Molecular Analysis of Antibiotic Resistance Determinants and Plasmids in Malaysian Isolates of Multidrug Resistant Klebsiella pneumoniae.

Al-Marzooq F1, Mohd Yusof MY1, Tay ST1.

1Department of Medical Microbiology, Faculty of Medicine, University of Malaya, Kuala Lumpur, Malaysia.

Abstract

Infections caused by multidrug resistant Klebsiella pneumoniae have been increasingly reported in many parts of the world. A total of 93 Malaysian multidrug resistant K. pneumoniae isolated from patients attending to University of Malaya Medical Center, Kuala Lumpur, Malaysia from 2010-2012 were investigated for antibiotic resistance determinants including extended-spectrum beta-lactamases (ESBLs), aminoglycoside and trimethoprim/sulfamethoxazole resistance genes and plasmid replicons. CTX-M-15 (91.3%) was the predominant ESBL gene detected in this study, aacC2 gene (67.7%) was the most common gene detected in aminoglycoside-resistant isolates. Trimethoprim/sulfamethoxazole resistance (90.3%) was attributed to the presence of sul2 (53.8%) and dfrA (59.1%) genes in the isolates. Multiple plasmid replicons (1-4) were detected in 95.7% of the isolates. Flik was the dominant replicon detected together with 13 other types of plasmid replicons. Conjugal plasmids (1-3 plasmids of ~3-100 kb) were obtained from 27 of 43 K. pneumoniae isolates. An ESBL gene (either CTX-M-15, CTX-M-3 or SHV-12) was detected from each transconjugant. Co-detection with at least one of other antibiotic resistance determinants [sul1, dfrA, aacC2, aac6'lb, aac(6')lb-cr and qnrB] was noted in most conjugal plasmids. The transconjugants were resistant to multiple antibiotics including β-lactams, gentamicin and cotrimoxazole, but not ciprofloxacin. This is the first study describing the characterization of plasmids circulating in Malaysian multidrug resistant K. pneumoniae isolates. The results of this study suggest the diffusion of highly diverse plasmids with multiple antibiotic resistance determinants among the Malaysian isolates. Effective infection control measures and antibiotic stewardship programs should be adopted to limit the spread of the multidrug resistant bacteria in healthcare settings.