Short Communication Journal of Food & Industrial Microbiology 2021
Vol.7 No.1

Increased rifampicin mono-resistance prevalence in Zimbabwe – Is the higher prevalence of codon 523 to 529 mutation in the rpoB gene an attributing factor?- Charambira K- International Union against Tuberculosis and Lung Disease

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Background: Zimbabwe conducted a second anti-tuberculosis drug resistance survey (TB-DRS) in 2015/16 using the Xpert MTB/RIF assay. This assay uses molecular beacons in five overlapping regions of the *rpoB* DNA region. The probes detect mutations in the codons 507 to 511 (Probe A), 511 to 518 (Probe B), 518 to 523 (Probe C), 523 to 529 (Probe D), and 529 to 533 (Probe E). We report the frequencies of mutations in *rpoB* gene of the *Mycobacterium tuberculosis* (MTB) among the TB-DRS samples with rifampicin resistance tuberculosis (RR-TB) detected.

Method: A retrospective review of data collected through the TB-DRS and using the GxAlert platform to check the actual probe details for those tests from samples that had RR-TB strains. Sputum smear positive samples had an Xpert MTB/RIF assay done followed by phenotypic culture and drug susceptibility testing (DST) in those that had RR-TB detected.

Results: A total of 60 specimens had RR-TB detected on Xpert MTB/RIF assay. Of these, 50 (83.3%) had *Mycobacterium tuberculosis* growth on culture with 48 (96.0%) confirmed RR-TB on phenotypic DST. Among those confirmed RR-TB on phenotypic DST, 23 (47.9%) had rifampicin mono-resistance (RMR) detected and 25 had additional isoniazid resistance (MDR-TB). Probe E mutations occurred in 46% (23/50), probe D 34% (17/50), probe B 10% (5/50), probe A 2% (1/50) and probe C 2% (1/50) of the specimens. Among the RMR, probe D mutation occurred in 54.5% (12/22), probe E 36.4% (8/22), probe A 4.5% (1/22) and probe B 4.5% (1/22).

Conclusion: There is increase in the RMR prevalence from zero percent to 48% between the 1994/5 and 2015/6 TB-DRS. Rifampicin (RMP) seems to be associated with mutations in codons 523 to 529 of the *rpoB* gene of MTB DNA. GxAlert makes it possible to conduct such surveillance remotely and there is need for further studies to cement this.

The S- The aureus isolates belonged to different types of sequences (STs) with the most common ST15 and ST152. All isolates carried the blaZ gene, and also observed low prevalence of tetK and dfrG genes. All the isolates were negative about mecA. The genes of the pvl were common and observed in distinct lines revealing diverse Sa2int phages. The genomics data at Korle-Bu Teaching Hospital revealed multiple transmission events involving S. Auroreus ST15 involves contamination of various surfaces in the emergency pediatric ward where the outbreak occurred.

Conclusion: Dissemination pattern of the ST15 clone in the Korle-Bu Teaching Hospital emergency ward illustrates a fundamental issue with the hospital's disinfection of environmental surfaces. Various phage populations rather than a single highly transmissible type of phage is likely to mediate the high prevalence of pvl genes among the genes S. aureusisolates.