suggests that phylotypes differ phenotypically. An accurate survey of genetic diversity and population structure will facilitate responsible selection of drug and/or vaccine targets for future treatments, and will enable better understanding of virulence factors contributing to the wide range of severity of symptoms associated with trichomoniasis.

P4-S3.08 DEVELOPMENT OF A NOVEL CHIMERIC PROTEIN CONSTRUCT FOR IMPROVED DIAGNOSIS OF SYPHILIS

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Objectives To develop a novel diagnostic protein in order to enhance early detection of syphilis infections and improve overall syphilis diagnosis.
Methods Using pooled serum samples from patients infected with syphilis, immunoreactive regions of two previously identified diagnostic protein candidates, Tp0326 and Tp0453, were elucidated. Focusing on these regions, a chimeric protein construct was created for expression in *Escherichia coli* and expression conditions were optimised to produce soluble protein expression. This Tp0326/Tp0453 chimeric construct was screened against serum samples from; patients with primary, secondary, latent, and neurosyphilis and uninfected individuals. These results were directly compared to the rapid plasma regain (RPR) test, and the microhemagglutination assay for *T pallidum* (MHA-TP).
Results Screening results show high degrees of sensitivity and specificity for the Tp0326/Tp0453 chimeric construct, identifying all stages of syphilis infection from early primary to late latent.
Conclusion The Tp0326/Tp0453 chimera shows promise as a new diagnostic antigen for detecting all stages of syphilis infection and for development into point-of-care diagnostic test formats.

P4-S3.09 THE PREVALENCE OF *TRICHOMONAS VAGINALIS* VIRUS (TVV) IN GLOBALLY DISTRIBUTED *TRICHOMONAS VAGINALIS* ISOLATES

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Objective *Trichomonas vaginalis*, a highly prevalent non-viral sexually transmitted infection, has been shown to be infected by a double-stranded RNA virus known as *T vaginalis* virus (TVV). The presence of this virus has been associated with increased trafficking of the immunogenic P270 to the surface of the parasite, and has therefore been hypothesised to be an important virulence factor in trichomoniasis. In the present study, we investigate the prevalence of TVV in globally distributed *T vaginalis* isolates and find an association between TVV infection and genetically distinct *T vaginalis* populations.
Methods 150 *T vaginalis* isolates from the USA, Mexico, Italy, Southern Africa, Papua New Guinea and Australia were screened for TVV infection by running total RNA extract on 1% agarose gels to detect the presence or absence of the diagnostic 4.5 kb dsRNA genome of the virus. The prevalence of TVV in genetically distinct *T vaginalis* phylotypes was compared using χ^2 tests.
Results TVV was found to be present in 37% of *T vaginalis* isolates. We find a difference in the prevalence of TVV infection between genetically distinct populations of parasites, with 3% of phylotype 1 isolates containing the virus vs 73% of phylotype 2 parasites (<0.001).
Conclusions TVV prevalence varies between *T vaginalis* phylotypes 1 and 2. This finding has implications suggesting that TVV is transmitted vertically among parasites, as more closely related *T vaginalis* strains are infected with TVV. Preliminary data also suggests that phylotype 2 parasites may show greater virulence, and further studies will be required in determining the role of TVV in this increased pathology.

P4-S3.10 A *TRICHOMONAS VAGINALIS* HUMAN VACCINE CANDIDATE: FREUND'S ADJUVANT VS ALUMINIUM HYDROXIDE ADJUVANT IN A BALB/c MOUSE VAGINAL INFECTION MODEL

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Background *Trichomonas vaginalis* is an underreported STD known to increase HIV transmission. Development of a vaccine against *T vaginalis* could greatly affect transmission of *T vaginalis* and HIV as well as reducing their global prevalence. Herein, we aim to investigate the feasibility of developing a *T vaginalis* vaccine using the human-safe adjuvant Alhydrogel compared against an already established Freund's adjuvanted vaccine in a BALB/c vaginal infection mouse model.
Methods A prime-boost vaccination schedule was employed with live, whole cell *T vaginalis* (1×107 Tv/ml) is injected in 2–200 ul aliquots 4 weeks apart and prior to vaginal infection challenge. Either Freund's, 0.5 mg Al/ml Alyhydrogel, or 0.75 mg Al/ml Alhydrogel were applied as adjuvants. Additionally, 0.75 mg Al/ml Alhydrogel sham and non-vaccinated groups serve as controls. The BALB/c vaginal environment was modified to mimic humans by adjustment of vaginal flora and estrogenisation prior to vaginal infection. The total IgG, IgG1 and IgG2a levels in serum were tested 3 weeks post each vaccine injection, then 2 and 4 weeks post-vaginal infection by ELISA. Groups were compared using Tukey's MCT (Post-Hoc one-way ANOVA; $\alpha<0.05$).
Results Alhydrogel adjuvanted groups showed comparable total IgG and IgG1 levels to Freund's adjuvanted group. These levels for all adjuvanted groups were significantly different from control groups at all time points following boost-vaccination. IgG2a levels were not as consistent with large SD seen within Freund's adjuvanted mice. Alhydrogel adjuvanted groups were not significantly different from control groups at any time point for IgG2a levels suggesting no induction of IgG2. Controls and sham vaccines showed no Ig response.
Conclusions Our data suggest that in line with expected Th2 skewed response from Alhydrogel adjuvant and Th1 skewed response from Freund's adjuvant there was a difference in IgG2a antibody production. Additionally, the Alhydrogel adjuvanted vaccines are otherwise similar to Freund's adjuvant in terms of total IgG and IgG1 levels suggesting the feasibility to pursue Alhydrogel as a vaccine candidate. Alhydrogel induces a significantly elevated immune response compared to natural infection antibody production (non-vaccinated control) and does not induce a nonspecific immune response.

Basic sciences poster session 4: Bacterial diversity

P4-S4.01 INVESTIGATION OF THE BACTERIAL DIVERSITY IN URINE OF URETHRITIS PATIENTS AND HEALTHY CONTROLS USING 454 HIGH-THROUGHPUT-SEQUENCING

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Background Non-gonococcal urethritis (NGU) is a common sexually transmitted disease in men but in 30–50% of NGU cases, no known organism is found. We have used 454 high throughput sequencing to analyse the micro flora in urine samples from cases of urethritis and from controls.