

(1) Submission ID#1539885

Phenotypic and genotypic analysis of *Neisseria gonorrhoeae* strains from matched men and women.

Author(s)

Ana Paula Lourenco Aran, PhD

Research Associate

Department of Immunology, Tufts University School of Medicine, Boston, USA

Jack Cartee, MS

Biologist

CDC

Wenjing Le, MSC.

Technologist-in-charge

Sexually Transmitted Disease Clinic, Institute of Dermatology, Chinese Academy of Medical Sciences and Peking Union Medical College, Nanjing, China

Xiaohong Su, MD, PhD

professor

Sexually Transmitted Disease Clinic, Institute of Dermatology, Chinese Academy of Medical Sciences and Peking Union Medical College, Nanjing, China

Paola Massari, n/a

Research Associate Professor

Department of Immunology, Tufts University School of Medicine

Caroline Genco, n/a

Provost and Senior Vice President ad interim, Arthur E. Spiller, M.D. Professor of Immunology

Tufts University

Background

The global emergence of antimicrobial resistance (AMR) in *Neisseria gonorrhoeae* strains has limited the therapeutic choices to treat gonorrhea.

Aim/Methods

To address this threat of gonococcal antimicrobial resistance, we have conducted detailed studies on a cohort of subjects with gonococcal disease attending the National Center for STD Control in Nanjing, China, where the AMR rate is high. We have obtained and analyzed *N. gonorrhoeae* strains collected from urethral and cervicovaginal swabs for AMR phenotypic and genotypic profiles.

Results

Phylogenetic analysis based on whole genome core single nucleotide polymorphisms of the *N. gonorrhoeae* isolates shows that 92% of subjects were infected by *N. gonorrhoeae* strains genetically identical to the strain infecting their matched partner. More than 80% of *N. gonorrhoeae* isolates were multidrug-resistant to penicillin, ciprofloxacin, and tetracycline. Resistance to azithromycin and reduced susceptibility to extended-spectrum cephalosporin were reported for 12% and 9% of *N. gonorrhoeae* isolates, respectively. AMR phenotypic profile corresponded to genotypic alterations. Variations in genes encoding resistance to antimicrobials in *N. gonorrhoeae*, such as *penA*, *ponA*, *porB*, *mtrR*, *gyrA*, *parC*, *rpsJ*, *erm*, *bla*, and 23s rRNA, were observed. Genotyping analysis as Multilocus Sequence Typing and NG-MAST revealed the circulation of *N. gonorrhoeae* lineages among the study population, including international lineages. *N. gonorrhoeae* specific lineages did not predominate in the study population; a few unmatched subjects were infected with the same *N. gonorrhoeae* lineage.

Conclusions

Our analysis showed no genetic changes after transmission and under different environmental conditions. Isolates from matched partners were genetically identical, suggesting that gonococcal gene expression may provide a survival benefit in these sex-specific niches.