Molecular Studies on the Antibiotic Sensitivity and Expression Analysis of npcRNA in Clinical Isolates of *Klebsiella pneumoniae*

ABSTRACT

Klebsiella pneumoniae (*K. pneumoniae*), a member of Enterobacteriaceae family, is an opportunistic pathogen that accounts for a significant proportion of nosocomial and community acquired infections. It causes pyogenic liver abscess, urinary tract infections, pneumoniae and soft tissue infection. Infections are often associated with high morbidity and mortality. The emergence of multidrug-resistant (MDR) and extended-spectrum β-lactamase (ESBL)-producing *K. pneumoniae* poses a serious antibiotic management problem as resistance genes are easily transferred from one organism to another. One hundred and twenty *K. pneumoniae* isolated from sporadic cases in three hospitals from Northern Malaysia were analysed by antimicrobial susceptibility testing, PCR detection of ESBL-encoding genes, Enterobacterial Repetitive Intergenic Consensus PCR (ERIC-PCR), Random Amplified Polymorphic DNA PCR (RAPD-PCR) and Northern Blotting for expression analysis of *Klebsiella pneumonia* gene. Hospitals which involved in this study were Hospital Taiping; Perak Darul Ridzuan, Hospital Pulau Pinang, Pulau Pinang and Hospital Sultan Abdul Halim, Sungai Petani; Kedah Darul Aman. Among 120 *Klebsiella* only 26 been confirmed *K. pneumoniae.* All the 26 *K. pneumoniae* harboured very prominent bands in PCR detection of ESBL-encoding genes, ERIC-PCR, and RAPD-PCR. Comparative analysis have done on recent identifications of novel npcRNAs in closely related bacteria to *Klebsiella pneumoniae* genera, those are *Salmonella enterica Typhimurium, Salmonella enterica Typhi* and *Escherichia coli*. Interestingly 40.54 % of *Salmonella enterica Typhimurium* npcRNAs are homologously present in *K. pneumoniae*, showing its evolutionary close relationship with

Salmonella. Moreover npcRNA from *E.coli* shows 90.0 % and Salmonella enteric Typhi 43.90% percentage are homologously present in *K. pneumoniae*. From the comparative analysis, five npcRNAs were randomly chosen for expression analysis using Northern blot technique. Through this study, we manage to identify the antibiotics to which *K. pneumoniae* isolates were resistant and manage to identify the relativity of npcRNAs from closely related species to *K. pneumoniae* and steps to be taken to solve this problem in near future.