

MULTIDRUG-RESISTANT *E. COLI* AND COLIFORMS IN CONFISCATED FOODS OF NON-SCHENGEN ORIGIN

RENÁTA KUGLER¹, AMA SZMOLKA¹, I. TÓTH¹, D. SVÁB¹, NÓRA SCHWEITZER², B. NAGY¹

¹Enteric Bacteriology and Foodborne Zoonoses, Institute for Veterinary Medical Research, Centre for Agricultural Research, Hungarian Academy of Sciences; ²Veterinary Diagnostic Directorate, National Food Chain Safety Office, Budapest, Hungary

Multidrug resistance (MDR) in Enterobacteriaceae is an increasing worldwide concern. The import of contaminated food may represent a food safety risk by the spread of pathogenic- and/or MDR bacteria and their determinants for antimicrobial resistance. As part of an EU collaborative research project (PROMISE), our studies aimed to identify and analyse pathogens like *Salmonella* spp., *Campylobacter* spp. and verotoxigenic *E. coli* (VTEC), and isolation of MDR *E. coli* from food samples from non-Schengen countries confiscated at Hungarian borders was also attempted. Detection of *Salmonella*, *Campylobacter* and VTEC bacteria was performed according to the appropriate ISO standards (ISO 6579:2002/*Salmonella*, ISO 10272-1:2006/*Campylobacter* and ISO 16654:2001/VTEC-O157). For the isolation of non-O157 VTEC strains the Ridascreen® method was also used. *E. coli* colonies were isolated by their phenotype on Chromocult Coliform selective agar plates (Merck) and their identity was confirmed by PCR based on the presence of *lacZ* and *uidA* genes. For the detection of MDR of *E. coli* a pre-selection was used: the isolates were tested for their resistance to ampicillin, cefotaxime and tetracycline, and those demonstrating resistance for at least one of these three antibiotics were tested by disc diffusion for 18 antimicrobials with clinical relevance. The interpretation was performed according to the CLSI recommendations, and isolates with intermediate resistance were considered as sensitive. Resistance phenotype was confirmed by the presence of the respective antimicrobial resistance genes by PCR. The integron content of the isolates was also identified. A total of 207 confiscated food samples were tested in this study. All of them proved to be negative for *Salmonella* and VTEC bacteria, and in one sample from raw chicken carcass *Campylobacter jejuni* was identified. From the 207 samples, 833 coliform bacteria were isolated (5-10 representatives/sample) according to the methods described above. There were 87 samples negative for the presence of coliforms. From the total of 833 coliform isolates 257 (31%) fulfilled the pre-selection criteria for MDR, and were subjected to the determination of the resistance phenotype. Among them 13 isolates showed resistance to at least three different antimicrobial classes thus were designated as MDR. They represented 11 different food samples: 4 porcine, 2 bovine, 2 chicken, 1 rabbit, 1 duck and 1 of sheep origin. In addition to the above 13 MDR isolates, 10 other isolates merits further analyses, being resistant to β -lactams and/or aminoglycosides. Class 1 integrons (1.0-1.5 kb) were found in 9 of the 13 MDR isolates, and majority of them showed an atypical structure lacking the *sul1* gene from their conserved segments 3'CS. Identification and detailed characterization of genes underlying above resistances mechanisms is in progress, and results will be analysed in comparison with those of international and our earlier national studies on antimicrobial resistance genotypes.

PRELIMINARY RESULTS OF A MANNANE-BASED SYMBIOTIC PROJECT

J. KUKOLYA¹, ERZSÉBET BAKA¹, Á. TÓTH¹, ILDIKÓ BATA-VIDÁCS¹, OLIVIA CSERNUS¹, TERÉZ BARNA², I. NAGY³, SZ. FERENCZY⁴, KRISZTINA J. KOVÁCS⁴

¹Department of Microbiology, Central Environmental and Food Science Research Institute, Budapest; ²Department of Genetics and Applied Microbiology, Faculty of Science, University of Debrecen, Debrecen, Hungary; ³Department of Molecular Structural Biology, Max Planck Institute of Biochemistry, Martinsried, Germany; ⁴Laboratory of