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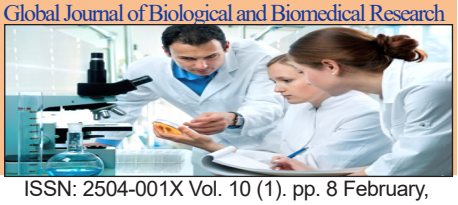

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Opinion Open Access

Listeria monocytogenes isolates by high-resolution melting curve

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ABOUT THE STUDY

Listeria Monocytagenes is a group of gram-positive, mobility, nonporous formation, and adherent patho-gens that can cause rituris with individuals, elderly and immune isomeric patients. *L. monocytogenes* is widely distributed in the environment and has the abil-ity to survive and grow under severe conditions such as low temperature and high salt levels. *L. Monocy-togenes* is an environmental organism that typically infected with the food processing industry, and 99% of human listeriosis infections are presumed to be caused by consumption of polluted food. Listeriosis is associated with a high hospitalization rate (85-90%), with a mortality rate of 2030% for this condition, which is higher than infections caused by other food-borne pathogens.

High Resolution Melting (HRM) is a real-time PCR (QPCR) -based method developed to detect chang-es in nucleic acid sequences. This method monitors changes in DNA sequences in response to changes in the melting temperature of real-time PCR prod-ucts. Through our study, five variable number tandem repeat (VNTR) loci were selected for genotyping of *Listeria monocytogenes* isolates. VNTR is a region of DNA that contains a short sequence of nucleotides called tandem repeats (TRs) in different numbers of different strains. Today, this difference in the number of VNTRs is used as a suitable target for assessing bacterial genotyping. In this study, we used the HRM method, which is a simple and rapid method for analyzing VNTR and genotyping the *Listeria monocyto-genes* strain.

Listeria monocytogenes isolates play an important role in identifying the source of infection and preventing the spread of this pathogen. Currently, different methods are used for molecular typing of *Listeria monocyto-genes* from different sources, such as PFGE, MLST, and more recently WGS, which requires a lot of labor and cost. MLVA (Multilocus Variablenumber Tandem-repeat Analysis) is another molecular typing technique that offers practical advantages such as speed and ease of use. This procedure uses capillary electropho-resis for diagnosis. The VNTR locus in the bacterial genome is frequently mutated, the number of tandem repeats changes, and the nucleic acid changes contin-uously. Changes in the number of VNTR repeats are used by the MLVA method for molecular typing of var-ious isolates. To evaluate the validity and suitability of the MLVA method for routine monitoring and subtyping of *Listeria monocytogenes* isolated from meat prod-ucts, and collected 113 isolates of *Listeria monocyto-genes* from meat.

In HRM, changes in nucleotide sequences and variations in chain length of PCR products are indicated by changes in the melting curve. One study performed an analysis of MLVA using the HRM method as an easy and rapid method for distinguishing *Listeria monocytogenes* isolates. The study also compared the ability of MLV-AHRMA, MLVA using capillary electrophoresis, and multilocus sequence typing (MLST) to distinguish strains. This study showed that the MLVA HRM method using capillary electrophoresis is more discriminating than MLST and MLVA. In studies on system generation analysis, MLST and MLVA were performed.