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High-Risk HPV Genotype Distribution in Karnataka, India: Implications for Screening and Vaccination Strategies

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ABSTRACT

Background: Cervical cancer remains a major cause of cancer mortality among women in India, driven primarily by persistent infection with high-risk human papillomavirus (HPV) genotypes. While HPV 16 and 18 are globally recognised as the most oncogenic, the prevalence of other high-risk types varies regionally, influencing prevention strategies. Methods: We conducted a cross-sectional study involving 923 women aged ≥30 years from diverse socio-economic backgrounds across urban and rural Karnataka. Cervical swabs were collected using the HC2 DNA

Collection Device following counselling by obstetricians and gynaecologists in their respective hospitals. All positive samples underwent extended genotyping. Co-testing with Pap smear cytology was performed for all participants. Women with normal cytology were advised to repeat HPV testing after one year and offered HPV vaccination if <45 years. Those with abnormal cytology were referred for colposcopy, biopsy, and further management. Results: Of the 923 women screened, 35 (3.79%) tested positive for high-risk HPV genotypes. The most prevalent types were HPV 66 (54.3%) and HPV 33 (34.3%), followed by HPV 16 (14.3%) and HPV 58 (14.3%). HPV 18, 35, 45, 51, and 52 were detected in ≤4 cases each. This pattern represents a marked deviation from the globally dominant HPV 16/18 profile. Conclusions: The predominance of HPV 33 and 66 in this cohort highlights the need for region-specific HPV surveillance, extended genotyping in screening programmes, and reconsideration of vaccination strategies to ensure coverage of locally prevalent oncogenic strains.

Keywords: HPV genotyping, cervical cancer, India, HPV 33, HPV 66, Pap smear, screening, vaccination policy, LMIC.

INTRODUCTION

Cervical cancer is the second most common cancer among Indian women, with an estimated 123,907 new cases and 77,348 deaths annually. Persistent infection with high-risk HPV genotypes is the principal cause of cervical cancer. While HPV 16 and 18 together account for ~70% of cervical cancers worldwide, other oncogenic genotypes such as HPV 33, 45, 52, 58, and 66 contribute substantially to the burden, particularly in low- and middle-income countries (LMICs). Global screening and vaccination strategies have largely been designed based on data from high-income countries (HICs), where HPV 16/18 predominate. However, emerging evidence from LMICs, including India, indicates variation in genotype distribution, underscoring the need for local data to guide effective interventions.

METHODS

Study Design and Participants

This cross-sectional study recruited 923 women aged ≥30 years from multiple hospitals across Karnataka, India. Participants represented a range of socio-economic backgrounds and resided in both urban and rural settings. Screening was conducted by practising obstetricians and gynaecologists following informed consent and pre-test counselling.

Sample Collection and Laboratory Testing

Cervical swabs were collected using the HC2 DNA Collection Device. All samples were analysed for high-risk HPV DNA, and positive cases underwent extended genotyping to determine the distribution of HPV types.

Cytology and Triage

All participants received Pap smear cytology as part of co-testing. Women with normal cytology were advised to repeat HPV testing after one year and were offered HPV vaccination if under 45 years of age. Women with abnormal cytology were referred to specialised centres for colposcopy, biopsy, and further management per standard guidelines.

RESULTS

Overall prevalence:
Total tested: 923 women.
High-risk HPV positive: 35 women (3.79%)

HPV Type	Number of Cases	Percentage (%)
66.0	19.0	54.3
33.0	12.0	34.3
16.0	5.0	14.3
58.0	5.0	14.3
18.0	4.0	11.4
35.0	1.0	2.9
45.0	1.0	2.9
51.0	1.0	2.9
52.0	1.0	2.9

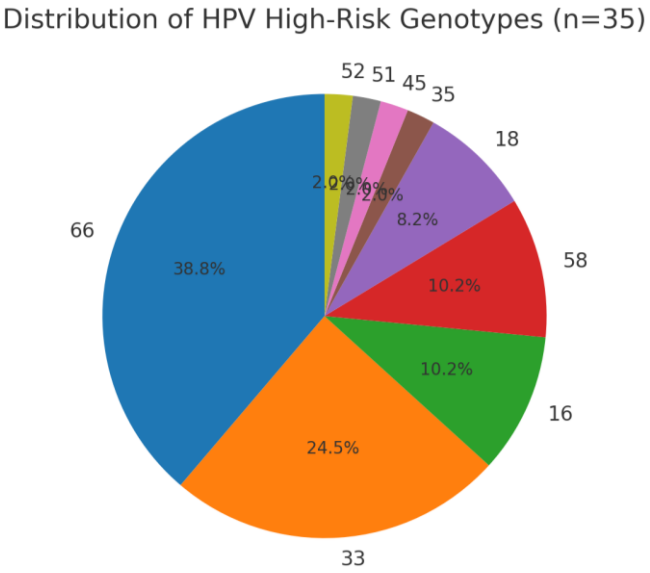

Figure 1: Distribution of high-risk HPV genotypes among positive cases (Pie chart).

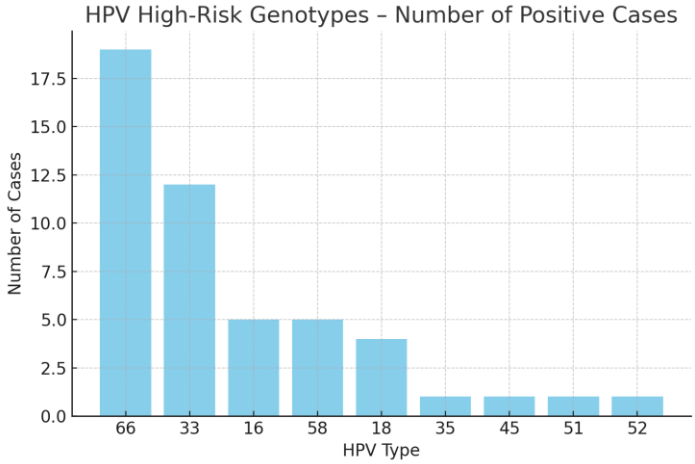

Figure 2: Number of positive cases per genotype (Bar chart).

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DISCUSSION

This study is among the first in Karnataka to demonstrate a predominance of HPV 33 and 66 over HPV 16 and 18 among women aged ≥30 years. Similar findings have been reported in other LMICs, where non-16/18 high-risk types contribute significantly to the oncogenic HPV burden. Implications for vaccination policy: Current bivalent and quadrivalent vaccines target HPV 16/18 (and 6/11 for quadrivalent), leaving HPV 33 and 66 uncovered. The nonavalent vaccine includes HPV 33, 45, 52, and 58 but excludes HPV 66, which in our cohort accounted for over half of positive cases.

Implications for screening: Programmes detecting only HPV 16/18 may underestimate risk in populations with high prevalence of other high-risk types. Extended genotyping, while costlier, can improve triage by identifying women at risk from non-16/18 oncogenic infections.

CONCLUSIONS AND RECOMMENDATIONS

- Region-specific HPV genotype data should inform national screening protocols.
- HPV vaccination strategies in India should consider broader genotype coverage.
- Integration of extended genotyping into screening programmes can enhance early detection.
- Policymakers should recognise that HIC-derived HPV data may not reflect Indian realities.

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