Role of the Microbiome in Porcine Respiratory Disease

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Microbiome

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

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Emerging Area of Study

- NIH Human Microbiome Project
  Understanding the microbiome in human health and disease (Peterson et al., 2009)

- National Microbiome Initiative
  Understanding the microbiome across different ecosystems (Bouchie, 2016)

"Human Microbiome"
$n = 33,458$ (1977-2017)

"Swine Microbiome"
$n = 714$ (1977-2017)
Sites of microbial colonization

The vast majority of microorganisms live in the GASTROINTESTINAL TRACT (10 microbes: 1 human cell)

Includes bacteria, viruses, fungi, protozoa, archeae
Roles of the Gut 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 spectrum disorders
Increased Clostridium species
(Kraneveld et al., 2016)

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

Gut-lung axis

Streptococcus pneumoniae
Decreased microbiome diversity
(Schuijt et al., 2016)

Mycobacterium tuberculosis
Increased Helicobacter species
(Arnold et al., 2015)

Obesity
Increased Helicobacter pylori
(Kallus and Brandt, 2012)
Microbiome

Weight

Immunity

Porcine Respiratory Disease (PRRSV/PCV2) co-infection
Are there microbiome characteristics associated with outcome after PRRSV/PCV2 co-infection?

$n = 95$

PRRSV/PCV2 Challenge

20 Pigs Selected for Best or Worst Clinical Outcome

Niederwerder et al., 2016
Are there microbiome characteristics associated with outcome after PRRSV/PCV2 co-infection?

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

**70 days post-infection** is associated with best clinical outcomes after PRRSV/PCV2 co-infection.

Niederwerder et al., 2016
Are there microbiome characteristics that **PREDISPOSE** outcome after co-infection?

Ober et al., 2017
Are there microbiome characteristics that PREDISPOSE outcome after co-infection?

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

Pre-infection is associated with high growth rates after PRRSV/PCV2 co-infection

Ober et al., 2017
Fecal Microbiota Transplantation

• Transplanting the feces from a healthy donor into a diseased individual (FMT)
  – Beneficial for a wide-range of diseases
    • *Clostridium difficile*, autism, ulcerative colitis, chronic fatigue syndrome, diabetes, multiple sclerosis, IBD
  – Increased microbial diversity, enhanced beneficial microbes
  – Phenotypes are transmissible through FMT

(Ridaura et al., 2013; Turnbaugh et al., 2006)
Can **fecal microbiota transplantation** prior to PRRSV/PCV2 co-infection improve outcome?
Experimental Design

3-week-old littermates

Control Group $n = 10$

Saline Mock Transplant

Microbiome Therapeutic Group $n = 10$

Beneficial Bacterial Transplant

PRRSV/PCV2d Challenge

Wt. -7 0 4 7 11 14 21 28 35 42
Summary

**Fecal microbiota transplantation** prior to co-infection with PRRSV/PCV2 is associated with:

1. Decreased morbidity and mortality
2. Improved weight gain
3. Decreased viral load
4. Increased antibody response
Characteristics of Improved Outcome

↑ Diversity
↓ Methanobacteriaceae
↑ Escherichia coli
↑ Average Daily Gain
↓ Clinical Disease
↓ Mortality
↑ Antibody Production

Fecal Microbiota Transplantation

↑ Streptococcaceae
↑ Ruminococcaceae
↓ Interstitial Pneumonia
↓ Virus Replication
Conclusion

The gut microbiome may be used as an **ALTERNATIVE TOOL** and novel prevention and treatment strategy for infectious respiratory disease
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