STD Prevalence and Incidence Among Black MSM in HPTN 061: Analysis Plan

Background: Bacterial STDs (syphilis, chlamydia and gonorrhea) can potentiate HIV transmission and acquisition through increasing genital and anorectal inflammation, recruiting more cells that can bind HIV in susceptible individuals and upregulating HIV concentrations in mucosal fluids and surfaces in HIV-infected individuals. Additionally, the presence of anogenital bacterial STDs can serve as a marker that individuals are engaging in unprotected anal intercourse. Although bacterial STDs can be transmitted through the same ways that HIV is transmitted, other behaviors may also be associated with bacterial STD transmission, particularly oral sex, which can transmit syphilis either through insertive or receptive exposure, and insertive penile-oral sex can result in the acquisition of gonorrhea or chlamydia. Prevalent STDs were associated with prevalent HIV infection in the baseline analysis of HPTN 061, and may be part of the multifactorial basis for the disproportionate burden of HIV among American Black MSM.

Study questions: The current analysis will address the following questions:

- 1. What are the correlates of prevalent syphilis, urethral or rectal gonorrhea or chlamydia infection among Black MSM enrolled in HPTN 061?
- 2. What is the incidence of syphilis, urethral or rectal gonorrhea and chlamydia at 6 months and at 12 months among Black MSM enrolled in HPTN 061?
- 3. What are the correlates of incident syphilis, urethral or rectal gonorrhea or chlamydia infection among Black MSM enrolled in HPTN 061?
- 4. Is incident syphilis, urethral or rectal gonorrhea or chlamydia infection associated with incident HIV infection at 6 or 12 months among Black MSM enrolled in HPTN 061?

Operational guidance for data analysis:

- 1. For the analysis of the correlates of prevalent syphilis, urethral or rectal gonorrhea or chlamydia infection the same variables that were used in the baseline paper that looked at the correlates of HIV infection will be used, with the demographic, social and behavioral variables coded the same way as for the baseline paper.
- 2. Variables that are found to be statistically significantly correlated with prevalent syphilis, urethral or rectal gonorrhea or chlamydia infection at the p</= 0.1 level will be analyzed in a multivariable model to assess those variables that remain statistically significantly associated with each STD.
- 3. A similar process will be used to assess the correlates of incident syphilis, urethral or rectal gonorrhea or chlamydia infection, using the same variables that were used in the baseline paper that looked at the correlates of HIV infection, with the demographic, social and behavioral variables coded the same way as for the baseline paper. For the incidence analyses, it will be presumed that an individual may acquire a new bacterial STD at 6 or 12 months, since

- participants with newly diagnosed gonorrhea or chlamydia were expected to be treated appropriately. For syphilis, the endpoint committee has determined whether an infection was new or not, and those determined endpoints should be used in these analyses.
- 4. Since individuals can have the same infection potentially 3 times during the study (e.g. rectal gonorrhea at baseline, 6 months and 12 months, a table will be constructed to show how many participants had each infection at baseline only, at 6 months only, at 12 months only, at baseline and 6 months, at baseline and 12 months, and at all 3 time points. However, for the correlates of incident bacterial STD infection, each specific infection diagnosed at 6 and/or 12 months in each individual will be the unit of analysis (e.g. person will be considered to have incident rectal gonorrhea if he was diagnosed with it at 6 and/or 12 months)
- 5. Variables that are found to be statistically significantly correlated with incident syphilis, urethral or rectal gonorrhea or chlamydia infection at the p</= 0.1 level will be analyzed in a multivariable model to assess those variables that remain statistically significantly associated with each STD.