

The Study of Genetic Relationship among Third Generation Cephalosporins-resistant *Salmonella enterica* Strains by ERIC-PCR

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Background & Objectives: *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 cephalosporins-resistant *Salmonella enterica* strains by Enterobacterial Repetitive Intergenic Consensus (ERIC)-PCR.

Methods: 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.

Results: Of 136 *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.

Conclusion: 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.

Keywords: *Salmonella enterica*; Enterobacterial Repetitive Intergenic Consensus; Antimicrobial Susceptibility