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

¹L Zhou, ²A Lopez Rodas, ²L Llangari-Arizo, ^{2,3}N Romero-Sandoval, ^{1,2}P Cooper, ¹S Sadiq*. ¹Applied Diagnostic Research and Evaluation Unit, Institute for Infection and Immunity, St George's, University of London, London, UK; ²School of Medicine, Faculty of Health and Life Sciences, Universidad Internacional del Ecuador, Quito, Ecuador; ³Grups de Recerca d'Amèrica i Àfrica Llatines, GRAAL, Barcelona, Spain

10.1136/sextrans-2021-sti.404

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.

P361

VAGINAL MICROBIOME PROFILING IN INDIAN WOMEN WITH AND WITHOUT BACTERIAL VAGINOSIS

¹A Challa*, ²G Kachhawa, ³S Sood, ¹S Gupta. ¹Department of Dermatology and Venereology, All India Institute of Medical Sciences, India; ²Department of Obstetrics and Gynaecology, All India Institute of Medical Sciences, India; ³Department of Microbiology, All India Institute of Medical Sciences, India

10.1136/sextrans-2021-sti.405

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*

spp., *P. timonensis* and *Eggerthella* spp., were strongly associated with all four clinical signs defined by Amsel's criteria.

Conclusion *Lactobacillus* species including *L. iners* and *L. gasseri* are the predominant vaginal species found in the vaginal tract of Indian women of reproductive age. A heterogeneous vaginal community marked by the presence of *G. vaginalis*, *Sneathia* spp., *Atopobium* spp., *Prevotella* spp., *Eggerthella* spp., is associated with BV and its clinical symptoms.

P364

ACCESS TO HIV-PREVENTION IN FEMALE SEX WORKERS IN UKRAINE BETWEEN 2009 AND 2017: COVERAGE, BARRIERS AND FACILITATORS

N Blumer*, J Burns, L Pfadenhauer. *Ludwig-maximilians-Universität Munich, Munich, Germany*

10.1136/sextrans-2021-sti.406

Background The comprehensive prevention package (PP) is an important intervention in reducing the burden of HIV amongst female sex workers (FSW) worldwide. According to the UNAIDS 90–90–90 goal, 90% of people at risk of HIV infection were to have access to the PP by 2020, however, in 2015 and 2017, only 46% and 48% of Ukrainian FSWs accessed the PP. Hence, we aimed to identify the barriers and facilitators associated with the access to HIV prevention amongst Ukrainian FSWs between 2009 and 2017.

Methods We began by conducting a comprehensive literature review to develop a literature-informed conceptual framework. We then conducted a document analysis to identify the items of the Ukrainian prevention package (PP). Identified by our conceptual framework, we then conducted descriptive analyses using the Integrated Bio Behavioural Surveillance Surveys, to explore PP coverage from 2009 to 2017 and the influence of factors associated with access to the PP.

Results Our conceptual framework illustrates that most thematic clusters which influence access to HIV prevention operate at the macrostructural level. 24 prevention items were included in the PP in 2012 and 2013, however this dropped to 7 items in 2014. Access to the Ukrainian PP increased from 2009 to 2013, where it peaked at 67.42%, however dropped to 32.10% in 2017. Our analyses of the IBBS identified that being a client of a non-governmental organisation, street and highway solicitation, non-condom use, and knowledge of HIV were associated with access to HIV prevention in the Ukrainian context.

Conclusions Our novel study calls for colleagues designing future HIV prevention interventions to strongly consider the barriers and facilitators identified in our conceptual framework and the multiple structural levels on which barriers and facilitators operate. Colleagues can draw upon our findings to bolster the level of access for FSWs in their own countries.

P365

GENDER AND SEX – WHAT SHOULD BE MEASURED AND HOW? LEARNINGS FROM BRITAIN'S NATIONAL SURVEY OF SEXUAL ATTITUDES AND LIFESTYLES

^{1,2}S Clifton, ³K Nambiar, ²M Karikoski, ¹L McDonagh, ¹J Gibbs*, ²C Lapham, ¹P Sonnenberg, ¹C Mercer. ¹University College London, London, UK; ²Natcen Social Research, London, UK; ³Brighton and Sussex University Hospitals NHS Trust, Brighton, UK

10.1136/sextrans-2021-sti.407

Background Many social surveys have purported to measure 'sex', but this has been through interviewers' observation of outward appearance (e.g. clothing, name). In previous rounds of the decennial large-scale probability sample surveys of the British general population (www.natsal.ac.uk), this approach was used to make assumptions about the respondents' anatomy in the rest of the questionnaire. This is not appropriate and results in some misclassification. Although often used interchangeably, sex and gender refer to different concepts, and can differ. Here, we consider what aspects of sex and gender are relevant for a sexual health survey, and how these can be measured in a way that captures diversity, is acceptable, and is comprehensible to the general population. This informed development of questions for Natsal-4.

Methods First, we reviewed international literature for questions about gender/sex in social surveys, censuses and sexual health research, including national (BASHH) recommendations. Second, we conducted stakeholder engagement. Third, we synthesised the findings from both activities into questions deemed appropriate for use with general population samples. Finally, questions were cognitively tested among 30 members of the general population (including three people who identified as trans/had a trans history).

Results Several questions from the literature had undergone general population testing, however, there were no definitive or 'harmonised' questions. No existing set of questions captured the elements of sex and gender most relevant for a sexual health survey. Few studies addressed how to tailor detailed sexual partnership questions to account for trans partners. Our developed questions were found to be well understood and accepted by both trans and non-trans people in cognitive testing.

Discussion We used a multi-stage process to identify a set of questions that seem to balance the needs of a diverse group of participants. These questions are subject to further piloting before being finalised for inclusion in Natsal-4.

P368

ETIOLOGY OF CERVICITIS – ARE THERE NEW AGENTS IN PLAY?

A Bhargava*, N Khunger, S Bansal, P Panchal, N Joshi. *VM Medical College and Safdarjung Hospital, New Delhi, India*

10.1136/sextrans-2021-sti.408

Background Considering the changing causative and resistance pattern of agents implicated in Sexually Transmitted Infections (STIs), etiological diagnosis is imperative especially in countries practicing syndromic management. This study was designed to diagnose cervicitis and to identify etiological agents associated with cervicitis.

Methods Female STI clinic attendees presenting with cervico-vaginal discharge were examined for presence of cervicitis as per standard protocol. Endocervical swabs were collected for gram staining and Real time PCR was performed for various bacterial and viral STI agents in patients presenting with cervical discharge and clinical signs of cervicitis. A vaginal swab was also evaluated for bacterial vaginosis by Nugent's criteria. **Results** Of 64 patients with clinical cervicitis, 26.6% and 12.5% patients complained of genital itching and lower abdominal pain respectively. Mean of 36.6 pus cells/hpf were observed, appreciably greater number in patients with *N.gonorrhoeae* (NG) and *C.trachomatis* infections (p value 0.0063 and 0.0032 respectively). Pus cells were high (mean 68 pus