S01.2 BACTERIAL VAGINOSIS, VAGINAL MICROBIOTA, AND FECUNDABILITYE Lokken*. *University of Washington, Seattle, USA*

10.1136/sextrans-2021-sti.20

Bacterial vaginosis (BV), high diversity vaginal microbiota, and presence of specific BV-associated bacteria have been associated with an increased risk of reproductive outcomes including pelvic inflammatory disease, miscarriage, and preterm birth. The effects of BV and vaginal microbiota on fecundity and fertility in the context of non-medically assisted reproduction is not yet fully characterized. In this session, we will summarize what is known about the relationship between vaginal microbiota disruption and fertility among infertile populations undergoing in-vitro fertilization, discuss results from a recently published study assessing BV and fecundability – the per menstrual cycle probability of pregnancy – among Kenyan women trying to conceive, and identify key considerations for future studies of how the vaginal microbiota may influence conception, implantation, and early pregnancy.

S01.3 NEW INSIGHTS INTO GARDNERELLA AND OTHER BV-ASSOCIATED BACTERIAN Cerca*. *University of Minho, Braga, Portugal*

10.1136/sextrans-2021-sti.21

Bacterial vaginosis (BV), the most common vaginal disorder in women of reproductive age, remains one of the most intriguing and controversial challenges in modern-day clinical microbiology. BV is associated with increased transmission of HIV and other STIs, and is characterized by the loss of normal vaginal flora and overgrowth of anaerobes such as *Gardnerella*. However, it is not clear which is the preceding step for BV development: the loss of resident lactobacilli that eventually allows the overgrowth of already resident *Gardnerella* species, or the colonization of *Gardnerella*, presumably acquired due to sexual transmission, which will lead to the displacement of vaginal lactobacilli. However, *Gardnerella* colonization does not always lead to BV. Importantly, a recent large genome sequencing study demonstrated that what was previously described as *G. vaginalis* are, in fact, distinct species of the genus *Gardnerella*. It has been hypothesized that the distinct *Gardnerella* species have different virulence potential and that this can explain why some *Gardnerella* are present in healthy women without developing BV.

While *Gardnerella* has been proposed as pivotal agents for BV development, other species are also found in the typical multi-species biofilms associated with BV. What is not known, so far, is if these other species are playing an active role in BV development or if are just a consequence of the lactobacilli depletion that occurs in the early stages of BV. In recent years, my research team has been working on elucidating how different bacterial species associated with BV might interact synergistically and enhance the polymicrobial biofilm observed in vivo. Our in vitro data has shown that (i) some species enhance *Gardnerella* mediated biofilms and (ii) different multi-species biofilm morphotypes are formed, with distinct tridimensional structures, which, in some cases, can explain why

antimicrobial therapy often fails, resulting in very high rates of recurrent BV.

S01.4 IMMUNE ACTIVATION BY THE GUT MICROBIOME IN HIV POSITIVE AND NEGATIVE MEN WHO HAVE SEX WITH MEN; POTENTIAL IMPLICATIONS FOR TRANSMISSION AND DISEASE PATHOGENESISC Lozupone*, B Palmer, C Neff, E Yamada, S Li, T Campbell. *University of Colorado, Anschutz Medical Campus, Aurora, USA*

10.1136/sextrans-2021-sti.22

Men who have sex with men (MSM) have differences in immune activation and gut microbiome composition compared with men who have sex with women (MSW). Gut microbiome differences have also been associated with HIV itself. Understanding whether gut microbiome composition impacts immune activation in HIV-negative and HIV-positive MSM has important implications since immune activation has been associated with HIV acquisition risk and disease progression. We have used both in vitro assays and gnotobiotic mouse models to show that MSM and HIV-associated gut microbiota increases immune activation, including T cell activation and expression of the HIV co-receptor CCR5. To investigate whether these findings could have implications for HIV replication, we infected primary human lamina propria cells stimulated with isolated fecal microbiota, and found that microbiota from MSM stimulated higher frequencies of HIV-infected cells than microbiota from MSW. We have also been mechanistically exploring the potential role of key correlated bacteria in both driving and suppressing gut T cell activation. This work has the potential to assist in efforts to reduce new HIV infections within the disproportionately affected population of MSM and to reduce chronic immune activation in this population.

S02.1 ANTIMICROBIAL RESISTANCE AND EXTRAGENITAL STIS – PHARMACOKINETIC CONSIDERATIONSF Kong*. *The University of Melbourne, Melbourne, Australia*

10.1136/sextrans-2021-sti.23

Rates of bacterial sexually transmitted infections (STIs) continue to rise, demanding treatments to be highly effective. However, curing infections faces significant challenges due to antimicrobial resistance for organisms such as *Neisseria gonorrhoeae* and especially at extragenital sites, such as for oropharyngeal gonorrhoeal infections. As few new treatments are entering the market, clinicians must optimize current available antibiotics, but robust data are lacking on how the antibiotic's properties or pharmacokinetics can be used to inform STI treatment regimens to improve treatment outcomes. This presentation discusses how factors related to the drug (e.g. penetration into tissue/fluids/cells, protein binding) and human (e.g. pH, site of infection, immune response) can affect treatment outcomes. The presentation will focus in oropharyngeal gonorrhoeal infections. It discusses the potential methods for measuring antibiotic concentration in novel oropharyngeal samples other than blood including saliva and gingival crevicular fluid and the role tissue pH may have on