

P584

FACTORS PREDICTING LIFETIME SEXUAL EXPERIENCE AMONG RURAL, RESERVATION-BASED NATIVE AMERICAN YOUTH

¹Lauren Tingey*, ²Rachel Chambers, ²Anne Rompalo, ²Anna Beach, ²Laura Melgar, ²Summer Rosenstock, ³Angelita Lee. ¹Johns Hopkins University, Johns Hopkins Center for American Indian Health, Baltimore, USA; ²Johns Hopkins Center for American Indian Health, Baltimore, USA; ³Johns Hopkins Center for American Indian Health, Whiteriver, AZ, USA

10.1136/sextrans-2019-sti.655

Background Early sexual initiation is a risk factor for sexually transmitted infection and unintended pregnancy. Native American youth initiate sex earlier than other U.S. youth contributing to current inequalities in sexual health. Identifying factors that predict lifetime sexual experience among Native youth can inform the development of primary prevention programming to delay sexual initiation and improve sexual health outcomes in this population.

Methods We analyzed cross-sectional data from 558 Native youth ages 11–19 from a rural, reservation-based community. Multivariate logistic regression models were used to estimate associations between lifetime sexual experience (vaginal and/or anal sex) and independent variables across eight categories: sociodemographic, knowledge, attitudes/perceptions, beliefs, intentions, skills, behaviors, and theoretical constructs.

Results The sample was 51.6% female, mean age 13.4 years ($SD=1.9$); and 8.0% were sexually experienced. In our final model, older age ($OR=2.04$; $p<0.0001$) and identifying as transgender ($OR=35.3$; $p=0.019$) predicted lifetime sexual experience. The notion that sometimes sex just happens ($OR=0.56$; $p=0.01$), and having condom use self-efficacy ($OR=0.47$, $p=0.026$) were negatively associated with lifetime sexual experience. Youth who intended to have sex in the next 6 months were more likely to be sexually experienced ($OR=3.18$; $p<0.0001$). Recent substance use including having smoked cigarettes ($OR=4.38$, $p=0.048$), and having smoked marijuana in the past 3 months ($OR=6.48$, $p=0.002$) predicted lifetime sexual experience.

Conclusion Results provide direction for future programming. Programs focusing on intentions to have sex while cultivating skills to promote condom use, in addition to being delivered stratified by age, may have the greatest impact. Substance use was a driving factor in sexual initiation; thus, sexual health education programs should simultaneously target substance use prevention. That identifying as transgendered predicted sexual experience is notable: despite research indicating transgendered youth of other ethnicities have heightened risk for negative sexual health outcomes, little research has been conducted with transgendered Native youth.

Disclosure No significant relationships.

P585

INUIT COMMUNITY READINESS: ADAPTING THE COMMUNITY READINESS MODEL WITH INUIT COMMUNITIES FOR HIV PREVENTION

¹Audrey Steenbeek*, ²Tracey O'Hearn, ³Jenny Rand, ³Janet Curran, ⁴Marni Amirault, ⁵Diane Sammutok, ⁴Reenee Masching, ⁵Igah Sanguya, ²Ashlee Pigford, ⁶Barbara Plested. ¹Dalhousie University, Nursing, Halifax, Canada; ²Pauktuutit, Ottawa, Canada; ³Dalhousie University, Nursing, Halifax, Canada; ⁴Canadian Aboriginal AIDS Network, Halifax, Canada; ⁵Nunavut Health and Social Services, Arviat, Canada; ⁶Colorado State University, Fort Collins, USA

10.1136/sextrans-2019-sti.656

Background With the highest rates of STIs in Canada, high mobility between North and South and a lack of adequate screening for STBIs, it is possible that Inuit communities could face an HIV epidemic. If no action is taken to scale up prevention efforts, an epidemic in Inuit communities in the North could soon be a reality. Therefore, gauging an Inuit community's level of readiness to develop and participate in community-based HIV prevention, education, screening, and ensuring approaches are culturally relevant is imperative.

Methods This current research project builds directly on priorities outlined by Inuit stakeholders, and is facilitated through strong partnerships between the three communities (Kugluktuk, Arviat, and Clyde River Nunavut), Pauktuutit Inuit Women of Canada, the Canadian Aboriginal AIDS Network, and Dalhousie University. The goal of this research project is to engage Inuit communities and organizations in adapting, piloting and using the Community Readiness Model (CRM) to improve readiness to engage in HIV-modalities at the community level. This presentation will outline the community engagement and integrated knowledge translation processes, progress to date, and next steps for this community-based research project.

Results This project has adopted *Inuit Qaujimajatuqangit (IQ)* as a framework, which supports personal wellness through a collective cultural sense of health. Consultations with the project advisory committee (Canadian Inuit HIV/AIDS Network (CIHAN)), Community Health Representatives from three respective Nunavut communities and the research team were held November 2015. We are working collaboratively to: (1) adapt the CRM; (2) ensure it is Inuit-specific; (3) pilot the adapted tool; and (4) determine the applicability of this tool. Representatives from Nunatsiavut, Nunavik and Inuvialuit will also be mentored on how to use the adapted CRM.

Conclusion By engaging knowledge users and communities, this project will address HIV prevention in Inuit communities by identifying factors that impact readiness for HIV interventions.

Disclosure No significant relationships.

P586

IKAJURNIQ: AN INUIT CASCADE OF CARE FRAMEWORK FOR SEXUALLY TRANSMITTED AND BLOOD BORNE INFECTIONS

Savanah Ashton, Sipporah Enuaraq. Pauktuutit Inuit Women of Canada, Ottawa, Canada

10.1136/sextrans-2019-sti.657

Background Introduction: Inuit in Canada are experiencing high rates of sexually transmitted and blood-borne infections (STBIs). While there is limited Inuit-specific statistical information, we know that chlamydia, gonorrhea and syphilis rates in Inuit regions are high. A central approach to reducing STBIs among Inuit communities is the development of effective methods to increase the number of Inuit being tested, diagnosed and treated before they spread infection to others.

Methods At its inaugural meeting in November 2017, the National Inuit Sexual Health Network, made up of sexual health experts and community representatives, developed an Inuit-specific STBI Cascade of Care framework called Ikajurniq – meaning “the act of helping”.

Results Ikajurniq builds on best practices in prevention and treatment of STBBIs in Canada, while recognizing both the particular challenges and the known enablers in reaching, testing and treating Inuit with STBBIs in northern communities.

Conclusions

Inuit experience high rates of STBBIs and face particular challenges in completing the testing and treatment journey. The enablers described in Ikajurniq can greatly increase the number of Inuit who successfully navigate the STBBI cascade of care.

Disclosure No significant relationships.

P587

ASSOCIATION BETWEEN VAGINAL BACTERIA AND HIV ACQUISITION RISK AMONG AFRICAN WOMEN PARTICIPATING IN THE VOICE STUDY

¹Sujatha Srinivasan*, ²Barbra Richardson, ¹Jacqueline Wallis, ¹Tina Fiedler, ³Noah Hoffman, ⁴Sean Proll, ⁵Z Chirenje, ⁶Edward Livant, ¹David Fredricks, ⁷Sharon Hillier, ⁸Jeanne Marrazzo. ¹Fred Hutchinson Cancer Research Center, Vaccine and Infectious Disease Division, Seattle, USA; ²University of Washington, Biostatistics, Seattle, USA; ³University of Washington, Laboratory Medicine, Seattle, USA; ⁴University of Washington, Medicine, Seattle, USA; ⁵University of Zimbabwe, College of Health Sciences Clinical Trials Research Center, Harare, Zimbabwe; ⁶Magee-Womens Research Institute, Pittsburgh, USA; ⁷University of Pittsburgh and Magee-Womens Research Institute, Obstetrics, Gynecology and Reproductive Sciences, Pittsburgh, USA; ⁸University of Alabama, Medicine, Birmingham, USA

10.1136/sextrans-2019-sti.658

Background We previously identified seven vaginal bacteria associated with increased HIV acquisition risk among African women using taxon-directed quantitative PCR (qPCR). We sought to extend the search for high-risk bacteria using a sequential PCR approach.

Methods African women participating in a randomized placebo-controlled trial of daily oral vs. vaginal tenofovir-based pre-exposure prophylaxis for HIV (VOICE study) provided vaginal samples. Cases (177 HIV pre-seroconversion visits from 150 women who acquired HIV) and controls (531 visits from 436 women who remained HIV uninfected) were matched by study arm and site. The vaginal microbiota was characterized using 16S rRNA gene PCR and sequencing to assess associations between relative abundances of bacteria and HIV risk; bacterial taxa were ranked in descending order by score statistic using logistic models run on each taxon until a p-value=0.1. Taxa prevalent at ≥5% were selected for measurement of concentrations by qPCR. Relationship between bacterial concentrations and HIV risk was analyzed using Generalized Estimating Equation models, and adjusted for potential confounders.

Results Vaginal bacterial diversity among cases was higher than controls (p=0.0044). Analysis of relative abundance data identified 12 bacterial taxa associated with HIV risk that were not previously described. Six of these 12 taxa were selected for taxon-specific qPCR measurements. Concentrations of five of six taxa were significantly associated with increased risk for HIV acquisition. These include bacterial vaginosis-associated bacterium 2 (adjusted odds ratio (aOR)=1.57; 95% CI 0.97, 2.56), Candidate Division TM7 (aOR=2.04; 95% CI 1.14, 3.65), *Prevotella amnii* (aOR=1.53, 95% CI 0.95, 2.46),

Porphyromonas Type 1 (aOR=2.04, 95% CI 1.27, 3.28), and *Peptinophilus lacrimalis* (aOR=1.55, 95% CI 0.98, 2.44). *Dialister microaerophilus* was not associated with HIV risk.

Conclusion A sequential PCR approach facilitated the identification of new bacteria associated with increased HIV acquisition risk. Interventions to decrease high-risk bacteria could be explored as one approach to reduce HIV risk in women.

Disclosure No significant relationships.

P588

A MULTI-SITE COMPARATIVE STUDY TO UNDERSTAND SOURCES OF VARIABILITY IN STUDIES OF THE VAGINAL MICROBIOTA

¹Jennifer Balkus*, ¹Sean Proll, ²Johanna Holm, ³Sujatha Srinivasan, ⁴Darrell Dinwiddie, ⁵Liam Van Der Pol, ¹Noah Hoffman, ⁵Elliot Lefkowitz, ¹James Hughes, ⁵Barbara Van Der Pol, ⁴Cosette Wheeler, ¹Anna Wald, ⁵Jeanne Marrazzo, ²Jacques Ravel, ³David Fredricks. ¹University of Washington, Seattle, USA; ²University of Maryland, Institute for Genome Sciences, Baltimore, USA; ³Fred Hutchinson Cancer Research Center, Vaccine and Infectious Disease Division, Seattle, USA; ⁴University of New Mexico – Albuquerque, Albuquerque, USA; ⁵University of Alabama at Birmingham, Medicine/Infectious Diseases, Birmingham, USA

10.1136/sextrans-2019-sti.659

Background The most common approach for describing bacterial communities is amplification of a taxonomically informative gene (e.g. 16S rRNA) followed by amplicon sequencing and taxonomic assignment of the sequences. Variability can arise from numerous steps in this process including DNA extraction, PCR amplification, and bioinformatics approaches for taxonomic assignment. To better understand sources of variation in describing the vaginal microbiota, we conducted a comparative study across four laboratories.

Methods A central laboratory prepared and distributed a specimen set including vaginal swabs from four women with a range of Nugent scores (*in vivo* samples), three mock communities of vaginal bacteria, and positive and negative controls. For *in vivo* and mock communities, each laboratory was also provided specimens that underwent DNA extraction by the central laboratory. Laboratories followed their standard laboratory and bioinformatics processes. Results were analyzed by a central group blinded to laboratory.

Results For mock and *in vivo* communities dominated by a mix of *Lactobacillus* species, all laboratories successfully detected each of the taxa in the sample and reported similar relative abundances. For mock communities containing BV-associated taxa, most laboratories detected all taxa; however, some taxa, including *Prevotella amnii* and *Atopobium vaginae*, were not detected by all laboratories and there was more variation in relative abundances across the laboratories (*P. amnii* relative abundance range=<1%–17%; mock community proportion of colony forming units=11%). Variations were observed between the relative abundances within laboratories compared to samples that underwent DNA extraction by the central laboratory, highlighting impact of DNA extraction method.

Conclusion Despite differences in methods, in most cases laboratories would have come to the same conclusion regarding dominant taxa in a sample, especially for *Lactobacillus*-dominant samples. Samples with more diverse communities had