GYRA AND PARC MUTATIONS IN FLUOROQUINOLONE-RESISTANT NEISSERIA GONORRHOEAE ISOLATES FROM KENYA

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Background Phenotypic fluoroquinolone resistance was first reported in Western Kenya in 2009 and later in Coastal Kenya and Nairobi. Until recently gonococcal fluoroquinolone resistance mechanisms in Kenya had not been elucidated. The aim of this paper is to analyze mutations in both GyrA and ParC responsible for elevated fluoroquinolone MICs in Neisseria gonorrhoeae (GC) isolated from heterosexual individuals from different locations in Kenya.

Methods Antimicrobial Susceptibility Tests were done on 84 GC in an ongoing STI surveillance program. Of the 84 isolates, 22 resistant to two or more classes of antimicrobials were chosen for analysis. Antimicrobial susceptibility tests were done using E-test and the results were interpreted with reference to European Committee on Antimicrobial Susceptibility Testing (EUCAST) standards. The isolates were sub-cultured and whole genomes sequenced using Illumina platform. Reads were assembled de novo using Velvet, and mutations in the GC Quinolone Resistant Determining Regions identified using Bioedict sequence alignment editor. Single Nucleotide Polymorphism based phylogeny was inferred using RaxML.

Results Double GyrA mutations; S91F and D95G/D95A were identified in 20 isolates. Of these 20 isolates, 14 had an additional E91G ParC mutation and significantly higher ciprofloxacin MICs (p=0.0044*). On the contrary, norfloxacin MICs of isolates expressing both GyrA and ParC QRDR mutations were not significantly high (p=0.82) compared to MICs of isolates expressing GyrA mutations alone. No single GyrA mutation was found in the analyzed isolates, and no isolate contained a ParC mutation without the simultaneous presence of double GyrA mutations. Maximum likelihood tree clustered the 22 isolates into 6 distinct clades.

Conclusion Simultaneous presence of mutations in ParC and GyrA has been reported to increase gonococcal fluoroquinolone resistance from different regions in the world. Our findings indicate that GyrAS91F, D95G/D95A and ParC E91G amino acid substitutions mediate high fluoroquinolone resistance in the analyzed Kenyan GC.

Disclosure No significant relationships.