## ABSTRACT

*Proteus* spp. which belongs to the *Enterobacteriaceae* family are rod shaped gram-negative bacteria that are widespread in the natural environment. *Proteus* spp. are opportunistic pathogens, which cause urinary tract infections (UTIs), wounds infections, meningitis in neonates or infants, and rheumatoid arthritis. These bacteria are also associated with nosocomial infections. They are frequently responsible for UTI in patients with a urinary catheter in place or with structural or functional abnormalities within the urinary tract, as well as after surgical intervention in the urogenital system. *Proteus* spp. possesses swarming ability when cultures onto solid media. Despite the recent advances in antimicrobial therapy, *Proteus* spp. infections cause high morbidity and mortality, especially among immunocompromised patients. The emergence of multidrug-resistant (MDR) and extended-spectrum β-lactamase (ESBL)-producing *Proteus* spp. poses a serious antibiotic management problem as resistance genes are easily transferred from one organism to another. In this study, various techniques were used to determine the antimicrobial resistance profiles of *Proteus* spp. strains isolated from two different hospitals in Northern Malaysia. Moreover by using simple and easy PCR-based fingerprinting methods Random Amplification of Polymorphic DNA (RAPD) and Enterobacterial Repetitive Intergenic Consensus Polymerase Chain Reaction (ERIC-PCR) the genetic diversity of the isolates was established. Despite the blooming data on bacterial ncRNAs, no studies have been reported on *Proteus vulgaris* and *Proteus hauseri* ncRNAs. Due to the non-availability of genome data of this two bacterial species, a comparative analysis of gram negative bacterial ncRNAs was previously performed in our laboratory against available genome data of *Proteus mirabilis* and this results was used in this current study to analyze the expression profile of 6 selected ncRNAs in *P. vulgaris* and *P. hauseri* using Northern blot technique. Interestingly, all 6 ncRNAs showed expression and with stage-specific regulation during growth of these two bacterial species. Additionally, these

ncRNAs were reverse transcribed into complementary DNAs and were submitted to NCBI for acquisition of reference number for future research purpose