HPV genotype analysis for women in Shaanxi Province of China

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ABSTRACT. The aim of this study was to examine the subtype distribution of human papilloma virus (HPV) in women in the Shaanxi Province of China. A DNA chip, along with polymerase chain reaction amplification and reverse dot blot technology, was adopted to analyze the HPV genotypes of 22,937 cases of cervical cell specimens. The HPV infection rate was 18.70%, wherein high-risk, low-risk, and high- and low-risk multiple infection rates were 15.75, 2.96 and 1.91%, respectively. High-risk infections accounted for 84.20% of total infections. The rate of HPV infection in women with rural residence, high school education or less, a low income, or age over 40 years was significantly higher than that in the control group (negative HPV infection women). Of the 18 detected high-risk HPV subtypes, the most common in single infections were, in the order of prevalence, HPV16, 58, 18, 52, 33, and 56. For multiple high-risk infections, the most common subtypes in the order of prevalence were HPV16, 52, 58, 18, 56, and 33. Age was a factor in the rate of infection, as the 41-
50-year age group had a significantly higher risk of infection than the other groups (P < 0.05). In multiple infections, double infections were common, accounting for 77.10% of multiple infections, and triple or more infections were more common in women aged 51-60 years. In Shaanxi Province, high-risk HPV infection in women was mainly attributed to rural residence, age over 40 years, low income, and low education level.

**Key words:** Age distribution; Human papilloma virus; Subtype distribution; Multiple infection; Cervical cancer