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The high frequency of uropathogenic *Escherichia coli* strains carrying aerobactin gene isolated from clinical cases

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Objectives: Uropathogenic *Escherichia coli* (UPEC) are one of the most important etiologic agent of urinary tract infection (UTI). UPEC stains have various types of virulence factors including adhesions, toxins and iron uptake systems. Virulence genes are mainly located on transmissible genetic elements and/or in particular locus on the chromosome called pathogenicity islands (PAI). The aim of this study was to investigate the frequency of uropathogenic *E. coli* strains carrying aerobactin gene recovered from the patients admitted to Baqiyatallah hospital in Tehran, Iran.

Methods: The urine samples were collected from hospitalized patients with UTI admitted to Baqiyatallah hospital, Tehran, Iran from April to October 2014. Standard microbiological and biochemical techniques were used to identify the *E. coli* strains. Total genomic DNA was extracted using boiling method. Polymerase chain reaction (PCR) using specific primers were used for detection of virulence gene encoding aerobactin among the strains. The PCR amplicons were visualized after electrophoresis and staining with ethidium bromide.

Results: Fifty *E. coli* strains were isolated and included in the study. The results obtained from PCR amplification showed that aerobactin gene was amplified successfully with the final size of 602 bp in all stains. The frequency of uropathogenic *E. coli* strains harboring aerobactin gene was %88.

Conclusion: Our finding indicated that the frequency of uropathogenic *E. coli* strains carrying aerobactin gene in the study is very high and can pose a threat for spreading of the organism in the hospital.

The study of genetic relationship among third generation cephalosporin-resistant *Salmonella enterica* strains

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Salmonella is an important food-borne pathogen responsible for disease in humans and animals. The aim of this study was to investigate the genetic relationship among third generation cephalosporin-resistant *Salmonella enterica* strains by Enterobacterial Repetitive Intergenic Consensus (ERIC)-PCR. The study included all *Salmonella* isolates obtained from clinical cases in a pediatric hospital in Tehran, Iran during 2006 to 2009. Antimicrobial susceptibility testing was performed according to the Clinical and Laboratory Standards Institute. The genetic relationship between third generation cephalosporins-resistant *Salmonella enterica* strains was determined using ERIC-PCR. Of all *Salmonella enterica* isolates recovered from pediatric patients, six isolates including four *Salmonella enterica* serotype Infantis and two *Salmonella enterica* serotype Enteritidis showed an extended-spectrum cephalosporins resistant phenotype. ERIC-PCR differentiated *Salmonella enterica* serotypes Infantis and Enteritidis into 2 distinct clusters arbitrarily named as E1 and E2. Profile E1 was found in two *Salmonella enterica* serotype Enteritidis isolates, and profile E2 was found in four *Salmonella enterica* serotype Infantis isolates. Extended-spectrum cephalosporins resistant *Salmonella* could be attributed to a few predominant serotypes including Enteritidis and Infantis in this study. Genetic analysis using ERIC-PCR showed that closely related clones are responsible for the occurrence of extended-spectrum cephalosporins resistant *Salmonella* infection in Tehran.