

**PHENOTYPIC AND GENOTYPIC CHARACTERIZATION  
OF *SALMONELLA* ISOLATES FROM  
FARM/ FIELD TO FORK IN TURKEY**

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*Salmonella* poses a significant threat to public health in the farm to fork chain. In order to assure the consumer safety, elimination of *Salmonella* from the farm to fork chain is a must. Although Turkey is a major world producer and exporter of agricultural products, there is lack of surveillance studies on transmission, ecology and evolution of foodborne pathogens. Therefore, the objective of this research is to use genotypic and phenotypic methods to have a better understanding on the *Salmonella* diversity in humans, animals and various foods, collected from the main agricultural region in Turkey in 2012. In each season of a year, one month was chosen as the sampling period, during which street food samples and animal feces, as well as isolates from human clinical cases were collected and investigated for the presence of *Salmonella*. A total of 163 *Salmonella* isolates were collected from human clinical cases, animal feces and different food samples. All *Salmonella* isolates were characterized using phenotypic (serotyping and antimicrobial resistance profiling) and genotypic (multilocus sequence typing [MLST], and pulsed field gel electrophoresis [PFGE]) methods. Serotyping analysis revealed a wide range of serotypes. We determined two novel STs in *Salmonella* database at University College Cork. PFGE represented the highest diversity among our isolate set. Interestingly, all *Salmonella* isolates collected from poultry products showed antimicrobial resistance profiles. This study has a great value not only for surveillance and outbreak detection, but also for gaining an improved understanding of evolutionary path and physiological diversity of *Salmonella* in Turkey.

Keywords: *Salmonella*, MLST, PFGE, antimicrobial resistance

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