Role of the Microbiome in Disease Outcome of Swine

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Microbiome

“…the ecological community of commensal, symbiotic, and pathogenic microorganisms that literally share our body space”

Emerging Area of Study

NIH Human Microbiome Project

Understanding the microbiome in human health and disease
(Peterson et al., 2009)

“Human Microbiome”

$n = 25,671$ (1978-2016)

“Swine Microbiome”

$n = 556$ (1978-2016)
Microbial colonization

The vast majority of microorganisms live in the GASTROINTESTINAL TRACT (10 microbes: 1 human cell)
Includes bacteria, viruses, fungi, protozoa, archaeae
Roles of the Microbiome

Absorption, metabolism and storage of calories

Development and Regulation of Immunity

Protective Barrier Function
Microbiome in Health and Disease

The role is complex and not well understood

Microbiome diversity and composition play a role in

1. Disease susceptibility
2. Response to pathogens
**Microbiome and Disease**

**Gut-brain axis**

**Autism**
- Increased *Clostridium* species
  (Kraneveld et al., 2016)

**Chronic fatigue syndrome**
- Decreased microbiome diversity
  (Giloteaux et al., 2016)

**Clostridium difficile**
- Decreased microbiome diversity
  (Ross et al., 2016)

**Gut-gut interactions**

**Obesity**
- Increased Firmicutes bacteria
  (Kallus and Brandt, 2012)
Are there microbiome characteristics associated with outcome during PRRSV/PCV2 co-infection?
Experimental Design

$n = 95$

9-10 pigs/pen

PRRSV/PCV2 Challenge

20 Pigs Selected for Best or Worst Clinical Outcome
Selection of Pigs

Best Clinical Outcome

$n = 10$ pigs

Worst Clinical Outcome

$n = 10$ pigs

0.90 kg
0 days

Average Daily Gain

Clinical Disease

0.15 kg
$\geq 10$ days
Weight Gain

Worst Performing Group: $0.475 \pm 0.153$ kg  
Best Performing Group: $0.837 \pm 0.042$ kg  
$p < 0.0001$

Niederwerder et al., 2016
Lung Lesions and PRRSV Viremia

Area Under the Curve (p = 0.04)
Worst = 153.5 Best = 116.2

Niederwerder et al., 2016
Microbiome

Lawrence Livermore Microbial Detection Array

Detects all sequenced microbes

3,856 viruses, 3,855 bacteria, 254 archaeabacteria, 100 fungi, 36 protozoa
Microbiome Diversity

$p = 0.017$

Number of Families

Worst Clinical Outcome

Best Clinical Outcome

Niederwerder et al., 2016
Microbiome Composition

Worst Clinical Outcome           Best Clinical Outcome

Bacteria

Acidaminococcus fermentans
Planococcus donghaensis
Dorea longicatena
Eubacterium rectale
Eubacterium eligens
Methanobrevibacter smithii
Lactococcus garvieae
Streptococcus galoltyicus
Streptococcus agalactiae
Corynebacterium renale
Prevotella copri
Treponema succinifaciens
Phascolarctobacterium sp.
Megasphaera elsdenii
Faecalibacterium prausnitzii
Lactobacillus acidophilus
Lactobacillus johnsonii
Bacillus cereus

Proteobacteria

Erwinia amylovora
Escherichia coli
Campylobacter lari
Dechlorosoma suillum
Mannheimia haemolytica

Percent

Niederwerder et al., 2016
Summary

1. Increased microbiome diversity
2. Increased fecal *Escherichia coli*

Associated with best clinical outcome 70 days after PRRSV/PCV2 co-infection
Do microbiome characteristics PREDISPOSE outcome following PRRSV/PCV2 co-infection?
Experimental Design

$n = 50$

9-10 pigs/pen

PRRSV/PCV2 Challenge

20 Pigs Selected for High and Low Growth Rates
Selection of Pigs

High Growth Rate  
\( n = 10 \) pigs

0.962 kg

Low Growth Rate  
\( n = 10 \) pigs

0.596 kg

Average Daily Gain

0 days  Clinical Disease  0 days
Summary

1. Increased microbiome diversity
2. Increased fecal *Streptococcaceae*
3. Increased fecal *Ruminococcaceae*
4. Decreased fecal *Methanobacteriaceae*

On **day 0** is associated with high growth rates after PRRSV/PCV2 co-infection
Characteristics of Improved Outcome

↑ MICROBIAL DIVERSITY

↓ Methanobacteriaceae  ↑ Streptococcus sp.
↑ Escherichia coli  ↑ Ruminococcus sp.
↑ Average Daily Gain  ↓ Interstitial Pneumonia
↓ Clinical Disease  ↓ PRRSV Viremia
Conclusion

The microbiome may be used as an **ALTERNATIVE TOOL** and novel intervention strategy for management of infectious disease in swine.
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