HBV acquisition, chronic HBV infection and HBV disease. Chronic HBV infection may pose a challenge among HIV infected individuals' eligible for antiretroviral therapy, increasing their risk of rapid HIV-disease progression. Early prevention of HBV infection by vaccinating HIV infected people is recommended. However, in most poor countries HBV vaccination is not routine and those opting for vaccination are rarely tested before vaccination. We sought to determine the prevalence of HBV infection and natural immunity against HBV infection among HIV discordant couples.

Methods The first 949 discordant heterosexual couples screened for eligibility into an HIV pre-exposure prophylaxis study had HBV surface antigen (HBsAg) and anti-HBs status determined. CD4 count was also performed for HIV infected potential subjects. None of these participants reported HBV vaccination history. SPSS version 17 software was used for statistical analysis.

Results Of 949 HIV positive subjects, 34.7% (329) were men thus women were more likely to be the HIV-positive spouse in these HIV-discordant relationships ($p<0.001$). 99 of 1898 subjects were positive for HBVsAg, resulting to 5.2% HBV prevalence, with men being more likely to be HBV infected compared to women ($p<0.05$). 40% (758) of 1898 subjects tested for anti-HBs were immune to HBV, with men being more likely to possess natural protective antibodies against HBV compared to women ($p<0.05$). Among HIV infected subjects, those with a CD4 count >250 cells/ml were more likely to possess immunity against HBV compared to those with a CD4 count <250 cells/ml ($p<0.001$). However, HIV status was not associated with either HBV infection ($p=0.302$) or immunity against HBV ($p=0.512$).

Conclusion Scaling-up routine vaccination after anti-HBs screening in resource limited settings could be cost-effective and easy to roll-out in HIV endemic Sab-Sahara Africa. This is because 40% of individuals are already immune to HBV. Validation of Anti-HBs rapid screening tests is urgently needed in this population.

P4-S2.02 REGULATORY T CELLS AND FOX P3 LEVELS IN NAIVE AND HAART TREATED HIV-1 INFECTED PATIENTS IN THAILAND

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Background The frequency and expression levels of FoxP3 in regulatory T-cells (T-regs) from advanced-stage HIV-infected patients are controversial. Thus, the aims of this study were to compare these parameters of T-regs from HIV infected patients and from healthy controls.

Methods T-reg population and expression levels of FoxP3 were assessed from 43 HIV-1 infected individuals and 12 healthy controls by using FACs flow cytometry.

Results Minor decrease in frequencies of T-regs was found in both infected groups (naïve and treated) compared with those from healthy controls ($p=0.02$, $p=0.01$, respectively). In contrast, a significantly increase in the ratios of T-regs: CD4 cells from HIV-infected patients was observed ($p=0.001$). In addition, FoxP3 expression levels in both treated and untreated HIV-1 infected patients were significantly higher than those in healthy controls ($p<0.001$ and 0.01 respectively).

Conclusions The decreased number of T-regulatory cells and the increased levels of FoxP3 in T-regs from HIV infected patients were associated with advanced stage of AIDS disease.

P4-S2.03 CALCULATING BMI IN HIV+ FEMALE ADOLESCENTS: A CASE OF SHAPING THE HEALTH OF ADOLESCENTS IN ZIMBABWE: SHAZ! PLUS PROJECT

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Background Body Mass Index (BMI) is a statistical measure which compares a person's weight and height. It is used to estimate a healthy body weight based on a person's height. This measure is pertinent to use in HIV positives since weight loss is used as a proxy measure for clinical progression of HIV disease in that more weight loss is associated with advancing disease and often precedes clinical symptoms. We sought to measure BMI among HIV+ female adolescents to see if this is the best tool to use in immune-compromised populations.

Methods Data were pulled out from an ongoing RCT entitled SHAZ! Plus. (N=650). It enrols HIV +ive female adolescents who are out of school. Data were collected at baseline, 6, 12 and 18-month follow-up visits, with the project facilitating ongoing care, ART and support to those in need of it. BMI was calculated using Adolphe Quetelet BMI calculator of weight in kg over height in m^2 (kg/m^2). BMI prime 25 was also calculated and used to compare the BMI results. Sample of xx used.

Results 64.5% of the cohort had BMIs falling within normal ranges 18.5 to 25. 33.8% had BMIs of <18.5 and 0.16% had a BMI of >25. 64.5% had BMI prime that fell within normal ranges of 0.74 and 0.99. 33.8% had BMI prime of <0.74 and 0.16% had a BMI prime of >1.00. The average BMI at baseline was 19.35 Weight ranged from 25 to 70 at baseline, average was 47.71.

Conclusion Results call for the need to come up with an adjusted BMI index for female adolescents who are immuno-compromised to use as a standard measure for optimal health. BMI however has it's shortcomings since it does not measure the actual body fat. In resource poor settings, a simple tool like weight lost or gained over time might be a good indicator of clinical progression of HIV as opposed to validated tools like the BMI.

Basic sciences poster session 3: ureaplasma, trichomonas and syphilis

P4-S3.01 MACROLIDE-RESISTANCE TESTING AND MOLECULAR SUBTYPING OF TREPONEMA PALLIDUM STRAINS FROM SOUTH AFRICA

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Objectives To determine whether the main 23S rRNA mutation (A2058G) that confers macrolide resistance in *Treponema pallidum* is present among DNA obtained from syphilitic ulcers in South Africa and to determine the strain subtype distribution using molecular methods.

Methods DNA was re-extracted from sixty ulcer swabs, previously shown to contain *T pallidum* DNA by in-house real-time multiplex PCR assay, using a MagNA Pure Compact DNA extraction system (Roche, Germany). The genital ulcer specimens were collected in South Africa between 2005 and 2009 during either national microbiological surveillance activities or as part of large episodic acyclovir treatment trial (HSV4294). The re-extracted DNA was screened for the A2058G point mutation in the peptidyltransferase region of the 23S rRNA subunit using a rapid PCR-based restriction digest assay.

Subtyping of *T pallidum*, using a previously-published technique, was based on the molecular characterisation of two variable treponemal repeat genes, arp and tpr.

Results Macrolide resistance profiles and the subtype distribution for all 60 DNA samples were obtained. The mean age of all participants was 27.4 years (range 18–43; SD 5.24) of which 55 (92%) were male and 5 (8%) were female. None of the samples analysed contained the 23S rRNA gene point mutation that confers macrolide resistance. A total of eight arp repeat sizes, 8 RFLP patterns and a combined total of 17 subtypes were identified in this study population. The most common subtypes were 14d (43%), followed by 17d (13%), 14b (7%), 22b (5%) and 23b (5%).

Conclusions This is the first South African study to examine both macrolide-resistance profiles and the subtype distribution of syphilis strains using molecular techniques. Macrolide-resistant *T pallidum* strains appear to be uncommon in South Africa compared to more developed countries. Our results indicated subtype 14d to be the predominant circulating *T pallidum* strain in South Africa and there seem to be a high degree of genetic heterogeneity within this population.

P4-S3.02 SUBTYPING OF TREPONEMA PALLIDUM STRAINS BY SEQUENCE ANALYSIS OF TP0279 AND TP0548

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Background The goal of the study was to evaluate two sequence-based subtyping methods for their ability to further differentiate Treponema pallidum strains characterised by the CDC typing system.

Methods 12 clinical specimens with the 14d strain type obtained from patients with GUD in Cape Town in 2000; 14 specimens with the 14d strain type from patients with primary or secondary syphilis in San Francisco collected between 2004 and 2007; and 12 clinical specimens with the 14d strain type collected between 2000 and 2002 from a syphilis outbreak in Vancouver were included in the study. Specimens were previously characterised using the CDC typing method which involves analysis of the sequence variability with tprE, G, and J and, the variable number of 60-bp tandem repeats within the arp gene. Subtyping was performed by PCR amplification of a homonucleotide G" tandem repeat within tp0279 and a variable region within tp0548. PCR amplicons were purified and directly sequenced using the BigDye® Terminator v3.1 cycle sequencing kit and an ABI 3130 sequencer.

Results Of the 12 samples from South Africa, sequence analysis of tp0279 revealed three subtypes (9G, 10G, 11G) and combining this data with the CDC typing method produced strain subtypes 14d9, 14d10, and 14d11. Sequence analysis of the variable region within tp0548 resulted in five subtypes designated a, c, f, k, and l among these samples and, combination with strain type using the CDC method produced subtypes 14d/a, 14d/c, 14d/f, 14d/k, 14d/l. All 14 samples from San Francisco had 9G tandem repeats within tp0279 resulting in subtype 14d9. Sequence analysis of the variable region within tp0548 resulted in 3 subtypes designated f, g and j among these 14 samples and incorporation of the CDC typing method produced subtypes 14d/f, 14d/g, and 14d/j. Of the 12 samples from Vancouver, sequence analysis of tp0279 produced two subtypes (8G, 9G) resulting in strain subtypes 14d8 (1/12) and14d9 (11/12). Sequencing of tp0548 also produced two subtypes (e, f) resulting in strain subtypes 14d/e (1/12) and14d/f (11/12).

Conclusions The tp0279 subtyping method further differentiated 14d strains into four subtypes while the tp0548 method differentiated 14d strains into eight subtypes. Subtyping of strains from the initial syphilis outbreak in Vancouver suggests clonal spread of *T pallidum*. Both subtyping methods enhanced the original CDC typing method and appear to be promising tools for molecular epidemiological studies on syphilis.

P4-S3.03 CHARACTERISATION OF *UREAPLASMA PARVUM* FROM SYMPTOMATIC AND ASYMPTOMATIC MEN ATTENDING A FAMILY PRACTICE IN PRETORIA, SOUTH AFRICA

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Background The genus Ureaplasma colonises human mucosal surfaces such as urogenital tract of men and women. In men it has been implicated in the aetiology of non-gonococcal urethritis and infertility. Although its pathogenesis is not yet fully understood, it has been suggested that certain serotypes are associated with disease. This study undertook to detect genital *Ureaplasma spp.* and to characterise *Ureaplasma parvum* in men with and without urogenital symptoms.

Methods Two hundred first void urine specimens were collected from symptomatic (100) and asymptomatic (100) men attending a private clinic. All specimens were cultured in U9 broth and subcultured on A2 agar medium for confirmation. All isolates were tested for susceptibility using the Mycofast Evolution 3 kit. DNA was extracted from all specimens and amplified using a multiplex TaqMan polymerase chain reaction assay targeting the multiple-banded antigen gene for the detection and serotyping of *U parvum*. *Ureaplasma urealyticum* was detected by a commercial real-time PCR kit.

Results Cultures were positive in 16/100 symptomatic and 12/100 asymptomatic men (p=NS). All isolates were susceptible to doxycycline, pristimycin, roxycycline and azithromycin. One *Ureaplasma spp.* from an asymptomatic male was resistant to ciprofloxacin and josamycin and intermediately resistant to ofloxacin and another was resistant to ofloxacin. An isolate from a symptomatic man was resistant to ciprofloxacin. There was no significant difference (p=0.16) between the *U parvum* isolated from symptomatic (11/100) and asymptomatic (18/100) men as well as for *U urealyticum* from symptomatic 16/100 and asymptomatic 15/100 men (p=0.86). Four men (two from each group) were colonised by both *Ureaplasma spp.*. The predominant serotype was six, followed by types 1, 14 and 3 with no significant difference between symptomatic and asymptomatic men (p=0.309).

Conclusions There is no data of circulating *U parvum* serotypes from South Africa. The prevalence rate was low and no significant differences were found between symptomatic and asymptomatic men for both *Ureaplasma spp.*. Serotype 6 was the most common type compared to reports from developed countries which suggests type 3 as being the most common. Macrolides and tetracyclines remain effective drugs for treatment of the Ureaplasma infections. Molecular techniques are valuable identification and characterisation of this fastidious group of bacteria.