Hospital from March to August 2011 and were followed for death or discharge from hospital stay. All variables were documented on a proforma and analyzed using SPSS version 13.0 and a P-value of <0.05 was considered statistically significant.

**Results:** The mean age of our patients was 53.7 ± 20 years. There were 53% males and 47% females. Among the co-morbidities, 81% of people with ischaemic heart disease had respiratory infec-
tion with Acinetobacter, as compared to 42% of those without ischaemic heart disease (p=0.020). The primary diagnosis of major-
ity of patients was sepsis (55%), followed by trauma (13%) and 
malignancy (10%). The most frequent source of positive culture 
was from Tracheal Aspirate (48%) followed by Urine culture (25%).
There was a significantly higher prior admission rate in patients 
with respiratory Acinetobacter infection as compared to non-
respiratory group (p=0.002). The most commonly used antibiotic 
was Polymyxin (62%), followed by carbapenems in 18%. In 83%
the Acinetobacter infection had been nosocomially acquired as 
opposed to 17% in whom it was community acquired. Out of 60 
patients, 19 expired (32%) whereas 41 (68%) were discharged from 
the hospital. Although greater proportion of patients died in the res-
piratory group (40%) compared to non-respiratory group (23%), the 
difference was not statistically significant (p=0.165). Mean length of stay was 18 days and among those who survived there was 23% 
readmission rate. Logistic regression did not reveal any modifier 
effect from age, gender, primary diagnosis, co-morbidities and use of 
antibiotics.

**Conclusion:** In this study, there was no significant difference in frequency of mortality between patients having respiratory versus non-respiratory acinetobacter infections.

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**Does genotypes and virulence profiles play role in classifying Staphylococcus aureus as infectious or colonizing strain?**

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**Background:** Staphylococcus aureus is one of the well-known pathogen in human medicine. *S. aureus* can cause asymptomatic colonisation as well as life-threatening infection. In the present study, we address the question does the genotype and virulence factors play role in making *S. aureus* as a pathogen or colonizer and whether the clinical outcome of *S. aureus* can be predicted by genotyping and virulence profiling.

**Methods:** A total of 18 *S. aureus* isolates collected from bloodstream, wound and healthy nasal carriers (6 from each group) were characterised by multilocus sequence typing (MLST), accessory gene regulator (agr) typing, staphylococcal protein A (spa) typing, pulsed field gel electrophoresis (PFGE) and virulent gene profiling (sea, seb, sec, seg, seh, sei, eta, etb, ACME, cna, fnbA, icaA, icaC, icaD, pvl, tsst).

**Results:** Molecular typing revealed that majority of infectious isolates belonged to ST1 and ST239. Most of the infectious and car-
rriage isolates shared the agr group III. Spa typing and PFGE patterns demonstrated high variance among *S. aureus* isolates, although with the similar clinical manifestation. On the other hand, isolates that shared similar genotype presented different clinical outcomes. Among the 18 isolates, mecA and pvl genes were only possessed by the invasive isolates, while virulence genes seb and seg enterotoxin b and g were often harbored by healthy carriage isolates. Bacteremia associated-isolates rarely harbored seh and sei when compared to wound infection and healthy carrier isolates.

**Conclusion:** Overall, the virulence genes were heterogeneously distributed among the isolates and propose an exchange of virulence genes between the *S. aureus* strains. Isolates which harbor most of the virulence genes (exclude pvl gene) do not mean that it can cause significant clinical manifestation in host. Further studies are needed to explain whether virulence gene expression and host factor may play a role in the clinical infection outcomes.

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**Antimicrobial susceptibility and genotypic characterization of clinical Salmonella enteritidis strains isolated from a tertiary hospital in Malaysia by using multilocus variable number of tandem repeat analysis and pulsed-field gel electrophoresis**

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**Background:** Salmonella enterica serovar enteritidis (*S. enter-
ritis*) causes non-typhoidal salmonellosis (NTS) in humans. Twenty-eight percent of NTS serovars identified and reported to the laboratory based surveillance database of Malaysian Ministry of Health in 2005 was *S. enteritidis*. The increasing occurrence of multidrug resistant (MDR) *S. enteritidis* complicates available ther-
apeutic options. Phage typing and pulsed-field gel electrophoresis (PFGE) are commonly used subtyping methods, but there are limits-
ations. The advent of multi-locus variable number of tandem repeats analysis (MLVA) provided a better discrimination of *S. enteritidis*. This study aimed to determine the antibiograms and genotypes of clinical *S. enteritidis* strains isolated from a tertiary hospital in Penang, Malaysia.

**Methods:** A retrospective study involving 16 clinical *S. enteritidis* strains isolated from 2005 to 2006 was conducted. The resistance of the strains against 14 antimicrobial drugs was examined, and the clonality of the strains was determined by both MLVA and PFGE of XbaI digested bacterial chromosomal DNA.

**Results:** Both invasive (n = 9) and non-invasive (n = 7) *S. enter-
ritis* were examined and a high percentage of multidrug resistance was observed (66% of invasive and 43% of non-invasive strains). MLVA (D = 0.77) yielded five distinct types (M1 to M5), which corre-
lated to antimicrobial resistance patterns of the strains. Strains of MLVA type M1 were resistant to tetracycline, type M2 resistant 
to nalidixic acid, types M3 and M4 resistant to both ampicillin and 
nalidixic acid, and type M5 resistant to sulfonamides, trimetho-
prim, trimethoprim-sulfamethoxazole and tetracycline. The VNTR loci were genetically homogeneous (Nei’s diversity index < 0.53) 
among the strains. PFGE (D = 0.94) subtyped all strains into 11 pul-
sotypes, showing high genetic homogeneity (0.84 < F < 1.00) among