

(1) Submission ID#1539487

Genomic analyses of African *Neisseria gonorrhoeae* isolates: identification of lineages distinct from the rest of the world

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Background

Along with *Chlamydia trachomatis*, *Neisseria gonorrhoeae* is one of the most widespread bacterial sexually transmitted infections (STIs) worldwide and is a global public health concern due to increasing resistance to multiple antimicrobials. Africa, in particular, suffers the greatest burden of STIs however, limited quality-assured data describing *N. gonorrhoeae* and *C. trachomatis* infections, their prevalence and/or antimicrobial resistance (AMR) profiles are available from this continent. This hinders our capacity to limit infections and the emergence of AMR globally. This study analysed publicly available whole genome sequence data (WGS) belonging to *N. gonorrhoeae* isolates originating from Africa and compared these with gonococci from the rest of the world.

Aim/Methods

WGS from 18,412 gonococci were extracted from PubMLST (<https://pubMLST.org/neisseria>). These data originated from all continents and dated from 1928 to 2022. Profiles from the typing schemes MLST, NG-MAST and NG-STAR, which are commonly used to delineate *N. gonorrhoeae* isolates, were extracted and minimum spanning trees were generated through comparison of the core genome (cgMLST). AMR genotypes were investigated and compared with phenotypic data where available.

Results

Of the 18,412 genomes, 11,233 (61%) isolates originated from Europe, 3,331 (18%) from North America, 1,519 (8%) from Asia, 1,219 (6%) from Oceania, 793 (4%) from South America and 323 (2%) from Africa. The majority of isolates dated from 2011 onwards. Analyses identified distinct genomic lineages circulating in Africa some of which highly resistant to ciprofloxacin, tetracycline and penicillin. In particular, a core genome

group, Ng_cgc300:498, identified using a 300 or fewer locus difference threshold, was found primarily consisting of African gonococci. In addition, these isolates belonged to NG-STAR clonal complexes CC 559, 958 and 1054, which were not prevalent in other continents.

Conclusions

These data improve our understanding of African gonococci and enhance public health initiatives. Searches of the PubMLST database allowed isolates to be examined in the context of existing data and compared with related gonococci. Analyses from this study demonstrate the advantages of using the *N. gonorrhoeae* cgMLST scheme to find related gonococci to carry out genomic analyses that enhance our understanding of the population biology of this important pathogen.