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Evaluation of rifampicin resistance and 81-bp rifampicin resistant determinant region of *rpoB* gene mutations of *Mycobacterium tuberculosis* detected with XpertMTB/Rif in Cross River State, Nigeria

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ABSTRACT

Objective/background: World Health Organization tuberculosis (TB) indices from 2014 to 2016 showed that Nigeria had the 6th highest prevalence, 4th highest incidence, and the highest mortality rate globally. In efforts to improve TB care, the XpertMTB/Rif (GeneXpert) technology, Cepheid, Sunnyvale, California, USA, which has revolutionized TB detection with concomitant rifampicin-resistance molecular detection, was introduced in Cross River State, South–South Nigeria, in 2014. The GeneXpert uses molecular beacons to detect five overlapping 81-bp regions in the rpoB gene known as the Rifampicin Resistant Determinant Region (RRDR). These probes are represented as Probe A (507–511), Probe B (512–518), Probe C (518–523), Probe D (523–529), and Probe E (529–533). Mutations in this region have been shown to account for about 93% of resistance to rifampicin, which is the most important drug in tuberculosis treatment. The objective of this study was to determine the frequency of rifampicin resistance and the commonly associated probes for various rpoB gene mutations within the 81-bp RRDR of Mycobacterium tuberculosis in Cross River State, Nigeria.
Method: We collated and analyzed data from the 10 Xpert MTB/Rif sites in Cross River State from June 2014 to June 2016 and determined the frequency of mutations associated with different probes designated A–E, which represent the RRDR of rpoB gene. All centers use XpertMTB/Rif version G4.
Result: In total, 973 tuberculosis cases were detected from 4671 cases tested. Rif resistance was detected in 6.0% (58/973) of cases. Probe E mutations were the most common, seen in 60.3% (35/58); followed by Probe D, 17.2% (10/58); and Probe B, 13.8% (8/58). Probe A occurred in 3.4% (2/58). No Probe C mutation was seen. Multiple mutation combinations involving probes B and D occurred in 3.4% (2/58), while one isolate had triple site mutations involving

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A, D, and E. One isolate that at initial testing showed a Probe A mutation displayed a Probe D mutation when tested in another site prior to treatment enrollment.
Conclusion: In our setting, 6.0% of tuberculosis isolates are rifampicin resistant. Mutations associated with probe E commonly due to codon 531 are the most predominant cause of rifampicin resistance. Mutations at probe C (codons 518–523) were uncommon. A change in mutation may have occurred in one of the patients.

Conflicts of interest

Non declared.

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