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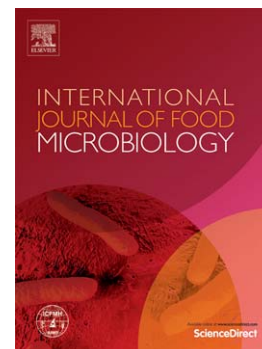
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Salmonella Diversity from Farm to Fork in Turkey

Phenotyping and Genetic Characterization of *Salmonella enterica* Isolates from Turkey Revealing Arise of Different Features Specific to Geography

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Abstract

192 food samples (commonly consumed 8 food types), 355 animal samples (animal feces of bovine, ovine, goat and chicken) and 50 samples from clinical human cases in Sanliurfa city, Turkey in a year were collected to determine the *Salmonella enterica* subsp. *enterica* mosaic in Turkey. 161 *Salmonella* isolates represented 17 serotypes, 20 sequence types (STs) and 44 PFGE patterns (PTs). 3 serotypes, *S. Enteritidis*, *S. Typhimurium* and *S. Kentucky*, were recovered from three different hosts. The highest discriminatory power was obtained by PFGE (SID=0.945), followed by MLST (SID=0.902) and serotyping (SID=0.885) for all isolates. The prevalence of antimicrobial resistance genes (*aadA1*, *aadA2*, *strA*, *strB*, *aphA_{1-tab}*, *bla_{TEM-1}*, *bla_{PSE-1}*, *tetA*) was highly correlated with phenotypic profiles of aminoglycoside, β -lactam and tetracycline groups ($\kappa > 0.85$). From our knowledge, this is the first study reporting spatial and temporal distribution of *Salmonella* species through phenotypic and genetic approaches over farm to fork chain in Turkey. Thus, our data provided further information for evolution, ecology and transmission of *Salmonella* in Turkey.

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