البحث الثانى:

عنوان البحث باللغة الانجليزية:

Whole-genome sequencing of Egyptian multidrug-resistant Klebsiella pneumoniae isolates: a multi-center pilot study

Abstract:

Multidrug-resistant (MDR) Klebsiella pneumoniae is a common infectious pathogen. We performed whole-genome sequencing (WGS) of 39 randomly selected, geographically diverse MDR K. pneumoniae from nine Egyptian hospitals. Clinical sources, phenotypic antibiotic resistance, and hyper-mucoviscosity were documented. WGS data were epidemiologically interpreted and tested for the presence of antibiotic resistance and virulence genes. Based on WGS data, we identified 18 classical multi-locus sequence types (MLST), the most common type being ST101 (23.1%) followed by ST147 (17.9%). Phylogenetic analyses identified small numbers of closely related isolates in a few of the centers, so we mostly documented independent nosocomial acquisition or import from public sources. The most common acquired resistance gene found was blaCTX-M-15, detected in 27 isolates (69.2%). Carbapenemase genes encountered were blaNDM-1 (n = 13), blaNDM-5 (n = 1), blaOXA-48 (n = 12), blaOXA-181 (n = 2), and blaKPC2 (n = 1). Seven strains (18%) contained more than a single carbapenemase gene. While searching for virulence-associated genes, sixteen wzi alleles were identified with wzi137, wzi64, and wzi50 most commonly found in ST101, ST147, and ST16, respectively. Yersiniabactin was the most common virulence factor (69.2%). Hyper-mucoviscosity was documented for 6 out of 39 isolates .

This is the first genomic study of MDR K. pneumoniae from Egypt. The study revealed a clear spread of well-known international clones and their associated antimicrobial resistance and (hyper)virulence traits. The clinical situation in Egypt seems to reflect the scenario documented in many other countries and requires close attention.