

Genetic Diversity of Motile *Aeromonas* spp. from Meat Samples

Seza ARSLAN, Fatma ÖZDEMİR, Rümeysa KÜÇÜKSARI

Department of Biology, Faculty of Arts and Science, Abant İzzet Baysal University, Turkey
arslan_s3@ibu.edu.tr

Aim of the study: *Aeromonas* spp. are frequently present in aquatic environments. These bacteria are commonly isolated from food, water and soil. In humans, *Aeromonas* species are responsible for various infections including gastroenteritis, chronic diarrhea, wound infections, respiratory tract infections, peritonitis, urinary tract infections, and septicemia. Enterobacterial repetitive intergenic consensus sequence-PCR (ERIC-PCR) method is useful for epidemiological studies and population genetic analysis of *Aeromonas* spp. In this study, the motile *Aeromonas* strains obtained from seawater fish (*Sparus aurata*), freshwater fish (*Oncorhynchus mykiss*) and ground beef were tested to determine the genetic relatedness by ERIC-PCR.

Material and Methods: A total of 44 motile *Aeromonas* strains including 8 strains of *A. hydrophila*, 27 strains of *A. caviae*, and 9 strains of *A. veronii* biovar *sobria* from fish and ground beef samples were examined for genotyping by ERIC-PCR method. Primer sequences, ERIC-1R and ERIC-2, were used for ERIC-PCR. PCR reactions were performed in a thermocycler with initial denaturation at 95°C for 7 min, followed by 30 cycles of denaturation at 90°C for 30 sec, annealing at 52°C for 1 min and extension at 65°C for 8 min, and a final extension at 65°C for 16 min. A 8 µl aliquot of each amplification reaction was analysed using electrophoresis on a 1.5% agarose gel and run in a 1X Tris-borate-EDTA buffer. The gel was stained with ethidium bromide and visualized with a UV transillumination. The band patterns of ERIC-PCR were analysed using the NTSYS-pc (version 2.10) software package. Each amplified ERIC band was marked as 1 for presence and 0 for absence. The similarity among the motile *Aeromonas* strains was calculated with Dice coefficient. The dendrogram was obtained by means of unweighted pair group method using average (UPGMA) clustering.

Results: In this study, a total of 45 *Aeromonas* strains including 44 motile *Aeromonas* strains isolated from fish and ground beef samples and one *A. hydrophila* ATCC 7966 as a reference strain were subjected to ERIC-PCR fingerprinting. Dendrogram constructed using ERIC-PCR fingerprint patterns showed that the 45 *Aeromonas* could be divided into 34 genotype. ERIC-PCR revealed 4 clusters consisting of 15 strains at the 100% similarity level.

Acknowledgements: This study was supported by Abant İzzet Baysal University, Scientific Research Projects (Project No. BAP-2011.03.01.405) to whom we would like to express our gratitude.

Keywords: *Aeromonas* spp., ERIC-PCR, Molecular typing, fish, ground beef.