

Evaluation of PAI_{usp} subtyping to characterize uropathogenic *E. coli* isolates

Abstract

Introduction: Uropathogenic virulence factors have been identified by comparing the prevalence of these among urinary tract isolates and environmental strains. The uropathogenic-specific protein (USP) gene is present on the pathogenicity island (PAI) of uropathogenic *Escherichia coli* (UPEC) and, depending on its two diverse gene types and the sequential patterns of three open reading frame units (orfUs) following it, there is a method to characterize UPEC epidemiologically called PAI_{usp} subtyping. **Methodology:** A total of 162 UPEC isolates from Sabah, Malaysia, were tested for the presence of the *usp* gene and the sequential patterns of three orfUs following it using polymerase chain reaction (PCR). In addition, by means of triplex PCR, the prevalence of the *usp* gene was compared with other two VFs of UPEC, namely alpha hemolysin (α -hly) and cytotoxic necrotizing factor (*cnf-1*) genes encoding two toxins. **Results:** The results showed that the *usp* gene was found in 78.40% of UPEC isolates, indicating that its prevalence was comparable to that found in a previous study in Japan. The two or three orfUs were also associated with the *usp* gene in this study. All the PAI_{usp} subtypes observed in Japan were present in this study, while subtype IIa was the most common in both studies. The *usp* gene was observed in a higher percentage of isolates when compared with α -hly and *cnf-1* genes. **Conclusions:** The findings in Japan and Sabah, East Malaysia, were similar, indicating that PAI_{usp} subtyping is applicable to the characterization of UPEC strains epidemiologically elsewhere in the world.