The study of genetic relationship among third generation cephalosporinresistant *Salmonella enterica* strains

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Background and 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 cephalosporin-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 Infantis 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 testing