Genomic Analysis of Pseudomonas aeruginosa Resistance to Carbapenem Isolates in Three Major Hospitals in Hanoi (2011-2015)

Tran, Hai Anh (School: High School for Gifted Students, Hanoi University of Science)
Nguyen, Minh Thao (School: High School for Gifted Students, Hanoi University of Science)

Purpose: Multidrug-resistant Pseudomonas aeruginosa is recognised as an important cause of hospital acquired infections listed among the WHO priority pathogens. The antibiotic resistance mechanisms of P. aeruginosa have been well documented. However, antibiotic resistance genes carried by P. aeruginosa differ markedly among communities and countries. Procedure: Whole genome sequence analysis was used to identify the antibiotic-resistance genes and phylogenetic structure of 72 carbapenem-resistant P. aeruginosa isolates from hospital acquired infection patients between 2011-2015 in three major hospitals in Hanoi-Vietnam. Results: All of P. aeruginosa strains carry different antibiotic resistance genes. Of these 48/72 strains carrying 3 variants of IMP genes, in which IMP-15 gene dominates (n= 34). Two strains were co-carried IMP-15+DIM-1 genes and 7 were positive to KPC-1. High MICs for imipenem may related to IMP-, DIM-1 and KPC-1 genes. Phylogenetic analysis has divided these isolates into 9 groups. Each group harbors characteristic drug resistance genes and genetic background. Sixteen STs, including 8 STs found in Vietnam and other continents; 8 STs only found in Vietnam and 2 novel STs were unidentified. The mobile genetic elements of IMP-51, DIM-1 and KPC-1 genes were similar to other countries in the world. Conclusions: These finding suggest high diversity and high proportions of carbapemem resistance among hospital isolates of P. aeruginosa and clonal expansion in hospitals associated with selection by antibiotic exposure. Most ST were described before in the region and world-wide suggesting global spread due to the globalization. Co-existence of IMP-15 + DIM-1 and KPC-1 genes in P. aeruginosa is first reported Vietnam.

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