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Investigation and Characterization of CRISPR-Cas system structure in *Salmonella enterica* Serovar *enteritidis*

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The aim of this study: *Salmonella enterica* is an enteric pathogen and one of the cause of bacterial foodborne illness in the world. It is known as enormously diverse species with six subspecies and over 2500 serovars. CRISPR- associated Cas proteins systems are found in 45% bacterial genomes including *Salmonellaspp*. which provide an adaptive immune system against bacteriophages and plasmids. Nowadays CRISPR loci could provide information useful for typing. *Salmonella* has two CRISPR loci (CRISPR1 and CRISPR2) and in this study, we analyze 15 isolates of *Salmonella enteica* serovar *enteritidis* with the aim of developing subtyping methods or understanding the *Salmonella* phylogeny better.

Material and method: In this study 15 isolates of *Salmonella enterica* serovars *enteritidis* were isolated from poultry in Izmir. We analyzed CRISPR1 and CRISPR2 loci of these isolates by PCR; the both DNA strands of amplicons of PCR products were sequenced. CRISPR loci sequences were aligned and the arrangement of spacersperformed by CRISPR finder and CRISPRcompar programs (http://crispr.i2bc.paris-saclay.fr/). MEGA 5 were used for phylogeny analysis and drawing genetic dendrogram.

Results: Both CRISPR1 and CRISPR2 loci were detected in 14 (93%); 12(80%) and 11(73%) of isolates. The direct repeat sequence is same in two CRISPR loci and different spacers sequences were found in an average of 5 spacers. This results shows that *Salmonella spp*. save themselves against the foreign DNAs like bacteriophages and plasmids and CRISPR-Cas systems play an important role in virulence, infection, and evasion of host immune system.

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