

P510 Phenotypic and genotypic characterisation of antimicrobial resistance in Turkish *Salmonella infantis* isolates from chicken and minced meat

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Objectives: Characterisation of the resistance (R) phenotypes and underlying molecular mechanisms in *Salmonella (S.) Infantis* strains isolated from Turkish foods.

Methods: 100 *Salmonella* isolates were isolated from foods bought in free markets in Ankara (2005–2006). One of the most prevalent serotypes was *Infantis* (13 isolates). Nine of these *S. Infantis* isolates were considered as epidemiological unrelated strains (different isolation date or place). The nine strains (7 from chickens and 2 from minced meat) were tested for susceptibility to 17 antimicrobial agents by broth microdilution. Resistant strains were screened for 16 R-genes, class 1 and 2 integrons and mutations in the quinolone-R determining regions. Strains were typed by XbaI-PFGE and plasmid profile.

Results: The strains showed two similar XbaI-PFGE-patterns (differences affecting two bands). Six strains showed PFP1 and 3 PFP2. One big plasmid (>200kb) was present in all of them. All strains were multiresistant, with resistances to 7–9 antimicrobials (6–7 R-determinants). Two phenotypic R-patterns were found: [kanamycin–neomycin–nalidixic acid–streptomycin–spectinomycin–sulfamethoxazole–tetracycline–trimethoprim–sulfamethoxazole/trimethoprim] in eight strains, and the same R-pattern without [kanamycin–neomycin] in one. One R-determinant was responsible for each resistance: aphA1 for kanamycin, aadA1-like for streptomycin-spectinomycin (no strA or strB were found); sul1 for sulfamethoxazole (no sul2 or sul3 were present); tet(A) for tetracycline (no tet(G) or tet(B)); and dfrA14 for trimethoprim (no dfrA1, A12, A7 or A17 were present). All strains harboured a class 1 integron carrying an aadA1 gene. No class 2 integrons were detected. All strains were resistant to nalidixic acid and showed reduced susceptibility to ciprofloxacin (0.25–0.5 microg/mL) conferred by mutations in the gyrA (Ser83 to Tyr83) and parC (Thr57 to Ser57) genes. No quinolone-R genes qnrA, qnrB or qnrS were found.

Conclusions: *S. Infantis* isolated from foods in Turkey exhibit a wide repertoire of genetic elements to survive under antimicrobial pressure. One specific PFGE-type carrying a big plasmid (>200 kb), and with the antimicrobial multi-R pheno/genotype [KAN-NEO]-[STR-SPE]-SUL-TET-[TMP-SXT]-NAL/aphA1-aadA1-sul1-tet(A)-dfrA14-[gyrA^{Tyr83}-parC^{Ser57}] is widespread. Since *S. Infantis* frequently causes human infections, the wide spread of such a multiresistant clone within foods should be considered as a public concern.

P511 *Salmonella enterica* serotype Typhimurium DT104 as a cause of infantile bacteraemia in Southern Mozambique

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Objectives: To report the presence of *Salmonella enterica* serotype Typhimurium DT104 as a cause of infantile bacteraemia in Southern Mozambique.

Methods: Bacterial infections surveillance has been carried out at Manhiça Health Research Centre since 1998, Maputo, Mozambique. One hundred seventy *Salmonella typhimurium* isolated from under 15 children admitted at Manhiça District Hospital (MDH) were analysed. Microbial identification was performed by biochemical methods, while serotype and phagotype were established following conventional methodologies. Antimicrobial susceptibility levels to ampicillin (Amp), amoxicillin plus clavulanic acid (AMC), ceftazidime (Caz) gentamicin (Gm), streptomycin (Str) cotrimoxazole (Sxt), tetracycline (Tc), chloramphenicol (Chl), nalidixic acid (Nal) and ciprofloxacin (Cip) were established by the method of Kirby-Bauer. Molecular mechanisms of resistance to β -lactams, chloramphenicol and tetracycline as well as the presence of type 1 integrons were detected by PCR and sequencing.

Results: Two isolates were identified as *S. typhimurium* DT104, which were resistant to Amp, Str, Chl and Tc, being susceptible to Sxt, Caz, Nal, Cip and Gm. One of the isolates was susceptible to AMC, while the other one was intermediate. The presence of the genes carb2, floR and tetG, as well as two integrons, that carry on the aforementioned carb2 gene and an aadA2 respectively were detected. Presence of the tetA, tetB, cmlA, tem-like, shv-like, oxa-1 like, oxa-2 like and oxa-5 like genes was not detected.

Conclusion: This is the first report of multi-drug resistant *Salmonella enterica* serotype Typhimurium DT104, as responsible for bacteraemia in rural Mozambican children. Bacterial surveillance studies are need in the country to monitor the emergence of multi-drug resistant *Salmonella* including this phagotype.

P512 Dissemination of antibiotic multi-resistant *Salmonella* isolates in Portuguese piggeries

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Objectives: To study susceptibility to different antibiotics and to characterise the genetic determinants of antimicrobial resistance in *Salmonella* isolated from Portuguese piggery in order to assess the contribution of this type of animal exploration to the burden of mobile resistance genes and multidrug resistant clones previously observed in human and food products.

Methods: Dry faeces samples collected in 2006 from 2 pig farms in the Center and South of Portugal were positive for the presence of *Salmonella* (reference method ISO 6579:2002). Antibiotic susceptibility was study by disk diffusion method (CLSI) to 10 antimicrobial agents. Different antibiotic resistant phenotypes were selected for further studies. Detection and characterisation of class 1 integrons was performed by PCR, RFLP (TaqI) and sequencing. Resistance genes were searched by PCR. Conjugation assays and clonality analysis (PFGE-XbaI) were performed.

Results: All the *Salmonella* isolates recovered were resistant to one (tetracycline) or more antimicrobial agents (streptomycin, gentamicin, ampicillin, nalidixic acid, chloramphenicol, tetracycline, sulfonamides or trimethoprim). Characterisation of class 1 integrons revealed the presence of an array of gene cassettes (dfrA12, aadA) in isolates of *S. typhimurium* which also carried sul1, sul2 and sul3 genes and in isolates of *S. Rissen*, carrying sul1. The isolates of both serotypes were clonally related to strains previously observed in human and foodborne isolates widely disseminated in Portugal. Interestingly, MDR isolates of the *S. Rissen* clone were recovered from both piggeries studied. Other resistance genes (blaTEM, aac(3)-IV, tetA) were identified in the MDR isolates, but not integrated as gene cassettes.

Conclusion: Piggeries are in our country a source of MDR *Salmonella* isolates. Intensive use of several antimicrobial agents in this type of animal production seems to contribute to the selection of widely disseminated MDR clones.

P513 Dissemination of a new gene cluster comprising sul3 (tnp-sul3-tnp) linked to class 1 integrons with an unusual 3'CS region (qacH) among *Salmonella* isolates

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Objectives: The objective of this study was to characterise the genetic background of sul3 gene, including their association to integron structures, in non-typhoid *Salmonella* isolates, in order to explain the dissemination of this sulfonamide resistance gene.

Methods: Forty-seven sul3-carrying *Salmonella* isolates from different sources (human, food products and environment) and serotypes were studied. Characterisation of class 1 integrons was done by PCR, RFLP (TaqI) and sequencing. Clonality analysis (PFGE-XbaI) and location of the sul3 gene by conjugation assays, plasmid analysis and Southern blot hybridisation (S1-PFGE) were performed.

Results: A gene cluster comprising sul3 and transposase-like sequences (tnpA-sul3-orf1-IS26) was linked to class 1 integrons with an unusual