Salmonella Enterica Serovar Typhimurium DT104 Invasion is Not Enhanced by Sub-Inhibitory Concentrations of the Antibiotic Florfenicol

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Abstract

The incidence of multi-drug resistant Salmonella has increased globally over the past several decades and has become a major public health concern. Isolates of Salmonella enterica serovar Typhimurium DT104 are resistant to five or more antibiotics, including florfenicol, and have been associated with enhanced virulence in livestock and humans. Because sub-inhibitory concentrations of some antibiotics have been found to modulate invasion of certain bacteria under specific conditions, the effect of florfenicol on S. Typhimurium DT104 invasion was evaluated. Three clinical bovine isolates were exposed to sub-inhibitory concentrations of florfenicol for 30 minutes to establish the initial response to the antibiotic. HEP-2 cellular invasion assays, as well as expression analyses of invasion-related genes, demonstrated that the invasiveness of the S. Typhimurium DT104 isolates was not enhanced after exposure to sub-inhibitory concentrations of florfenicol. These results suggest that cattle and swine can be treated with florfenicol for respiratory illness without exacerbating Salmonella Typhimurium DT104 virulence in carrier animals.

Keywords: Salmonella Typhimurium DT104; Florfenicol; Sub-inhibitory; Invasion; Virulence, FloR

Introduction

Multi-drug resistant Salmonella enterica serovar Typhimurium DT104 isolates have increased in frequency worldwide over the past several decades [1] and have been associated with enhanced virulence in livestock and humans [2,3]. Isolates of Salmonella Typhimurium DT104 are typically resistant to ampicillin, chloramphenicol/ florfenicol, streptomycin, sulfonamides, and tetracycline, but may harbor additional resistance genes [4]. Antibiotic resistance in bacteria is problematic as treatment of an infection can be ineffective, but also because sub-inhibitory concentrations of certain antibiotics may enhance virulence in some bacteria [5]. For example, at sub-inhibitory levels, florfenicol increases the adherent phenotype of Staphylococcus aureus [6], fluoroquinolones increase expression of host-colonization factors in Clostridium difficile [7], and β-lactams increase hemolytic activity in Staphylococcus aureus [8]. Few studies have reported on the effect of sub-inhibitory concentrations of antibiotics on isolates of S. Typhimurium DT104, and none have examined the initial effect of florfenicol exposure.

Florfenicol is a broad-spectrum bacteriostatic antibiotic analog of chloramphenicol and is used to treat respiratory disease in cattle and swine [9]. A previous study indicated that invasion was not increased after S. Typhimurium DT104 was grown to stationary phase in the presence of florfenicol or tetracycline [10]. However, another study demonstrated that invasion was enhanced in S. Typhimurium DT104 grown to late-log phase in the absence of antibiotics and subsequently exposed to tetracycline for 30 minutes [11]. The discrepancy between these two studies regarding invasion is likely due to the different experimental conditions, which has been observed in studies of Pseudomonas aeruginosa virulence that tested the same antibiotics and found contradictory results [12]. Because florfenicol is a drug used for clinical treatment of respiratory illness in animals that are known to be asymptomatic carriers of Salmonella, it is important to determine the effect florfenicol exposure has on S. Typhimurium DT104 invasion. It is also important to evaluate the initial effect of florfenicol as this antibiotic is administered to the host only when necessary, in contrast to antibiotics used in feed that provide a constant source of exposure.

In this study, we grew S. Typhimurium DT104 to late-log phase and exposed the bacteria to florfenicol for 30 minutes to determine whether these conditions enhance invasion.

Materials and Methods

Bacterial strains and florfenicol exposure

Three isolates of Salmonella Typhimurium DT104 (530, 745, and 19823) originally collected from cattle were selected at random from our NADC strain library. The floR gene [13], which confers florfenicol/chloramphenicol resistance, was deleted in isolate 745 by recombination and resulted in strain BBS 650 (745floRΔ) [14]. For each experiment, a single bacterial colony from a Lennox L (LB) agar plate (Invitrogen, Carlsbad, CA) was selected and grown in LB broth under agitation for 6 hours at 37°C. A 1:100 dilution of the 6 hour culture was made in LB and grown statically to stationary phase at 37°C overnight. A 1:100 dilution of the overnight culture was made in LB containing 1% NaCl and divided into 16×100 glass tubes. To induce invasion [15], these cultures were grown statically for 3 hours at 37°C until late-log phase. Florfenicol (Nuflox, Schering-Plough Animal Health) was added at final concentrations of 0, 1, 5, or 30 μg/ml, and the cultures were incubated statically for 30 minutes at 37°C. 0 μg/ml was the control, 1 μg/ml was sub-inhibitory for growth for all strains, 5 μg/ml was sub-inhibitory for strains 530, 745, and 19823 but was inhibitory for 745floRΔ and 30 μg/ml was inhibitory for all strains. The invasion and gene expression results were based on a minimum of 4 experiments using each strain.

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Salmonella invasion assays

After the 30 minute incubation with or without florfenicol, 1 ml of each sample was centrifuged at 16,000 x g for 2 minutes and resuspended in fresh LB broth to remove the florfenicol. Invasion assays were performed using HEp-2 cells as previously described [16] at a multiplicity of infection of ~40. Percent invasion was calculated by dividing CFU/ml recovered by CFU/ml added. Differences in invasion were determined by a one-way ANOVA with Dunnett's post-test to assess pair-wise differences between the no-antibiotic control and the other sample conditions using GraphPad Prism 5 (GraphPad Software, San Diego, CA).

Real-Time PCR assays

Aliquots for RNA analysis were taken from each bacterial culture immediately after the 30 minute florfenicol incubation and placed in RNAProtect (QIAGEN, Germantown, MD). RNA was isolated using the RNeasy Mini Kit (QIAGEN), and genomic DNA was removed using the Turbo DNase DNA-free kit (Ambion, Austin, TX) according to the directions from the manufacturer. Reverse transcription was carried out using the Applied Biosystems High capacity cDNA reverse transcription kit on total RNA using random primers. Real-Time PCR was performed in a Chromo4 Real-Time PCR Detection System (BioRad Laboratories, Hercules, CA) using the SYBR Green Master Mix (Applied Biosystems, Foster City, CA). Primer sets were used to evaluate the 16S rRNA, floR, hilA, sopB, and pnp genes (Table 1). For control assays, reverse transcriptase was not added to parallel mixtures for each sample. Amplification was performed using the following cycle conditions for each primer set: 95ºC for 10 min; 40 cycles of 95ºC for 15 s, 55ºC for 30 s, 72ºC for 30 s; melting curve analysis from 65ºC to 95ºC. Amplification was performed using the following cycle conditions for each primer set 

<table>
<thead>
<tr>
<th>gene</th>
<th>forward primer</th>
<th>reverse primer</th>
<th>Reference</th>
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<tr>
<td>16S</td>
<td>GGGGGAGGAGGTGTTGTTG</td>
<td>GAGCCCGGGGAATTTCACATC</td>
<td>[25]</td>
</tr>
<tr>
<td>floR</td>
<td>CCACAAATTTGGCTGGATGGCCTCA</td>
<td>TGGTCTGTTATCGGCGGAGAT</td>
<td>[26]</td>
</tr>
<tr>
<td>hilA</td>
<td>CGCTGGCAATGCTACCTC</td>
<td>AGCCCCAGTAATCTAAAGCC</td>
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</tr>
<tr>
<td>sopB</td>
<td>CGTTGTGGAGGTAAGAG</td>
<td>GAGGTCTGAAATACATTAGCG</td>
<td>This study</td>
</tr>
<tr>
<td>pnp</td>
<td>TGAAACGACCTCCTTC</td>
<td>GAGATCCAGCGAGAG</td>
<td>This study</td>
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**Table 1**: Real-time PCR primers (5'-3').

Figure 1: Effect of florfenicol on S. Typhimurium DT104 invasion. Isolates were grown to late-log and then exposed to 0, 1, 5, or 30 μg/ml florfenicol for 30 minutes. Invasion assays were performed in HEp-2 cells.
μg/ml florfenicol was observed, it was not significant compared to the controls. Unexpectedly, strain 19823 was not invasive; however, this is now a valuable strain to use as a control for future investigations.

The floR, hila, sopB, and pnp genes were chosen to assess the effect of florfenicol exposure on expression of invasion-related genes by real-time PCR for the following reasons: FloR mediates florfenicol/chloramphenicol resistance through an efflux pump [13]; Hila is a transcriptional activator that controls genes on the Salmonella pathogenicity island 1 (SPI-1), is required for invasion, and is regulated by changes in environmental conditions [19]; SopB is an inositol phosphate phosphatase and is necessary for invasion, but it is located outside of SPI-1 and is not directly regulated by Hila [20,21]; PNPase is a polynucleotide phosphorylase that negatively regulates invasion genes in SPI-1 [22,23]. Up-regulation of hila and sopB gene expression is associated with increased invasion, while up-regulation of pnp gene expression is associated with decreased invasion. Statistical differences in expression for each gene were determined relative to the no-antibiotic controls. Unexpectedly, strain 19823 was not invasive; however, this is now a valuable strain to use as a control for future investigations.

In summary, parallel phenotypic and transcriptional analyses indicate that S. Typhimurium DT104 invasion was not enhanced after exposure to the antibiotic florfenicol. Concern that using florfenicol to treat respiratory illness will impact the invasiveness of S. Typhimurium DT104 in carrier animals is not supported by these results.

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References

resistant *Salmonella enterica* subsp. *enterica serovar Typhimurium* DT104.


