THE ROLE OF *INVA*-GENE IN THE DETERMINATION OF *SALMONELLA* SPP. CONTAMINATION OF FOOD

Emilia BEHTA[1,2]

[1]*Doctoral School of Food Sciences, Economics and Management, Technical University of Moldova,* ***Moldova***
[2] *"Nicolae Testemitanu" State University of Medicine and Pharmaceutics, Chișinău,* ***Moldova***

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In recent decades, the incidence of salmonellosis has been increasing worldwide. Contamination of food with *Salmonella* spp. And, as a consequence, the development of salmonellosis is a common bacterial disease that affects the intestinal tract and a severe foodborne toxic infection, it is a serious threat that requires great attention to the control of the microbiological purity of food, the development of quick and accurate methods for the detection and identification of *Salmonella* spp. in food in order to ensure their quality in a timely manner and safety, as well as avoidance of economic losses. Currently, *Salmonella* spp. is detected by standard microbiological methods, which are usually laborious and time-consuming. Nowadays, molecular techniques are becoming more and more important for the detection and typing of *Salmonella*.

The modern scientific literature on the mechanisms of development of *Salmonella* infections at the genetic level has been analyzed. The ability of *Salmonella* to penetrate into phagocytes and enterocytes within a few minutes after ingestion of infected food and follow spread throughout the body is provided by a set of effectors whose coordinated expression promotes intracellular survival and replication of bacteria. One of the earliest stages of the pathogenic cycle is the invasion of intestinal epithelial cells. The genetic locus *inv*, which allows *Salmonella* spp. to penetrate intestinal epithelial cells, has been identified. The *invA* gene is a part of this locus and an important component of the inner membrane of the Type III Salmonella Secretion System (T3SS) apparatus, which is responsible for regulation of the export of virulence protein in pathogenic bacteria. Bacterial genome of *Salmonella* includes almost 4.5 thousand genes and consists of one circular chromosome and a number of plasmids. Have been identified the most common genes, and the most detectable gene was the *invA* gene. In the studies of many authors, PCR is used to identify *Salmonella* spp. For this, using special programs, primers are created and implemented that target the *invA* gene, as a conservative and specific indicator of the *Salmonella* genome. These primers are the most selective. The *invA* gene contains unique sequences specific to the genus *Salmonella* and has established itself as a specific target for PCR. To obtain a more accurate profile of the prevalence of *Salmonella* spp, it is appropriate to use the PCR-RT method and to develop primers specific for the *invA* gene. This approach can be considered as a good alternative to the traditional culture method.