

Phylogenetic Analysis of Klebsiella Species from Clinical Specimens from Nelson Mandela Academic Hospital in Mthatha, South Africa

Authors : Sandeep Vasaikar, Lary Obi

Abstract : Rapid and discriminative genotyping methods are useful for determining the clonality of the isolates in nosocomial or household outbreaks. Multilocus sequence typing (MLST) is a nucleotide sequence-based approach for characterising bacterial isolates. The genetic diversity and the clinical relevance of the drug-resistant Klebsiella isolates from Mthatha are largely unknown. For this reason, prospective, experimental study of the molecular epidemiology of Klebsiella isolates from patients being treated in Mthatha over a three-year period was analysed. Methodology: PCR amplification and sequencing of the drug-resistance-associated genes, and multilocus sequence typing (MLST) using 7 housekeeping genes *mdh*, *pgi*, *infB*, *FusAR*, *phoE*, *gapA* and *rpoB* were conducted. A total of 32 isolates were analysed. Results: The percentages of multidrug-resistant (MDR), extensively drug-resistance (XDR) and pandrug-resistant (PDR) isolates were; MDR 65.6 % (21) and XDR and PDR with 0 % each. In this study, *K. pneumoniae* was 19/32 (59.4 %). MLST results showed 22 sequence types (STs) were identified, which were further separated by Maximum Parsimony into 10 clonal complexes and 12 singletons. The most dominant group was *Klebsiella pneumoniae* with 23/32 (71.8 %) isolates, *Klebsiella oxytoca* as a second group with 2/32 (6.25 %) isolates, and a single (3.1 %) *K. varriicola* as a third group while 6 isolates were of unknown sequences. Conclusions/significance: A phylogenetic analysis of the concatenated sequences of the 7 housekeeping genes showed that strains of *K. pneumoniae* form a distinct lineage within the genus *Klebsiella*, with *K. oxytoca* and *K. varriicola* its nearest phylogenetic neighbours. With the analysis of 7 genes were determined 1 *K. variicola*, which was mistakenly identified as *K. pneumoniae* by phenotypic methods. Two misidentifications of *K. oxytoca* were found when phenotypic methods were used. No significant differences were observed between ESBL *bla*CTX-M, *bla*TEM and *bla*SHV groups in the distribution of Sequence types (STs) or Clonal complexes (CCs).

Keywords : phylogenetic analysis, phylogeny, klebsiella phylogenetic, klebsiella

Conference Title : ICCEMID 2017 : International Conference on Clinical, Experimental Microbiology and Infectious Diseases

Conference Location : Kyoto, Japan

Conference Dates : April 27-28, 2017