

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.