Distribution and positive predictive value of high-risk HPV genotypes in histologically confirmed high-grade cervical intraepithelial neoplasia (CIN2+): Implications for clinical triage and vaccination strategies

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ABSTRACT

Introduction: While HPV genotypes 16 and 18 account for a substantial proportion of cervical cancer cases globally, emerging evidence highlights the contribution of other high-risk HPV genotypes to CIN2+. Understanding the broader genotype distribution is essential for informing screening strategies and vaccine policy. **Objective:** This study aims to identify the most prevalent HPV genotypes associated with histologically confirmed high-grade cervical intraepithelial neoplasia (CIN2+). **Materials and Methods:** This cross-sectional study was conducted at the University Malaya Medical Centre in Malaysia from July 2018 to June 2024. A total of 671 women referred for colposcopy following a positive HPV screening were enrolled. Cervical samples were tested using the BD Onclarity HPV assay for extended genotyping, and histological diagnoses were obtained based on colposcopy-guided biopsies. Descriptive statistics were used to determine genotype distribution and calculate genotype-specific positive predictive values (PPVs) for CIN2+ and CIN3+. **Results:** Among 58 women with confirmed CIN3+, HPV16 was the most prevalent genotype (41.4%) and had the highest PPV for CIN3+ (28.6%). HPV16, HPV18, HPV52 and HPV33/58 collectively contributed to 81.1% of CIN3+. HPV52 and HPV33/58, despite having lower PPVs (~16%), ranked the second and third frequently observed genotypes in CIN3+. **Conclusion:** These findings support genotype-informed triage algorithms and underscore the value of vaccines that include prevalent genotypes like HPV52 and 33/58, alongside HPV16 and 18, in high-grade lesions. PPV can be useful for clinicians to assess an individual woman's risk when HPV-positive, while the prevalence of specific genotypes serves to inform public health policy.