ABSTRACT

Surgical site infection is a leading cause of morbidity and mortality of all hospital-acquired infections worldwide. To date, there have been no studies reported on antimicrobial susceptibility pattern of bacterial isolates and plasmid analysis of the resistant strains in Kedah State Malaysia. Hence, the aim of the study was to determine antimicrobial susceptibility pattern of the bacterial isolates and plasmid analysis of the resistant strains. Prospective cross-sectionally designed hospital-based study was conducted on patients who underwent surgery in the surgical ward, obstetrics/gynaecology ward and orthopaedic ward of Hospital Sultan Abdul Halim between December 2016 and June 2017. Clinical history and demographic characteristics of the study participants were collected using a structured questionnaire. Pus swabs were collected using cotton swabs that were moistened in sterile Amies transport medium and processed for bacterial isolation, identification and testing sensitivity using the standard procedure. Multidrug resistance bacterial isolates were randomly selected for plasmid analysis. Descriptive statistics and Chi-square test were used to analyse the data using SPSS. A total of 164 patients, males 77 and females 87 with age ranging from 15-70 years were included in the study. A hundred and twenty-six (76.8%) of the 164 specimens collected, had positive bacterial growth. The most predominant isolate was *Staphylococcus aureus* (25.2%) followed by *Klebsiella pneumoniae* (17.0%), *Escherichia coli* (12.2%), *Pseudomonas aeruginosa* (10.2%), *Acinetobacter baumanii* (7.5%) and Coagulase-negative *Staphylococcus aureus* (6.0%). *Klebsiella pneumoniae* and *Escherichia coli* 17% and 16% respectively were extended-spectrum ß-lactamases producers. The study showed that Gram-negative bacteria causing surgical site infections were susceptible to Imipenem, Ertapenem, Meropenem, Amikacin and Gentamicin while the Gram-positive bacteria were susceptible to Cotrimoxazole, Rifampin and Clindamycin. The isolates showed resistance to antibiotics like Ampicillin and Ampicillin/Sulbactam in the present study. The overall multidrug-resistant pattern of the bacterial isolates was seen in 56 (38.0%) isolates. Pan-resistance was also recorded in all of the of the *Acinetobacter baumanii* isolated. Association was not found between the patients' age, gender, ward of care and hospital stay with multidrug resistance organisms statistically significant difference. The plasmids size found in the study had higher molecular weight than 1kb of which falls around 11,000bp to 12,000bp. About one-third of the bacteria causing SSIs in this hospital were multidrug resistant, of which 50.5% were Gram-negative bacteria and 14% were Gram positive bacteria.

It is presumed that some of these plasmids could have contributed to the multi drug resistance pattern. Current study showed presence of plasmids in the multi drug resistant strains, however the study did not relate the plasmids to antibiotic resistance. Future studies in plasmid sequencing of these isolates will enhance our knowledge and understanding of the specific resistance genes in these isolates.