

Role of the Microbiome in Disease Outcome of Swine

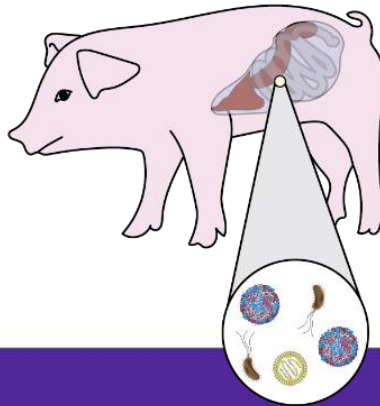
Megan C. Niederwerder, DVM, PhD

Assistant Professor

Department of Diagnostic Medicine/Pathobiology

Kansas State Veterinary Diagnostic Laboratory

Kansas State University



Microbiome

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

antigenome	immunogenome	plastidome
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	

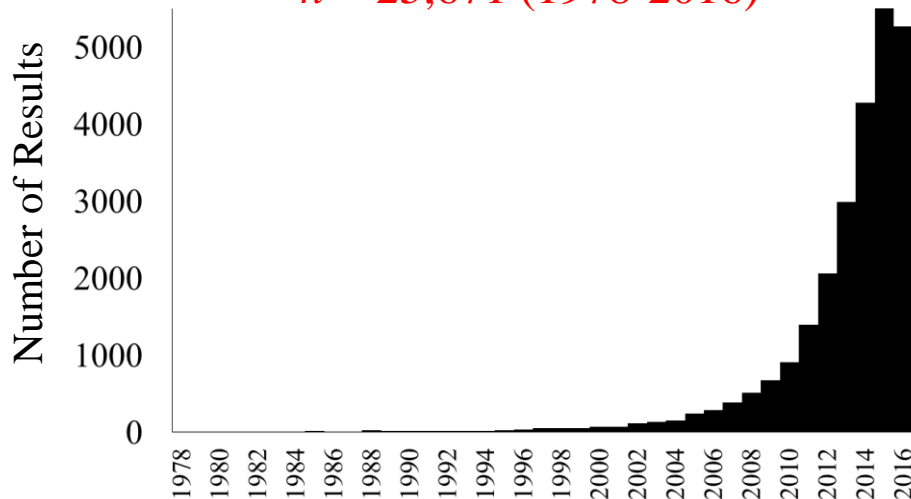
Emerging Area of Study

NIH Human Microbiome Project

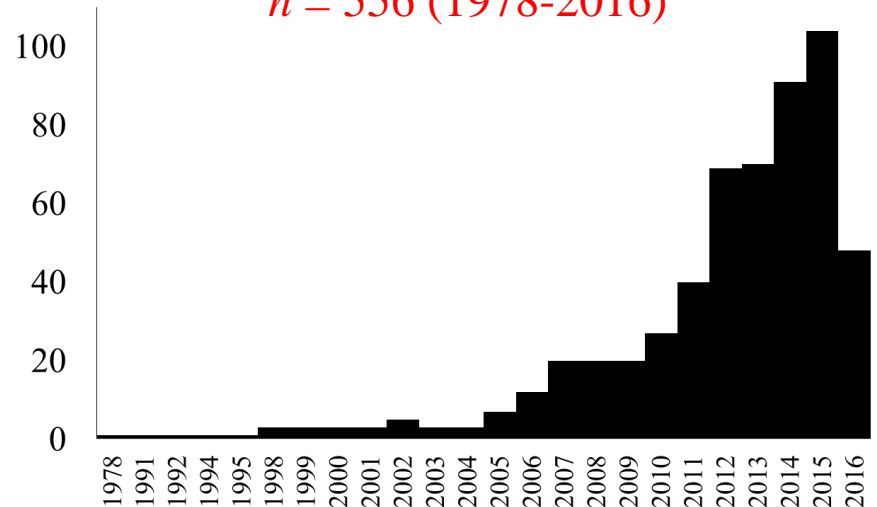
Understanding the microbiome in human health and disease

(Peterson et al., 2009)

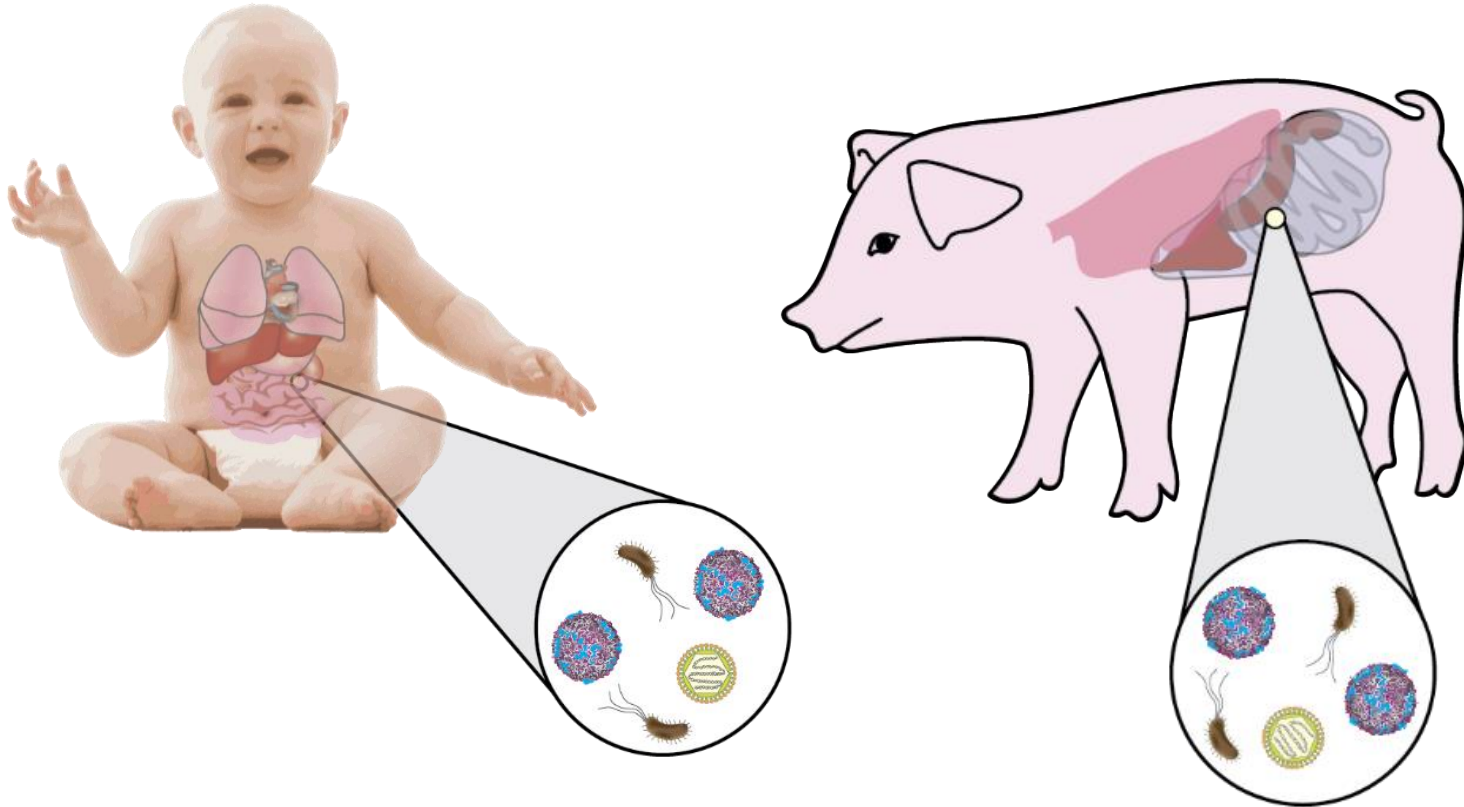
“Human Microbiome”
 $n = 25,671$ (1978-2016)



“Swine Microbiome”
 $n = 556$ (1978-2016)

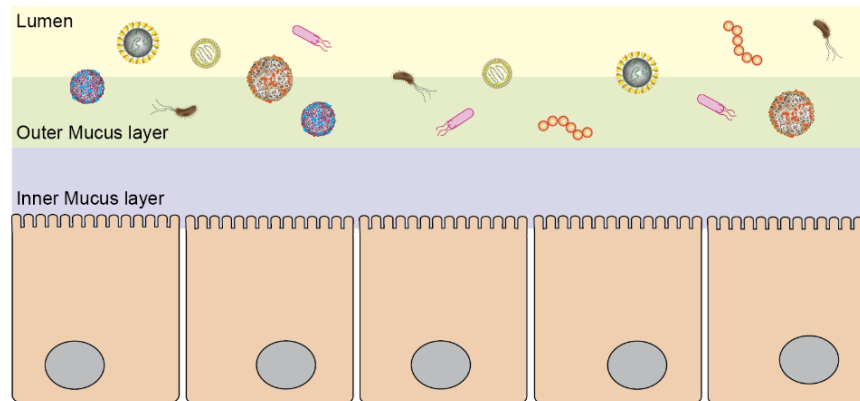
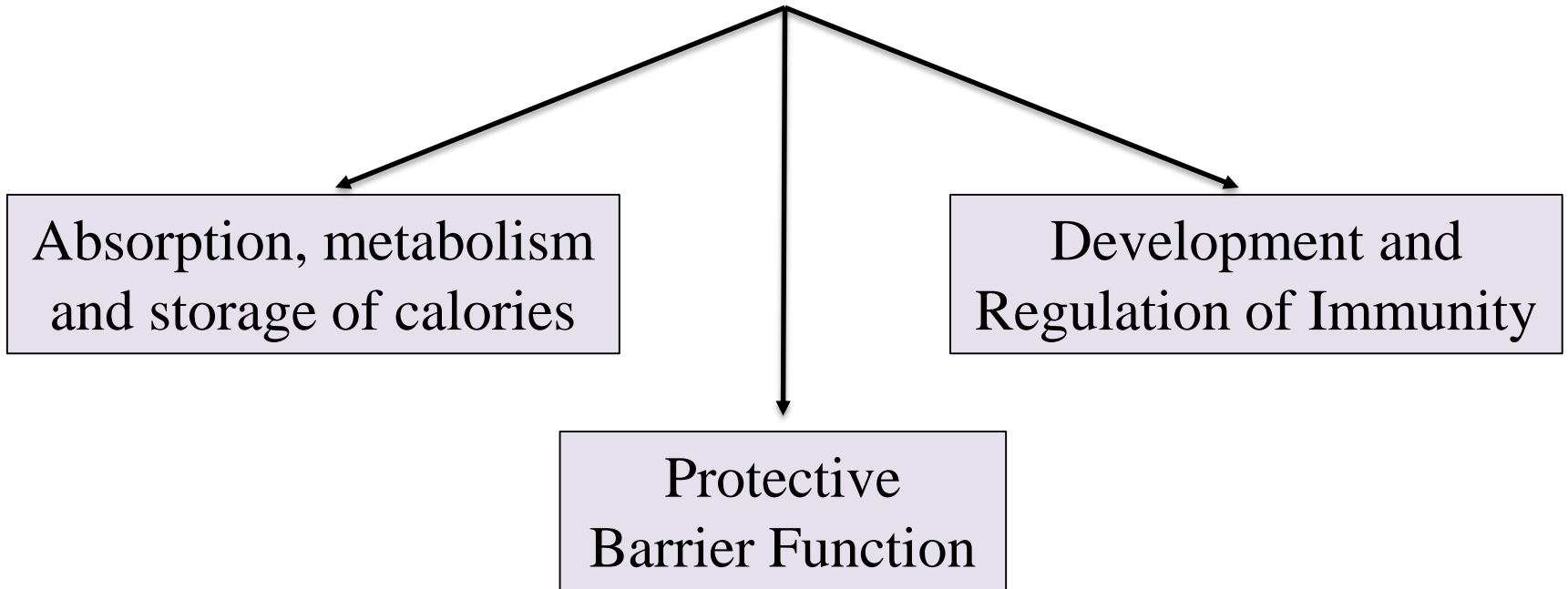


Microbial colonization



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

Roles of the Microbiome

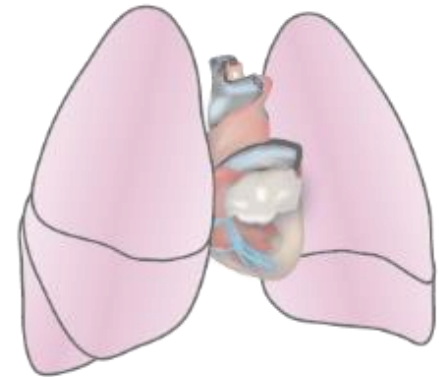
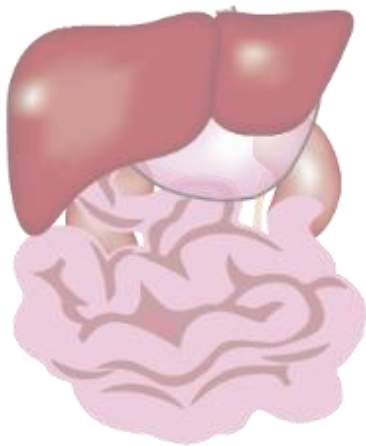


Microbiome in Health and Disease

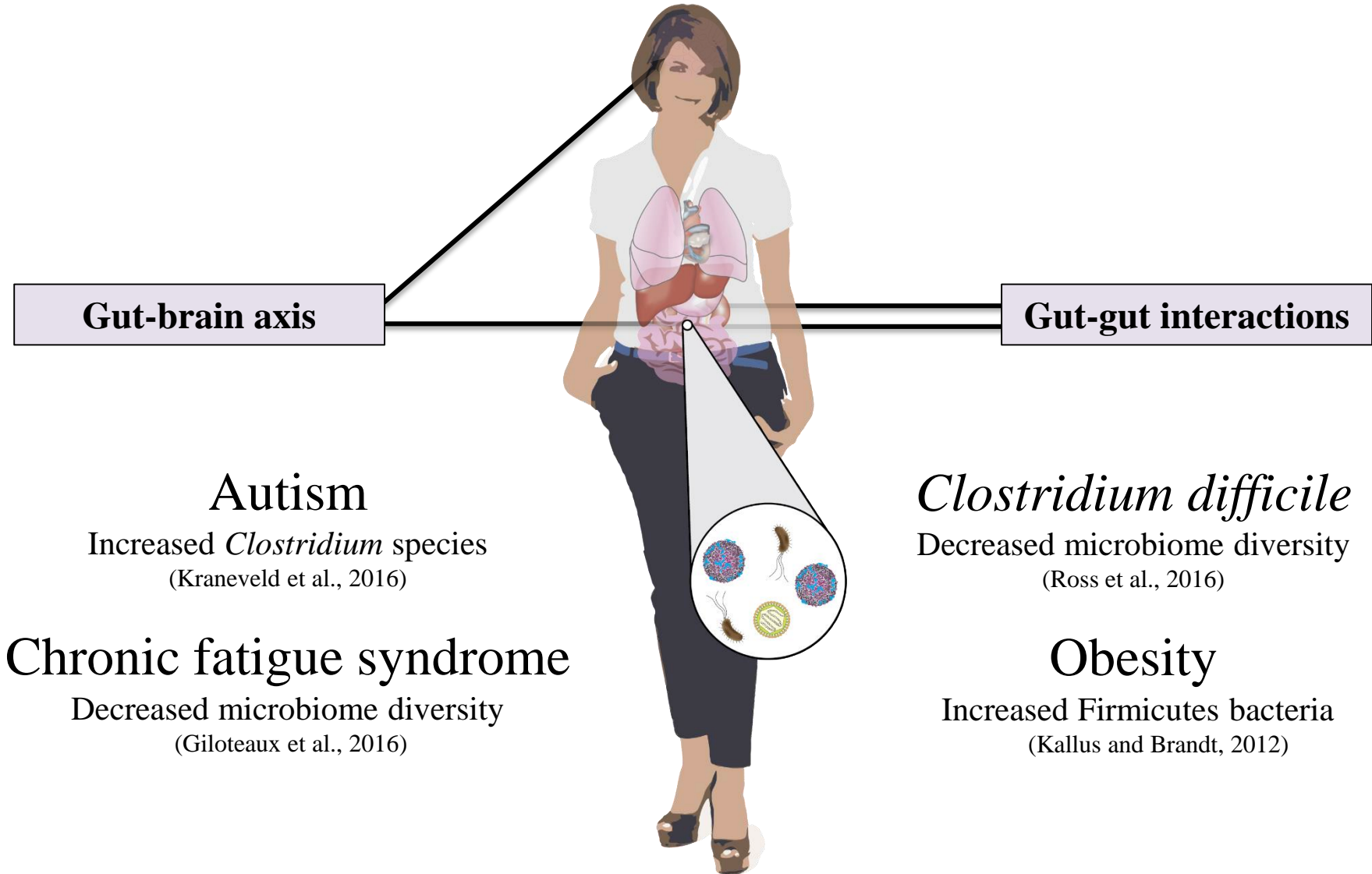
The role is complex and not well understood

Microbiome diversity and composition play a role in

1. Disease susceptibility
2. Response to pathogens



Microbiome and Disease



Gut-brain axis

Gut-gut interactions

Autism

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

Chronic fatigue syndrome

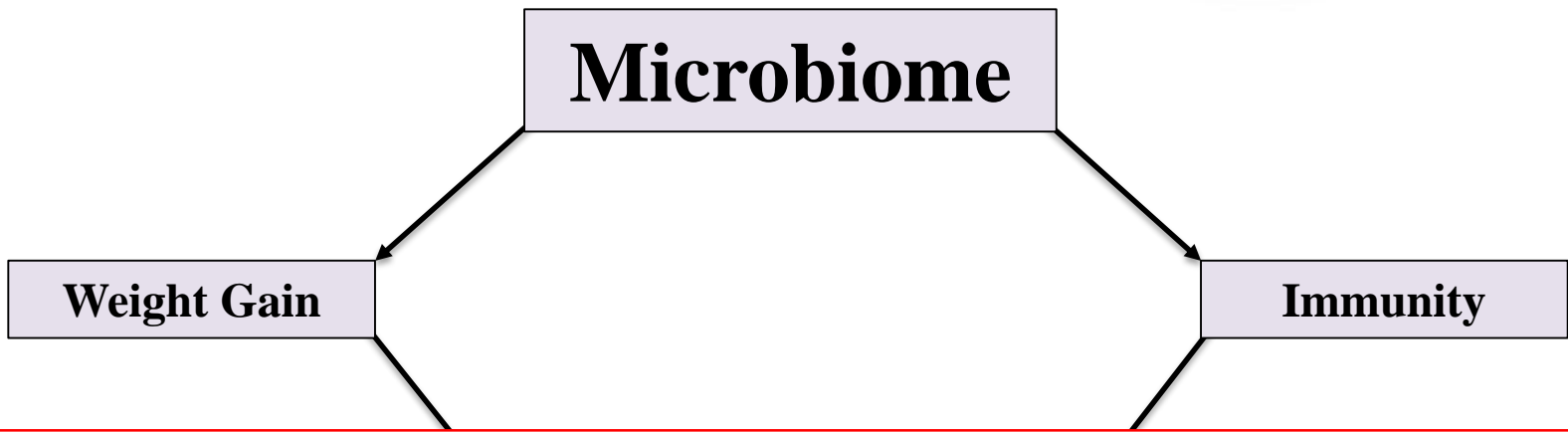
Decreased microbiome diversity
(Giloteaux et al., 2016)

Clostridium difficile

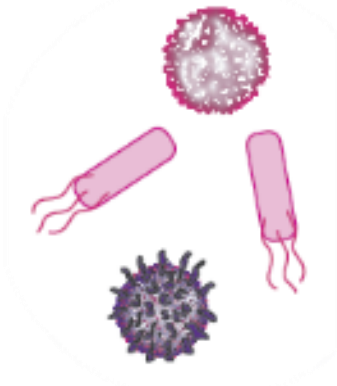
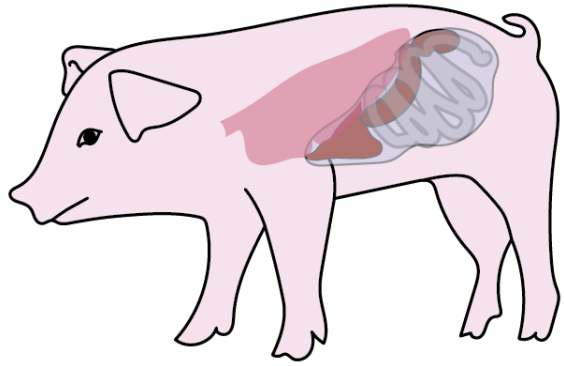
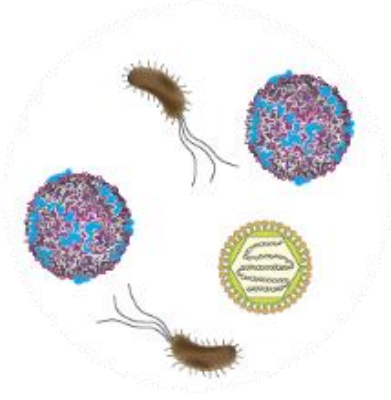
Decreased microbiome diversity
(Ross et al., 2016)

Obesity

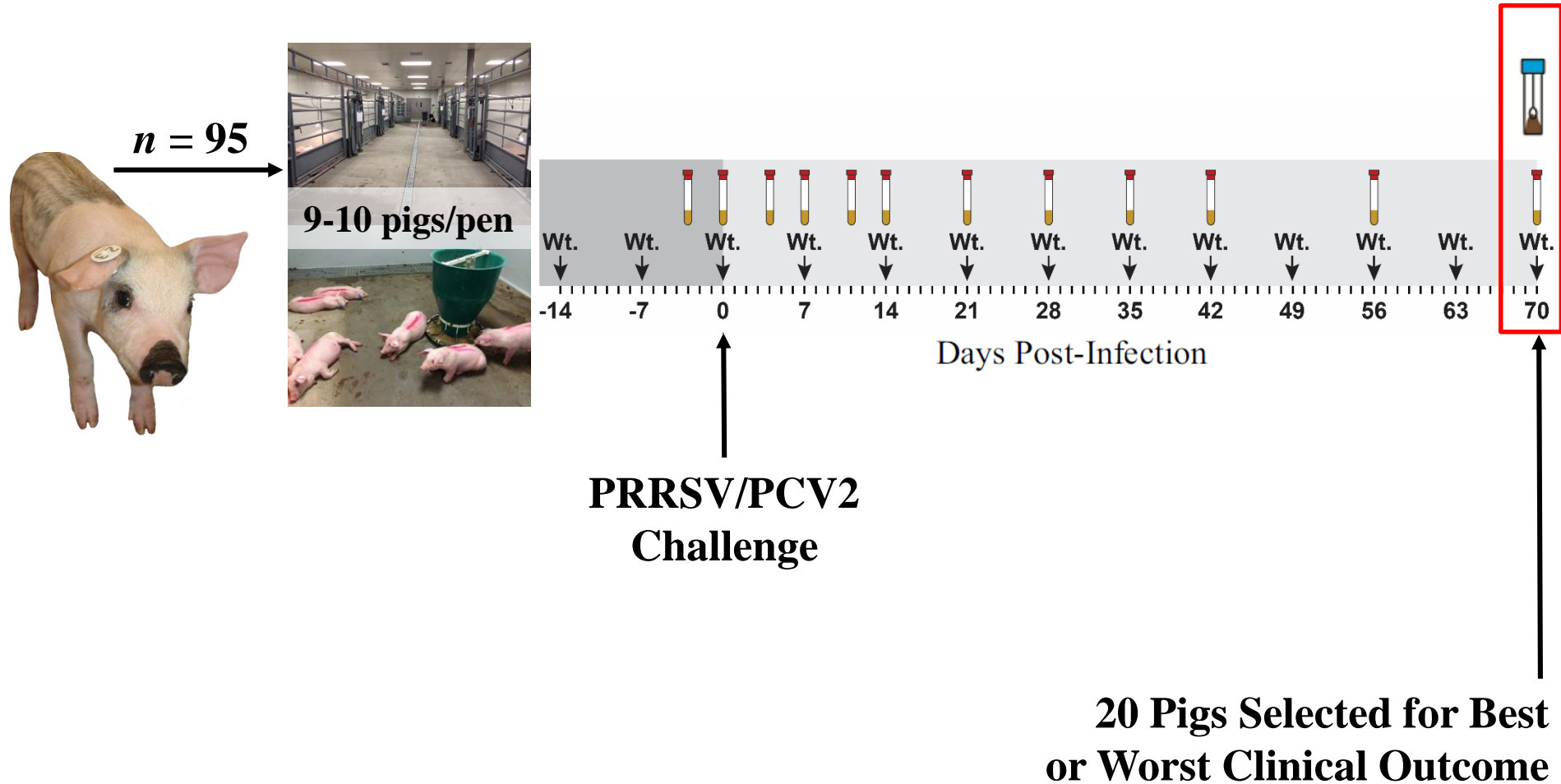
Increased Firmicutes bacteria
(Kallus and Brandt, 2012)



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



Experimental Design



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

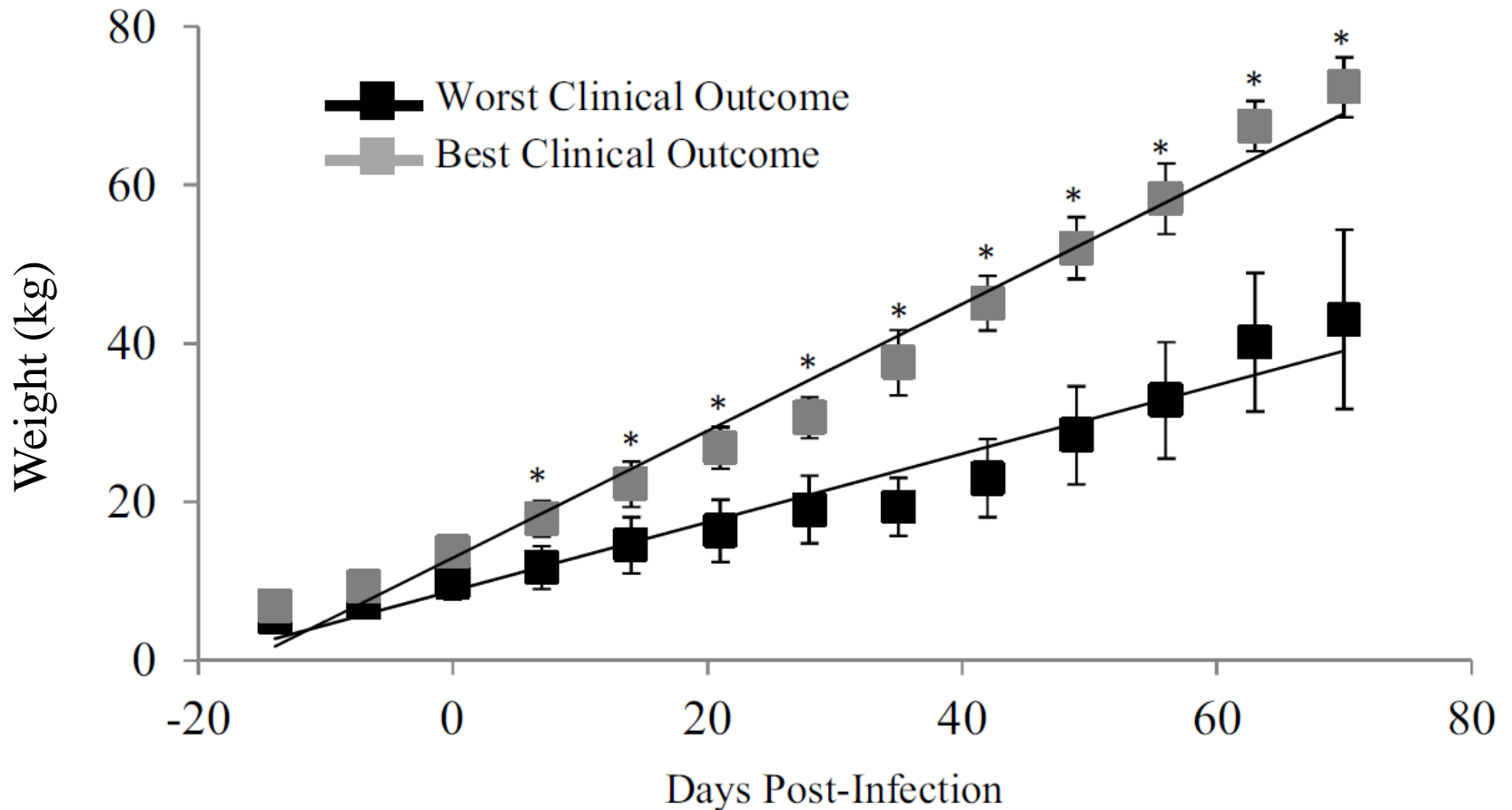
0.15 kg

≥ 10 days

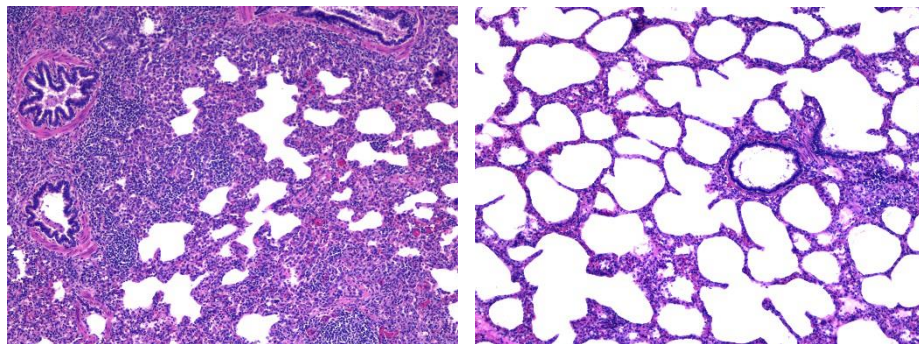
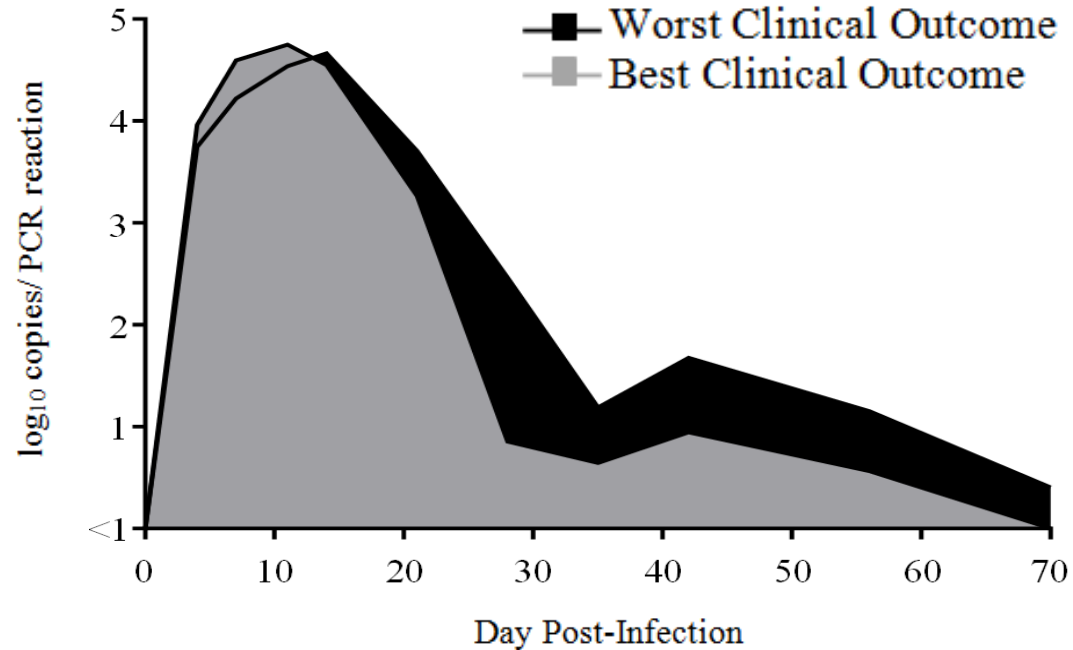
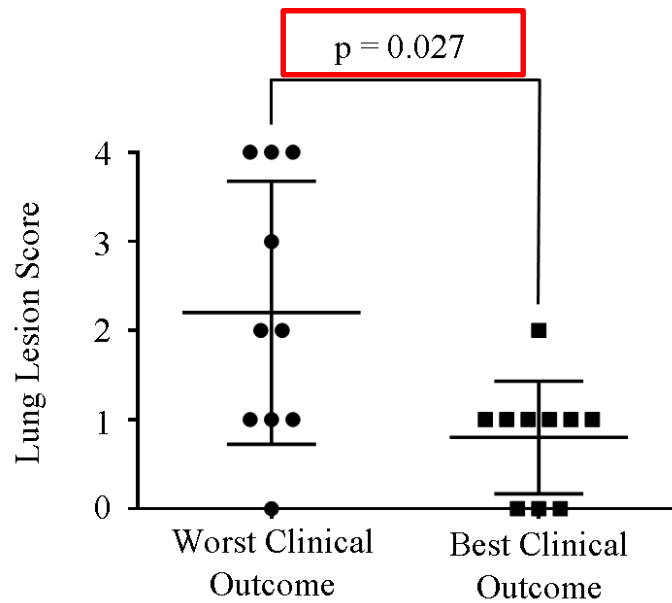


Weight Gain

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



Lung Lesions and PRRSV Viremia



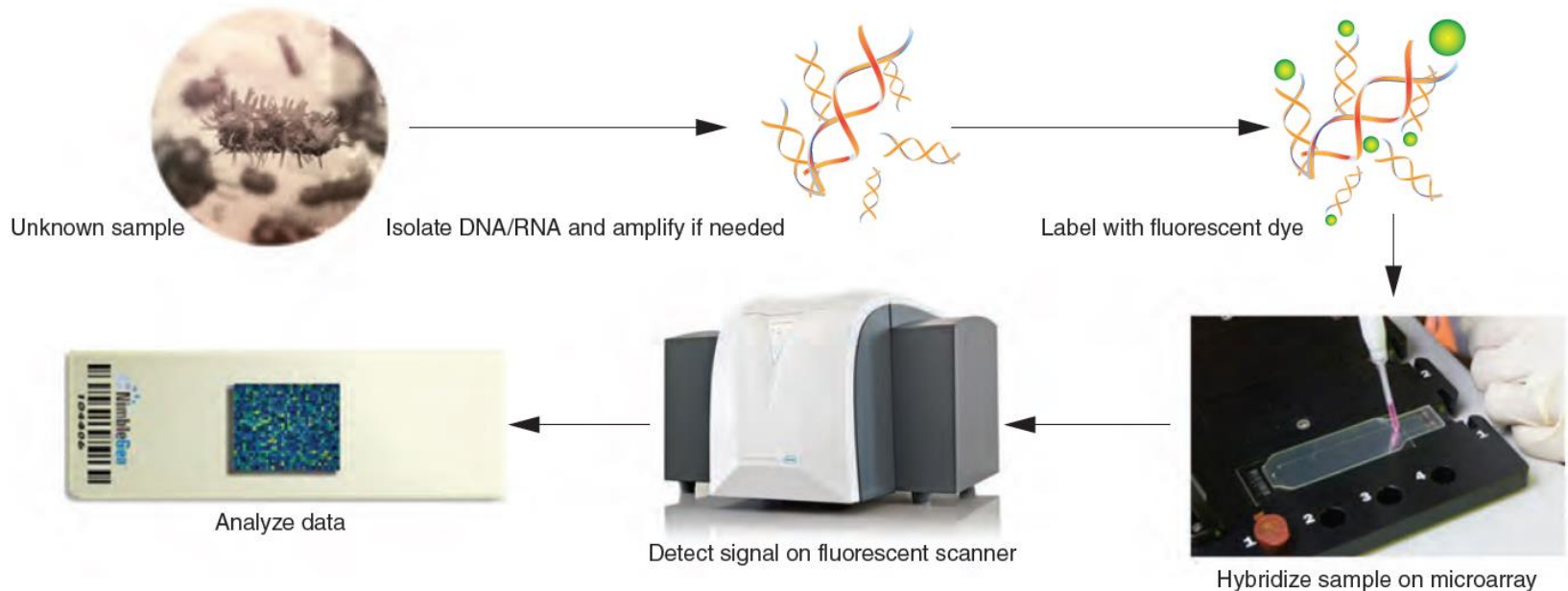
Area Under the Curve (p = 0.04)
Worst = 153.5 Best = 116.2

Microbiome

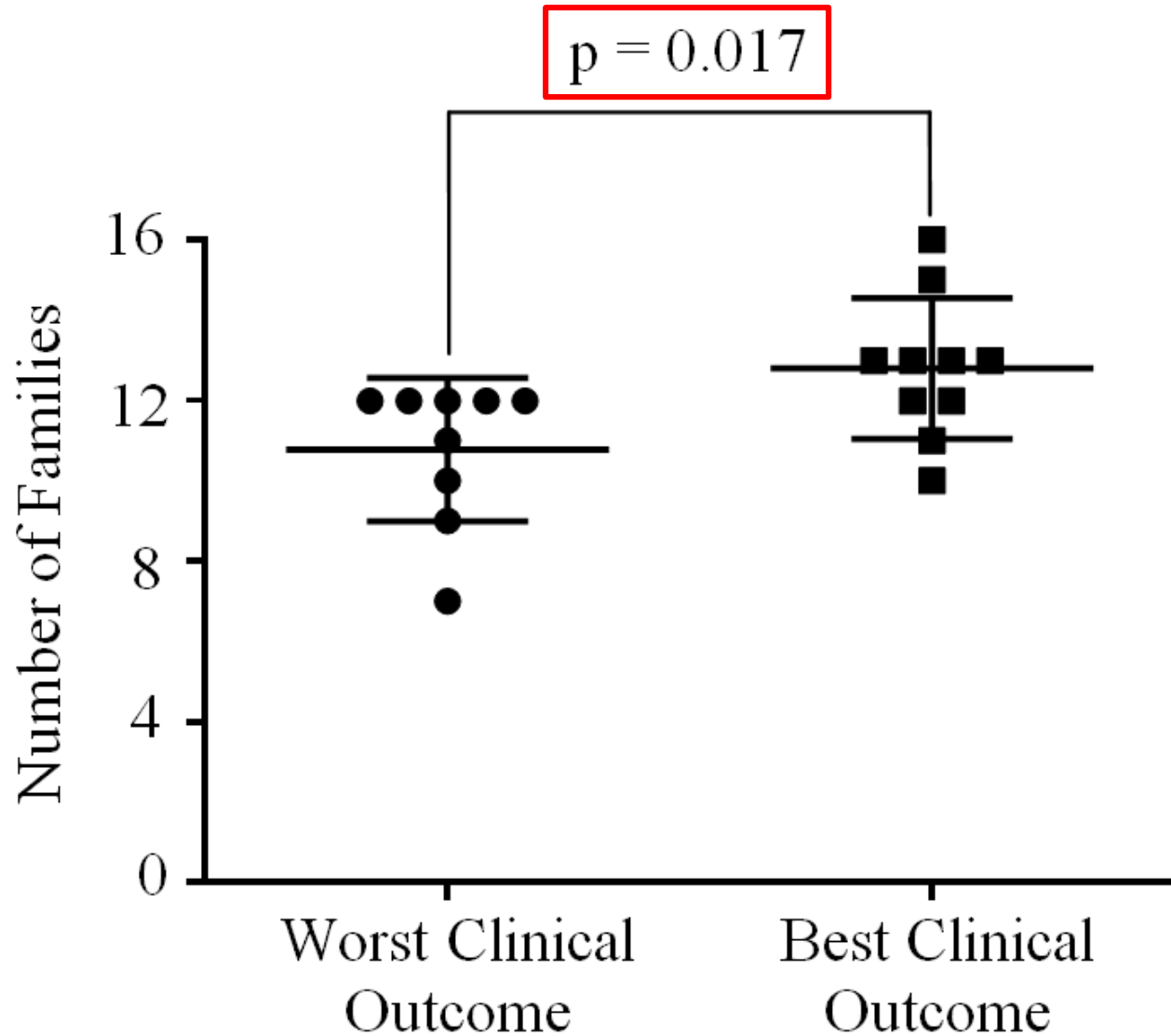
Lawrence Livermore Microbial Detection Array

Detects all sequenced microbes

3,856 viruses, 3,855 bacteria, 254 archaeobacteria, 100 fungi, 36 protozoa



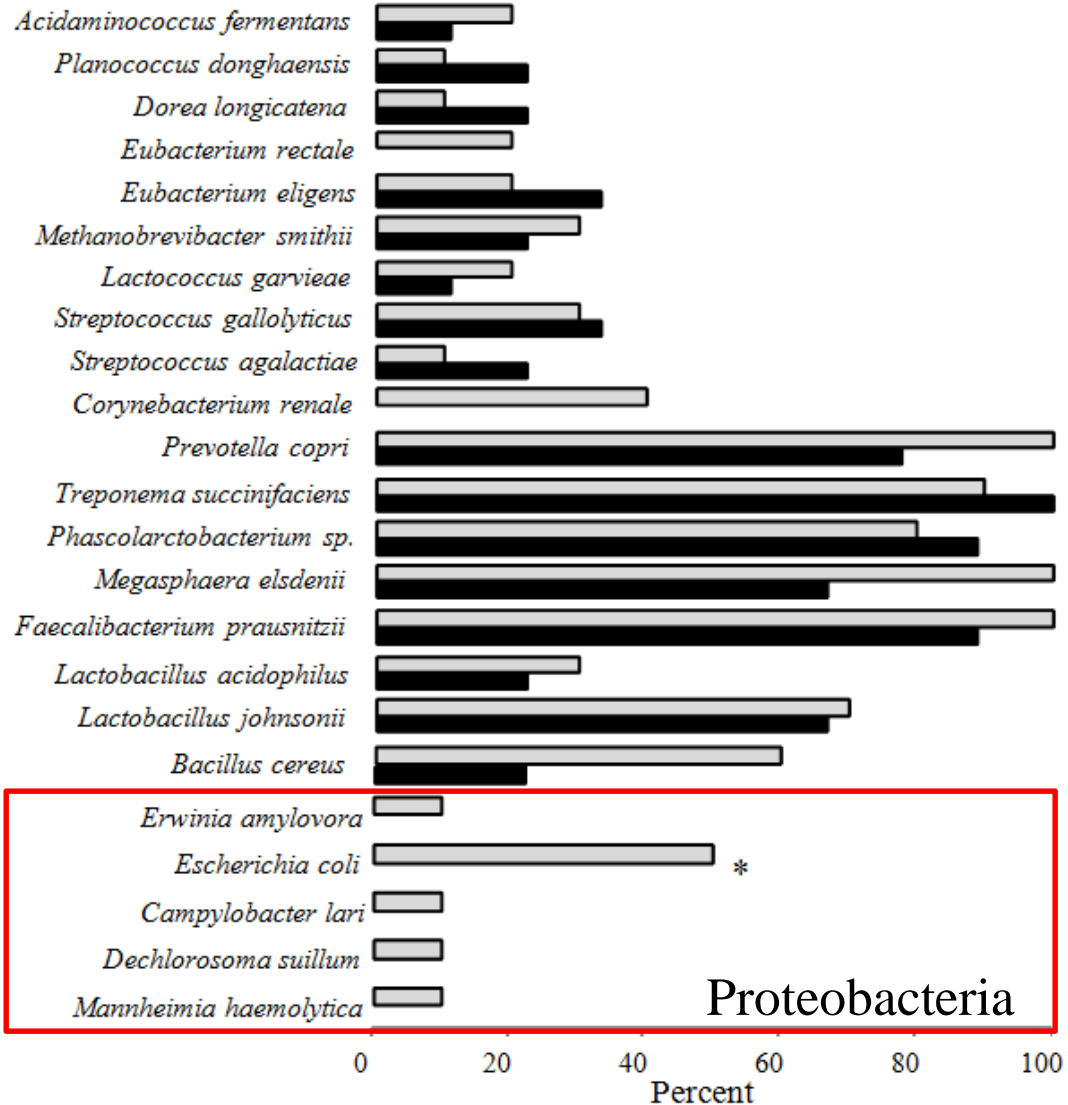
Microbiome Diversity



Microbiome Composition

Worst Clinical Outcome
 Best Clinical Outcome

Bacteria

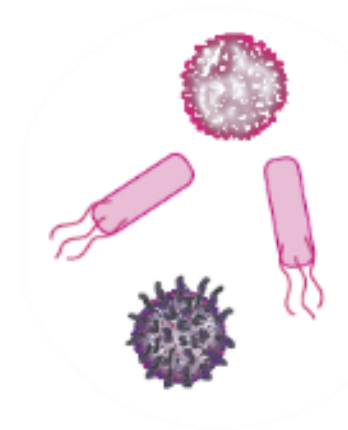
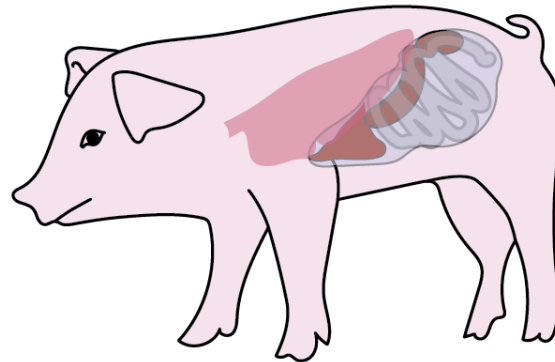
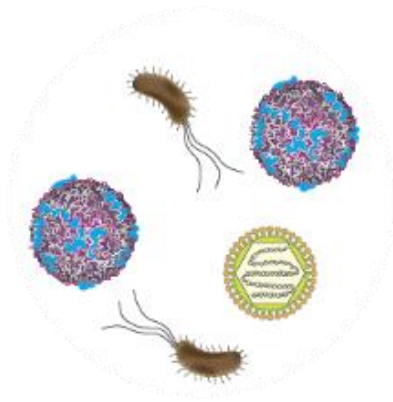


Summary

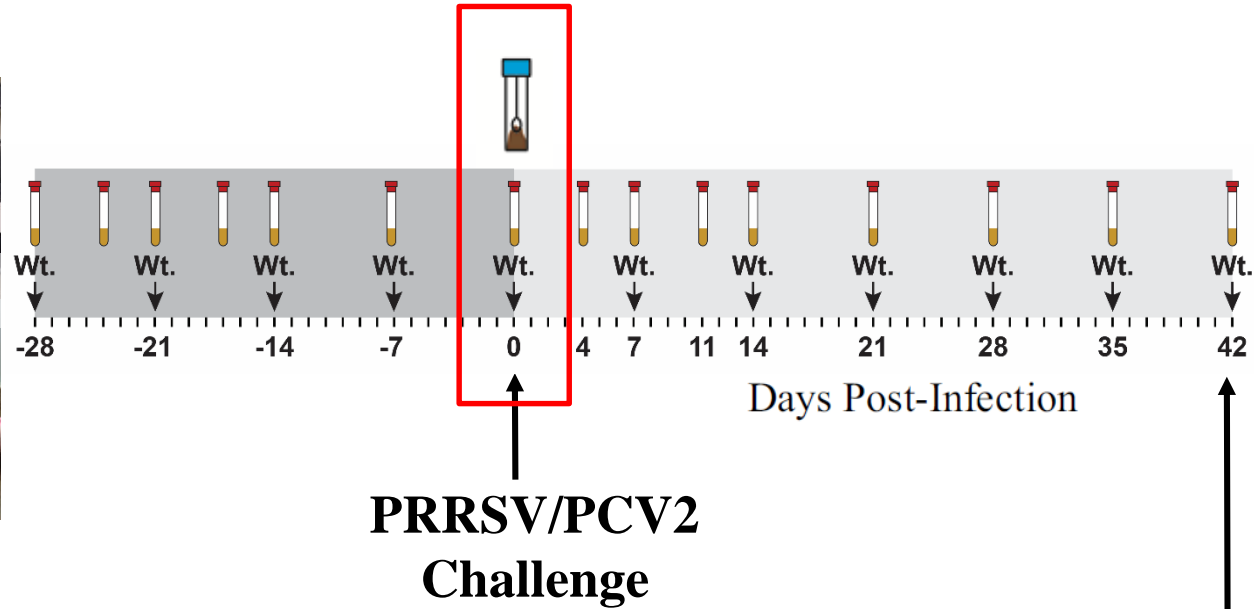
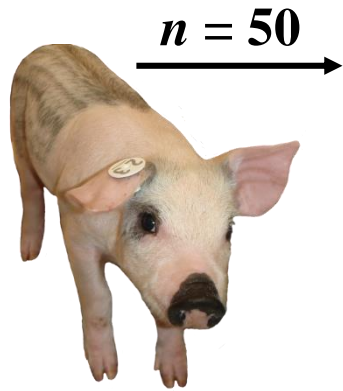
1. Increased microbiome diversity
2. Increased fecal *Escherichia coli*

Associated with best clinical outcome **70 days**
after PRRSV/PCV2 co-infection

Do microbiome characteristics **PREDISPOSE** outcome following PRRSV/PCV2 co-infection?



Experimental Design



20 Pigs Selected for High and Low Growth Rates

Selection of Pigs

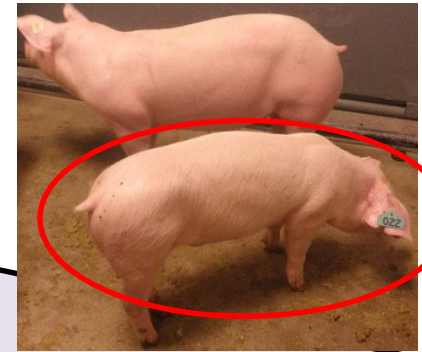
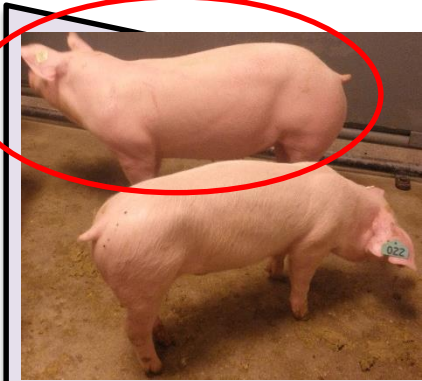
High Growth Rate
***n* = 10 pigs**

Low Growth Rate
***n* = 10 pigs**

0.962 kg

Average Daily Gain

0.596 kg



0 days

Clinical Disease

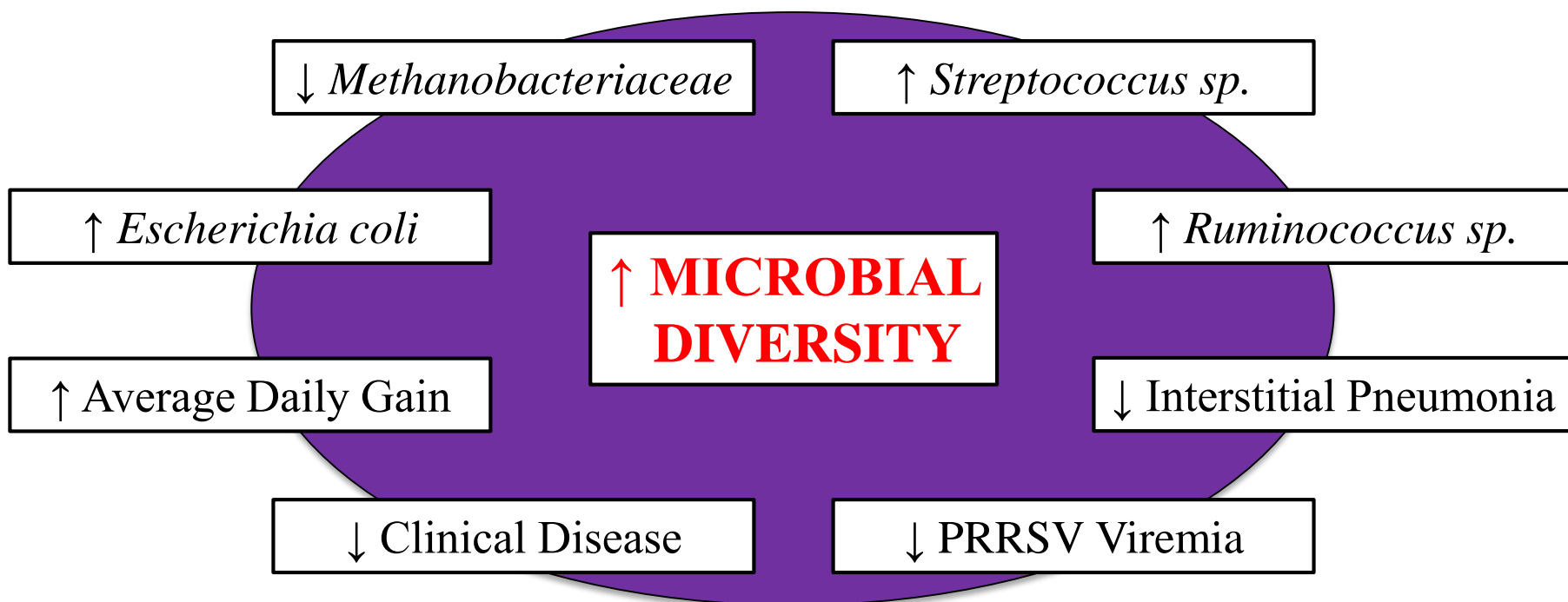
0 days

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



Conclusion

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

Acknowledgements

This work was supported by the USDA NIFA Award #2013-68004-20362, the State of Kansas National Bio and Agro-Defense Facility Fund, and by the Lawrence Livermore National Laboratory Derived Research and Development effort (14ERD081)

Bob Rowland

Benjamin Tribble

Rebecca Ober

James Thissen

Maureen Kerrigan

Nick Monday

Giselle Cino

Kevin McLoughlin

Becky Eaves

Ni Wang

Michelle Mazur

Joan Lunney

Ross Wahl

Mal Hoover

Crystal Jaing

Jack Dekkers

Mallory Phillips

Vlad Petrovan



Lawrence Livermore National Laboratory