P3-21 Integrons and Antimicrobial Resistance Genes of Multidrug Resistant* Escherichia coli *and Coliform Bacteria from Foods of Animal Origin Confiscated at the Hungarian Borders

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Introduction: The import of contaminated food may represent a food safety risk by the spread of pathogenic and/or multidrug resistant (MDR) bacteria and their determinants for virulence and antimicrobial resistance.

Purpose: Here we aimed to isolate and characterize MDR *E. coli* and coliform bacteria from food samples from non-Schengen countries confiscated at the Hungarian borders.

Methods: *E. coli* and coliform colonies were isolated based on their phenotype on Chromocult® Coliform selective media. Furthermore, API®, PCR and 16S rDNS sequencing were used for species identification. Resistance phenotypes were determined by disc diffusion method for 18 antimicrobials with animal and human clinical relevance. Corresponding antimicrobial resistance and virulence gene patterns were identified using PCR microarray systems AMR05 and Ec03, respectively. The gene cassette arrangements of the integrons were defined by amplicon sequencing.

Results: From the total of 207 confiscated food samples, 833 coliform isolates were collected. Among them 17 (13 *E. coli* and 4 coliforms identified as *Enterobacter spp.*) showed resistance to at least three different antimicrobial classes thus were designated as MDR. The 17 strains represented 14 different food samples. Resistance genes *strA, strB, sul2,* $bla_{TEM-1,}$ *tet* (A) predominantly occurred, but in general the prevalence of the virulence genes was low. The identification of genes *qnrB, aac(6')-Ib,* bla_{OXA-7} in some of the isolates indicated the presence of certain emerging antimicrobial resistance plasmids. Class 1 integrons were found in 10 of the 17 MDR isolates (9 *E. coli*, 1 coliform), and in the majority of them the *sul1* gene was absent from their 3' conserved segment (CS). Interestingly, in one of the pork samples we detected a non-typical class 1 integron carrying the *sul3*gene on its 3'CS.

Significance: Above results showed that these illegal foods may frequently carry MDR *E. coli* and coliform bacteria with some unusual or new antimicrobial resistance traits.

P3-22 Which Virus may be Used as Process Control for Diagnosis of Hepatitis A Virus and Norovirus in Food and Water?

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Introduction: The two main viruses most frequently involved in foodborne infections worldwide are norovirus (genogroup I (NoV GI) and genogroup II (NoV GII) and hepatitis A virus (HAV). They are mainly transmitted through fecal–oral route, by person-to-person contact or by consuming contaminated water and foods. Detection methods used in the field of food virology are currently based on a final detection of the viral genome using real-time reverse transcriptase PCR (RT-qPCR). One of the general requirements for viral diagnosis in food concerns the use of a process control virus to monitor the quality of the entire viral extraction procedures as described in the CEN/ISO/TS 15216-1 standard published in 2013. The selected virus should exhibit morphological and physicochemical properties similar to the pathogen viruses, thus providing comparable extraction efficiency.

Purpose: The aim of this study was to determine which virus is most likely to choose as process control, murine norovirus (MNV-1) or mengovirus, for detecting HAV, NoV GI and NoV GII in bottled water, salads and semi-dried tomatoes.

Methods: Food samples were spiked with HAV, NoV GI or NoV GII alone or in presence of MNV-1 or mengovirus. Recovery rates of each pathogen virus were compared to those of both potential process controls using a multiple comparison procedure.

Results: Both process control viruses did not influence the recovery of pathogen virus regardless of the food matrices. MNV-1 was the most adapted to validate the detection of HAV and NoV GII in the three food matrices as well as NoV GI in salads. Mengovirus seems the most adapted for NoV GI detection in bottled water and semi-dried tomatoes.

Significance: The process control virus is essential for validation of viral diagnosis in food and its choice is dependent of food type and pathogen virus.

P3-23 Comparison of the New TEMPO® BC Method with the ISO 7932 Method for Rapid Enumeration of Bacillus cereus Group in Food and Environmental Samples

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