chemiluminescent microparticle immunoassay (CMIA, private laboratories). The non-treponemal Venereal Disease Research Laboratory (VDRL) assay was used to screen patients previously-treated for syphilis. An in-house PCR assay tested ulcer-derived DNA extracts for TP. The study received Ethics Committee approval.

Results 93 primary syphilis cases (92 with ulceration, 1 with inguinal lymphadenopathy) were diagnosed in the study period. TP PCR was performed in 84/92 (91%) cases and positive in 76/84 (90%) cases. Overall, syphilis serology detected 79/93 (85%) primary syphilis cases. 75/93 (81%) cases had no laboratory evidence of prior syphilis; 18 cases (19%) had previous reactive treponemal serology. Treponemal antibodies were present in 63/75 (84%) first-episode syphilis cases; 12/75 (16%) had non-reactive treponemal serology. Most cases with previously-treated syphilis had reactive VDRL tests (16/18, 89%). There were 64 PCR positive/serology reactive cases, 12 TP PCR positive/serology non-reactive cases, 7 PCR negative/serology reactive cases and one clinically-diagnosed case (negative TP PCR/non-reactive serology). Serology was reactive in all 9 cases where TP PCR was not performed (8 EIA reactive, 1 VDRL reactive).

Conclusion Primary syphilis is best diagnosed using a combined approach with TP PCR and syphilis serology.

P357 A NEW MEASURE OF SEXUAL WELLBEING FOR COMMUNITY SURVEYS: DEVELOPMENT AND VALIDATION OF THE THE NATSAL-SW

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Background Sexual wellbeing is intrinsic to public health but long-standing conflation of sexual health and sexual wellbeing has limited our ability to address everyday sexual issues. This study proposed a seven-domain model, and developed and validated a brief measure for community surveys.

Method Domains of sexual wellbeing were determined through critical engagement with wide-ranging literature and 40 semi-structured interviews to explore resonance with lived experiences. Measure development involved 7 cognitive interviews and two web-based surveys of general population samples (n=590, n=814), to assess performance of individual items, conduct exploratory and confirmatory factor analysis, and examine whether the resultant measure was associated with external variables as hypothesised. A sub-sample (n=113) completed the survey again after two weeks to test re-test reliability.

Results We proposed seven domains of sexual wellbeing: security and safety; respect; self-esteem; resilience; forgiveness of past sexual experiences; self-determination and comfort. Semi-structured interviews confirmed the relevance of these domains to lived experiences of sex and sexuality. Drawing on the semi-structured and cognitive interviews we drafted a 25-item measure to capture these domains. Based on individual item assessment and exploratory and confirmatory factor analyses, we trimmed the measure to 13-items. The confirmatory factor analysis indicated that a 'general specific model' had best fit (RMSEA: 0.064; CFI: 0.975, TLI: 0.962), and functioned equivalently across age groups, genders, sexual orientation and

relationship status. The final measure was associated with external variables in the directions hypothesised (all $p < 0.001$), including sexual functioning (coefficient = 0.924), mental wellbeing (0.454), self-esteem (0.564), sexual esteem (0.563), body image (0.232), depression (-0.384), anxiety (-0.340), sexual satisfaction (0.680) and sexual distress (-0.615) and demonstrated good test-retest reliability (ICC = 0.78).

Conclusion Our conceptual model and 13-item measure distinguishes sexual wellbeing from sexual health and enables sexual wellbeing to be quantified and understood within and across populations.

P358 ASSESSING SEXUAL HEALTH SERVICES AT A PUBLIC UNIVERSITY IN THE UNITED STATES

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Background The American National College Health Association reports that college students have frequent, condomless sex. Student health and wellness clinics (SHWC) offer sexual health services, but few have dedicated sexual health clinics (SHC). We evaluated screening service use at a university SHWC after implementation of a SHC two half-days per week.

Methods This was a retrospective analysis of data from patients receiving sexual health screening at the University of Alabama at Birmingham (UAB) SHWC from 2015 to 2019. Demographic variables and rates of STIs were extracted from the electronic medical record and were compared by clinic (SHC vs. SHWC). Univariate models were fit, and multi-variable models will be fit, selecting variables with p values of 0.1 or less. Odds ratios with corresponding 95% confidence intervals for univariate analysis are presented.

Results A total of 5025 STI screenings were performed. Males (OR 4.13; 3.61–4.72), undergraduates (OR 1.33; 1.15–1.54), and persons reporting sex with the same sex (OR 1.88; 1.56–2.28), were significantly more likely to seek care at the SHC. Students with symptoms were more likely to seek care at the SHWC (OR 0.53; 0.47–0.61), while persons who reported contact with STIs were more likely to seek care at the SHC (OR 2.88; 2.22–3.74). The overall percentage of positive screenings was 9.3% for chlamydia (CT), 3.0% for gonorrhea (GC), 0.8% for trichomoniasis (TV), 0.7% for syphilis, and 0.3% for HIV with higher percentages of positive for CT (OR 1.60; 1.30–1.96) and GC (OR 2.02; 1.44–2.85) in the SHC.

Conclusion Embedding a dedicated SHC within a university SHWC may expand populations reached for STI screening. With higher percentages of patients testing positive for CT and GC, a SHC may allow for greater diagnosis and treatment of STIs in general screening and persons presenting as contacts.

P359 OPTIMIZED METHODS TO MODEL MYCOPLASMA GENITALIUM REPRODUCTIVE TRACT INFECTION IN PIG-TAILED MACAQUES

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Background *Mycoplasma genitalium* (MG) is a sexually transmitted bacterial pathogen implicated in urogenital disease of both men and women. Of importance, MG is associated with upper reproductive tract sequelae in women such as pelvic inflammatory disease (PID). In earlier studies, we have defined pig-tailed macaques as a suitable animal model for chronic lower reproductive tract infection, though only a subset of the primates remained persistently infected after cervical inoculation. Building on our previous findings, we refined our inoculation methods to increase infection rates, extended the course of infection, and measured the ascension of MG to the upper reproductive tract to model PID.

Methods Three female pig-tailed macaques were infected with an MG inoculum (2×10^9 genomes) prepared to minimize cell aggregates. Lower reproductive tract specimens were collected over 18 weeks. MG infection status was determined by culture in SP4 broth, Vero cell co-cultures, and qPCR. Humoral and cervical antibody responses to MG whole-cell lysates were analyzed through immunoblots.

Results All three primates were persistently infected, one for 8 weeks and two for >14 weeks. Primates that cleared the infection were re-infected to promote ascension to the upper reproductive tract. Humoral and cervical antibodies to the immunodominant MgpB and MgpC adherence proteins were detected after three weeks but were unable to clear MG infection.

Conclusion In prior experiments, MG persisted in only 4/9. In this pilot study, all three primates maintained persistent infection. MG-specific antibodies detected from both serum and cervical specimens will provide an important resource for the optimization of serologic tests that may elucidate immune mechanism of evasion in the genital tract. Future experiments will discern MG pathogenesis, including upper reproductive tract sequelae, as well host-pathogen interactions in a relevant animal model.

P360

SINGLE GENE TARGETED NANOPORE SEQUENCING FOR SIMULTANEOUS IDENTIFICATION AND ANTIMICROBIAL RESISTANCE DETECTION OF SEXUALLY TRANSMITTED INFECTIONS

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Background World Health Organization guidelines to treat sexually transmitted infections (STIs) with the right antibiotic, at the right dose and the right time are undermined by spread of antimicrobial resistance (AMR). Accurate and rapid diagnostics simultaneously predicting antibiotic susceptibility and diagnosis may help address this challenge. We report early data from a novel approach using single gene targeted nanopore sequencing for simultaneous STI identification and AMR detection among female sex workers (FSWs) in Ecuador.

Methods Real-time PCR (RT-PCR) was performed on vulvo-vaginal swab samples from 200 FSWs to identify *Neisseria gonorrhoeae* (NG), *Chlamydia trachomatis* (CT), *Mycoplasma genitalium* (MG) and *Trichomonas vaginalis* (TV) infections. Samples positive and negative (controls) for these STIs were amplified and barcoded by PCR, targeting genes: *gyrA* (NG),

ntf6 (TV) and 23S rRNA (MG), which confer resistance to fluoroquinolones, metronidazole and macrolides respectively, and *omp1* (CT). A DNA library, constructed from a pool of these barcoded samples, was sequenced on Oxford Nanopore Technologies (ONT) MinION sequencer controlled by the smartphone operated 'MinIT' hand-held processor. Data were analysed using ONT AMR workflow, with manual BLAST confirmation.

Results Among PCR positives analysed, 25/26 of CT, NG or MG infections were clearly distinguishable from controls using sequence read counts, but discrimination of TV positives from controls was challenging as many had low pathogen loads (RT-PCR: cycle threshold >35) with associated low sequence read counts. Manual BLAST confirmed 3/3 NG, 2/10 TV, and 0/11 MG had fluoroquinolone, metronidazole and macrolide resistance-associated mutations respectively. Overall library preparation and sequencing time took approximately about five hours.

Conclusions Single gene targeted nanopore sequencing for diagnosing and simultaneously identifying key AMR markers for four common STIs shows promise. Further work to optimise accuracy, reduce costs and improve speed may allow sustainable approaches for managing STIs and emerging AMR in resource poor and laboratory limited settings.

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VAGINAL MICROBIOME PROFILING IN INDIAN WOMEN WITH AND WITHOUT BACTERIAL VAGINOSIS

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Background Bacterial vaginosis (BV), a common condition among reproductive age women is associated with an imbalance of vaginal microbiota composition. It has been implicated in numerous adverse reproductive outcomes and increased risk of sexually transmitted infections. The vaginal ecology varies widely among women from various geographic and ethnic backgrounds. Our study aimed to explore the spectrum of bacterial communities in Indian women with and without BV and the association of individual species with Amsel's clinical diagnostic criteria.

Methods 16S rRNA gene PCR and V3-V4 sequencing were performed on vaginal swabs from 38 women with BV (mean age = 30.84 years, Nugent score ≥ 7) and 16 healthy controls (mean age = 28.25 years, Nugent score ≤ 3). BV was assessed by Amsel's clinical criteria and confirmed by Nugent scoring of Gram stained vaginal smears. Taxonomic classification was performed using SILVA reference database.

Results The vaginal community composition of women with BV was highly heterogeneous and characterized by species diversity and richness. Women with BV harbored high concentrations of *Gardnerella vaginalis* (>99% women), *Atopobium* spp (81.6%), *Prevotella timonensis* (73.7%), *Sneathia amnii* (73.7%) and *Sneathia sanguinegens* (63.2%). On the contrary, in healthy women with no evident symptoms of vaginitis, *Lactobacillus* species dominated the vaginal flora wherein *L. iners* and *L. gasseri* were the two most frequently detected species. Interestingly, *L. iners* was noted in all women, irrespective of their BV status. The presence of *Atopobium* spp., *Sneathia*