Increase in incidence of resistance to ampicillin, chloramphenicol and trimethoprim in clinical isolates of Salmonella serotype Typhimurium with investigation of molecular epidemiology and mechanisms of resistance

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Antimicrobial resistance patterns of Salmonella serotype Typhimurium isolates obtained during the period 1987–1994 were examined and the molecular epidemiology and the mechanisms of resistance to ampicillin, chloramphenicol and trimethoprim were investigated in 24 strains isolated during 1994. Resistance to ampicillin increased from 18% to 78%, to chloramphenicol from 15% to 78%, to tetracycline from 53% to 89% and to co-trimoxazole from 3% to 37%, whereas resistance to norfloxacin remained at 0%. Of Salmonella serotype Typhimurium strains isolated during 1994, all ampicillin-resistant strains had an MIC > 256 mg/L, except one strain in which the MIC was 64 mg/L. Twelve strains (52%) had a TEM-type β-lactamase, nine (39%) a CARB-type β-lactamase and two strains (8%) had an OXA-type β-lactamase. Chloramphenicol acetyl-transferase activity was detected in only nine (47%) of 19 chloramphenicol resistant strains, whereas all eight trimethoprim-resistant strains produced a dihydrofolate reductase type Ia enzyme. Three different epidemiological groups were defined by either low-frequency restriction analysis of chromosomal DNA and pulsed-field gel electrophoresis or repetitive extragenic palindromic-PCR. The latter technique provided an alternative, rapid and powerful genotyping method for S. Typhimurium. Although quinolones provide a good therapeutic alternative, the multiresistance of S. Typhimurium is of public health concern and it is important to continue surveillance of resistance levels and their mechanisms.

Introduction

Gastro-enteritis is the most common clinical manifestation of salmonella infection [1]. The two most common causes of non-typhoidal salmonellosis are serotypes Enteritidis and Typhimurium. Although infection with non-Typhi Salmonella often causes mild self-limiting illness, serious sequelae including death may occur, especially in immunocompromised patients [2]. In this sense Salmonella serotype Typhimurium is an important cause of diarrhoea and bacteraemia in HIV-positive patients and normally they require antimicrobial treatment [3].

The antimicrobial resistance of Salmonella has an impact through the recognised association between drug-resistant salmonellae and the routine clinical use of antimicrobial agents for infections other than salmonellosis. There are three facets of this association: (i) antimicrobial-resistant salmonella infections can complicate antimicrobial treatment of other infections; (ii) prior antimicrobial therapy allows fewer numbers of antimicrobial-resistant Salmonella to cause symptomatic infections; (iii) an increase in the proportion of salmonella that are antimicrobial-resistant will increase the overall frequency of salmonellosis [4].

Various typing techniques have been used in epidemiological studies to discriminate strains of Typhimurium. These include biotyping [5], phage typing [6, 7], antimicrobial susceptibility testing [8], plasmid
P-Lactamase activity was quantified by the spectrophotometric assay of nitrocefin hydrolysis [19] in 0.1 M phosphate buffer (pH 7.0); β-lactamases were detected by two different methods – iso-electric focusing and the genes encoding them by PCR. For iso-electric focusing, cell-free lysates were obtained by ultrasonication of exponential cultures grown at 37°C in LB broth containing ampicillin 50 mg/L. Analytical iso-electric focusing was done by applying the crude sonic extracts to Phast gels (pH gradient 3–9) in a Phast System (Pharmacia AB, Uppsala, Sweden). Several strains carrying β-lactamases of known pI were used as controls and focused in parallel with the extracts. Nitrocefin (50 mg/L) was used for detection. Three different sets of primers were used to detect β-lactamase genes by PCR, one specific for blaTEM gene amplification and another for blacARB gene amplification [20]. The third set was designed according to the blaOXA-1 gene and comprised 5'-GGCACCAGATTGATTTATCCTGATATTCCATGGAGTG-3' and 5'-TTTTTCTTGGCTTTTATCTCGGCTTTTATGGCTTG-3'.

Chloramphenicol acetyl-transferase detection

The chloramphenicol acetyl-transferase activity was assayed by the radiometric method of Robinson et al. [21] and by a modification of a rapid method developed by Azemun et al. [22]. Briefly, the strains were grown overnight on MacConkey agar. A heavy suspension of bacteria in 0.2 ml of 1 M NaCl, 0.01 M EDTA and SDS 0.05% (pH 8.0) was incubated in an eppendorf tube at 37°C for 60 min. After a short centrifugation in a microfuge, 50 µl were transferred to a microtitration plate. Duplicate wells were prepared with each strain and 50 µl of a solution containing two parts of 0.2 M Tris-HCl, pH 8.0, 2 mM acetylco-enzyme A and one part of 10 mM 5',5'-dithiobis(2-nitrobenzoic acid) (DTNB) in 0.1 M Tris-HCl, pH 8.0, were added to each well. A 50-µl amount of 5 mM sterile chloramphenicol (dissolved in water) was added to one well (test reaction), and an equivalent amount of water was added to the duplicate well (control). The plate was reincubated at 37°C for 5 min. The reaction was stopped by adding 1 N H2SO4 and read spectrophotometrically.

Detection of trimethoprim resistance genes

Samples (1.5 ml) of overnight cultures were centrifuged for 1 min at 12 000 g in a microcentrifuge. The cells were resuspended in 100 µl of sterile saline and 5-µl volumes were dotted on to a Qiabranse Nylon Plus Membrane (Hybaid, Twickenham) and allowed to dry in air. Cell lysis and denaturation of DNA for subsequent hybridisation experiments were as described by Maniatis et al. [23]. The biotin-labelled oligonucleotide used as a probe for the type Ia dihydrofolate reductase (DHFR) gene [24] was as follows: 5'-CGGGAAATGGCCCTGATATTCCATGGAGTGTCG-3'. The probe was custom-synthesised and 5'-biotinylated by British Biotechnology Products (Abingdon). Pre-treatment of membranes with proteinase K was as described previously [25]. Subsequent pre-hybridisation, hybridisation and washing conditions were those recom-
Positive hybridisation results were detected by the BluGENE Detection System (Gibco/BRL, Paisley) with the conditions and washes recommended by the manufacturer.

**Low-frequency restriction analysis of chromosomal DNA by pulsed field gel electrophoresis (PFGE)**

Genomic DNA was extracted by a slightly modified version of the method of Matushek et al. [26]. Briefly, 3 ml of an overnight culture were centrifuged and resuspended in 0.5 ml of lysis 2X buffer (1X, 6 mM Tris-HCl, pH 7.4, 1 M NaCl, 10 mM EDTA, pH 7.5, Brij 0.5%, deoxycholate 0.2%, sodium lauryl sarcosinate 0.5%) to which lysozyme (Sigma) 0.5 mg/ml and RNAase (Sigma) 10 μg/ml were added. Genomic DNA was prepared in agarose plugs as described previously [27]. It was then incubated with 3 ml of 1X lysis solution at 37°C for 2 h with gentle shaking. After incubation, the lysis solution was replaced with ESP (10 mM Tris-HCl, pH 7.4, 1 mM EDTA), to which proteinase K (Sigma) at a final concentration of 100 μg/ml and SDS 1% were added; the plugs were incubated at 50°C for 1 h. Protein digestion products were removed by washing the plugs three times with TE buffer (10 mM Tris-HCl, pH 7.4, 0.1 mM EDTA) at 50°C for 5, 30 and 30 min.

A plug slice 4 mm wide was suspended in 500 μl of restriction buffer for 1 h at 37°C. The buffer was then replaced with 250 μl of fresh restriction buffer and it was incubated overnight with 20 U of XhoI (Promega) following the manufacturer’s recommendations. The DNA fragments were separated by PFGE in an agarose 1% gel (BioRad) that was prepared and run in Tris-borate-EDTA (TBE) buffer on a contour-clamped homogeneous field apparatus (CHEF-DR2, BioRad). The conditions for electrophoresis were 200 V for 21 h, with pulse time from 5 to 8 s. Thereafter, the gels were stained with ethidium bromide and photographed.

**Repetitive extragenic palindromic (REP) PCR**

Bacteria were grown on MacConkey agar overnight. Half a colony of each isolate was suspended in 25 μl of reaction mixture containing 20 mM Tris-HCl (pH 8.8), 100 mM KCl, 3.0 mM MgCl₂ and gelatin 0.1%; 400 μM dNTPs and 1 μM primer were added, together with 2.5 U of Taq polymerase (Gibco-BRL). The reaction mixture was overlaid with mineral oil and amplified with the following programme: 30 cycles at 94°C for 1 min, 40°C for 1 min and 65°C for 8 min, with a single final extension at 65°C for 16 min. Samples (10 μl) of each PCR end-product were analysed on agarose 1.5% w/v gels. One set of primers was used as indicated by Vila et al. [28].

**Statistical test**

Percentages of antimicrobial resistance among different years were compared by Fisher’s exact test with Epi-Info, version 6.02.

**Results**

During the study period, 292 Typhimurium strains were isolated. The origins of the Salmonella isolates were stool (85%), blood (13%) and urine (2%). The increase in the resistance of Typhimurium isolates to several antibiotics during the period 1987–1994 is summarised in Fig. 1. In this period, the resistance of Typhimurium clinical isolates to ampicillin increased from 18% to 78% (p < 0.00007), to chloramphenicol from 15% to 78% (p < 0.00007), to tetracycline from 53% to 89% (p < 0.01) and to co-trimoxazole from 3% to 37% (p < 0.007); all these increases in resistances were highly significant. Meanwhile, resistance to norfloxacin
remained at 0%. In 1994, 83% of the strains were multiresistant.

Twenty-four Typhimurium strains isolated during 1994 were used for detailed investigations of the mechanisms of resistance to ampicillin, chloramphenicol and trimethoprim alone. Although a strain that is sensitive to co-trimoxazole is not necessarily sensitive to trimethoprim alone, all subsequent studies on trimethoprim resistance mechanisms were performed with strains shown to be resistant to trimethoprim alone in MIC tests. Thirteen of these 24 strains were resistant to ampicillin and chloramphenicol; six were resistant to ampicillin, chloramphenicol and trimethoprim; three were resistant only to ampicillin; one strain was resistant only to trimethoprim; and one strain was resistant to ampicillin and trimethoprim. The MICs of ampicillin, chloramphenicol and trimethoprim for these strains are shown in Table 1. All the ampicillin-resistant strains had an ampicillin MIC >256 mg/L, except for one strain in which the MIC was 64 mg/L. All the strains resistant to chloramphenicol and trimethoprim also had MICs >256 mg/L. On the basis of antibiotic susceptibility, five phenotypes could be defined. Thirteen strains belonged to phenotype I (AmpR, CmR, TmS), six to phenotype II (AmpR, CmR, TmR), three to phenotype III (AmpR, CmS, TmS), one strain to phenotype IV (AmpR, CmS, TmR) and one strain to phenotype V (AmpR, CmR, TmR).

Iso-electric focusing was used first to detect β-lactamase production. The results are shown in Table 1. β-Lactamase activity was detected in crude extracts from 96% of the strains resistant to ampicillin. Twelve strains (52%) showed a β-lactamase with a PI of c. 5.4, nine strains (39%) with a PI c. 5.6 and two (8%) with a PI c. 7.0. To corroborate the results of isoelectric focusing a PCR technique with specific primers for amplification of the genes encoding TEM-, CARB- and OXA-type β-lactamasess was used. The PCR results are also shown in Table 1. All the strains that produced a β-lactamase of PI 5.4 showed a positive amplification result with TEM-specific primers, probably corresponding to TEM-1 β-lactamase, whereas all the strains with a β-lactamase of PI 5.6 failed to amplify with the TEM primers, but were positive with CARB-specific primers, corresponding to carbenicillinase and not to TEM-2 β-lactamase as originally thought. The PCR products obtained with both TEM-specific primers and CARB-specific primers had the expected sizes of 503 bp for TEM and 586 bp for CARB (Fig. 2). Both strains with a β-lactamase of PI 7.0 showed a positive reaction (PCR product 598 bp) with the OXA-1 primers.

Chloramphenicol acetyl transferase activity was detected in only 9 (47%) of the 19 chloramphenicol-resistant strains with either the radioactive or spectrophotometric assay (Table 1). All eight strains resistant to trimethoprim gave a positive result with the oligonucleotide probe for DHFR type la gene (Table 1).

The 24 clinical isolates were typed by PFGE and REP-PCR. Three completely different restriction fragment patterns were observed among the 24 isolates of Typhimurium studied when the DNA was digested with XhoI (Table 2 and Fig. 3a). The profiles

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**Table 1. Characteristics of Salmonella serotype Typhimurium clinical isolates**

<table>
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<th>Strain no.</th>
<th>MIC (mg/L)</th>
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CAT: chloramphenicol acetyl-transferase; DHFR, dihydrofolate reductase.

*Radiometric assay to detect CAT.

¹Spectrophotometric assay to detect CAT.
generated with REP primers contained several bands of 0.3–2.5 kb. REP-PCR analysis also revealed three different banding patterns (Table 2 and Fig. 3b). There was very good correlation between the techniques and in both cases the clinical isolates studied could be distributed into three different groups with 15, 6 and 3 strains in each group, respectively (Table 2). However, the results with the fingerprinting techniques did not correlate with the results obtained by antimicrobial susceptibility tests.

Discussion

Salmonella enteritis in man is usually a self-limiting disease and antimicrobial treatment is seldom required; but should spread beyond the intestine occur, effective antimicrobial treatment is essential. Furthermore, HIV-positive patients frequently develop bacteraemia with S. Typhimurium [3, 29–34]. Under these circumstances, a knowledge of the likelihood of resistance to commonly available drugs could be of considerable value to the clinician.

The overall increase in resistance observed in Typhimurium is in agreement with that shown in other geographical areas of Spain [35–38] and other countries [39, 40], except that resistance to trimethoprim-sulphamethoxazole in this study was 37%, compared with 2–11% in other developed countries. It should be noted that a strain that is sensitive to co-trimoxazole is not necessarily sensitive to trimethoprim alone, but all strains studied in detail that were resistant to trimethoprim-sulphamethoxazole in disk tests also showed resistance to trimethoprim alone in MIC tests.

Resistance to β-lactam antibiotics in gram-negative bacilli is mainly associated with β-lactamase production [41]. In the present study, the overall percentage (96%) of β-lactamase-producing strains was similar to that found by others [42]. The ampicillin resistance of strain no. 1694 (ampicillin MIC 64 mg/L) could be associated with changes in permeability. Three types of β-lactamases (TEM, CARB and OXA) were detected. The percentage of strains with either TEM or CARB type β-lactamase was very similar; however, the percentage of strains producing TEM-1 was lower.
than found in the study by Roy et al. [42] who found 27 (87%) TEM-1 β-lactamase-producing strains from a total of 31 ampicillin-resistant strains of Salmonella spp. In the present study, a CARB-type β-lactamase originally isolated from P. aeruginosa was found in 36% of the strains analysed, and this type of β-lactamase has been shown previously in Typhimurium [43]. A plasmid-mediated OXA-type β-lactamase with a pl of 7.0 has also been described in this microorganism [44] and it was found in 8% of the strains of the present study.

The percentage of chloramphenicol-resistant strains producing chloramphenicol acetyl-transferase was very low, suggesting the presence of other mechanism(s) of chloramphenicol resistance. Toro et al. [45] found that the lack of OmpF played a major role in the high level of chloramphenicol resistance in a S. Typhi strain. In this strain, chloramphenicol acetyl-transferase activity was not detected. A similar mechanism could occur in the strains investigated in the present study and further studies to identify possible other mechanism(s) of chloramphenicol resistance are in progress.

All the strains resistant to trimethoprim showed a DHFR type Ia gene, in agreement with the fact that DHFR type Ia is common in trimethoprim-resistant Enterobacteriaceae in many European countries [46,47], but in contrast to the results presented by Agodi et al. [48]. These authors studied the occurrence of trimethoprim resistance in different Salmonella species isolated from human patients and water samples in Sicily and found that only four of 14 trimethoprim-resistant Typhimurium clinical isolates analysed produced a type Ia DHFR, whereas the remaining 10 strains did not produce dihydrofolate reductases belonging to groups Ia, II, IV or V.

No resistance was observed to quinolones or third-generation cephalosporins (data not shown). However, recently there has been an increasing number of reports of strains of Typhimurium that are either resistant, or have decreased susceptibility, to these antimicrobial agents. Resistance to quinolones was rare, although a strain of Typhimurium producing a SHV-2 β-lactamase was detected in France [53,54].

Typhimurium is commonly associated with cattle, but it has also been associated with sheep, pigs, goats, chickens and turkeys, with an association between illness and the consumption of several food items made from the above-mentioned animals demonstrated in a case-control study [55]. Probably the use of antimicrobial agents in veterinary medicine and animal husbandry selects multiresistant Typhimurium, although it is surprising that this dramatic increase in the antimicrobial resistance has not been observed in Enteritidis, which also has an animal reservoir.

Phage typing has been the most useful typing technique to investigate outbreaks of Typhimurium infection; however, its requirement for a collection of specialised phages and the appropriate bacterial strains for their propagation means that it is routinely used in only a few reference laboratories. Some genotyping methods, such as RFLP of 16S rRNA and IS200 and low-frequency restriction analysis of chromosomal DNA with PFGE have proved to be helpful for the epidemiological typing of Typhimurium [56]. PFGE may provide evidence of minor genetic heterogeneity which cannot be detected readily by such RFLP-based techniques as ribotyping and IS200 fingerprinting. However, these techniques are time-consuming and labour-intensive procedures and unsuitable for routine epidemiological analysis of a large number of isolates. A PCR-based fingerprinting technique widely applied in epidemiological investigations uses consensus primers to amplify sequences located between successive repetitive extragenic palindromic elements (REP-PCR) [57]. In the present study, REP-PCR had the same power of discrimination as PFGE.

The strains could be distributed into three different groups based on REP-PCR and PFGE analysis. However, if the different mechanisms of resistance to ampicillin, chloramphenicol and trimethoprim shown by the strains studied are considered, together with the epidemiological markers, 13 different groups were defined. Two groups (AmpR, CmR, TmR, CARB+, REP-PCR-1, PFGE-A and AmpR, CmR, TmR, TEM+, CAT+, DHFR+, REP-PCR-2, PFGE-B) were the most frequent with seven and four strains, respectively. Some strains belonging to a different group showed the same susceptibility pattern and the same mechanism of resistance to β-lactam antibiotics, whereas other strains from the same group showed different mechanisms of antimicrobial resistance. The evolutionary divergence observed is probably due to the acquisition of different mobile genetic elements, such as plasmids, transposons or integrons carrying resistance genes.

In conclusion, REP-PCR analysis provides an alternative, rapid and powerful genomic typing method for Typhimurium. The multiresistance in this microorganism is of public health concern and although third-generation cephalosporins and quinolones currently provide a very good alternative for clinical treatment it is important to continue surveillance of resistance levels and mechanisms of resistance in this species.

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References


