INTRODUCTION

Pseudomonas aeruginosa is a common pathogen that causes nosocomial infections in intensive care units (ICUs) ***(NNIS, 2000; Wisplinghoff et al., 2004)***. In spite of significant changes in the spectrum of organisms causing nosocomial infections in ICUs, *Ps. aeruginosa* has held a nearly unchanged position as an important pathogen. Today, the organism is isolated as the second most frequent organism causing ventilator-associated pneumonia, the fourth causing catheter-associated urinary tract infections, the fifth causing surgical site infections and the seventh causing central line–associated bloodstream infections ***(Hidron et al., 2008)***.

Ps. aeruginosa has inherent resistance to many drug classes, can acquire resistance to all relevant treatments via mutations, and can harbor integrons with multiple resistance genes, as those coding for metallo-β-lactamases (MBLs), which can cleave the most active antimicrobial agents against *Ps. aeruginosa* and Enterobacteriaceae: the carbapenems ***(Livermore, 2002)***.

Optimal control of *Ps. aeruginosa* outbreaks may require rapid identification and strain differentiation. *Ps. aeruginosa* has traditionally been typed on the basis of its phenotypic characteristics ***(Pitt, 1988)***. However, strain typing by traditional phenotypic methods may lack discriminatory power and stability. Molecular techniques offer a considerable improvement, and can complement phenotypic data to obtain a better understanding of bacterial diversity ***(Olive and Bean, 1999)***.

Pulsed field gel electrophoresis (PFGE) is commonly employed, and has achieved widespread recognition as the ‘gold standard’ for *Ps. aeruginosa* Deoxyribonucleic acid (DNA) typing ***(Spencker et al., 2000; Bertrand et al., 2001; Douglas et al., 2001)***. However, this method is limited by technical complexity, expense and

prolonged turnaround times for results ***(Olive and Bean, 1999)***. As an alternative to PFGE, repetitive-element-based polymerase chain reaction (rep-PCR) and arbitrary-primed polymerase chain reaction (AP-PCR) have shown considerable potential as DNA typing tools in the laboratory ***(Kersulyte et al., 1995; Olive and Bean, 1999)***.

Rep-PCR assays utilize primers targeting highly conserved repetitive sequence elements in the bacterial genome ***(Versalovic et al., 1991)***. In AP-PCR, or randomly amplified polymorphic DNA (RAPD), DNA synthesis is primed at low stringency with single oligonucleotides of arbitrarily chosen sequence from sites in genomic DNA to which the oligonucleotide is fortuitously matched or almost matched, and strain-specific arrays of amplified DNA fragments are obtained from pairs of closely spaced sites ***(Kersulyte et al., 1995)***.