related to resistance and epidemiological characteristics was performed. We analysed 143 isolates (69 resistant and 74 susceptible); 81% was from men who have sex with men (MSM). Azithromycin resistant isolates had significantly more often C2611T mutations of 23S rRNA (n=62, 89.9%, p<0.001), an NG-MAST genogroup G2992 (p<0.001), G5108 (p<0.001), or G359 (p=0.02), and were more often part of NG-MLVA clusters (p<0.001). Two resistant isolates (2.9%) had A2059G mutations, and five (7.3%) were wild-type 23SrRNA. Four of the five NG-MLVA clusters contained resistant and susceptible isolates, and isolates from HIV-positive and HIV-negative patients. Two of the clusters consisted mainly of resistant isolates and were strains from MSM, heterosexual men and women. Co-occurrence of resistant and susceptible strains in NG-MLVA clusters and frequent occurrence of resistant strains outside of clusters suggests that azithromycin resistance develops independently from the 'background genome'.

013.3

VACCINE DEVELOPMENT TO COMBAT ANTIMICROBIAL RESISTANT GONORRHOEA

kate L Seib, Evgeny A Semchenko. Institute for Glycomics, Griffith University

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Introduction Neisseria gonorrhoeae, the causative agent gonorrhoea, is a major public health problem worldwide with an estimated global incidence of 106 million cases/yr. If left undiagnosed or untreated, infection can lead to severe sequelae that include pelvic inflammatory disease, infertility, neonatal complications, and an increased risk of HIV. It recognised by WHO and CDC as an urgent threat to global health due to the emergence of multi-drug resistant gonococcal strains. There is currently no vaccine, and no new antibiotics or new vaccine candidates in late-stage development.

Methods To facilitate gonococcal vaccine development, we performed mathematical modelling to predict the impact of different vaccine scenarios. We have also identified and characterised a series of potential vaccine candidates.

Results Mathematical modelling of different vaccine scenarios indicates that even a modestly efficacious vaccine could have a substantial impact on gonorrhoea prevalence and sequelae. We have also characterised 2 highly conserved and immunogenic candidate vaccine antigens. In vitro assays, using wild type, knock-out and complemented strains, have shown that NGO1958 (gonococcal homologue of the Neisseria heparin binding antigen (NHBA) present in the serogroup B meningococcal vaccine) is involved in serum resistance and adherence to cervical epithelial cells. Similar assays show that NGO2139 (methionine uptake receptor) is involved in resistance to killing by human serum, monocytes and macrophages, as well as adherence and invasion of cervical epithelial cells. Antibodies to these proteins are bactericidal and can block gonococcal infection of cervical epithelial cells. Additional studies are underway to determine if antibodies to these proteins can protect again infection in a mouse model.

Conclusion We present two antigens that elicit both bactericidal and functional blocking antibodies, which are valid candidate antigens for possible inclusion in an urgently needed vaccine for the prevention of gonorrhoea.

013.4

MULTIPLE CYTOKINE GENE EXPRESSION DETECTED AFTER HPV VACCINATION

¹Ana Paula Ferreira Costa, ²Paulo César Giraldo, ¹Paula Renata Lima Machado, ¹Kleber Juvenal Silva Farias, ¹Janaina Oliveira Crispim, ³José Eleutério Júnior, ⁴Steven S Witkin, ¹Ana Katherine Gonçalves. ¹Federal University of Rio Grande do Norte, Brazil; ²University of Campinas, Brazil; ³Federal University of Ceará, Brazil; ⁴Cornell University, USA

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Introduction Human papillomavirus (HPV) infection does minimal damage and does not induce the production of immune mediators by host epithelial cells. The induction of a proinflammatory immune response is necessary to break the tolerance induced by HPV. Therapeutic interventions with vaccines to induce an effective immune response have the potential to treat latent infection as well as clinically apparent lesions. The aim of this study was to evaluate the influence of the human papillomavirus (HPV) vaccination on peripheral blood mononuclear cell (PBMC) proliferation and cytokine gene transcription.

Methods PBMCs isolated after immunisation were incubated with HPV vaccine, phytohemagglutinin (PHA) or buffer. Cell proliferation was assessed by MTT reduction assay. RNA was extracted from PBMCs, and the relative concentration of cytokine messenger RNA (mRNA) transcripts (IFN-b, IFN-c, IL-12, TNF-a, IL-6, IL-17, or IL-10) relative to transcription of the b-actin gene was determined by real-time polymerase chain reaction.

Results PBMC proliferation in response to HPV vaccine and PHA were greater than that observed in unstimulated cells (p<0.001). Cytokine mRNAs were upregulated in stimulated PBMC cultures. The median increase in vaccine-stimulated cultures was: IFN-b=334.4 fold; IL-12=46.33 fold; IFN-c=12.64 fold; IL-6=9.07 fold; IL-17=7.33 fold; IL-10=6.47 fold; and TNF-a=2.36 fold.

Conclusion The IFN-b expression was significantly higher (p<0.05). Proliferative PBMC responses and multiple cytokine gene expression were detected in women who received the HPV vaccine.

013.5

CORE GROUPS OF INDIVIDUALS WITH CHLAMYDIA AND/OR GONORRHOEA REINFECTIONS HAVE INCREASED ODDS OF DIAGNOSIS WITH INFECTIOUS SYPHILIS: A POPULATION-BASED RETROSPECTIVE COHORT STUDY IN BRITISH COLUMBIA, CANADA, 2006–2015

Heming Jiang, Christine Lukac, Gina Ogilvie, Mark Gilbert, Troy Grennan, Jason Wong. British Columbia Centre for Disease Control, Canada

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Introduction The incidence of infectious syphilis (primary, secondary, or early latent) has increased in British Columbia (BC). Identifying core groups at risk for syphilis can inform public health programming. We assessed the odds of syphilis infection among individuals with repeat *Chlamydia trachomatis* (CT) and/or *Neisseria gonorrhoeae* (GC) infections in this population-based analysis.

Methods Surveillance records for all BC residents diagnosed with ≥ 2 CT (CT reinfection) or ≥ 2 GC (GC reinfection) or ≥ 2 infections including CT and GC (CT/GC reinfection) from 1/1/2006 to 12/31/2015 were linked with all infectious syphilis cases from the same time period. Logistic regression models

were used to measure the odds of acquiring syphilis with greater number of CT and/or GC reinfections, adjusted for age, ethnicity and population (e.g., men who have sex with men).

Results Of 1 03 115 people having a CT infection, 11 458 (11.1%) had CT reinfection; of 14 713 people with a GC infection, 1514 (10.3%) had GC reinfection. Overall, 4989 individuals had CT/GC reinfection. Among these three reinfection groups (CT, GC, CT/GC), 80.9%/72.9%/63% had 2 infections, 14.4%/15.9%/19.5% had 3 infections, 3.2%/6.1%/ 8.9% had 4 infections and 1.6%/5.1%/8.6% had 5+ infections. Of all syphilis cases in BC, 7.4%/9.4%/12.3% were diagnosed among individuals with CT reinfection, GC reinfection and CT/GC reinfection. The odds of syphilis increased with greater number of infections, which persisted after adjustment in all three groups. Among the group with CT/GC reinfection, individuals with 3, 4 and 5+ infections had increased odds of syphilis compared to individuals with 2 infections (OR=2.2 (95%CI 1.6, 3.0), OR=2.5 (95%CI 1.7, 3.6) and OR=4.1 (95%CI 3.0, 5.7) respectively).

Conclusion Increasing number of CT and/or GC reinfections is strongly and independently associated with a syphilis diagnosis. Targeting public health interventions to a core group of individuals with CT/GC reinfections may be an effective syphilis prevention strategy.

013.6

UNDERSTANDING HEALTH FACILITY BARRIERS TO THE IMPLEMENTATION OF OPTION B+ GUIDELINES IN AN URBAN HOSPITAL IN GHANA: A QUALITATIVE ANALYSIS OF VIEWS AND PERSPECTIVES OF HEALTH PROVIDERS

¹AS Laar, ²PA Dalinjong. ¹Ghana Health Service/PATH-GHANA, PMB CT 307, Cantonments, Accra, Ghana; ²Navrongo Health Research Centre, Navrongo, Upper East Region, Ghana

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Introduction Full implementation of Option B+ guidelines in line with the World Health Organisation's recommendation could avert as many as 3 million AIDS-related deaths and 3.5 million new HIV infections by 2025. This study explored health providers' perspectives on health systems barriers affecting the implementation of Option B+ at the health facility level in Ghana.

Method A total of 17 in-depth interviews and two focus groups were conducted with health providers providing (prevention of mother to child transmission (PMTCT) services at Greater Accra regional hospital between April and May 2016. The Health providers were interviewed to obtain their perspectives on barriers for delivering Option B+ services. Interviews were tape-recorded and analysed using a thematic framework approach.

Results The findings highlight health system barriers that hinder optimal implementation of Option B+ guidelines. These comprise: inadequate work space for the provision of PMTCT services; limited laboratory capacity (lack of certain equipment for results confirmation); inadequate staff; lack of transport (for follow ups on defaulters) and training to upgrade staff knowledge. The supply of antiretroviral drugs was however not seen to be a challenge in this study.

Conclusion There are still some health system gaps that need to be addressed and strengthened to improve initiation, adherence and retention of clients in Option B+ care. Tackling these specific challenges will contribute towards the elimination of mother to child transmission (MTCT) of HIV, and improve maternal and child health outcomes in Ghana and the world at large.

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014.1

RISK OF HIV FOLLOWING REPEAT SEXUALLY
TRANSMISSIBLE INFECTIONS AMONG MEN WHO HAVE
SEX WITH MEN IN VICTORIA, AUSTRALIA

¹BrendanHarney, ¹Agius P, ²Roth N, ³Tee BK, ⁴Fairley CK, ⁴Chow Epf, ⁵D Leslie, ¹Stoové M, ¹El-Hayek C. ¹Burnet Institute, Melbourne, Australia; ²Prahran Market Clinic, Melbourne, Australia; ³The Centre Clinic, Melbourne, Australia; ⁴Melbourne Sexual Health Centre, Melbourne, Australia; ⁵Victorian Infectious Disease Reference Laboratory, Melbourne, Australia

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Introduction HIV notifications have increased significantly in Victoria since 2000. The majority of these are among men who have sex with men (MSM). Chlamydia, gonorrhoea and syphilis notifications have also increased among MSM in Victoria and reinfection occurs in approximately 15%–30% of MSM retested after a positive diagnosis of syphilis, chlamydia or gonorrhoea. Sexually transmissible infections (STI) have been associated with an increased risk of HIV acquisition. We aimed to test whether repeat infection increased the risk of HIV infection among MSM.

Methods A retrospective analysis of sentinel surveillance data was conducted. HIV negative MSM who attended three high case load clinics in Victoria from 2007 to 2014 with two or more HIV tests were eligible for inclusion. STI diagnosis and behavioural exposures were lagged to a patient's prior test event and an individual level discrete-time survival analysis using generalised linear modelling estimated the cumulative effect of repeat STI diagnoses on HIV diagnosis risk.

Results 8941 individuals were included in the analysis among whom 2.5% (n=227) were diagnosed as HIV positive. After adjustment for number of sexual partners and condom use in the previous six months, repeat rectal gonorrhoea infection (adjusted hazard ratio [aHR]: 6.24, 95% confidence interval [95% CI]: 2.68–14.50), single-event rectal gonorrhoea (aHR: 2.09, 95% CI: 1.15–3.79), rectal chlamydia (aHR: 1.89, 95% CI: 1.12–3.18) and syphilis (aHR: 1.99, 95% CI: 1.00–3.96) infections were associated with an increased risk of HIV diagnosis. Repeat rectal chlamydia infection (aHR: 1.62, 95% CI: 0.73–3.59) and repeat syphilis infection (aHR: 0.93, 95% CI: 0.11–7.65) were not associated with an accumulated increased risk of HIV diagnosis.

Conclusion In addition to increased risk due to a single STI, repeat rectal gonorrhoea infection was strongly associated with an accumulated increased risk of HIV diagnosis. These findings suggest MSM with repeat rectal gonorrhoea infection represent a higher risk group for whom preventive interventions are encouraged.