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Phenotypic and genotypic characterisation of *Neisseria gonorrhoeae* isolates from Yaoundé, Cameroon, 2019 to 2020

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Background

Neisseria gonorrhoeae has evolved into a superbug exhibiting resistance to all recommended antimicrobials. It is, as a result, a major global public health concern. In Cameroon, few studies have determined the molecular determinants of resistance in *N. gonorrhoeae*. We therefore investigated this in isolates from Yaoundé, Cameroon, dating from 2019 to 2020.

Aim/Methods

N. gonorrhoeae was cultured using on chocolate GC Selective Agar. Minimal inhibitory concentrations results were obtained by E-test for ciprofloxacin, ceftriaxone, tetracycline, azithromycin and benzylpenicillin. Whole genome sequence data (WGS) were obtained and, using a threshold of 300 or fewer locus differences in the *N. gonorrhoeae* cgMLST scheme, four distinct core genome lineages were identified. Publicly available WGS from 1,355 gonococci belonging to these same lineages were retrieved from the PubMLST database allowing the Cameroonian isolates to be examined in the context of existing data and compared with related gonococci.

Results

Antimicrobial resistance to tetracycline, penicillin and ciprofloxacin was observed although none of the isolates had reduced susceptibility to azithromycin, cefixime or ceftriaxone. Examination of AMR genotypes in this dataset found an association between the core genome and AMR with, for example, isolates belonging to the core genome group, Ng_cgc_300:21, possessing *gyrA* and *parC* alleles with amino acid substitutions conferring high-level resistance to ciprofloxacin while lineage Ng_cgc_300: 41 and Ng_cgc_300:243 were predicted to be susceptible to several antimicrobials. A core genome lineage, Ng_cgc_300:498, was observed which largely consisted of gonococci originating from Africa. Five different MLST STs were identified and ST-15667 has only been identified in Africa (Malawi and Cameroon). All of the isolates had distinct NG MAST profiles, four of which newly identified in this study. The remaining NG STAR profiles were not widely found with four of the six isolates possessing NG STAR STs unique to Cameroon.

Conclusions

This study confirms that resistance to ciprofloxacin is prevalent in Cameroon despite this antibiotic still recommended for gonorrhoea in Cameroon. 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.