

P643 ADVERSE PREGNANCY AND NEONATAL OUTCOMES ASSOCIATED WITH *NEISSERIA GONORRHOEA*: A SYSTEMATIC REVIEW AND META-ANALYSIS

¹Dianne Egli-Gany*, ²Lisa Valley, ²Handan Wand, ²Andrew Valley, ¹Nicola Low. ¹University of Bern, Institute of Social and Preventive Medicine (ISPM), Bern, Switzerland; ²University of New South Wales, Kirby Institute, Sydney, Australia

10.1136/sextrans-2019-sti.711

Background *Neisseria gonorrhoeae* (NG) infections during pregnancy have been reported to be associated with a range of adverse pregnancy outcomes, but systematic information is lacking. The objective of this study was to systematically review data about associations between NG and: preterm birth (PTB); low birth weight (LBW); premature rupture of membranes; spontaneous abortion; perinatal mortality; and ophthalmia neonatorum.

Methods We searched Medline, Excerpta Medica, Cochrane Library and the Cumulative Index to Nursing and Allied Health Literature databases up to October 2017. Two researchers selected studies, extracted data and assessed risk of bias independently. We used meta-analysis to calculate summary odds ratios (OR with 95% confidence intervals, CI) separately for unadjusted and adjusted results, stratified by study design. We assessed heterogeneity using the I^2 statistic.

Results We screened 2,290 articles and included 15 studies, published from 1976–2017, of which seven were from low or lower-middle income countries. For PTB, the summary unadjusted OR was 1.47 (95% CI 1.17–1.78, $I^2=0\%$) in four case-control studies, 1.93 (1.24–2.63, $I^2=86\%$) in two cross-sectional studies and 0.78 (0.49–1.06, $I^2=0\%$) in three cohort studies. Adjusted ORs were only available in three case-control studies, summary OR 1.14 (0.85–1.44, $I^2=16\%$). For LBW, the summary unadjusted OR was 1.57 (1.15–1.99, $I^2=53\%$) in three case-control studies, 1.20 (0.30–4.30) in one cross-sectional study and 0.99 (0.73–1.25, $I^2=47\%$) in two cohort studies. The adjusted summary OR was 1.33 (0.96–1.71, $I^2=0\%$) in the case-control studies. For other outcomes, unadjusted summary ORs varied, generally being lower for cohort than cross-sectional or case-control studies.

Conclusion In this systematic review of observational studies, the strength of associations between NG and adverse pregnancy outcomes were weaker than expected and, where data were available, attenuated after adjusting for confounding. Ongoing randomised controlled trials will now determine whether screening and treatment of NG in pregnancy reduces adverse outcomes.

Disclosure No significant relationships.

P644 ANALYZING THE GENOMES OF *NEISSERIA GONORRHOEA* ISOLATES USING A NOVEL INTEGRATED BIOINFORMATIC PIPELINE: GEN2EPI

¹Nidhi Parmar*, ¹Reema Singh, ²Irene Martin, ¹Sumudu Perera, ²Walter Demczuk, ³Anthony Kusalik, ⁴Jessica Minion, ¹Jo-Anne Dillon. ¹University of Saskatchewan, Biochemistry, Microbiology and Immunology, Saskatoon, Canada; ²National Microbiology Laboratory, Winnipeg, Canada; ³University of Saskatchewan, Computer Science, Saskatoon, Canada; ⁴Saskatchewan Health Authority, Regina Qu'appelle Health Region, Regina, Canada

10.1136/sextrans-2019-sti.712

Background Whole genome sequencing (WGS) is a high-resolution approach for tracking the transmission and antimicrobial

susceptibility (AMS) of *Neisseria gonorrhoeae* (Ng). Multiple bioinformatics tools currently used for the analysis of WGS data for Ng complicate their application in clinical settings. We determined the genomic epidemiology and AMS of Ng from Saskatchewan (SK) using our integrated pipeline, Gen2-Epi, previously validated on 1484 publicly available Ng genome datasets.

Methods WGS was performed on 99 Ng isolates (2017–2018) from SK submitted to the Roy Romanow Provincial Laboratory. Genomic DNA was isolated using the DNAeasy mini kit (QIAGEN) and sequenced using MiSeq (Illumina). MICs were determined by agar dilution. Gen2Epi includes read assembly, scaffolding, strain typing (ST) by MLST and NG-MAST, plasmid identification, and, identification of mutations in antibiotic resistance genes by NG-STAR.

Results Nine MLST/NG-MAST/NG-STAR (M/M/S) STs comprised 75.6% (75/99) of the isolates; other M/M/S STs (24.3%, 24/99) comprised single isolates. M/M/S ST 1901/10451/90 predominated (21.3%, 21/99), carrying mosaic *penA* type 34.001 and mutations in *mtrR/porB/ponA/gyrA/parC*. These isolates were chromosomally resistant to penicillin (38%, 8/21), tetracycline (95.2%, 20/21), and ciprofloxacin (90%, 19/21); they were susceptible to ceftriaxone and 38% (8/21) had cefixime MICs of 0.125 mg/L. The second-most prevalent ST was 1584/7638/160 (18/99); most of these isolates (16/18) were susceptible to all antibiotics. Overall, 57.6% (57/99) of the isolates were tetracycline resistant; 29.8% (17/57) of these were from Regina and carried a *tetM* gene (M/M/S ST 12462/5985/42). One sporadic isolate was azithromycin resistant (23S rRNA-A2059G), carried *tetM* and was M/M/S ST 7822/304/515.

Conclusion Gen2Epi is a one-stop pipeline that both assembles and annotates raw reads and simplifies the analysis of transmission markers and AMS in Ng. We showed the emergence of M/M/S ST 1901/10451/90 as the predominant ST in SK. NG-MAST ST 10451 is similar (≤ 2 bp) to ST 1407 which is implicated in reduced susceptibility to cefixime.

Disclosure No significant relationships.

P645 PERUVIAN GONOCOCCAL STRAINS REVEAL NOVEL NG-MAST TYPES AND FALSE-POSITIVE β -LACTAMASE ISOLATES WITH *BLA*_{TEM} GENE MUTATIONS

¹Adriana Le Van*, ¹Nazia Rahman, ¹Nelson Dozier, ²Patrick Mc Gann, ³James Regeimbal, ³Andrea Mccoy, ⁴Olusegun Soge, ⁵Eric Garges, ¹Ann Jerse. ¹Uniformed Services University of the Health Sciences, Microbiology and Immunology, Bethesda, USA; ²Walter Reed Army Institute of Research, Multidrug Resistant Organism Repository and Surveillance Network (MRSN), Silver Spring, USA; ³U.S. Naval Medical Research Unit Number 6, Lima, Peru; ⁴University of Washington, Global Health, Seattle, USA; ⁵USUHS, Bethesda, USA

10.1136/sextrans-2019-sti.713

Background The Global Emerging Infectious Surveillance Program of the U.S. Department of Defense, Armed Forces Health Surveillance Branch supports a repository for *Neisseria gonorrhoeae* (GC) clinical isolates recovered from routine care at U.S. Military Treatment Facilities in the continental US (CONUS) and at several overseas (OCONUS) labs through collaborative surveillance projects. Here we report the use of phenotypic data in conjunction with molecular typing and whole genome sequencing (WGS) of GC to describe the antimicrobial resistance trends from isolates collected from three geographically different clinics in Lima, Callao and Iquitos, Peru.