Multilocus Sequence Typing and Phylogenetic Analysis of Campylobacter Isolated from Conventional and Antimicrobial-Free (ABF) Swine and their Environment

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ABSTRACT

Campylobacter is one of the leading pathogens causing foodborne illnesses in the US. Epidemiological evidence has indicated that food animals, including pigs, act as reservoirs of Campylobacter strains that can infect humans. The purpose of this study is to determine the clonality or diversity of Campylobacter coli isolated from the conventional and ABF production systems at farm, slaughter and environment using multilocus sequence typing (MLST). A total of 129 C. coli isolates were selected from fecal, environmental and carcass samples of ABF (N = 71) and conventional (N = 58) production systems. Seven housekeeping genes (aspA, glaA, gltA, gltB, pgm, tkt, uncA) were amplified using PCR and the amplified product was sequenced. Sequence data was analyzed for the determination of allelic profiles and identification of sequence types (STs). Dendrograms and minimum spanning trees were generated to establish the relationships between the genotyped isolates. Isolates with similar sequence types were found between the pigs and their environment at farm and slaughter (ABF: 13, Ia = 0.1308; Conventional: 20, Ia = 0.1357). Higher genotypic diversity was observed among isolates from the conventional swine production systems (ABF: 0.3455 +/- 0.0901; Conventional: 0.3929 +/- 0.0805). Phylogenetic analysis revealed a genotypically diverse C. coli population with the presence of C. coli isolates sharing a common ancestry in both production systems. Overall, MLST of C. coli isolates from two distinct production systems unveils a weak clonal population and diverse genetic makeup of this species.

INTRODUCTION

Campylobacter is one of the leading causes of foodborne diarrhea illness in the US and a significant public health concern worldwide. Antimicrobial resistant Campylobacter have been shown to be shed by swine and constitute a major risk factor for contaminating swine carcasses during slaughter (Thakur et al., 2006; Thakur and Gebreyes, 2005). Campylobacter is known to have a hypervariable genome (Parkhill et al., 2000). Therefore, MLST is a useful technique in epidemiologic investigation of Campylobacter jejuni strains that can infect humans. The purpose of this study is to determine the clonality or diversity of Campylobacter coli isolated from the conventional and ABF production systems at farm, slaughter and environment using MLST.

OBJECTIVES

➢ To determine how clonal/diverse are the Campylobacter coli populations in the two production systems
➢ To determine Campylobacter coli clonal complexes of the two production systems

MATERIALS & METHODS

Housekeeping Genes

PCR amplification

DNA from ABF and Conventional Swine and Environment

Campylobacter coli isolates N=129

Sequence Data

Submitted at

www.mlst.net

Sequence Type (ST)

Ex : ST-828

Allelic Frequency

33 12 178 48 182 68 17

RESULTS

A) C. coli Clonal Complex Determination

A.1) Conventional System (N = 58)

ST - 2508 presumed founder

A.2) ABF System (N = 71)

ST - 828 presumed founder

B) Phylogenetic Diversity in C. coli from ABF & Conventional Swine Production Systems

C. coli from Conventional Systems

C. coli from ABF Systems

C) Genetic Diversity and Ia Analysis

<table>
<thead>
<tr>
<th>Production System</th>
<th>Unique STs</th>
<th>Ia</th>
</tr>
</thead>
<tbody>
<tr>
<td>Conventional (N = 58)</td>
<td>20</td>
<td>0.1357</td>
</tr>
<tr>
<td>ABF (N = 71)</td>
<td>13</td>
<td>0.1308</td>
</tr>
</tbody>
</table>

Ia: Index of Association

REFERENCES


SUMMARY

➢ Preliminary results clearly highlight a higher genotypic diversity among isolates from the conventional swine production at both farm and slaughter.
➢ C. coli has a genotypically diverse population with a hyper-variable genome.
➢ Phylogenetic analysis reveals the presence of C. coli isolates sharing a common ancestry in both of the production systems.

CONCLUSIONS

➢ Overall, MLST of C. coli isolates from two pig production systems highlights a weak clonal population and diverse genetic makeup of this species.

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