

A Cross Sectional Study to Determine the Prevalence of HPV Genotypes in women of reproductive age “at risk for HIV” who present for screening for ASPIRE

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Rationale

- HPV is a common STI
- Annual incidence of 6.2 million worldwide
 - 1 in 4 in adult Zimbabwean women infected
- Burden of HPV disease ranges from genital warts to cervical intraepithelial neoplasia (CIN) to carcinoma
- High-risk (HR)HPV is responsible for the vast majority of cervical cancers
 - Leading cause of cancer death in adult Zimbabwean women
 - Preventable disease with immunization

Rationale

- Interaction between HIV and HPV manifests as:
 - Susceptibility to HPV-related pathology
 - High rates of relapse after treatment of HPV-related diseases
 - Increased frequency, virulence and disease progression of HPV infections
- HPV more commonly detected in women with lower CD4 cell counts and high viral loads

Primary Objective

- To determine the prevalence of HPV genotypes in women of reproductive age “at risk for HIV” who present for screening for ASPIRE.

Secondary Objectives

- To determine the predictive value of HR-HPV in relation to abnormal cervical cytology.
- To determine the relationship between CD4+ levels and occurrence of HR-HPV genotypes
- To compare the proportion of HR-HPV types between HIV infected women and HIV-uninfected women
- To determine the association between Chlamydia (CT), Gonorrhea (GC), Syphilis, *Trichomonas vaginalis* (TV) and HPV detection



Methodology

- **Study design:** Cross sectional
- **Study population:** Women screening for ASPIRE at Harare, 700 HIV-ve and 400 HIV +ve
- Informed consent and eligibility verification
- Socio-demographic information and sexual practices
- **STI testing** for CT/GC, Syphilis and TV
- Vaginal and ecto/endocervical fluid swabs for **HPV PCR** using a qualitative in-house assay for both LR and HR-HPV
- Ecto/endocervical specimens for **PAP test**.
- **CD4** count for HIV-infected.
- **Statistical analysis**

Statistical Analysis

- Prevalence of HPV genotypes
- Proportions between HIV +ve and HIV-ve will be compared using (χ^2 - tests) for
 - HPV genotypes
 - cytological abnormalities
- Associations between
 - HPV genotypes and CD4+ cell count in HIV +ve participants
 - CT, GC, TV and syphilis with HPV
 - Women's socio-demographic characteristics and HPV detection
- Risk factors/rates for HPV acquisition (follow up group)

Public Health Implications

- Knowledge of distribution of HPV genotypes will improve implementation of HPV vaccination program in Zimbabwe
- Combining HPV testing and cytology will produce multiple risk strata which will range from very low to very high absolute risk (positive predictive value) of prevalent CIN3 or carcinoma

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