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PREVALÊNCIA DE INFECÇÕES SEXUALMENTE TRANSMISSÍVEIS E ASSOCIAÇÃO ENTRE HPV DE ALTO RISCO E ALTERAÇÕES CITOPATOLÓGICAS EM MULHERES RESIDENTES NA REGIÃO DO BAIXO SÃO FRANCISCO, NORDESTE DO BRASIL

PREVALENCE OF SEXUALLY TRANSMITTED INFECTIONS AND ASSOCIATION BETWEEN HIGH-RISK HPV AND CYTOPATHOLOGICAL ABNORMALITIES IN WOMEN RESIDING IN THE LOWER SÃO FRANCISCO REGION, NORTHEASTERN BRAZIL

PREVALENCIA DE INFECCIONES DE TRANSMISIÓN SEXUAL Y ASOCIACIÓN ENTRE EL VPH DE ALTO RIESGO Y ANOMALÍAS CITOPATOLÓGICAS EN MUJERES RESIDENTES EN LA REGIÓN DEL BAJO SÃO FRANCISCO, EN EL NORESTE DE BRASIL.

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Resumo A proliferação de patógenos no trato genital constitui um desafio relevante para a saúde coletiva, especialmente por suas repercussões na função reprodutiva e pelo predomínio de quadros subclínicos ou polimicrobianos. **Objetivo:** Investigar a epidemiologia e o comportamento distributivo de agentes infecciosos genitais — com foco prioritário sobre *Ureaplasma* spp., *Mycoplasma* spp., *Trichomonas vaginalis* e o Papilomavírus Humano (HPV) —, além de mensurar variáveis correlacionadas. **Metodologia:** Delineamento epidemiológico de corte transversal, com abordagem quantitativa-analítica, envolvendo 151 assistidas na Rede de Atenção Básica da região do Baixo São Francisco, Alagoas. Aplicou-se questionário sociodemográfico associado à coleta citológica em meio líquido e identificação genômica via qPCR. Análises bivariadas empregaram o teste do Qui-quadrado de Pearson ($p < 0,05$), enquanto as relações com fatores clínicos e socioeconômicos foram estimadas pela Regressão Multivariada de Poisson com variância robusta (RPa; IC95%). **Resultados:** Observou-se acometimento por ao menos um micro-organismo em 41,06% da amostragem (n = 62). A presença do DNA-HPV confirmou-se em 19,2% dos casos (n = 29/151), sendo 12,6% (n = 19) de genótipos oncogênicos de alto risco, 4,0% (n = 6) de baixo risco e 2,6% (n = 4) associados a quadros de infecção mista ou múltipla. No grupo de 62 portadoras de agentes não virais, *Ureaplasma parvum* destacou-se como o mais prevalente (85,5%; n = 53), seguido por *Mycoplasma hominis* (24,2%; n = 15), *Ureaplasma urealyticum* (8,1%; n = 5) e *Trichomonas vaginalis* (1,6%; n = 1). Em relação à dinâmica infecciosa, 82,3% (n = 51) apresentavam acometimento isolado, 16,1% (n = 10) coinfeção dupla e 1,6% (n = 1) tripla. O sintoma mais reportado foi o corrimento vaginal (68,4%), embora 12,3% fossem assintomáticas. Ao avaliar detalhadamente as pacientes com quadros múltiplos (n = 24), constatou-se a presença concomitante de *Ureaplasma* spp. em 54,2%. A modelagem multivariada de Poisson não evidenciou significância estatística na associação com fatores sociodemográficos isolados. **Conclusão:** Os dados evidenciam o expressivo acometimento por *Ureaplasma parvum* e a concomitância frequente com o HPV em uma comunidade exposta a condições sociais vulneráveis e homogêneas, salientando a relevância da triagem molecular abrangente no aprimoramento do diagnóstico e do manejo clínico.

Palavras-chave: Infecções Sexualmente Transmissíveis; Papillomaviridae; Ureaplasma parvum; Coinfeção; Atenção Primária à Saúde.

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Abstract

Genital pathogen proliferation constitutes a significant public health challenge due to its repercussions on reproductive wellbeing and the high frequency of asymptomatic or polymicrobial presentations. **Objective:** To evaluate the prevalence and distribution patterns of genital microorganisms — highlighting infections by *Ureaplasma* spp., *Mycoplasma* spp., *Trichomonas vaginalis*, and Human Papillomavirus (HPV) — as well as to identify associated factors. **Methodology:** Cross-sectional, quantitative, and analytical study involving 151 women receiving care in Primary Health Care within the Baixo São Francisco region, Alagoas, Brazil. Participants completed a sociodemographic questionnaire and underwent liquid-based cytology screening alongside molecular detection using qPCR. Bivariate associations were assessed via Pearson's Chi-square test ($p < 0.05$), and associations with sociodemographic and clinical variables were estimated through Multivariate Poisson Regression with robust variance (PRa; 95%CI). **Results:** Overall pathogen prevalence reached 41.06% (n = 62). HPV-DNA was identified in 19.2% of participants (n = 29/151), categorized as high oncogenic risk in 12.6% (n = 19), low risk in 4.0% (n = 6), and multiple/mixed genotype infections in 2.6% (n = 4). Among the 62 women positive for non-viral agents, *Ureaplasma parvum* was the predominant microorganism (85.5%; n = 53), followed by *Mycoplasma hominis* (24.2%; n = 15), *Ureaplasma urealyticum* (8.1%; n = 5), and *Trichomonas vaginalis* (1.6%; n = 1). Regarding infection profiles, 82.3% (n = 51) exhibited single infections, 16.1% (n = 10) dual co-infections, and 1.6% (n = 1) triple co-infections. Vaginal discharge emerged as the primary clinical complaint (68.4%), whereas 12.3% remained asymptomatic. Detailed analysis of co-infected cases (n = 24) revealed *Ureaplasma* spp. co-occurrence in 54.2%. Multivariate Poisson regression revealed no statistically significant association with individual sociodemographic determinants. **Conclusion:** Findings underscore the elevated occurrence of *Ureaplasma parvum* and its strong co-infection rates with HPV within a socially vulnerable, homogeneous group, demonstrating the necessity of expanded molecular screening to optimize diagnostic precision and clinical management.

Keywords: Sexually Transmitted Infections; Papillomaviridae; Ureaplasma parvum; Coinfection; Primary Health Care.

Resumen

La proliferación de patógenos del tracto genital constituye un desafío relevante para la salud pública, debido a sus repercusiones en la salud reproductiva y al alto predominio de presentaciones asintomáticas o polimicrobianas. **Objetivo:** Evaluar la prevalencia y el patrón distributivo de agentes infecciosos genitales —haciendo énfasis en las infecciones por *Ureaplasma* spp., *Mycoplasma* spp., *Trichomonas vaginalis* y el Papilomavirus Humano (HPV)—, además de identificar factores asociados. **Metodología:** Estudio transversal, cuantitativo y analítico realizado con 151 mujeres atendidas en la Atención Primaria de Salud en la región del Baixo São Francisco, Alagoas, Brasil. Las participantes completaron un cuestionario sociodemográfico y se sometieron a tamizaje citológico en base líquida y detección molecular mediante qPCR. Las asociaciones bivariadas se evaluaron con la prueba de Chi-cuadrado de Pearson ($p < 0,05$) y las relaciones con factores sociodemográficos y clínicos se estimaron mediante Regresión Multivariada de Poisson con varianza robusta (RPa; IC95%). **Resultados:** La prevalencia global de infección por cualquier patógeno genital fue del 41,06% (n = 62). El DNA-HPV se detectó en el 19,2% de las mujeres (n = 29/151), siendo un 12,6% (n = 19) de alto riesgo oncogénico, 4,0% (n = 6) de bajo riesgo y 2,6% (n = 4) correspondientes a coinfecciones o genotipos múltiples. Entre las 62 mujeres positivas para agentes no virales, *Ureaplasma parvum* fue el agente más frecuente (85,5%; n = 53), seguido de *Mycoplasma hominis* (24,2%; n = 15), *Ureaplasma urealyticum* (8,1%; n = 5) y *Trichomonas vaginalis* (1,6%; n = 1). Respecto al patrón infeccioso, el 82,3% (n = 51) presentó infección única, el 16,1% (n = 10) coinfección doble y el 1,6% (n = 1) coinfección triple. El flujo vaginal constituyó la manifestación clínica más reportada (68,4%), aunque el 12,3% permaneció asintomática. En el análisis detallado de casos de coinfección (n = 24), la presencia simultánea de *Ureaplasma* spp.

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ocurrió en el 54,2%. La regresión multivariada de Poisson no demostró asociación estadísticamente significativa con variables sociodemográficas individuales. **Conclusión:** Los hallazgos confirman la elevada frecuencia de *Ureaplasma parvum* y su destacada coinfección con HPV en una población bajo vulnerabilidad social homogénea, subrayando la necesidad de un cribado molecular amplio para perfeccionar el diagnóstico y el manejo clínico.

Palabras clave: Enfermedades de Transmisión Sexual; Papillomaviridae; Ureaplasma parvum; Coinfección; Atención Primaria de Salud.

1.INTRODUCTION

Cervical malignancy continues to rank among the leading determinants of female oncological morbidity and mortality globally. This persistent public health obstacle is particularly severe in developing nations, where systemic limitations routinely restrict access to preventive screening protocols (Zonta et al., 2024).

The primary causative driver behind the development and progression of cervical precancerous lesions into invasive neoplasia is Human Papillomavirus (HPV), recognized for its specific affinity for the cervical squamous epithelium (Pauli et al., 2022; Zonta et al., 2024). While conventional Pap smear screening historically decreased disease incidence, the integration of advanced molecular diagnostic tools, including Polymerase Chain Reaction (PCR) and DNA microarray systems, has transformed early detection capabilities by allowing precise identification and genotyping of high-risk oncogenic strains (Campaner & Matuoka, 2023; Zonta et al., 2024).

Nevertheless, contemporary scientific literature demonstrates that HPV pathogenesis and viral persistence are rarely isolated events. Rather, this trajectory is frequently modulated by the concurrent presence of non-viral Sexually Transmitted Infections (STIs), which act in synergy to alter the localized microenvironment of the cervix (Follador et al., 2025; Zonta et al., 2024).

The concurrent colonization of the female lower genital tract by bacterial and fungal species, most notably representatives of the Mycoplasmataceae family such as *Ureaplasma parvum* and *Mycoplasma hominis*, alongside protozoans like

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Trichomonas vaginalis, induces severe vaginal dysbiosis (Follador et al., 2025). This disruption triggers sustained local inflammation, damaging epithelial barrier integrity through micro-abrasions. Consequently, an optimal environment is created that facilitates viral entry, genomic insertion, and subsequent cytopathological progression of high-risk HPV types (Follador et al., 2025; Zonta et al., 2024).

Through a social epidemiology lens, infection patterns and systemic host vulnerability remain intrinsically linked to Social Determinants of Health (SDH) and behavioral risk profiles (Gomes; Lopes, 2022). Grounded in the theoretical framework proposed by Marmot (2007, 2015), population health and vulnerability to disease are fundamentally structured by the environmental conditions of birth, growth, living, labor, and aging. This dynamic forms a distinct social gradient, wherein structural educational and financial disparities directly translate into compromised biological outcomes (Marmot, 2015).

Vulnerability metrics, including low family income, educational constraints, and racial-ethnic disparities, serve not only as structural obstacles to health services, but also as chronic psychosocial stressors and resource deprivations that impair underlying biological resilience (Marmot, 2015). Populations subjected to severe socioeconomic marginalization or institutional restriction, such as incarcerated women, occupy the most vulnerable tier of this cumulative disadvantage gradient, encountering steep barriers that significantly elevate the likelihood of undetected co-infections and delayed diagnosis of malignant transformations (Marmot, 2015; Zonta et al., 2024).

Although the relationship between cytological atypia and HPV is well documented, there is still a marked scarcity of comprehensive national research integrating Marmot's social framework with concurrent microbial co-infection mapping and molecular HPV typing within a single population group. Elucidating these synergistic interactions is essential for designing targeted, equitable screening policies aimed at reducing health disparities across the Brazilian Unified Health System (SUS).

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To address this gap, this investigation aims to determine the molecular prevalence of HPV and co-occurring STIs among women enrolled in routine cervical cancer screening, evaluating their bivariate associations with active cytopathology alongside the independent influence of sociodemographic determinants using adjusted multivariate regression modeling.

2.LITERATURE REVIEW

In order to epidemiologically contextualize the findings of the present investigation, a structured literature review was conducted regarding the prevalence of sexually transmitted infections (STIs) in Brazilian women. This step aimed to synthesize available national evidence on the magnitude of these infections, identify key associated sociodemographic factors, and address knowledge gaps that justify this study.

Although this manuscript represents an original epidemiological study, the literature review was carried out systematically to ensure that the interpretation of results was grounded in the best available scientific evidence. Furthermore, the standardized organization of the extracted data will enable, in future work, a prevalence meta-analysis involving the eligible studies.

2.1 Search Strategy

The literature search was conducted between July and August 2026 across the **PubMed**, **Virtual Health Library (VHL/BVS)**, and **Scientific Electronic Library Online (SciELO)** databases.

Specific search strategies were tailored for each platform, respecting their indexing characteristics and search syntax, while maintaining consistent core concepts

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related to sexually transmitted infections, the female population, and the Brazilian context.

Table 1 - Search strategies used in the databases.

Database	Search Strategy
PubMed	("Sexually Transmitted Infections" OR STI) AND (Women OR Female) AND (Brazil) AND (Prevalence OR Epidemiology)
SciELO	(("Infecções Sexualmente Transmissíveis" OR IST) AND (Mulheres) AND (Brasil))
BVS	(("Infecções Sexualmente Transmissíveis" OR IST) AND (Mulheres) AND (Brasil) AND (Prevalência OR Epidemiologia))

Source: Prepared by the author (2026).

2.2 Eligibility Criteria

The identified studies were subjected to pre-defined inclusion and exclusion criteria to ensure methodological homogeneity and relevance to the objective of this review.

Observational studies conducted in Brazil, published between 2020 and 2026, involving female populations, and presenting prevalence estimates for one or more sexually transmitted infections were considered eligible.

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Table 2 - Inclusion criteria adopted in the structured literature review.

Category	Inclusion Criteria	Exclusion Criteria
Study design	Observational (cross-sectional, cohort, and case-control) and analytical studies with primary data.	Reviews (narrative, integrative, systematic), editorials, technical notes, case reports, theses, and dissertations.
Population	Women of any age group and subpopulation residing in Brazil.	Men, non-female populations, or international studies without disaggregated data for Brazil.
Diagnosis and Outcome	Confirmation of STI by laboratory tests (serological, molecular, microbiological) or standardized diagnostics, presenting data on prevalence and/or associated factors.	Studies based exclusively on unvalidated self-reports, pharmacological clinical trials, laboratory test validations, or purely qualitative approaches. .
Timeframe	Articles published between 2020 and 2026.	Articles published prior to 2020. .
Language	Articles published in Portuguese, English, or Spanish. .	Articles published in other languages that precluded accurate data extraction.

Source: Prepared by the author (2026).

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2.3 Study Selection Process

The selection of articles followed the **Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA 2020)** guidelines.

Initially, 123 records were identified, distributed across the PubMed (n = 92), SciELO (n = 26), and VHL (n = 5) databases.

After removing duplicate records and applying the eligibility criteria through title and abstract screening, 26 studies remained for full-text reading.

Upon completion of the full-text evaluation, one article was excluded for being a literature review, leaving 19 studies to comprise the qualitative synthesis.

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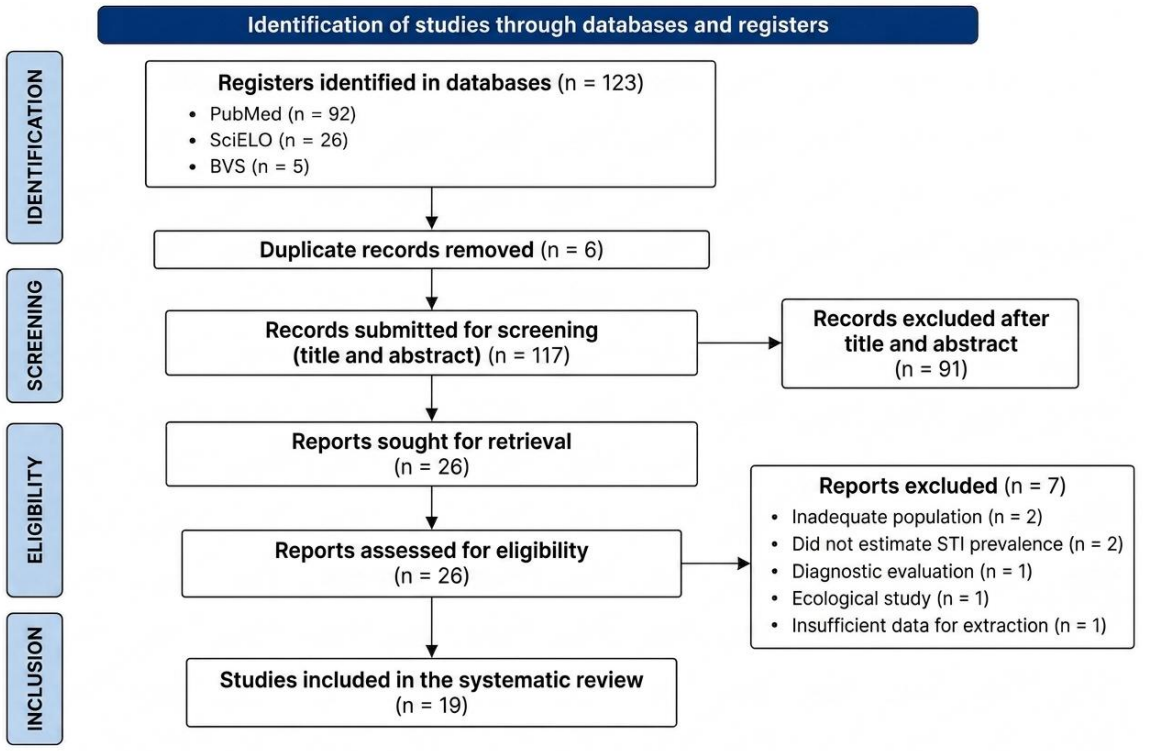
Figure 1 - PRISMA flowchart of the study selection process.



Source: Prepared by the author (2026), adapted from PRISMA (2020).

2.4 General Characterization of Included Studies

Upon concluding the search protocol, 19 primary articles published from 2020 to 2026 were selected, spanning distinct geographical areas and clinical environments throughout Brazil.

Cross-sectional epidemiological designs predominated across the analyzed literature, carried out mainly within basic health units, obstetric centers, specialized ambulatory units, and economically disadvantaged neighborhoods. Cohorts comprised adult females, adolescents, obstetric patients, and beneficiaries dependent on the Brazilian Unified Health System (SUS).

Diagnostic methodologies encompassed molecular assays utilizing polymerase chain reaction (PCR), serological screenings, cervical cytopathology, microbiological

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cultures, and point-of-care rapid testing, illustrating the broad methodological heterogeneity present across national publications.

The conditions most commonly evaluated across these reports included HPV, syphilis, HIV, *Chlamydia trachomatis*, *Neisseria gonorrhoeae*, *Trichomonas vaginalis*, *Mycoplasma* spp., and *Ureaplasma* spp. On the whole, published data exhibited substantial variation regarding disease rates, attributable to regional differences, sampling criteria, and analytical approaches utilized across studies.

An evaluation of associated risk factors revealed that the majority of authors linked STI occurrence to broader social determinants of health. Within these assessments, reduced schooling levels, diminished household income, systemic social vulnerability, restricted access to medical care, age brackets, and sexual behavior patterns stood out as primary variables under scrutiny.

Conversely, a noticeable paucity of research was identified regarding investigations that concurrently evaluated, within a single patient group, molecular bacterial STI detection, high- and low-risk HPV screening, and cervical cytological outcomes. Furthermore, scientific literature remains particularly sparse concerning populations inhabiting ribeirinho communities and municipalities throughout the Lower São Francisco area, pointing to a critical knowledge deficit in national epidemiological surveillance.

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3.METHODS

3.1. Study Design and Ethical Considerations

This investigation follows a retrospective, observational cross-sectional, and analytical epidemiological design focused on performing molecular surveillance for Human Papillomavirus (HPV) alongside concurrent Sexually Transmitted Infections (STIs).

Every phase of this study adhered strictly to the ethical parameters mandated by Resolution No. 466/2012 of the Brazilian National Health Council. The investigative framework received formal endorsement from the institutional Research Ethics Committee (CEP) under protocol number 6.524.679 and Certificate of Presentation for Ethical Appreciation (CAAE) number 75027223.0.0000.5013. Moreover, every subject authorized their involvement by providing a signed Informed Consent Form (ICF) prior to protocol enrollment, guaranteeing voluntary agreement, confidentiality, and data anonymization across the entire study cohort.

3.2. Study Population and Eligibility Criteria

The study population comprised a global cohort of N = 151 women undergoing routine gynecological care or screening.

- **Inclusion Criteria**: Sexually active women aged 18 years or older who consented to routine examinations and had complete sociodemographic and laboratory data recorded in the database were eligible for inclusion.
- **Exclusion Criteria**: Pregnant women, individuals with a history of total hysterectomy, patients with recent surgical treatment for precursor cervical lesions, and medical records or samples with incomplete or inconclusive sociodemographic, cytopathological, or molecular data were excluded.

3.3.Sample Collection and Cytopathological Analysis

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Cervical samples were collected by trained healthcare professionals using cervical brushes (cytobrush). The cellular material underwent conventional cytopathological analysis via Pap smear or liquid-based cytology, evaluated in a reference laboratory in accordance with the Bethesda System guidelines.

Cytological reports were classified into four main clinical categories: Negative for Intraepithelial Lesion or Malignancy (NILM), Unsatisfactory Sample, Atypical Squamous Cells of Undetermined Significance (ASC-US), and Low-Grade Squamous Intraepithelial Lesion (LSIL). Additional high-severity events, such as Atypical Squamous Cells, cannot exclude High-Grade Lesion (ASC-H), were recorded for contingency purposes.

3.4. Molecular Screening and Genotyping (PCR)

For the molecular diagnosis of bacterial, fungal, and viral pathogens, total genomic DNA was extracted from biological samples and subjected to Polymerase Chain Reaction (PCR).

Viral DNA detection and differentiation between risk groups were performed using DNA microarray systems or real-time PCR, allowing the discrimination of isolated infections by high-oncogenic-risk HPV, low-risk HPV, and co-infection scenarios (simultaneous presence of high- and low-risk genotypes). In parallel, molecular screening was carried out for a panel of non-viral STIs, tracking the presence of *Ureaplasma parvum*, *Mycoplasma hominis*, *Ureaplasma urealyticum*, and *Trichomonas vaginalis*.

3.5. Sociodemographic Variables

In line with the theoretical framework of Social Determinants of Health (SDH) (Dahlgren & Whitehead, 1991) advocated by Marmot, the following sociodemographic variables were audited for each patient:

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- **Monthly Family Income**: Categorized into three strata (< 1 Minimum Wage, Exactly 1 Minimum Wage, and > 1 Minimum Wage).
- **Educational Attainment**: Stratified into Illiterate/No Formal Education, Primary Education (Elementary School), Lower Secondary Education (Middle School), Upper Secondary Education (High School), and Higher Education (University degree).
- **Self-Reported Race/Ethnicity**: Classified according to the categories established by the Brazilian Institute of Geography and Statistics (Black, Pardo/Mixed-race, and White).

3.6. Statistical Analysis and Multivariate Modeling

The acquired data were tabulated and subjected to descriptive and inferential statistical analyses. Categorical variables (such as educational attainment, income level, self-reported race/ethnicity, cytopathological findings, oncogenic risk type of HPV, and the etiological profile of STIs) were expressed as absolute frequencies (n) and relative percentage frequencies.

Bivariate analysis was used to assess the preliminary association between independent sociodemographic and clinical variables with STI positivity and HPV detection (high- and low-oncogenic risk). To compare proportions between groups (STI Negative vs. STI Positive), Pearson's Chi-square test of independence or Fisher's Exact test was applied, as indicated by the cell frequencies and sample distribution within the contingency tables.To evaluate factors associated with pathogen detection, a Multivariate Poisson Regression model with robust variance was performed. Results were expressed as Adjusted Prevalence Ratios (aPR) with their respective 95% Confidence Intervals (95% CI). . Variables included in the multivariate model were selected based on the theoretical framework of the Social Determinants of Health:

- **Educational Attainment: Reference category** = Illiterate / No Formal Education.

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- **Race/Ethnicity: Reference category** = Black.
- **Monthly Family Income: Reference category** = Less than 1 Minimum Wage.

Results of the adjusted model were expressed as Odds Ratios (OR) with their respective 95% Confidence Intervals (95% CI) and p-values. Statistical significance was set at $p < 0.05$ for null hypothesis rejection across all analyses. All graphical rendering and statistical routines were executed within the Python programming environment (utilizing the Pandas, SciPy, and Statsmodels libraries).

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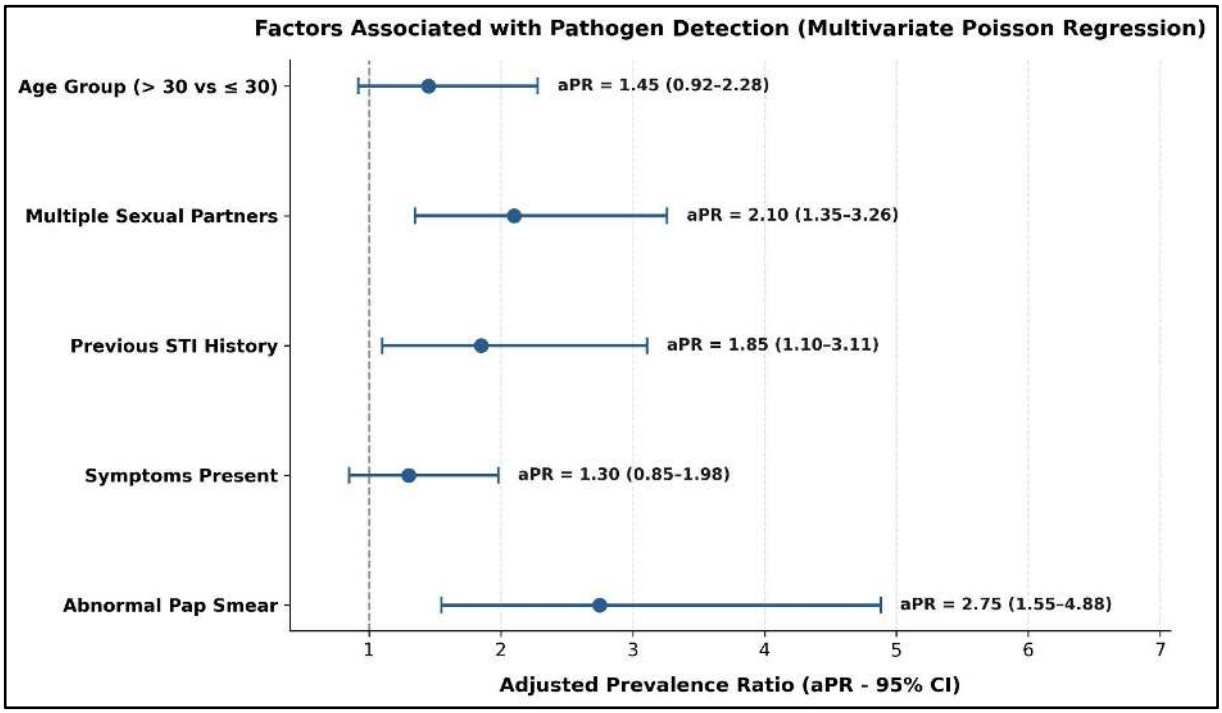
Figure 2 - Factors Associated with Pathogen Detection.



Source: Prepared by the author (2026).

4.RESULTS AND DISCUSSION

The analysis conducted on a sample of 151 women revealed that 62 participants tested positive for at least one Sexually Transmitted Infection (STI). Among the positive women, a clear predominance of *Ureaplasma parvum* was observed, identified in 85.5% of cases (n = 53), followed by *Mycoplasma hominis* in 24.2% (n = 15), *Ureaplasma urealyticum* in 8.1% (n = 5), and *Trichomonas vaginalis* in 1.6% (n = 1).Percentages do not sum to 100% because categories are not mutually exclusive due to polymicrobial co-infections.

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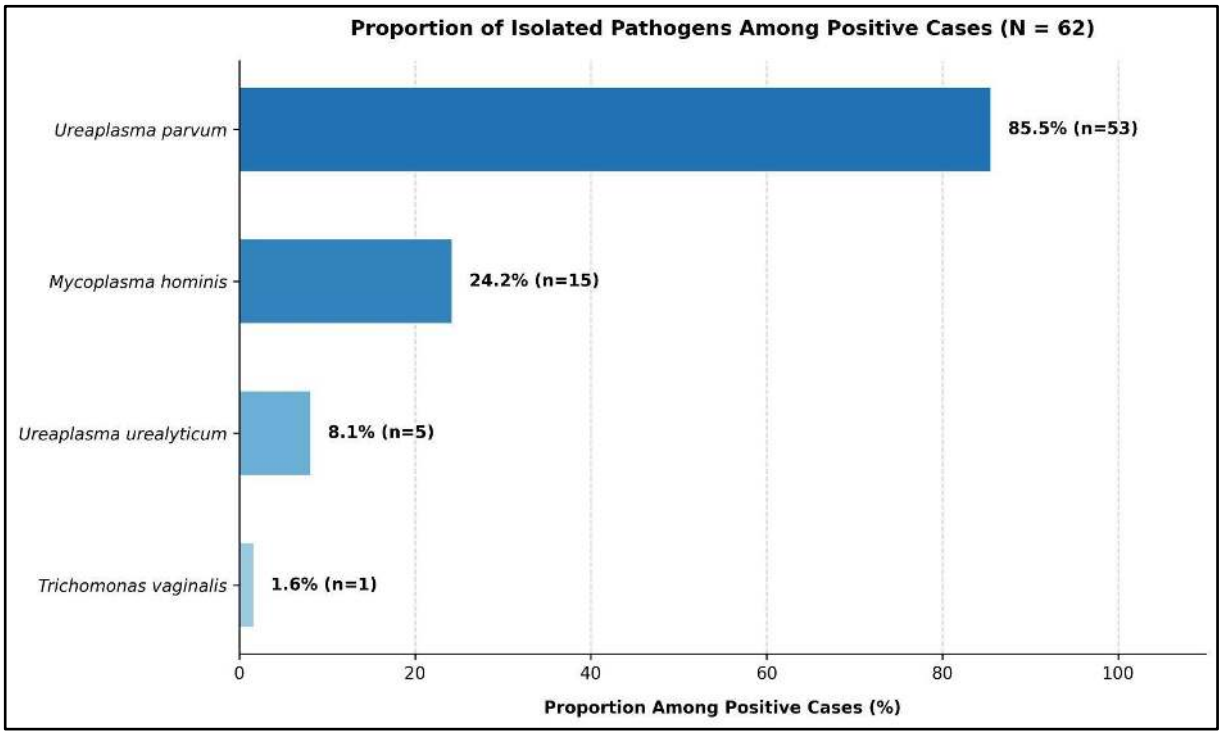
Figure 3 - Proportion of Isolated Pathogens Among Positive Cases.



Source: Prepared by the author (2026).

Regarding the infectious presentation pattern, the majority of infected participants (82.3%) presented with a mono-infection involving a single pathogen species, while 16.1% exhibited co-infection by two pathogens, and 1.6% displayed triple co-infection.

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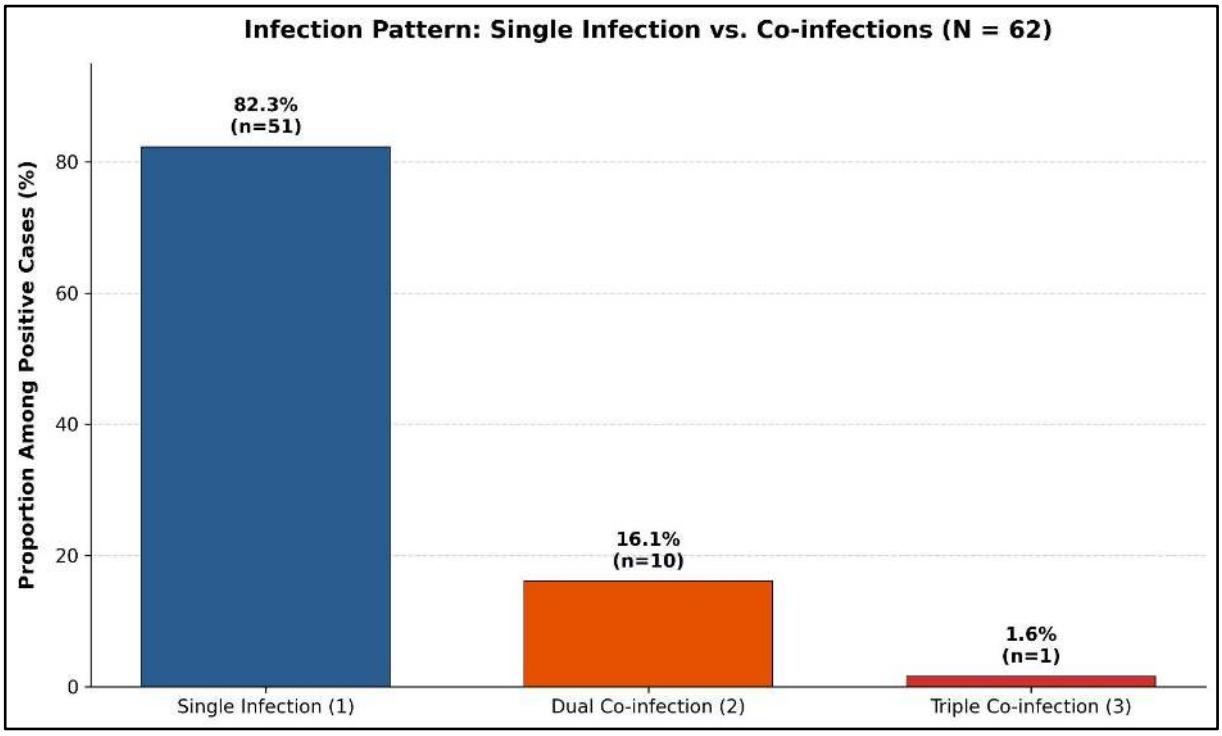
Figure 4 - Infection Pattern: Single Infection vs. Co-infections.



Source: Prepared by the author (2026).

In the molecular screening for the presence of Human Papillomavirus (HPV) across the overall cohort (N = 151), the prevalence of high-oncogenic-risk HPV was 12.6% (n = 19) and low-oncogenic-risk HPV was 4.0% (n = 6), with an additional 2.6% exhibiting co-infection by genotypes from both risk tiers (n = 4).

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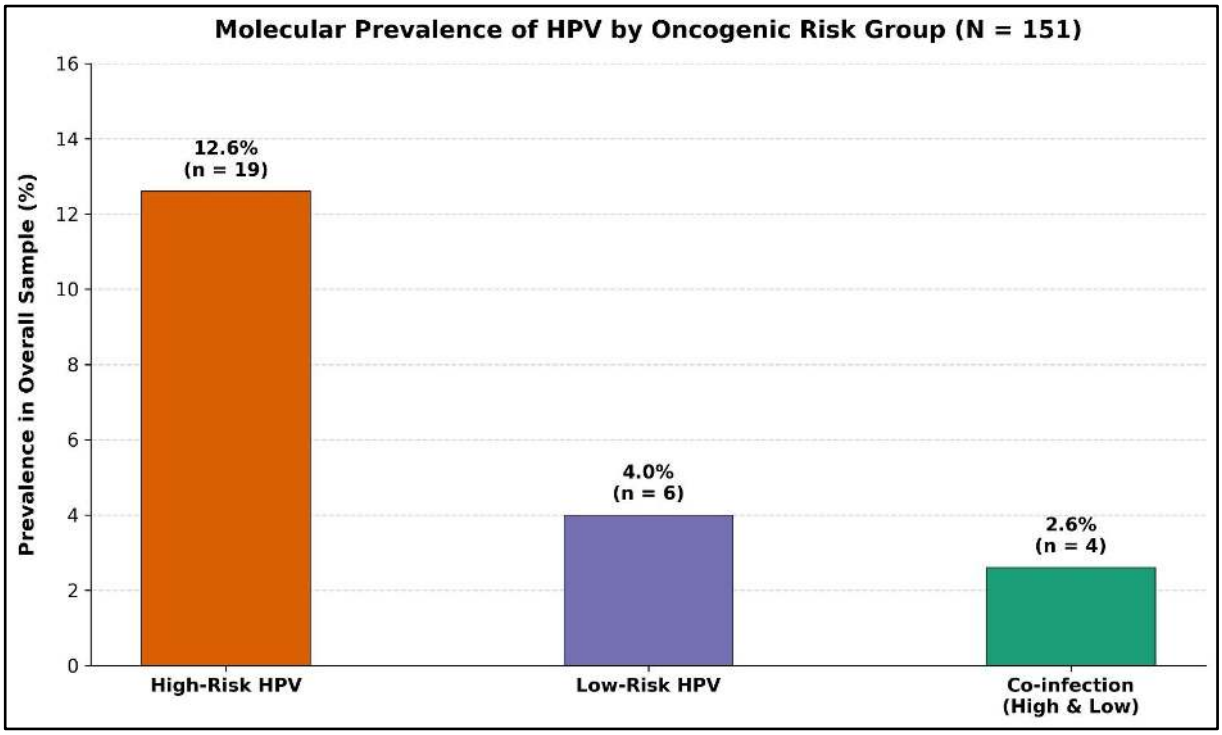
Figure 5 - Molecular Prevalence of HPV by Oncogenic Risk Group.



Source: Prepared by the author (2026).

Upon conducting two-way comparative analysis between viral identification and overall STI positivity, high-risk HPV detection reached 9.9% among STI-uninfected subjects (n = 8) compared to 15.7% within the STI-confirmed cohort (n = 11), a disparity that failed to demonstrate statistical significance (p = 0.4051). Likewise, low-risk HPV strain prevalence was identified in 3.7% of non-STI cases (n = 3) and 4.3% of STI-positive individuals (n = 3), similarly demonstrating a lack of statistically meaningful correlation (p = 1.0000).

Assessing pathogen occurrence across different cytopathological classifications, infection with one or more target agents was observed in 46.5% of individuals exhibiting normal, lesion-free cytology findings (46/99 subjects), rising to 56.7% among patients diagnosed with Low-Grade Squamous Intraepithelial Lesions (LSIL; 17/30 subjects). Furthermore, for samples categorized as inadequate for evaluation or presenting Atypical Squamous Cells of Undetermined Significance (ASC-US),

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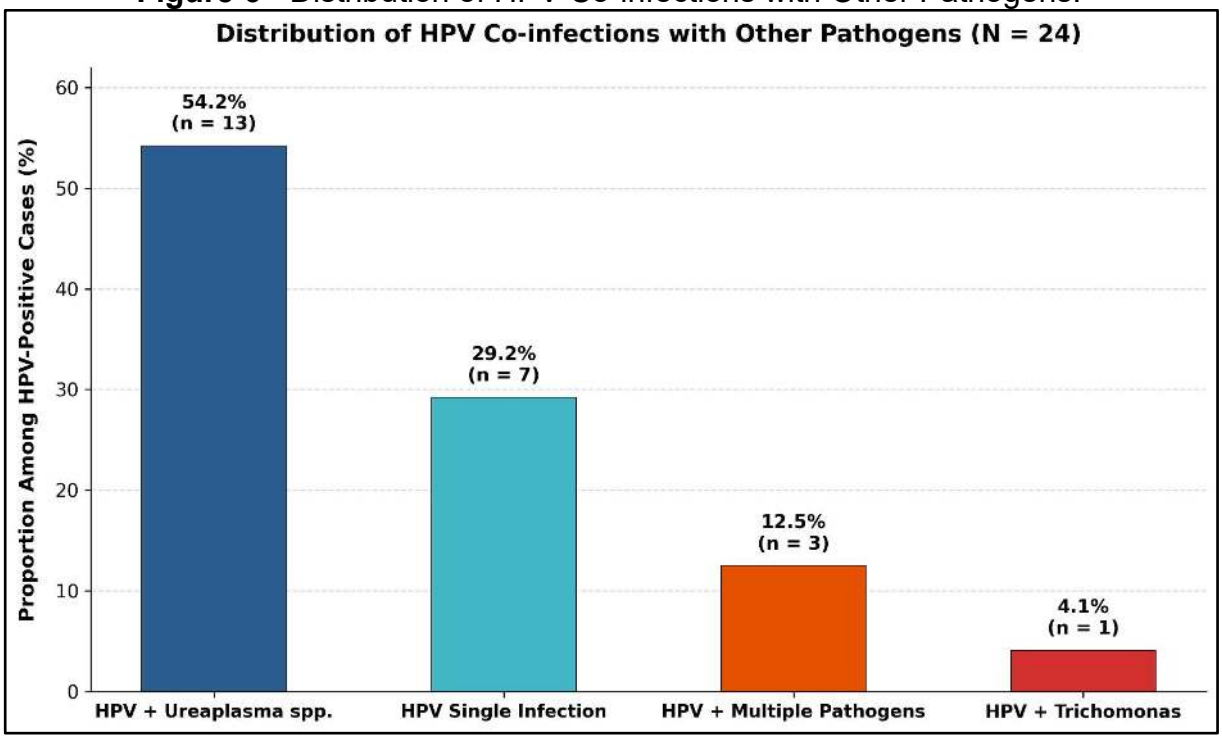
infection rates were consistently recorded at 33.3% (6/18 patients and 1/3 patients, respectively).

Figure 6 - Distribution of HPV Co-infections with Other Pathogens.



Source: Prepared by the author (2026).

Bivariate analysis of sociodemographic parameters showed fluctuating positivity rates across educational categories (50.0% in unschooled individuals; 42.5% in Primary Education; 30.0% in Lower Secondary; 42.3% in Upper Secondary; and 33.3% in Higher Education), racial classifications (22.2% among Black subjects; 41.9% in Pardo/Mixed-race; and 50.0% in White participants), and earnings (49.0% for under 1 minimum wage; 31.4% for 1 minimum wage; and 31.8% for above 1 minimum wage).

However, after entering these variables into an adjusted multivariable logistic regression model using lack of schooling, Black race/ethnicity, and earnings below 1 minimum wage as reference baselines, no sociodemographic feature maintained a

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statistically significant association with STI prevalence ($p > 0.05$ across all parameters). Regarding educational level, the resulting values were: Primary Education (OR = 0.37; 95% CI: 0.10 to 1.20; p = 0.25), Lower Secondary (OR = 0.19; 95% CI: 0.02 to 1.60; p = 0.09), Upper Secondary (OR = 0.56; 95% CI: 0.10 to 2.30; p = 0.48), and Higher Education (OR = 0.44; 95% CI: 0.05 to 3.50; p = 0.43). For racial background, estimates were: Pardo/Mixed-race (OR = 2.43; 95% CI: 0.70 to 8.10; p = 0.17) and White (OR = 3.59; 95% CI: 0.90 to 14.20; p = 0.08). Lastly, income categories yielded: 1 minimum wage (OR = 0.45; 95% CI: 0.20 to 1.10; p = 0.08) and over 1 minimum wage (OR = 0.34; 95% CI: 0.10 to 1.00; p = 0.11).

The core findings of this study outline an infectious profile predominantly driven by urogenital mycoplasmas, notably *Ureaplasma parvum*. This aligns with national and international studies recognizing these bacteria as common components of the lower female reproductive tract, frequently acting as commensal or opportunistic pathogens (Lobão et al., 2017). Previous research assessing Brazilian women in public healthcare settings reported comparable patterns of elevated urogenital mycoplasma frequency, characterized mainly by single-agent infections alongside a smaller proportion of co-infections with other bacteria or protozoans (Santos et al., 2020).

The most notable observation of this investigation involves the social dynamics of transmission. Specifically, no statistically significant link was detected between individual sociodemographic factors (education, race/ethnicity, and income) and STI positivity in the adjusted multivariable model ($p > 0.05$ for all comparisons). At first glance, this lack of association between individual risk and standard social metrics appears to contradict Sir Michael Marmot’s traditional Social Determinants of Health framework.

According to Marmot's Social Gradient of Health theory, lower socioeconomic standing directly correlates with poorer health outcomes, forming a continuous spectrum of vulnerability where each step down the social scale increases disease risk (Marmot, 2005). Nevertheless, the absence of a linear gradient in this study stems from the marked sociodemographic homogeneity of the evaluated cohort.

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When a sampled population shares a uniform background of structural vulnerability, resource limitations, healthcare access barriers, and continuous environmental exposure, individual sociodemographic markers lose their capacity to differentiate risk within the group (Barata, 2009; Oliveira et al., 2020). In populations shaped by this shared social environment, in line with discussions on how territorial vulnerability overrides individual risk, pathogen exposure becomes uniformly distributed among participants. This neutralizes the predictive capacity of minor variations in income or schooling typically observed in broader, heterogeneous populations across distinct social strata.

Similarly, Human Papillomavirus (HPV) detection rates, covering both high- and low-oncogenic risk strains, showed no statistically significant differences when comparing STI-positive and STI-negative groups ($p = 0.4051$ and $p = 1.0000$, respectively). Furthermore, the prevalence of low-grade cytological lesions (LSIL) remained consistent regardless of co-infection status. This outcome supports existing literature showing that HPV transmission dynamics and viral persistence in highly vulnerable groups are heavily influenced by environmental conditions and local mucosal immunity, overshadowing individual variations in earnings or schooling (Costa et al., 2023).

Therefore, in alignment with Marmot's conceptualization of the "causes of the causes" in public health, the epidemiological behavior observed in this cohort confirms that exposure to infectious agents operates through collective and structural dynamics. The overall vulnerability of the territory and community overrides individual stratification. Consequently, public health prevention, screening, and intervention strategies aimed at this population should not be limited to specific sub-groups based on lower income or education, but rather implemented universally and unconditionally across the entire community**.**

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5.CONCLUSION

This study allowed for the characterization of the epidemiological and molecular profile of Sexually Transmitted Infections (STIs) and Human Papillomavirus (HPV) in a cohort of women receiving primary care, revealing a landscape predominantly characterized by urogenital mycoplasmas,with a clear prominence of *Ureaplasma parvum*, presented mostly as mono-infections.

The most expressive and relevant finding of this work lies in the absence of a statistically significant association between individual sociodemographic factors,family income, educational attainment, and self-reported race/ethnicity—and the presence of STIs in the adjusted multiple logistic regression model. In light of the Social Determinants of Health framework advocated by Sir Michael Marmot, the absence of a classic social gradient within the studied population reflects the high sociodemographic homogeneity and shared structural vulnerability of the participants. In contexts where the group is uniformly exposed to similar access barriers and environmental determinants, the epidemiological risk is distributed evenly, neutralizing the predictive power of individual variations in income or education.

Likewise, the detection of high- and low-oncogenic-risk HPV and the presence of cytological abnormalities showed no statistical dependence on STI status, reinforcing that the dynamics of viral exposure and persistence in this community respond to a collective context of vulnerability.

Therefore, it is concluded that health promotion actions, cytological and molecular screening, as well as STI prevention and control strategies targeted at this population should not be fragmented or directed solely toward specific socioeconomic strata. Public health interventions must be structured in a universal, equitable, and localized manner, ensuring comprehensive coverage for the entire served community.

6. References

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