Antimicrobial susceptibility and occurrence of resistance genes among Salmonella enterica serovar Weltevreden from different countries

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Objectives: This study was conducted to investigate the occurrence of antimicrobial resistance among Salmonella Weltevreden isolates from different sources in South-East Asia (Indonesia, Laos, Malaysia, Taiwan, Thailand, Vietnam), Australia, Denmark, New Zealand and the USA.

Methods: A total of 503 isolates were examined for susceptibility to antimicrobial agents, and resistant isolates were examined for the presence of selected resistance genes by PCR.

Results: Only 48 (9.5%) of the isolates were resistant to one or more of the antimicrobial agents tested. A low frequency of resistance was found towards ampicillin (1.8%), chloramphenicol (1.6%), florphenicol (0.4%), nalidixic acid (1.6%), neomycin (0.6%), streptomycin (4.4%), sulfamethoxazole (4.2%), tetracycline (4.0%) and trimethoprim (1.4%), whereas all isolates were susceptible to co-amoxiclav, ceftiofur, ciprofloxacin, colistin and gentamicin. All nine ampicillin-resistant isolates contained a sequence similar to the blaTEM-1b gene, one of the eight chloramphenicol-resistant isolates a sequence similar to the catA1 gene, all three neomycin-resistant isolates a sequence similar to the aphA-2 gene, 16 (73%) of the 22 streptomycin-resistant isolates a sequence similar to the aadA gene, the remaining six (27%) a sequence similar to the strA gene, and all 21 sulfamethoxazole-resistant isolates a sequence similar to the sul2 gene. Thirteen (65%) of the 20 tetracycline-resistant isolates contained the tet(A) gene, four (20%) the tet(B) gene, and one (5%) the tet(C) gene.

Conclusions: This study showed a low frequency of resistance among Salmonella Weltevreden isolated from humans and other reservoirs in South-East Asia and elsewhere. There was no major difference in the occurrence of resistance between source or geographical origin.

Keywords: Salmonella Weltevreden, antimicrobial resistance, genes, South-East Asia

Introduction

Salmonella enterica is one of the most common causes of human gastroenteritis worldwide. More than 2500 different serovars of S. enterica have been identified, and most of them have been described as the cause of human infections. A few serovars are responsible for the majority of human infections. S. enterica serovar Typhimurium and S. enterica serovar Enteritidis have been implicated, in particular, as causes of human salmonellosis. However, in South-East Asia, S. enterica serovar Weltevreden has been reported as a frequent and increasing cause of human infection, and is the predominating serovar in both Malaysia and Thailand.1,2

In recent years, an increase in the occurrence of antimicrobial resistance among S. enterica has been observed in several countries, but there is only limited information on the occurrence of antimicrobial resistance among Salmonella Weltevreden. Boonmar et al.2 reported a very low frequency of resistance among 111 Salmonella Weltevreden from human infections in 1993 in Thailand, which was in contrast to the frequent occurrence of resistance observed among other serovars. However, in 1994, they reported a much...
higher occurrence of resistance among 139 isolates. Thong et al. examined 95 isolates from different sources in Malaysia and found a low frequency of resistance.

This study was conducted to investigate the occurrence of antimicrobial resistance, and the distribution of resistance genes, among 503 Salmonella Weltevreden isolates from different sources in 10 countries, most of them from South-East Asia.

Materials and methods

Bacterial isolates

A total of 503 isolates were received from laboratories in South-East Asia [Indonesia (45), Laos (6), Malaysia (105), Taiwan (7), Thailand (197), Vietnam (19)], Australia (46), Denmark (16), New Zealand (40) and the USA (22). The isolates were collected during 1995–2001. Most isolates originated from humans (282), but some were from animals (59), food products (114) and water, the environment or other sources (48).

Susceptibility testing

Susceptibility to antimicrobial agents was performed as MIC determinations. As described in NCCLS guidelines, a commercially prepared, dehydrated panel (Sensititre) was used for the following antimicrobial agents: ampicillin, ceftiofur, chloramphenicol, ciprofloxacin, co-amoxiclav, ceftiofur, ceftriaxone, cefuroxime, colistin, gentamicin. A total of the antimicrobial agents tested. All isolates were susceptible to all the antimicrobial agents tested. Only 48 (9.5%) of the 503 isolates were resistant to one or more of the antimicrobial agents tested. All isolates were susceptible to co-amoxiclav, cefuroxim, ciprofloxacin, colistin and gentamicin. A low frequency of resistance was found towards ampicillin (1.8%), co-amoxiclav, ceftiofur, ciprofloxacin, colistin, gentamicin (1.6%), chloramphenicol (1.6%), floxuridine (0.4%), nalidixic acid (1.6%), neomycin (0.6%), streptomycin (4.4%), sulfamethoxazole (4.2%), tetracycline (4.0%) and trimethoprim (1.4%) (Table 1). Resistance was observed most frequently among isolates from Laos and Malaysia, but otherwise the occurrence of resistance was so low that no major difference between country or isolate origin could be found.

All nine ampicillin-resistant isolates gave positive amplicons for theblaTEM gene. DNA sequencing revealed 100% identity to the sequence of theblaTEM gene. One of the eight chloramphenicol-resistant isolates contained thecatA gene, all 22 streptomycin-resistant isolates contained thestrA gene and six (27%) thestrB gene, and all 21 sulfamethoxazole-resistant isolates the sul2 gene. Thirteen (65%) of the 20 tetracycline-resistant isolates contained thetet(A) gene, four (20%) thetet(B) gene, and one (5%) thetet(C) gene. None of the four tetracycline-resistant genes could be detected in two tetracycline-resistant isolates.

Table 1. Occurrence of antimicrobial resistance among Salmonella Weltevreden isolates from different countries

<table>
<thead>
<tr>
<th>Country</th>
<th>No. of isolates</th>
<th>AMP</th>
<th>CHL</th>
<th>FLO</th>
<th>NAL</th>
<th>NEO</th>
<th>STR</th>
<th>SUL</th>
<th>TET</th>
<th>TMP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Australia</td>
<td>46</td>
<td>2.2</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>2.2</td>
<td>2.2</td>
<td>2.2</td>
<td>2.2</td>
<td></td>
</tr>
<tr>
<td>Denmark</td>
<td>16</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Indonesia</td>
<td>45</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>2.2</td>
<td>2.2</td>
<td>6.7</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Laos</td>
<td>6</td>
<td>17.7</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>50</td>
<td>17.7</td>
<td>33.3</td>
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</tr>
<tr>
<td>Malaysia</td>
<td>105</td>
<td>0</td>
<td>2.9</td>
<td>0</td>
<td>0.9</td>
<td>8.5</td>
<td>6.6</td>
<td>9.4</td>
<td>1.0</td>
<td></td>
</tr>
<tr>
<td>New Zealand</td>
<td>40</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>2.5</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Taiwan</td>
<td>7</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
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<td></td>
</tr>
<tr>
<td>Thailand</td>
<td>197</td>
<td>3.0</td>
<td>2.0</td>
<td>0.5</td>
<td>2.0</td>
<td>5.1</td>
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<td>0</td>
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<td></td>
</tr>
<tr>
<td>USA</td>
<td>22</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>4.5</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Vietnam</td>
<td>19</td>
<td>5.3</td>
<td>5.3</td>
<td>5.3</td>
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<td>0</td>
<td>5.3</td>
<td>0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>503</td>
<td>1.8</td>
<td>1.6</td>
<td>0.4</td>
<td>1.6</td>
<td>0.6</td>
<td>4.4</td>
<td>4.2</td>
<td>4.0</td>
<td>1.4</td>
</tr>
</tbody>
</table>

Results

Only 48 (9.5%) of the 503 isolates were resistant to one or more of the antimicrobial agents tested. All isolates were susceptible to co-amoxiclav, cefuroxim, ciprofloxacin, colistin and gentamicin. A low frequency of resistance was found towards ampicillin (1.8%), chloramphenicol (1.6%), floxuridine (0.4%), nalidixic acid (1.6%), neomycin (0.6%), streptomycin (4.4%), sulfamethoxazole (4.2%), tetracycline (4.0%) and trimethoprim (1.4%) (Table 1). Resistance was observed most frequently among isolates from Laos and Malaysia, but otherwise the occurrence of resistance was so low that no major difference between country or isolate origin could be found.
Antimicrobial resistance was exclusively mediated by the sul2 gene, which has been found widespread among other Gram-negative bacteria. Tetracycline resistance was mainly mediated by tet(A), but a few isolates contained tet(B) and a single isolate contained tet(C). tet(A) is located frequently on transposons such as Tn1721, and the gene has been found widespread among Gram-negative bacteria including salmonella. Resistance to sulfamethoxazole was exclusively mediated by sul2. In the past, the sul1 gene has been found mainly in connection with integrons, whereas sul2 is located usually on a variety of plasmids. All neomycin-resistant isolates contained aphA-2, which also has been found in several Gram-negative species. Both aadA and strA have been found frequently among streptomycin-resistant isolates, as has Salmonella Typhimurium in Denmark. Class I integrons containing the aadA gene have been observed often among clinically important Enterobacteriaceae. However, the class I integrons normally contain genes have been observed often among clinically important Enterobacteriaceae. No major differences between country or source could be observed.

Discussion

A very low frequency of resistance was detected among the 503 Salmonella Weltevreden isolates. This could be because this serovar does not easily acquire resistance, or because the natural reservoirs were not exposed to large amounts of antimicrobial agents. It is not known which hypothesis is correct. Boonmar et al. reported a low occurrence of resistance among Salmonella Weltevreden isolated from humans in Thailand in 1993, and a major increase in resistance in 1994. Such an increase was not observed by us among isolates from Thailand in 1994. We found an infrequent occurrence of resistance, more in agreement with the observed frequency in Thailand in 1993, and that reported by Thong et al. from different sources in Malaysia.

A number of different resistance genes were detected among the 48 resistant isolates. All ampicillin-resistant isolates contained a sequence similar to blaTEM. The catA1 gene has been detected previously in Salmonella isolates, but is also widespread among other Gram-negative bacteria. Tetracycline resistance was mainly mediated by tet(A), but a few isolates contained tet(B) and a single isolate contained tet(C). tet(A) is located frequently on transposons such as Tn1721, and the gene has been found widespread among Gram-negative bacteria including salmonella. Resistance to sulfamethoxazole was exclusively mediated by sul2. In the past, the sul1 gene has been found mainly in connection with integrons, whereas sul2 is located usually on a variety of plasmids. All neomycin-resistant isolates contained aphA-2, which also has been found in several Gram-negative species. Both aadA and strA have been found frequently among streptomycin-resistant isolates, as has Salmonella Typhimurium in Denmark. Class I integrons containing the aadA gene have been observed often among clinically important Enterobacteriaceae. However, the class I integrons normally contain sul1; this gene was not observed in any strains in this study.

In conclusion, this study showed a low frequency of resistance among Salmonella Weltevreden isolated from humans and other reservoirs in South-East Asia and elsewhere. Resistance was encoded by genes previously widespread in other Enterobacteriaceae. No major differences between country or source could be observed.

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References


