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BRIEF COMMUNICATION

Gynecology

Prevalence and distribution of high-risk HPV genotypes in Indigenous Maya women in Guatemala

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In Guatemala, cervical cancer ranks second among gynecologic cancers, with 1761 cases and 973 deaths reported in 2022.[1] Furthermore, less than 40% of women in Guatemala undergo screening for cervical cancer, with this proportion (and subsequent clinical outcomes) being even worse for the country's large population of Indigenous Maya women.[2] According to the most recent National Maternal and Child Health Survey (ENSMI 2014–2015), only about 36% of Indigenous women reported having been screened within the last 3 years.

The WHO recommends human papillomavirus (HPV) DNA testing as the primary screening method, and Guatemala is slowly transitioning towards HPV-based screening, with increases in both public and private HPV-based screening options. In addition, since 2018 the Guatemalan Ministry of Health has been prioritizing HPV vaccination, although overall coverage remains low. Currently, primarily the quadrivalent HPV vaccine (genotypes 6, 11, 16, 18) is administered.

A number of studies from Latin America have now suggested that the distribution of HPV genotypes in the region may be distinct from other world regions, with a higher prevalence of high-risk HPV genotypes in screening and biopsy samples other than those included in the 4- and 9-valent vaccines (e.g., 6, 11, 16, 18, 31, 33, 45, 52, and 58).[3–5] However, there is limited HPV genotype data from Guatemala, which is badly needed given the burden and disparities of cervical cancer in the country.

In January 2024, our clinical laboratory at Wuqu' Kawoq|Maya Health Alliance transitioned to HPV-based testing for cervical cancer screening. Maya Health Alliance is a nonprofit primary care organization working primarily with Indigenous Maya populations in central and western Guatemala. Detection and identification were performed using real-time PCR with the GeneFinder HPV-HR RealAmp Kit, manufactured by Osang Healthcare Co., Ltd., and analyzed using the SLAN-48P Real-Time PCR System thermocycler, manufactured by Xiamen Zeesan Biotech Co., Ltd.[6] On this diagnostic platform, HPV-16 and HPV-18 are each detected individually, whereas 12 other high-risk HPV genotypes (types 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, and 68) are detected in aggregate.

We conducted a retrospective chart review of all cervical cancer screening samples obtained from launching the platform (January 1, 2024 to August 31, 2025). The protocol was approved by the Maya Health Alliance Institutional Review Board, which granted a waiver of informed consent as all data were de-identified prior to analysis. A total of 2128 resulted samples from women aged 30–65 years, were analyzed.

Among all samples, 20.6% ($n=438$) were positive for one or more high risk HPV genotype listed above, which is similar to the positivity rates reported from other studies in the Latin America region and smaller studies within Guatemala.[7] Positivity rate was 21% among women 30–39 years old ($n=993$); 20.1% in 40–49 year olds ($n=658$); 19.9% in 50–59 year olds ($n=392$); and 23.5% ($n=85$) in 60–65 year olds.

Regarding genotyping, non-16 non-18 high risk HPV genotypes predominated, at 69.2% of all positive samples. HPV-16 was detected in 11.9%, and HPV-18 in 3.4% (Figure 1), and coinfection with HPV-16 or −18 and another high-risk genotype in a smaller proportion of samples.

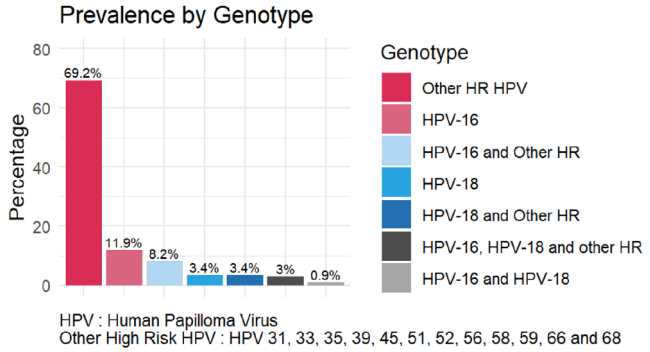

FIGURE 1 Prevalence of human papillomavirus (HPV) by genotype.

To our knowledge, this is the first report of HPV genotype data from a large sample of primarily Indigenous Maya women in Guatemala, who bear one of the highest burdens of cervical cancer morbidity and mortality in the country. We found a majority of non-16 non-18 high risk genotype infections, as well as coinfections with HPV-16 and -18. Smaller studies in non-indigenous Guatemalan women have also demonstrated high proportions of infections by other genotypes, including 39, 58, 52, and 45, although 16 and 18 still predominate in invasive cancer specimens.[7,8]

A major limitation of our findings is that our current clinical platform does not disaggregate multiple non-16 non-18 HPV genotypes. In future work we will be exploring individually genotyping of these subtypes. We will also correlate HPV genotypes to final biopsy-proven diagnoses, including carcinoma in situ and invasive cervical cancer. Our findings have significant implications for the Government of Guatemala's HPV vaccination strategy using only the quadrivalent vaccine.

AUTHOR CONTRIBUTIONS

Design: E.C.A.; and P.R; data analysis: E.C.A; C.V.M.; E.R.G. and P.R.; conduct: C.V.M.; E.R.G.; E.C.A. and P.R manuscript writing: E.C.A.; A.I.F.A.; C.V.M.; E.R.G. and P.R.

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CONFLICT OF INTEREST STATEMENT

The authors report no conflicts of interest.

DATA AVAILABILITY STATEMENT

Research data are not shared.

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