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以臨床微生物報告偵測 AB 菌院內感染的資料探勘研究

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A Data Mining Study to Detect Acinetobacter baumannii Nosocomial Infections from the Analysis of Clinical Microbiology

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Nosocomial infection is a serious problem within the hospital. Bacteria that coexist harmlessly with the human body could become a virulent source of infection due to multidrug resistance. Results of clinical microbiologic test are important for detection of nosocomial infection, which is difficult to be proved in early stages. This study seeks to formulate effective association rules about nosocomial infection by clinical microbiologic results from a medical center in central Taiwan. Combined with data of Acinetobacter baumannii and records of nosocomial infections, however, the huge amount of data accumulated from that analysis made it difficult to detect the nosocomial infections in early stages. The purpose of this study is to use data mining to extract effective associative rules about nosocomial infections as references for detecting nosocomial infections in hospital. We look for associated rules in different aspects among in-patient's sex, age, hospital ward, antimicrobial susceptibility testing results and nosocomial infections. There are 50 association rules ,that will be very valuable for nosocomial infections early detection. We create a real time laboratory information system for analyzing the microbiological analysis results and to early identify infection pattern. It is useful in healthcare .

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鮑氏不動桿菌分離菌株 β-lactam 類抗生素抗藥性染色體基因型研究

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Genotyping of OXA carbapenemases genes of Multidrug-Resistant Acinetobacter baumannii Isolates

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The emergence and rapid spread of the important nosocomial pathogens drug-resistant Acinetobacter spp., in particular Acinetobacter baumannii (A. baumannii), are of great concern worldwide. More than half of the drug-resistant Acinetobacter spp. are resistant to at least 3 classes of antibiotics, and designated as multidrug-resistant (MDR) Acinetobacter spp.. The antimicrobial agent carbapenems have been relied upon for treating infections caused by MDR A. baumannii. However, carbapenems resistance in Acinetobacter spp. is particularly a significant public health concern, leaving clinicians with few therapeutic options remaining. The OXA carbapenem-hydrolysing β-lactamases (carbapenemases; belonging to molecular class D OXA enzymes) of Acinetobacter spp. are divided into 4 phylogenetic subgroups: OXA-23-like (subgroup 1), OXA-24-like (subgroup 2), OXA-51-like (subgroup 3) and OXA-58 (sharing less than 50% amino acid identity to the other subgroups). In this study, 192 PDR A. baumannii isolates were collected, and distribution of genes encoding the 4 subgroups of OXA carbapenemases among the isolates was examined by multiplex polymerase chain reaction. All the 192 isolates have OXA-51-like gene while no OXA-58-like gene was detected. The frequency of OXA-23-like and OXA-24-like gene was 96.35% and 0.52%, respectively. No significant association between the genotyping of A. baumannii isolates and clinical parameters was observed. Our results provided the genotypic information of drug-resistant A. baumannii isolated in central Taiwan which, hopefully, would be beneficial to the understanding of microbial genetic background of antibiotic resistance as well as to the controlling the cognate infection of MDR A. baumannii in medical care and service.