(1) Submission ID#1526550

Genomic analysis of concurrent multisite gonococcal infections from eGISP and SURRG, 2018-2021

Author(s)

Noah A. Burg, n/a
Laboratory Leadership Service Fellow
Centers for Disease Control and Prevention

Jennifer Reimche, PhD
Biologist
CDC

Arvon Clemons, MS
ORISE Fellow, Bioinformatics
CDC

Apurva Shrivastava, n/a
ORISE Fellow
Centers for Disease Control and Prevention

Eric Tran, n/a
ORISE Fellow
Centers for Disease Control and Prevention

Sancta St Cyr, MD
Public Health Physician
CDC

Emily Learner, PhD, MPH
Epidemiologist
CDC

Matthew Schmerer, Dr
Team Lead
cdc

Kim Gernert, PhD
Biologist

CDC

Ellen Kersh, Dr

Chief

CDC

Sandeep J. Joseph, PhD, MPH

Lead, GC Bioinformatics and Advanced Molecular Detection Activity

Division of STD Prevention, STD Research and Reference Branch, CDC

Background

Concurrent multisite gonococcal infections (CMGI) occur when more than one anatomic site tests positive for Neisseria gonorrhoeae (Ng) in the same individual during the same infection episode. In this study we used data from the CDC's enhanced Gonococcal Isolate Surveillance Project (eGISP) and Strengthening the US Response to Resistant Gonorrhea (SURRG) program to identify cases with CMGI Ng isolates, to investigate if genetic differences were present among isolates within a CMGI.

Aim/Methods

From 2018-2021, a subsample of eGISP and SURRG isolates collected each month were submitted for whole-genome sequencing (WGS) and antimicrobial susceptibility testing (AST) at the regional Antimicrobial Resistance (AR) Laboratory Network laboratories, with some additional sequencing at CDC. CMGI isolates were sampled primarily from the oropharynx, rectum, urethra, endocervix, and vagina. Genomic analyses were performed at CDC to identify common strain types (ST) using multi-locus sequence typing (MLST).

Results

From 01/2018–01/2021, 1712 isolates (n=647 eGISP; n=1065 SURRG) submitted for WGS from CMGIs yielded viable sequences. These 1712 isolates represented 811 isolate pairs (i.e., two anatomic sites) (n=1622) and 30 triplets (i.e., three anatomic sites) (n=90). 88.2% of the pairs (n=1430) represented the same MLST within each pair, while 11.8% of pairs (n=192) showed differing MLSTs for each of the anatomic sites sampled. Of the 90 triplets, 77.7% (n=69) displayed identical MLSTs, while 23.3 % (n = 21) had one or more members of the triplet with a discordant MLST from the others. Some pairs and triplets also had discordant AST results.

Conclusions

Our results indicate the presence of different STs causing CMGIs in individuals with >10% of all sampled pairs and >20% of sampled triplet body site isolates carrying different Ng MLSTs. These findings suggest that persons can be infected with multiple STs of Ng at different anatomic sites simultaneously, along with discordant AST profiles. This study was limited to WGS from culture isolation and therefore likely represents an underestimation of STs present in CMGIs; culture-independent sequencing might identify more strain variation. These results have public health implications and may be used in selection of appropriate anatomic sites for development of diagnostic screening strategies and for development of treatment recommendations.