Genotypic Characterization of Extended Spectrum β-lactamases Producing *Klebsiella pneumoniae* Strains Isolated in Malaysia

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Klebsiella pneumoniae is an important opportunistic pathogen that causes urinary tract infections, intra-abdominal infections and pneumonia in immunocompromised individuals. The prevalence of multiple antibiotic resistant isolates has been increasing worldwide. Fifty one clinical strains obtained from tracheal aspirates, urine, blood, and swabs of patients from various public hospitals in Malaysia were analyzed by antimicrobial susceptibility test and DNA fingerprinting techniques. PCR detection of several resistance genes was also carried out. Using disk diffusion, the rates of resistance among the isolates were as follows: ampicillin 96%, piperacillin 61%, aztreonam 45%, ceftazidime 41%, cefriaxone 35%, gentamicin 27%, tetracycline 16%, amoxicillin, clavulanate and ciprofloxacin, 10% each, and cefepime 8%. Among them, 31 isolates were multi-drug resistant (MDR; resistant to 2 or more classes of antimicrobial agents). Most MDR isolates were resistant to cefriaxone and aztreonam compared to non-MDR isolates. Using PCR, bla_{SHV}, $bla_{CTX\text{-}M}$, bla_{TEM} and bla_{OXA} genes encoding for extended spectrum β-lactamases (ESBL) were detected in 46, 19, 4 and 5 isolates, respectively. 41% of the strains produced 2 or more ESBLs. Pulsed-field gel electrophoresis (PFGE) and random amplified polymorphic DNA (RAPD) were used to subtype these microorganisms to determine their genetic diversity. The clinical *K. pneumoniae* strains obtained from sporadic cases of infections were very diverse as determined by 2 DNA fingerprinting techniques. PFGE and RAPD-PCR generated 47 PFGE profiles (F = 0.53—1.0) and 49 PCR patterns (F = 0.30—1.0). Only two of the K. pneumoniae strains were indistinguishable by DNA fingerprinting. There were no correlation between the occurence of MDR and their DNA fingerprints. Imipenem seems to be the most active agent against Klebsiellae. In conclusion, 61% of the *K. pneumoniae* were MDR and the DNA fingerprinting indicated that the strains were very heterogeneous.

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Antimicrobial Resistance Genes among *Salmonella enterica* isolates from Poultry and Swine in Thailand

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A total of 184 *Salmonella enterica* isolated from poultry and swine were classified as resistant to at least one antibiotic and the presence of class 1 integrons and inserted resistance gene cassettes were investigated in our previous All the isolates were screened for the presence of class 2 and 3 integrase genes and 18 resistance genes corresponding to their resistance phenotypes. Ampicillin-resistant isolates ($n = 103$) were screened for the presence of bla_{PSE} and bla_{TEM}. Chloramphenicol-resistant isolates ($n = 59$) were investigated for *catA*, *catB* and *cmlA*. Gentamicin-resistant strains ($n = 26$) were screened for *aadB*. All strains resistant to tetracycline ($n = 86$) were examined for the presence of *tetA* and *tetB*. Trimethoprim-resistant isolates ($n = 69$) were investigated for *dfrA1*, *dfrA10* and *dfrA12*. Spectinomycin-resistant isolates ($n = 103$) were screened for *aadA1* and *aadA2* and streptomycin-resistant strains ($n = 127$) were additionally tested for the presence of *strA* and *strB*. All the strains resistant to sulphonamides ($n = 139$) were screened for *sul1*, *sul2* and *sul3*. The results revealed that none carried class 2 and 3 integrons. The investigated resistance genes were responsible for resistance in 78% of the isolates. All the strains harboring more than one resistance gene were resistant to three or more antibiotics. The bla_{TEM}, *cmlA*, *tetA*, *dfrA12*, *sul3*, *aadA1* genes were detected in the majority of strains resistant to ampicillin (87%), chloramphenicol (63%), tetracycline (86%), trimethoprim (42%), sulphonamides (42%) and streptomycin/spectinomycin (61%), respectively. The presence of different genes within the same strains, encoding resistance to the same antibiotics, was detected in 98 isolates. In conclusion, the results indicated that the resistance genes play a major role in conferring resistance among the *Salmonella* isolates investigated.

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Prevalence of *qnr* and *aac(6′)-Ib-cr* Genes in Community-Acquired *Enterobacteriaceae* Isolated in Healthy Volunteers in Hochiminh City

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Background: Multi-drug resistance in Gram-negative microorganisms is emerging. Data on the prevalence of multi-drug resistant organisms in the community are sparse, particularly in developing countries. We studied the carriage of multi-drug resistant *Enterobacteriaceae* in healthy volunteers in Hochiminh city, Vietnam, and determined the prevalence of genes encoding transferable quinolone resistance.

Methods: Strains were isolated from stool samples or rectal swabs of 27 healthy adults, 77 healthy children (aged 5—15) and 100 healthy neonates (aged 1—3 days). Samples were cultured on MacConkey agar supplemented with gentamicin (8 mg/ml), ceftazidime (2 mg/ml), or nalidixic acid (16 mg/ml). One colony representative of each morphology, was subcultured before identification by API 20E. Antibiotic resistance was determined by disc diffusion test and E-test. Quinolone resistance genes *qnrA*, *qnrB*, *qnrS*, and *aac(6′)-Ib-cr* were detected by PCR and sequencing.