INTRODUCTION

Post-weaning diarrhea
• Commonly caused by enterotoxigenic E. coli
• Often leads to weight loss and possibly death
• Economical losses

Bacillus subtilis
• Potential alternatives to antibiotics
• Gram positive, aerobic bacteria
• Dietary supplementation of B. subtilis affected weaned pigs challenged with F18 E. coli (Kim et al., 2019)
  • Improved growth rate
  • Reduced leaky gut
  • Enhanced gut barrier function
• Supplementation of B. subtilis alters fecal microbiome of weaned pigs challenged with pathogenic E. coli (Jinno et al., 2020)
  • Fecal microbiome altered differently between antibiotics and B. subtilis supplementation

OBJECTIVE

To observe the effects of supplementing Bacillus subtilis on intestinal microbiota of weaned pigs experimentally infected with F-18 E. coli.

MATERIALS & METHODS

Animal experiment
• 48 weaned pigs (~6.17 kg)
• Design: RCBD with BW x gender as blocking factors

Treatment (12 pigs per treatment)

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<thead>
<tr>
<th>Treatment</th>
<th>NC</th>
<th>Negative control</th>
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<tbody>
<tr>
<td>Sham</td>
<td>PC</td>
<td>Positive control</td>
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<tr>
<td>F18 E. coli challenge</td>
<td>AGP</td>
<td>50 mg/kg carbadox</td>
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<tr>
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<td>DFM</td>
<td>500 mg/kg B. subtilis</td>
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• Pigs were housed individually and had access to feed and water ad libitum for 28 days
• After 7 days adaptation period, pigs were orally inoculated with 3 mL F18 E. coli (10^10 CFU/dose) for 3 consecutive days from d 0 post-inoculation (PI)
• Pigs were euthanized d 21 PI
  • Fecal samples and digesta from jejunum, ileum, and colon were collected

16S rRNA analysis

• DNA extraction
• Amplification using PCR at the V4 region
• Illumina MiSeq 250PE
• sabre for demultiplexing
• QIIME2 (2019.4) for processing data
• R program for data visualization and statistical analysis

Analysis
• Alpha diversity
• Beta diversity
• Relative abundance

Library preparation

Data processing

Alpha diversity

Beta diversity

Relative abundance

Sampling mean: 14,345 Total number of taxa: 3,430

Statistical analysis

Alpha diversity and taxonomic analysis were analyzed with Kruskal-Wallis and Conover test using agricolae package in R.

RESULTS

Alpha diversity

Beta diversity

Relative abundance

CONCLUSION

• Supplementation of B. subtilis and carbadox modified intestinal microbiota of weaned pigs challenged with F18 E. coli differently from each other
• Further study should investigate the gut microbiome of weaned pigs challenged with F18 E. coli supplemented with B. subtilis using metagenomic sequencing

REFERENCES