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### GONOCOCCAL ANTIMICROBIAL SUSCEPTIBILITY FROM THE THAILAND ENHANCED GONOCOCCAL ANTIMICROBIAL SURVEILLANCE PROGRAM, 2015–2018

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**Background** Antimicrobial resistant *Neisseria gonorrhoeae* (NG) surveillance is critically important to determine patterns of resistance and to ensure national treatment guidelines for gonorrhoea remain effective. The Thailand Ministry of Public Health, the U.S. Centers for Disease Control and Prevention, and the World Health Organization began the first Enhanced Gonococcal Antimicrobial Surveillance Programme (EGASP) in 2015 to monitor gonococcal antimicrobial susceptibility in Thailand.

**Methods** We describe gonococcal antimicrobial susceptibility results from November 2015 to October 2018. Symptomatic men with urethral discharge or dysuria who attended one of two sentinel sites in Thailand, Bangrak Hospital and Silom Community Clinic @TropMed, provided specimens for culture and completed a questionnaire. Antimicrobial susceptibility testing (AST) was performed on all NG isolates to determine Minimum Inhibitory Concentrations (MIC) for Ceftriaxone (CRO), Cefixime (CFM), Azithromycin (AZI), Gentamicin (GEN), and Ciprofloxacin (CIP) using E-test®.

**Results** A total of 2,390 specimens were collected during 2015–2018; 1,373 (57.4%) had AST results. Only one isolate had an elevated MIC ( $\geq 2$  µg/mL) to AZI, 1,262 isolates (91.9%) were resistant (MIC  $\geq 1.0$  µg/mL) to CIP, and no isolate had elevated MICs to CRO ( $\geq 0.125$  µg/mL), CFM ( $\geq 0.25$  µg/mL), or GEN ( $\geq 16$  µg/mL). The overall and each year MIC<sub>50</sub> and MIC<sub>90</sub> were stable for CRO (MIC<sub>50</sub>/MIC<sub>90</sub> = 0.004/0.008 µg/mL), CFM (MIC<sub>50</sub>/MIC<sub>90</sub> = 0.016/0.016 µg/mL) and GEN (MIC<sub>50</sub>/MIC<sub>90</sub> = 4/8 µg/mL). The overall MIC<sub>50</sub>/MIC<sub>90</sub> for AZI was 0.125/0.25 µg/mL. The MIC<sub>50</sub> for AZI remained relatively stable only changing from 0.032 µg/mL in 2015 to 0.125 µg/mL during 2016–2018; the MIC<sub>90</sub> for AZI fluctuated between 0.125 (2015) and 0.5 (2017) µg/mL.

**Conclusion** Although CIP resistance was common, most isolates collected through EGASP appeared susceptible to CRO and CFM supporting the continued use of these antimicrobials to treat gonorrhoea in Thailand. Continued surveillance for antimicrobial resistance is important for monitoring the emerging threat of NG resistance.

**Disclosure** No significant relationships.

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### WHOLE GENOME SEQUENCING OF *N. GONORRHOEA* DECONVOLUTES SEXUAL BEHAVIOUR, POPULATION STRUCTURE AND TRANSMISSION IN SINGAPORE

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**Background** Gonorrhoea is the third most commonly notified sexually transmitted infection (STI) in Singapore. In 2012, there were 1781 notifications, with an incidence rate of 33.53 per 100,000 population with more males than females being diagnosed. While most of the cases occur in people aged between 20 and 39 years of age, gonorrhoea is the most common STI among teenagers and among men who have sex with men (MSM) in Singapore. The aim of this study was to use whole genome sequencing to gain insights into the patterns of transmission that exist within and between different subpopulations in Singapore and internationally.

**Methods** We sequenced 676 samples from 544 patients infected with gonorrhoea between 2014–2016. Sequencing reads from *N. gonorrhoeae* genomes were mapped to a common reference and recombination masked, followed by phylogenomic, Bayesian clustering and pairwise network analyses. We correlated genetic relatedness with detailed clinical parameters.

**Results** *N. gonorrhoeae* circulating in Singapore is polyphyletic, and we defined 31 circulating sub-lineages. We detected distinct patterns of sexual behaviour associated with different genetic lineages: some lineages are strongly associated with MSM groups, whilst other lineages have increased rates of reported contact of commercial sex workers. It is likely that these associations reflect the underlying population within the transmission networks. We further correlate these genomic and behavioural subpopulations according to genetically determined antimicrobial resistance patterns.

**Conclusion** The analysis shows distinct transmission clustering within Singapore groups based on sexual preference and commercial sex worker use. Through the use of multiple isolates from single individuals, we established expected within patient diversity levels based on pairwise sequence differences and used this to infer both putative transmission events and also possible bridging between distinct transmission networks. Further work is required to increase the prediction accuracy of the transmission networks and relate this to predicted microbial resistance patterns.

**Disclosure** No significant relationships.