

Genotyping of *Yersinia enterocolitica* Strains from Various Food Products by Enterobacterial Repetitive Intergenic Consensus (ERIC) - PCR

Fatma ÖZDEMİR, Seza ARSLAN

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

Aim of the study: *Yersinia enterocolitica* belongs to *Enterobacteriaceae* family. *Y. enterocolitica* which is an important food-borne enteropathogen can cause gastrointestinal infections in humans, ranging from mild diarrhea to mesenteric adenitis, evoking appendicitis and septicemia. Various molecular methods are available for genetic analysis of *Enterobacteriaceae* isolates. Enterobacterial repetitive intergenic consensus (ERIC)-PCR is a powerful method to reveal genetic differences among the strains. Recently, the number of studies on genetic typing of *Y. enterocolitica* by ERIC-PCR method is scarce. Therefore, the purpose of this study to investigate the genetic relationship between the *Y. enterocolitica* strains isolated from meat and milk products through ERIC-PCR technique.

Material and Methods: A total of 18 *Y. enterocolitica* strains were isolated from 300 samples including chicken meat (n=60), minced meat (n=60), homemade white cheese traditionally made from raw milk (n=60), open (unpackaged) white cheese made from pasteurized milk (n=60), and raw milk (n=60). Identification of *Y. enterocolitica* strains from various foods was performed by both conventional and 16S RNA sequencing method. *Y. enterocolitica* strains were analyzed for typing by ERIC-PCR method. The extracted genomic DNA of the strains was maintained -20°C and used for molecular characterization. The amplified DNA bands of ERIC-PCR were recorded as 1 in case of presence of band, 0 when there is no band. ERIC-PCR genotype analysis was performed using the NTSYS-pc (version 2.10) software package. Similarity between the fingerprints was calculated by Jaccard coefficient. Cluster analysis of similarity matrices was carried out by the unweighted pair group method with arithmetic mean (UPGMA) analysis.

Results: The results of our study indicated the fingerprints of *Y. enterocolitica* strains consisted of 2 to 12 amplification bands. The 18 *Y. enterocolitica* strains from meat and milk products and one *Y. enterocolitica* ATCC 23715 reference strain could be divided into 18 different genotypes with %81 similarity. Among the *Y. enterocolitica* strains, the genetic similarity of only two strain was 100%. Consequently, we did not detect a direct relationship among the ERIC-PCR fingerprint patterns in terms of their sampling source.

Acknowledgements: This study was supported by Abant İzzet Baysal University, Scientific Research Projects Fund (Project No. BAP-2011.03.01.460) to whom we would like to express our gratitude.

Keywords: *Yersinia enterocolitica*, ERIC-PCR, meat products, milk products.