Molecular Detection of Salmonella Serovar Isolated from Eggs

Monadi, M. (MSc) MSc of Microbiology, Department of Microbiology, Islamic Azad University, Jahrom Branch Jahrom, Iran

Kargar, M. (PhD) Associate Professor of Microbiology, Department of Microbiology, Islamic Azad University, Jahrom Branch Jahrom, Iran

Naghiha, A. (PhD) Assistant Professor of Microbiology, Department of Animal Science, College of Agriculture, Yasuj University, Yasuj, Iran

Najafi, A. (MSc) PhD Student of Marine Microbiology, The Persian Gulf Marine Biotechnology Research Center, Bushehr University of Medical Sciences, Bushehr, Iran

Mohammadi, R. (MSc) MSc of Microbiology, Herbal Medicine Research Center, Faculty of Medicine, Yasuj University of Medical Sciences, Yasuj, Iran

Corresponding Author: Kargar, M.

Email: mkargar@jia.ac.ir

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Abstract

Background and Objective: Salmonellosis is the most common type of food poisoning in developed and developing countries that is caused by *Salmonella* serotype. Hence, we aimed to identify the Salmonella serovars in eggs obtained from Kohgiluyeh and Boyerahmad province and to evaluate antibiotic resistance of the isolated strains.

Material and Methods: In this study, 210 eggs were collected from Kohgiluyeh and Boyerahmad Province. The bacteria were isolated and identified using biochemical tests. After extraction of genomic DNA, Salmonella gender, *Salmonella enteritidis* and *Salmonella typhimurium* were investigated by invA, fliC and sefA primers, respectively, using Multiplex PCR method.

Results: of 210, 14 (6.66%) were contaminated with *Salmonella*. Of these, 12 (5.71%) were *Salmonella typhimurium* and 2 (0.95%) were related to Salmonella spp. None of the samples were contaminated with *Salmonella enteritidis*. The highest resistance was related to penicillin (100%) and neomycin (78.57%).

Conclusion: *Salmonella typhimurium* is the predominant serovar causing contamination in the eggs of this Province. Given the wide spread of antibiotic resistance in different serotypes of *Salmonella*, we recommend avoiding of indiscriminate use of antibiotics in livestock and poultry.

Keywords: *Salmonella*, Drug Resistance, Antibiotic, Multiplex PCR, Kohgiluyeh and Boyerahmad