Molecular epidemiology of virulence and antimicrobial resistance determinants in Klebsiella pneumoniae from hospitalised patients in Kilimanjaro, Tanzania

This study aimed to use whole-genome sequencing to determine virulence and antimicrobial resistance genes in K. pneumoniae isolated from patients in a tertiary care hospital in Kilimanjaro. K. pneumoniae isolates from patients attending Kilimanjaro Christian Medical Centre between August 2013 and August 2015 were fully genome-sequenced and analysed locally. Sequence analysis was done for identification of virulence and AMR genes. Plasmid and multi-locus sequence typing and capsular or capsular (K) typing were performed and phylogeny was done to ascertain K. pneumoniae relatedness. Stata 13 (College Station, TX, 77845, USA) was used to determine Cohen’s kappa coefficient of agreement between the phenotypically tested and sequence-predicted resistance. A total of 16 (47.1%) sequence types (STs) and 10 (29.4%) K types were identified in 30 (88.2%) and 17 (50.0%) of all analysed isolates, respectively. K. pneumoniae ST17 were 6 (17.6%). The commonest determinants were blaCTX-M-15 in 16 (47.1%) isolates blaSHV in 30 (88.2%), blaOXA-1 in 8 (23.5%) and blaTEM-1 in 18 (52.9%) isolates. Resistance genes for aminoglycosides were detected in 21 (61.8%) isolates, fluoroquinolones in 13 (38.2%) and quinolones 34 (100%). Ceftazidime and ceftriaxone showed the strongest agreement between phenotype- and sequence-based resistance results: 93.8%, kappa = 0.87 and p = 0.0002. Yersiniabactin determinant was detected in 12 (35.3%) of K. pneumoniae. The proportion of AMR and virulence determinants detected in K. pneumoniae is alarming. WGS-based diagnostic approach has showed promising potentials in clinical microbiology, hospital outbreak source tracing virulence and AMR detection at KCMC.

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