

Role of the Microbiome in Porcine Respiratory Disease

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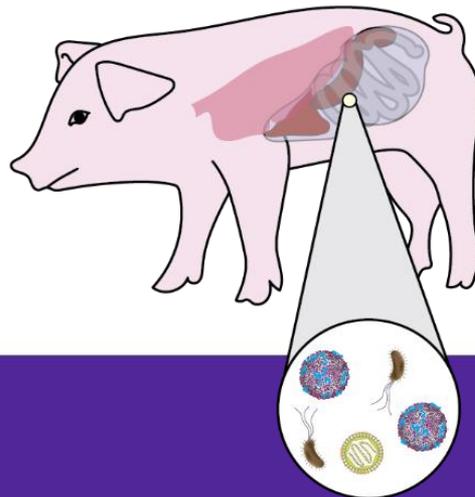
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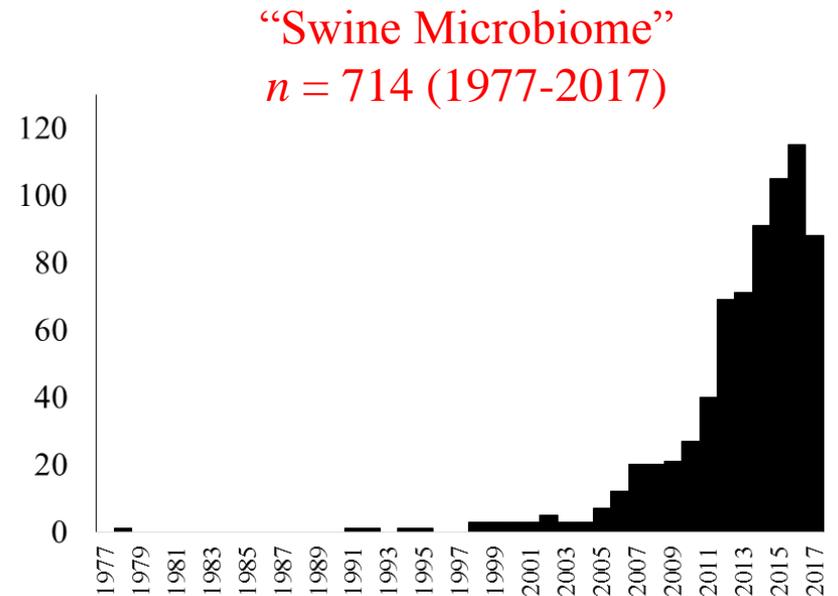
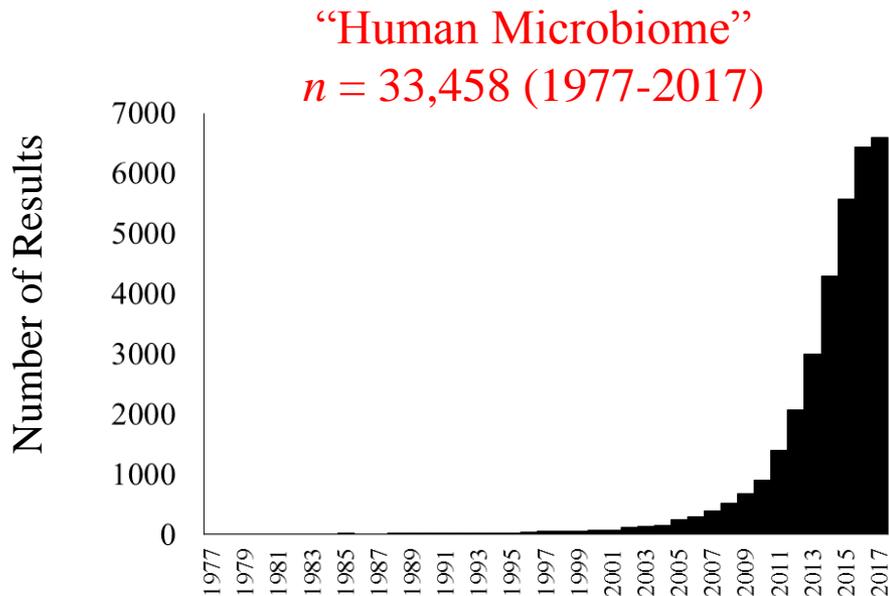
Microbiome

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

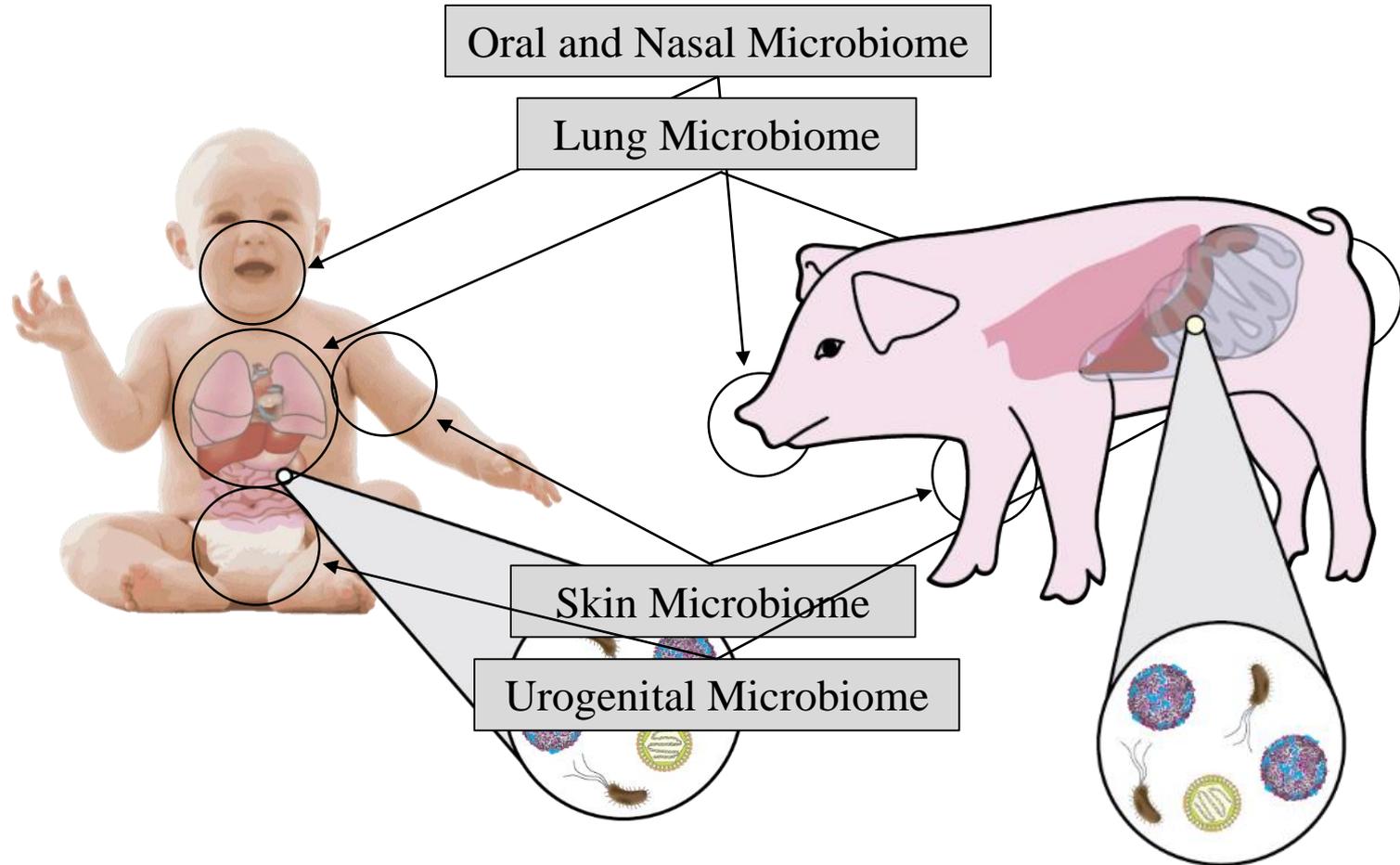
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bacteriome	immunome	plerome
basidiome	haptenome	proteinome
biome	karyome	proteome
cardiome	leptome	psychome
caulome	microbiome	regulome
chondriome	mnemome	rhabdome
cladome	mycetome	rhizome
coelome	neurome	stereome
epigenome	odontome	thallome
erythrome	osteome	tracheome
genome	pharmacogenome	transcriptome
geome	phenome	trichome
hadrome	phyllome	vacuome
histome	physiome	

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)

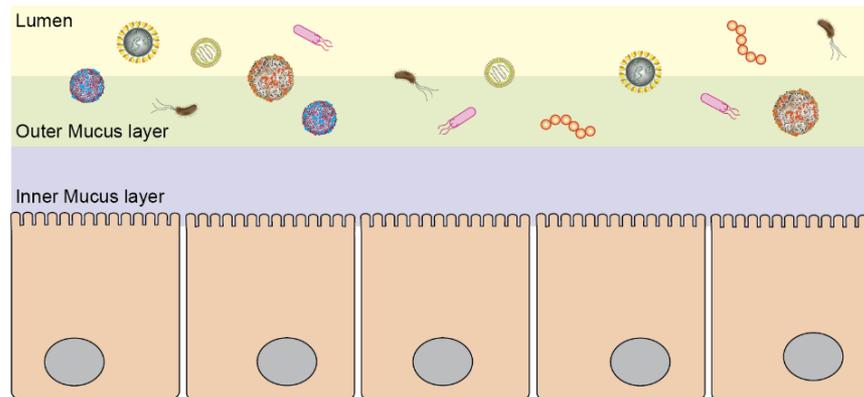
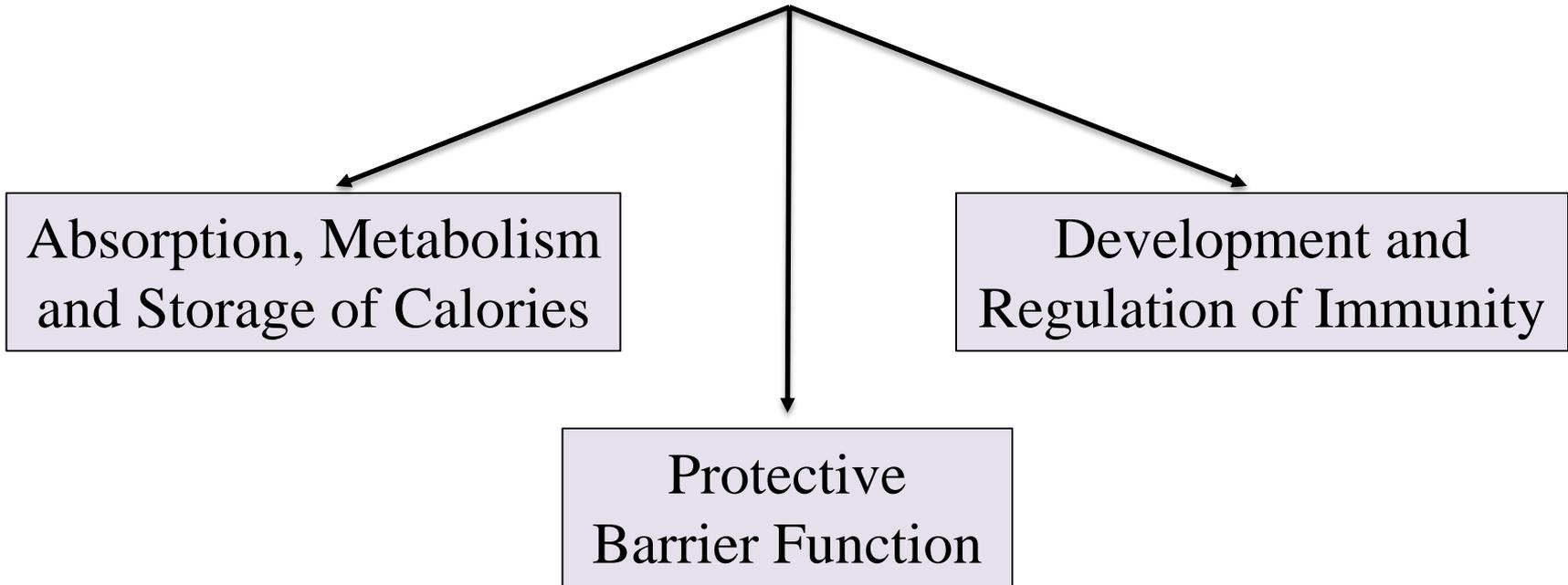


Sites of microbial colonization



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

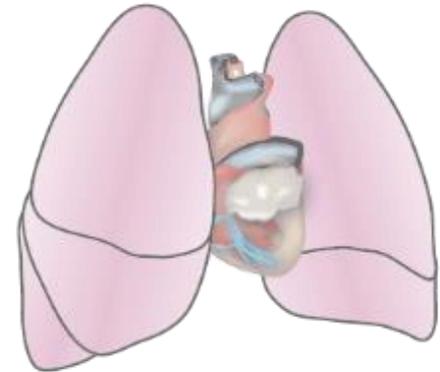
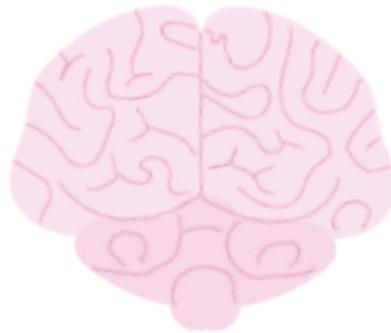
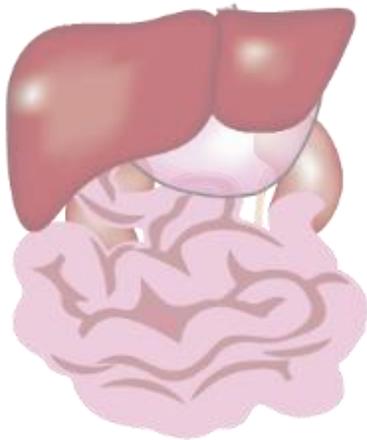


Microbiome in Health and Disease

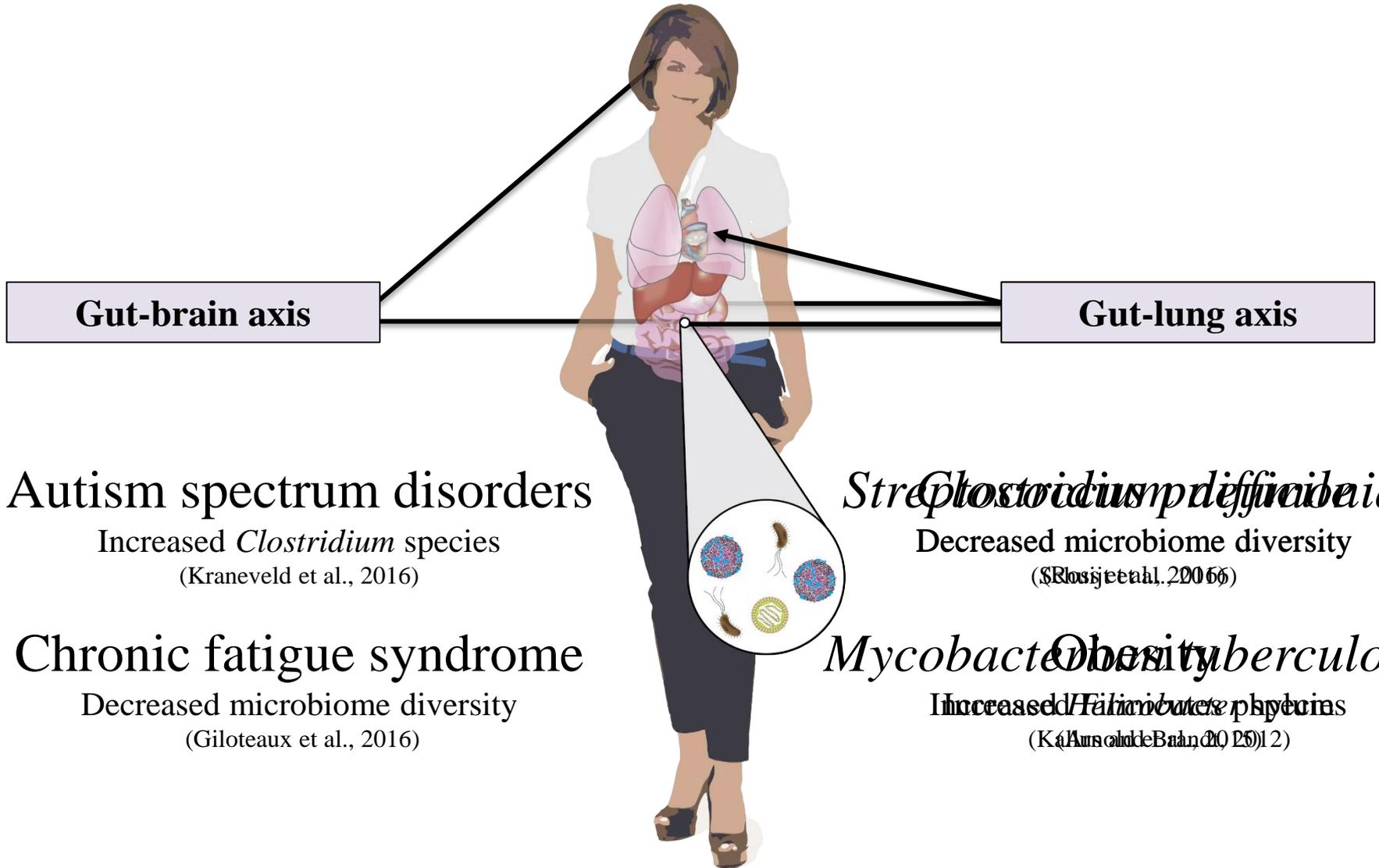
The role is complex and not well understood

Microbiome diversity and composition play a role in

1. Disease susceptibility
2. Response to pathogens



Microbiome and Disease



Gut-brain axis

Gut-lung axis

Autism spectrum disorders

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

Chronic fatigue syndrome

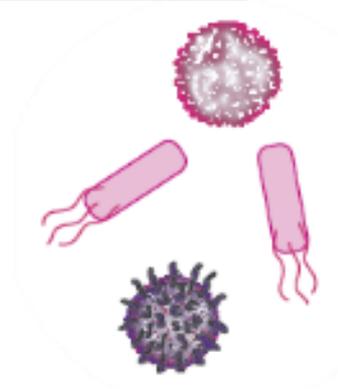
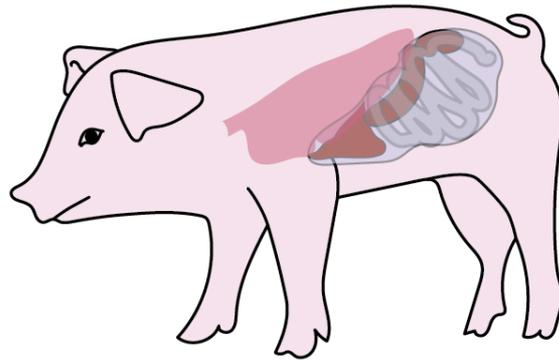
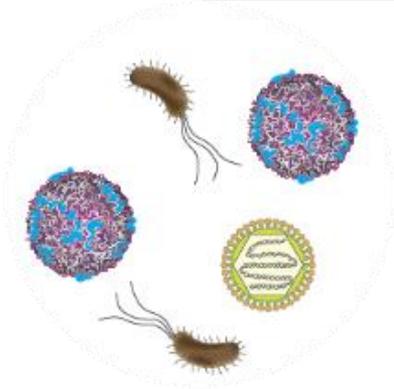
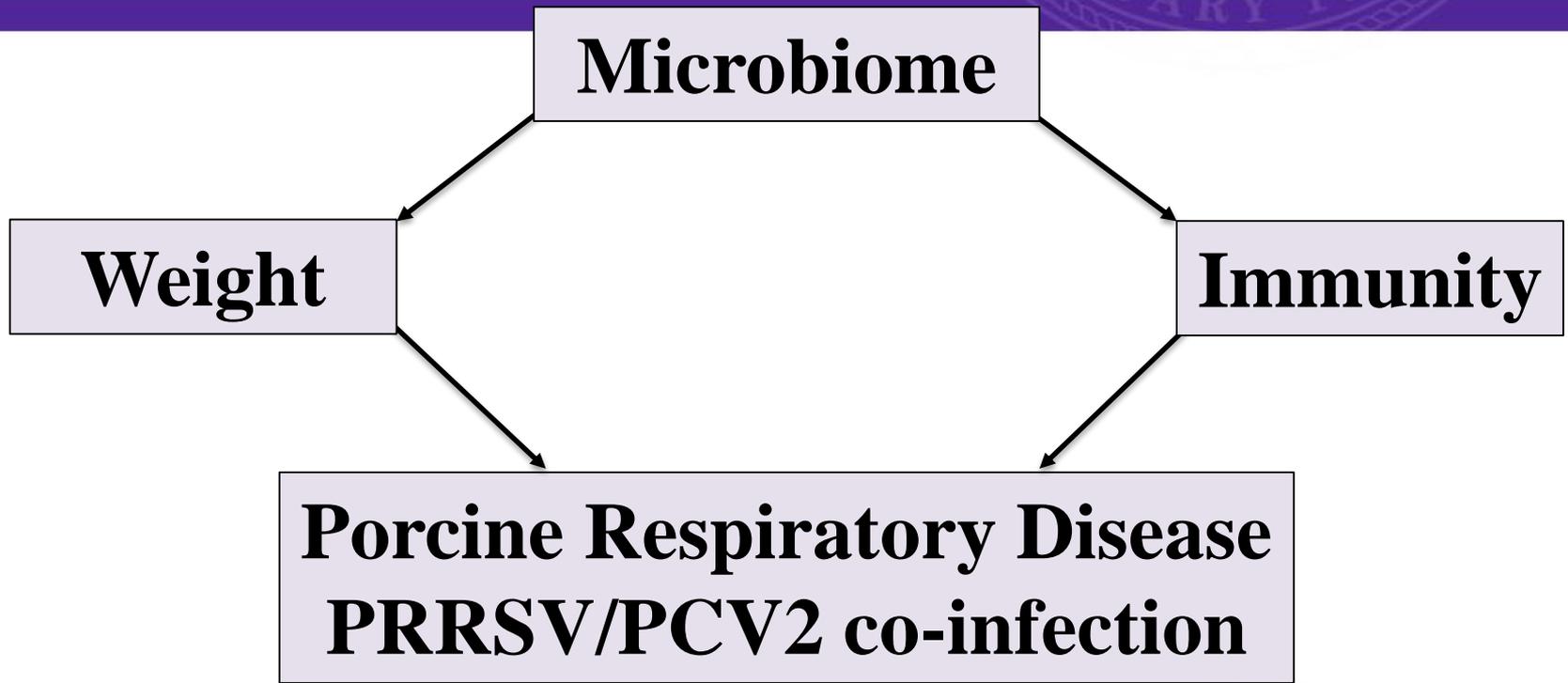
Decreased microbiome diversity
(Giloteaux et al., 2016)

Streptococcus pneumoniae

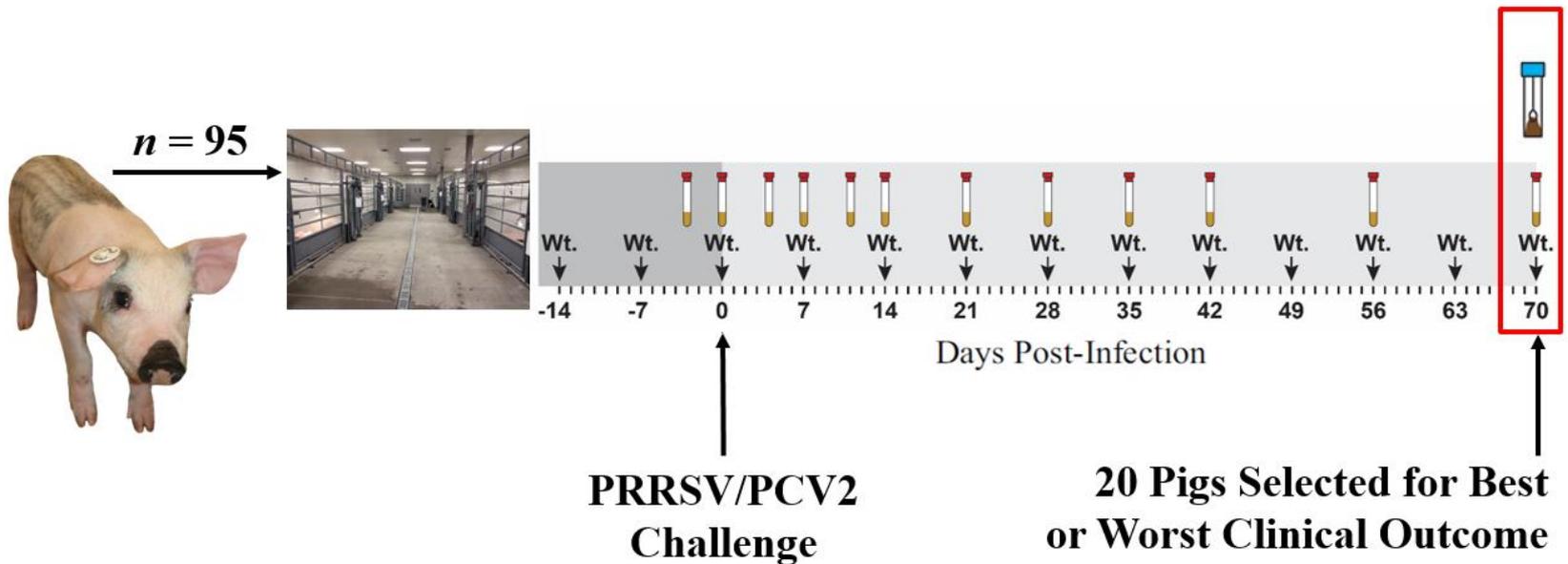
Decreased microbiome diversity
(Slosij et al., 2006)

Mycobacterium tuberculosis

Increased *Firmicutes* phylum
(K. Amadori et al., 2012)



Are there microbiome characteristics associated with outcome after PRRSV/PCV2 co-infection?



Niederwerder et al., 2016

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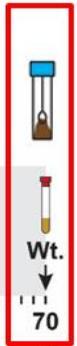
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1. Increased microbiome diversity
2. Increased *Escherichia coli*

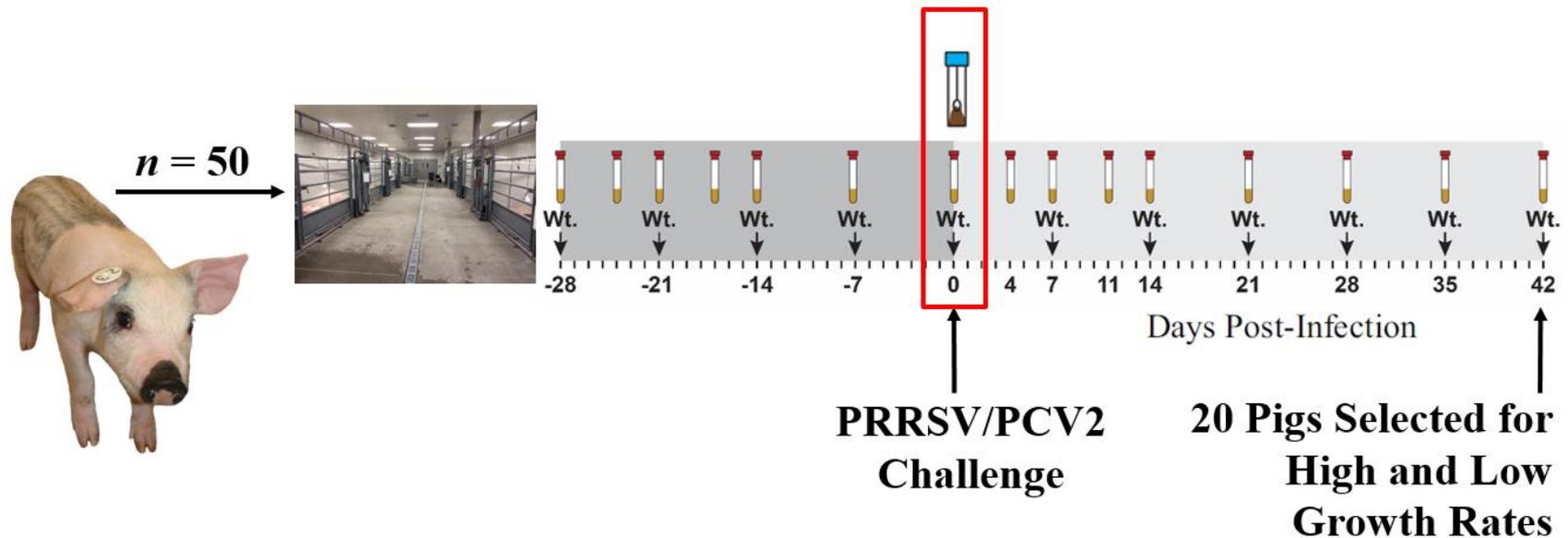
70 days post-infection is associated with best clinical outcomes after PRRSV/PCV2 co-infection

PRRSV/PCV2
Challenge

20 Pigs Selected for Best
or Worst Clinical Outcome



Are there microbiome characteristics that **PREDISPOSE** outcome after co-infection?



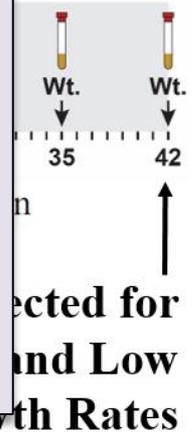
Ober et al., 2017

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

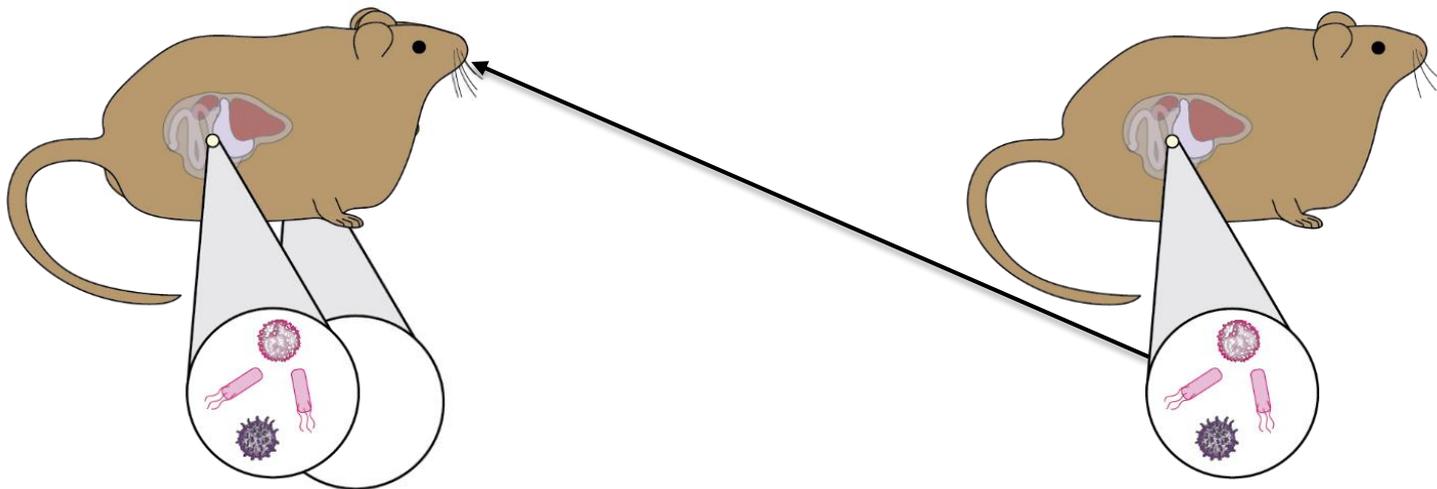


Ober et al., 2017

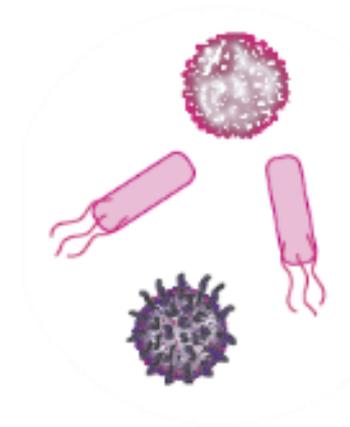
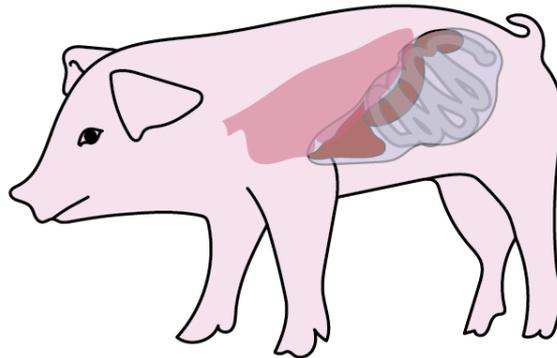
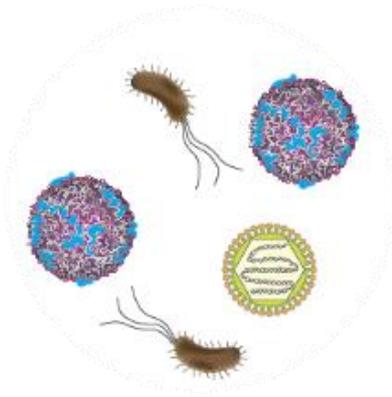
Fecal Microbiota Transplantation

- 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

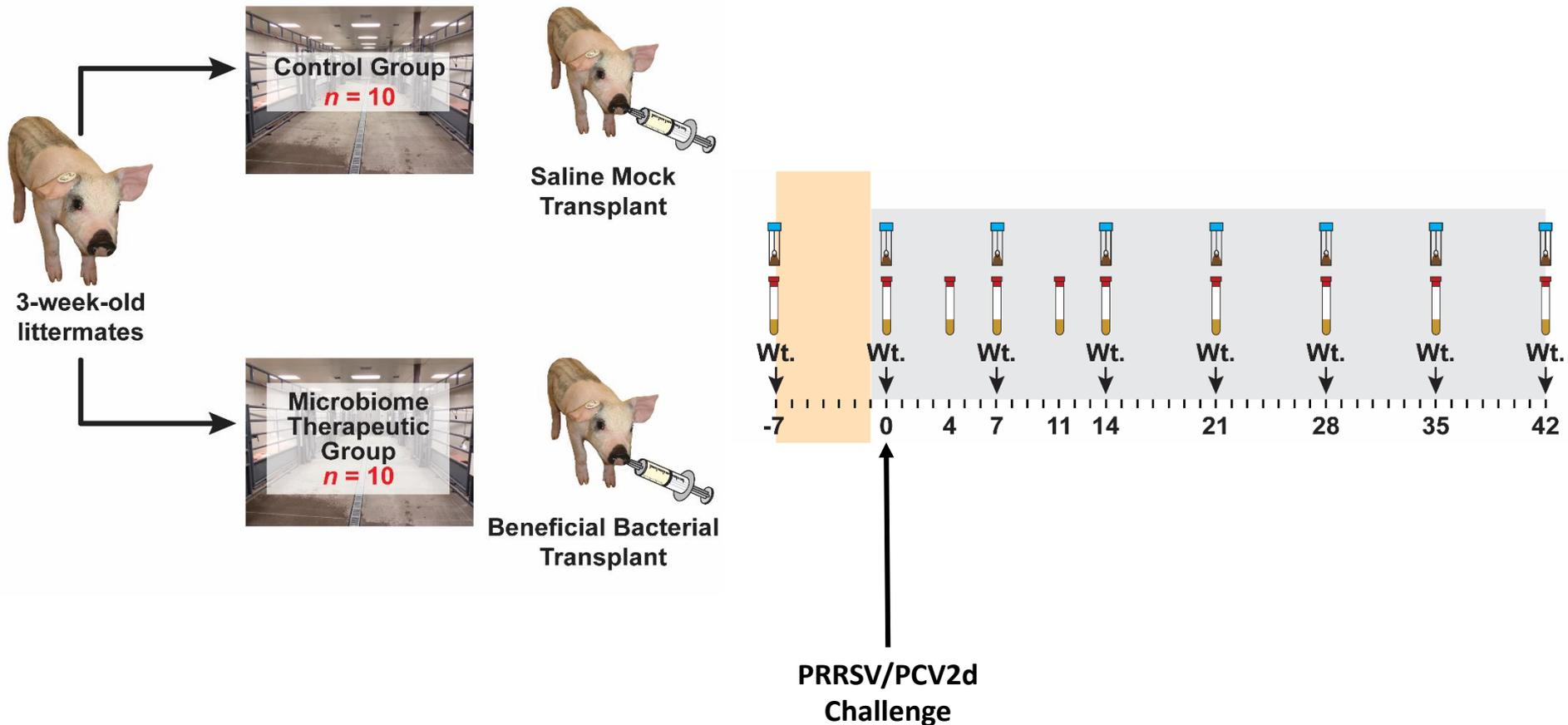
(Ridaura et al., 2013; Turnbaugh et al., 2006)



Can **fecal microbiota transplantation** prior to PRRSV/PCV2 co-infection improve outcome?



Experimental Design

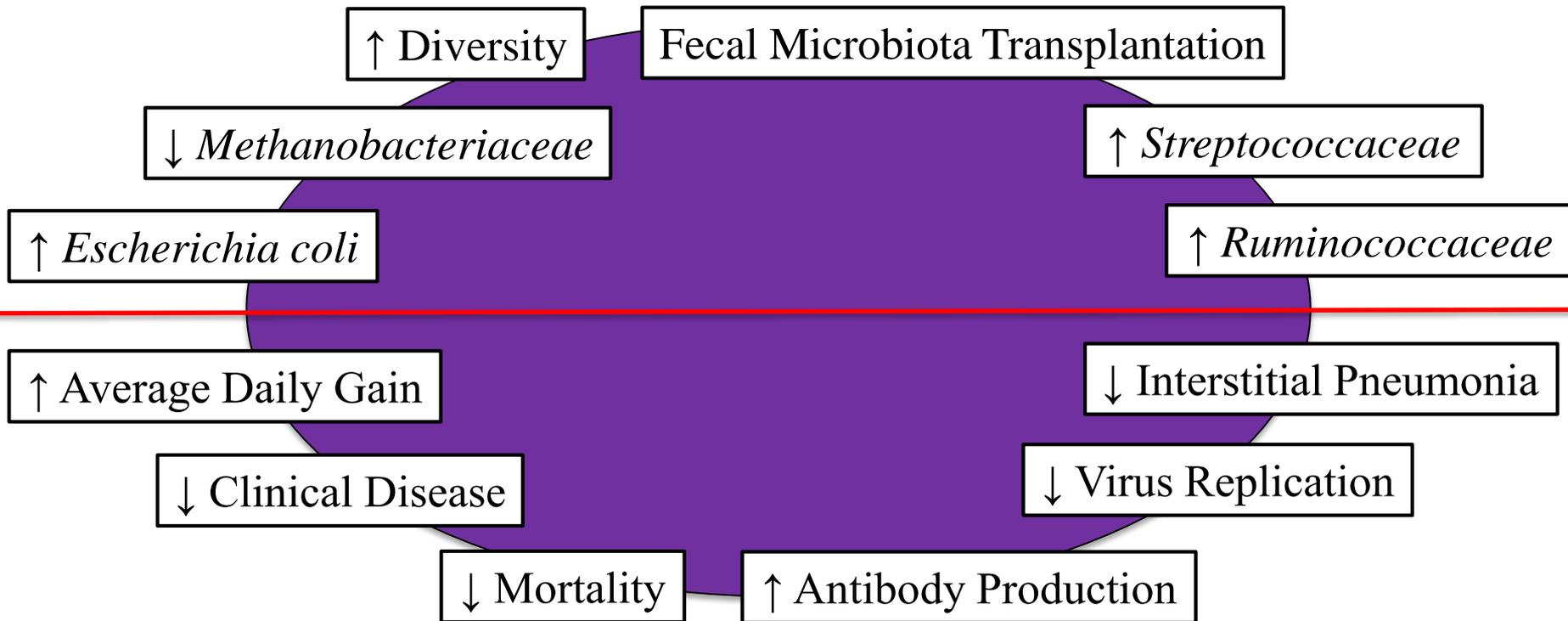


Summary

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



Conclusion

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

Acknowledgements

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