

recognize the strengths of individuals as active agents in their health, and not merely passive recipients of health services.

To support WHO normative guideline on innovative self-care strategies for sexual and reproductive health and rights (SRHR), a conceptual framework was developed and the evidence base was evaluated on interventions in transition from provision by facility-based, healthcare providers to delivery in the self-care environment, including STI and HPV self-sampling. While further research is needed on user understanding, uptake and access, our reviews suggest that STI and HPV self-sampling are effective strategies to increase STI and HPV testing uptake respectively.

Challenge remain, however, for vulnerable, marginalized and socioeconomically underprivileged populations, who have the poorest health outcomes globally, to access quality health innovations, including self-care interventions. The WHO guideline on self-care interventions for SRHR is framed around key principles of human rights, gender equality and a holistic, people-centred approach to health and well-being. The potential benefits of such an approach includes the creation of a safe and supportive enabling environment which can potentially increase health coverage, access and quality of services; and thereby reduce health inequities. There is already widespread and rapidly growing use of self-care interventions. When these interventions are people-centred, and evidence-driven, even vulnerable populations will be able to exercise their rights to health, to information, to autonomous decision-making.

**Disclosure** No significant relationships.

## S11 – RESEARCH ON THE VAGINAL MICROBIOME: ADVANCES & CONTROVERSIES

Tuesday, July 16, 2019  
10:45 AM – 12:15 PM

### S11.1 INTRODUCTION TO THE VAGINAL MICROBIOME PRE-CONFERENCE SYMPOSIUM

Jeanne Marrazzo\*. *University of Alabama, Medicine, Birmingham, USA*

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This will comprise an introduction to this session.

**Disclosure** No significant relationships.

### S11.2 LESSONS LEARNED FROM THE PRE-MEETING SYMPOSIUM ON CHARACTERIZING THE VAGINAL MICROBIOTA THROUGH A BLINDED MULTI-LABORATORY COLLABORATION

Jennifer Balkus\*. *University of Washington, Department of Epidemiology, Seattle, USA*

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In studies of the microbiome, variability can arise from numerous steps in the microbial profiling process, including DNA extraction, PCR amplification, and bioinformatics

approaches for taxonomic assignment. This variability may contribute to issues with reproducibility in clinical and epidemiologic studies. Others have described the contribution of different steps in the microbial profiling process to measurement variability in samples comprised of bacteria from the human gut. We conducted a comparative study across four laboratories to better understand sources of variation in describing the human vaginal microbiota. In this session, we will share highlights from the pre-conference symposium that presented lessons learned from this comparative project and discuss implications for future vaginal microbiota research.

**Disclosure** No significant relationships.

### S11.3 THE VAGINAL MICROENVIRONMENT PRIOR TO INCIDENT STI

Rebecca Brotman\*. *University of Maryland School of Medicine, Institute of Genome Sciences, Baltimore, USA*

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We sought to evaluate microenvironmental factors in the vagina that drive protection against STIs. We conducted a nested case control study in the Longitudinal Study of Vaginal Flora to assess the vaginal microenvironment of 397 cases at the visit before an incident genital STI (*Chlamydia trachomatis*, *Neisseria gonorrhoea*, or *Trichomonas vaginalis*) and 1,794 STI-negative controls. Controls were matched to cases on age, race and follow-up time. Vaginal lavages and surveys were collected every three months for one year. Vaginal microbiota, metagenomes, metabolites, and lactic acid isomers were assessed as factors associated with incident STI. Bacterial community state types (CSTs) were assigned by hierarchical clustering of vaginal microbiota. Metagenomes of 708 participants were characterized using VIRGO. We used conditional logistic regression with covariate adjustment (partner concurrency, number of sex partners, condom use). Women with a CST-IV-A profile, low-*Lactobacillus* with high relative abundance of BVAB-1, had the highest odds of incident STI. CST-I (*L. crispatus*-dominated), CST-II (*L. gasseri*-dominated), CST-III-A, and CST-III-C (both *L. iners*-dominated; the latter has other *Lactobacillus* spp.) had >50% lower odds of STI than women in CST IV-A (all  $p < 0.01$ ). CST-II had the lowest point estimate (72% lower odds,  $p = 0.02$ ). Metagenomic analyses confirmed these findings and revealed a cluster of *G. vaginalis* sub-species with 40% lower odds of STI than the BVAB-1 dominated cluster ( $p = 0.02$ ). Higher bacterial absolute abundance had lower odds of STI in each CST ( $p < 0.001$ ). High D-lactic acid concentration was associated with lower STI, irrespective of L-concentration ( $p < 0.05$ ). Of the 185 metabolites that were significantly associated with incident STI ( $q\text{-value} < 0.05$ ), 13 metabolites, including taurine and kynurenine (microbial metabolites with immunomodulating properties), were associated with  $\geq 20\%$  lower odds of STI per fold change. Multi-omic interrogation revealed protection against STI acquisition was associated with vaginal microenvironments containing immunomodulatory metabolites, as well as *Lactobacillus* spp. that produce D-lactic acid.

**Disclosure** No significant relationships.