P0933 Antimicrobial resistance and virulence features in Salmonella sp. strains isolated from community-acquired infections

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Background: Salmonella represents the most common etiological agent of foodborne diarrheal illnesses, with emerging resistance and virulence. The aim of this study was to reveal the antibiotic resistance and virulence determinants occurred in community acquired Salmonella infections.

Materials/methods: The study included 97 recently isolated (2017) Salmonella sp. from ambulatory patients (4 months – 63 years) in Synevo Central Laboratory, Medicover, Bucharest, Romania. All isolates were recovered from digestive infections, identified by mass spectrometry using the MALDI Biotyper and their antibiotic susceptibility profile was determined by agar disk diffusion (CLSI, 2017). Virulence phenotypes were assessed by performing enzymatic tests for the expression of eight soluble virulence factors. Evaluation of the bacterial adherence to cellular substrata was performed using Cravioto’s adapted method. Simplex and multiplex PCR was performed on genomic DNA to identify the β-lactam (TEM like; CTX-M-like, NDM-like and OXA-48-like), tetracycline resistance genes (tetA, tetB, tetC, tetD), fluoroquinolone resistance (QnrA, QnrB and QnrS), sulfonamide resistance genes (sul1, sul2, sul3), class 1 integrons and virulence genes (invA, spvC, sefA, pefA).

Results: The analyzed Salmonella strains expressed various resistance rates to tetracyclines (27.83%), quinolones (22.68% to ofloxacin), β-lactams: ampicillin (18.55%), ampicillin-sulbactam (16.49%), piperacillin (15.46%), amoxicillin-clavulanic acid (8.24%), aztreonam, ceftriaxone, cefotaxime and cefpodoxime (6.18%); trimethoprim sulphamethoxazole (8.24%). Only resistance genes to non-β-lactam antibiotics were detected, respectively: tetA-like, tetB-like – 100%, tetC-like – 26.08%, tetD-like-4.34%, Sul1 – 60.86%, Sul2 – 43.47%, QnrA-like - 4.34%. Integrase was found in more than 70% of the studied strains. Regarding the soluble virulence factors, the most frequently expressed were amylase (13%) followed by DN-ase, while 95% of isolates were positive for spvC gene and 26.8% harboured the invA gene, which is related to the invasion potential of Salmonella strains. Isolates exhibited different indexes of adherence to the cellular substratum represented by HeLa cells, ranging from 2 to 20 %. The diffused-localized pattern was the most frequent.

Conclusions: These results could help clinicians to achieve correlations between clinical manifestations, virulence and resistance markers in Salmonella sp. infections for a more personalized therapy.