 66 (5.76%), 33 (4.74%), 68 (3.92%), 31 (3.60%), 53 (3.13%), 59 (3.00%), 35 (2.53%), 51 (2.00%), 73 (1.08%), 45 (0.94%), 83 (0.84%), 39 (0.69%), 18 (0.61%), and MM4 (0.04%). Four low-risk HPV types were detected; HPV 43 (11.34%) was the most common, followed by 6 (5.17%), 42 (4.76%), and 11 (3.35%). Type 44 was not detected. Among the women positive for HPV, 71.17% (2538/3566) had a single type of infection; of these, 54.66% (1949/3566) had high-risk and 16.52% (589/3566) had low-risk infections. A total of 28.83% (1028/3566) had multiple HPV infec-

tions, of which 20.11% (717/3566) had double HPV infections. One peak in HPV prevalence occurred among women younger than age 25; a second peak occurred among women older than age 55. The overall prevalence of HPV infection in the Henan Province was 23.98%, of which the most common type was high-risk HPV and a single type of infection. The leading genotypes were HPV 16, 43, 58, 52, and 56.

Key words: Human papillomavirus; Genotypes; Vaccine; Cervical cancer