

R2798

Abstract (publication only)

**Antimicrobial resistance and virulence phenotypes and genes in food-borne bacterial strains**

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**Objectives:** The aim of this study is the investigation of virulence and resistance features in bacterial strains isolated from different food products. **Methods:** A number of 54 bacterial strains belonging to Enterobacteriaceae and Listeriaceae families were isolated and identified according to the latest ISO standards concerning food safety. **Phenotypic assays:** i) adherence to eukaryotic HeLa cells (Cravioto's adapted method); ii) biofilm development on the inert substratum (slime production assay); iii) evaluation of soluble enzymatic factors expression (pore-forming enzymes, proteases, siderophore-like production); iv) antibiotic susceptibility testing (disk diffusion method). **Genotypic PCR detection of:** i) virulence genes for the classical *E. coli* pathovars (eaeA, bfpA, eaf, AggR, EAggE, afa, pap, sfa, VT1, VT2, EAST1); ii) other virulence genes for *E. coli* (pldA -phospholipase A, helD- helicase IV); iii) virulence genes for *Salmonella* sp. (spvC, invA); iv) and for *Listeria* sp. (hlyA, prfA); v) antibiotic resistance genes (FOX, MOX, blaTEM, blaCTX-M, CIT, DHA, ACCM, EBCM, tetA, tetB, tetC, tetD). **Results:** The analyzed enterobacterial strains exhibited different adherence patterns to the cellular and inert substrata, and the following soluble virulence factors: proteases (caseinase, gelatinase), pore-forming toxins and enzymes (haemolysins, lecithinase, lipase), DN-ase, amylase, esculin hydrolysis, while *Listeria* sp. strains expressed only haemolysins, amylase and esculin hydrolysis. A significant number of enterobacterial strains showed resistance to beta-lactams and/or tetracyclines, while only a few expressed resistance to aminoglycosides, and *Listeria* sp. strains were resistant to trimethoprim-sulfamethoxazole. The molecular assay revealed that many of the analyzed strains possess multiple virulence genes and also genes that confer resistance to different antibiotics. **Conclusion:** The use of an enlarged panel of virulence and resistance markers allowed us to demonstrate that food borne bacteria could represent a major microbiological risk factor for the consumer's health, especially for people with a weak immune system, due to the presence of multiple virulence and resistance features and of corresponding encoding genes.