Anatum (16.1 %, 9 farms) followed by Rissen (14.5 %, 7 farms), Typhimurium (11.3 %, 7 farms), Derby (9.7 %, 3 farms), Tilburg (8.1 %, 2 farms), Goldcoast (8.1 %, 1 farm), Typhimurium variant 4,5,12:i:- (6.5 %, 4 farms). Serotypes Bovismorbificans, Bredeney, Diarizonae, Grumpensis, Infantis, Kapemba, Kedougou, Ohio, Settenberg and Virchow were also isolated although less than three times each. Antimicrobial susceptibility analysis showed that the highest level of resistance was against tetracycline (68.8 %). Sulphonamides and their combination with trimethoprim were only active against 67.7 % and 53.1 % of the strains, respectively. Regarding β-lactams, 41.6 % of the strains were resistant to ampicillin and 18.7 % were resistant to the combination of amoxycillin and clavulanic acid. Finally, 17.7 % of strains were resistant to cloramphenicol. Sixty-two percent of the strains showed resistance to three or more antimicrobial agents and 46 % were resistant to five or more drugs. The maximum number of compounds to which one strain was resistant was 10 (corresponding to a 4,5,12:i:- strain). In addition 3 strains were resistant to eight or nine compounds. None of the strains was resistant to colistin or ceftriaxone and 12 strains were susceptible to all antimicrobial agents tested (serotypes Anatum, Goldcoast, Kapemba and Ohio). These results indicate that sub-clinical infection with Salmonella can be produced by multidrug resistant strains. In addition, with very few exceptions, most of the detected serotypes were able to be resistant to more than three drugs. This fact suggests that antimicrobial resistance in Salmonella isolates from pigs is not an exclusive property of a given serotype, for instance Typhimurium, but a widespread characteristic. However, the wider spectrum of resistance is usually found in the 4,5,12:i:- variants of Typhimurium (De la Torre et al., 2002). Taking together, these results show that antimicrobial resistance is a real problem in swine isolates of Salmonella and reinforce the notion than an improved knowledge of the impact of antimicrobial agents used in swine is required.

References:
Recent suggestions that pigs reared in modern production systems do not reap the performance benefits of growth promotant antibiotics (Ice et al., 1999; Dritz et al., 2002) has increased the scrutiny over this antimicrobial use. In the US >60% of swine production units routinely incorporate growth promotants in the daily ration for pigs. (Anonymous, 2002) There is a paucity of controlled, prospective intervention studies in modern US commercial production settings to evaluate the impact of sub-therapeutic antimicrobial use on AR. The goal this study was to evaluate, in a controlled manner, the impact of sub-therapeutic antimicrobial use on AR in market age swine using S. enterica and the aerobic Gram-negative fecal flora as indicator organisms.

**Methods:** Within each of 3 farms, treatments were assigned to temporally matched finisher barn pairs based on pig placement dates. For each matched pair, a barn was assigned to the treatment (50g chlortetracycline/ton of feed) or control (no antibiotics in the feed). A total of 22 barns were enrolled. Fecal samples were collected from 96 individual pigs per barn prior to slaughter. All samples were cultured for S. enterica, and isolates were tested for resistance to 17 antimicrobials. For the gram-negative fecal flora, 48 individual 1g fecal samples per barn were serially diluted (2, 10-fold dilutions) and plated onto MacConkey agar. One hundred colonies per sample were selected to create a master plate for replica plating. Master plates were replicated onto 5 agar plates each containing ampicillin, ceftriaxone, gentamycin, or tetracycline at NCCLS breakpoint concentrations. Comparison of Salmonella prevalence between treatment and non-treatment groups was conducted using Wilcoxon Signed Rank test (SPSS 11.5, SPSS, Inc). A binary logistic regression model (SPSS 11.5, SPSS, Inc) was initially constructed with individual colony resistance as the dependent variable and treatment and farm and an interaction term entered as independent variables. The final model was then analyzed in MLwIN 1.1 to assess the contribution of clustering to variance components.

**Results:** The overall prevalence of S. enterica was low (<1.0%). Salmonella were isolated from only one temporally matched barn pair, with 1.3% prevalence in the treatment barn and 0.09% prevalence in the control barn. For the gram-negative fecal flora, there was a statistically significant difference (p<0.05) between treatment groups for the frequency of antimicrobial resistance in the gram negative flora with pigs receiving chlortetracycline having a greater frequency of isolates resistant tetracycline, gentamicin, and ceftriaxone, and a lesser proportion of isolates resistant to ampicillin (Table 1). Resistance to >1 antibiotics was more common in the treatment groups (29.0% and 18.2% for treatment and control respectively, p<0.05). Results of multi-level modelling are pending. Preliminary results suggest that short-term changes in chlortetracycline selection pressure do not alter S. enterica prevalence and resistance, but are associated with statistically significant changes in the frequency of resistance in the fecal flora.

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**References:**
Table 1. Proportion of aerobic gram-negative fecal flora isolates resistant to each of 4 antimicrobials in pigs receiving chlortetracycline and pigs not receiving chlortetracycline.

<table>
<thead>
<tr>
<th>Antimicrobial</th>
<th>Pigs fed chlortetracycline (50g/ton)</th>
<th>Pigs not fed chlortetracycline</th>
</tr>
</thead>
<tbody>
<tr>
<td>ampicillin</td>
<td>16.2</td>
<td>20.1</td>
</tr>
<tr>
<td>ceftriaxone</td>
<td>0.3</td>
<td>0.7</td>
</tr>
<tr>
<td>gentamycin</td>
<td>1.6</td>
<td>1.7</td>
</tr>
<tr>
<td>tetracycline</td>
<td>84.3</td>
<td>97.5</td>
</tr>
</tbody>
</table>

ANTIMICROBIAL RESISTANCE OF Salmonella ISOLATES FROM SWINE

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Summary: The aim of this study was to report the antimicrobial resistance pattern of 27 Salmonella strains previously isolated from swine feces and lymph nodes collected in a slaughter-house in S. o Paulo State, Brazil. The antibiotics tested were ampicillin (Amp), cephalothin (Cfl), ceftriaxone (Cro), streptomycin (Est), neomycin (Neo), gentamicin (Gen), amikacin (Ami), tobramycin (Tob), nalidixic acid (Nal), ciprofloxacin (Cip), norfloxacin (Nor), tetracycline (Tet), sulphazotrim (Sut) and chloramphenicol (Clo). Resistance to each antibiotic was determined by the Kirby-Bauer disk susceptibility test. Thirteen isolates (48.14%) were resistant to two or more antibiotics. Resistance to Tet was commonly seen among the isolates (55.5%). Total or intermediate resistance to Est (59.25%) were also commonly seen in the isolates. The high frequency of isolates resistant to Est and Tet may reinforce the possible link to the long-term therapeutic use of such drugs in pig production.

Keywords: Antibiotic, Kirby-Bauer, streptomycin, tetracycline, pigs

Introduction: Worldwide surveillance of Salmonella enterica serotyping and antimicrobial resistance is necessary in order to monitor emerging phenotypes. Furthermore, it permits to identify emerging clones and evaluate transmission of strains between regions (Petersen et al., 2002). The aim of this study was to determine the antimicrobial resistance patterns of some Salmonella strains isolated from swine in a commercial slaughterhouse located in S. o Paulo State, Brazil.

Material and Methods: The antibiotics tested were extended spectrum penicillin (ampicillin-Amp), broad-spectrum cephalosporins (cephalothin-Cfl and ceftriaxone-Cro), aminoglycosides (streptomycin-Est, neomycin-Neo, gentamicin-Gen, amikacin-Ami and tobramycin-Tob), narrow-spectrum quinolone (nalidixic acid-Nal), broad-spectrum quinolones (ciprofloxacin-Cip, norfloxacin-Nor), tetracycline-Tet, sulphazotrim-Sut and chloramphenicol-Clo. Resistance to each antibiotic was determined by the Kirby-Bauer disk susceptibility test. The reference strains used were E. coli ATCC 25922 and P. aeruginosa ATCC 27853. After the incubation period, the strains were finally interpreted as resistant, intermediate or susceptible to each antibiotic.