

IPVSBb

In-depth & functional characterization of the lower airways' microbial community in sick finisher pigs using a novel shotgun metagenomics approach

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PathoSense



Universiteit
Antwerpen

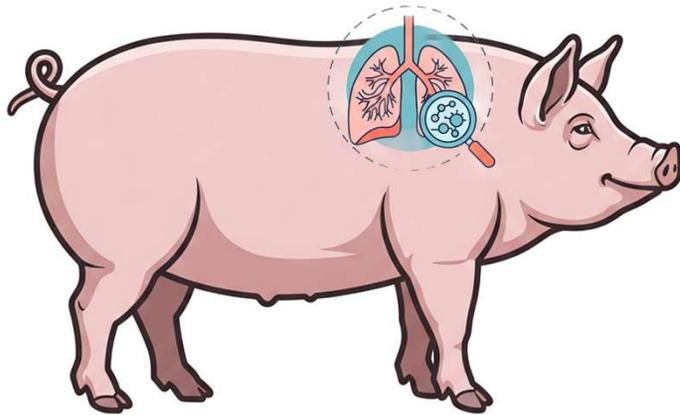
Introduction



- MSc in Molecular and Cellular Biology, University of Pisa (2021)
- Currently: **PhD student** at **PathoSense & Antwerp University** (promoters Prof. Sarah Lebeer and Dr. Sebastiaan Theuns) with a strong focus on the **respiratory microbiome of pigs** and **interactions between gut and lung microbiome**
- **Research Scientist** at PathoSense

Introduction

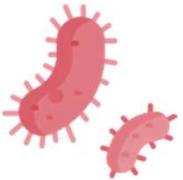
What do we know about disease-causing microorganisms in pigs?



Viruses



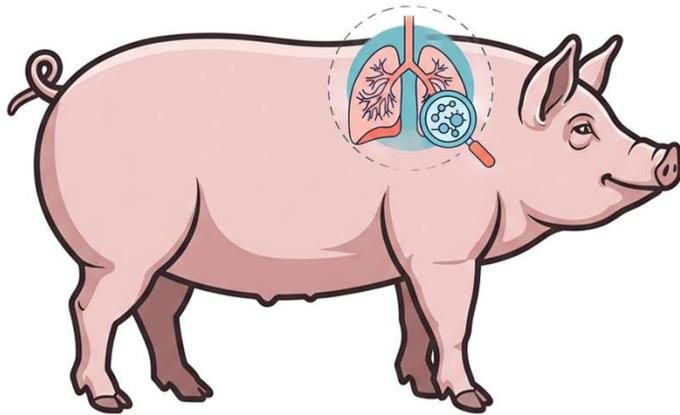
Bacteria → pathogenic?
→ part of microbiome?



Viral-bacterial interactions?

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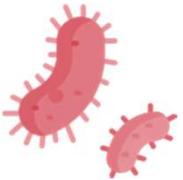
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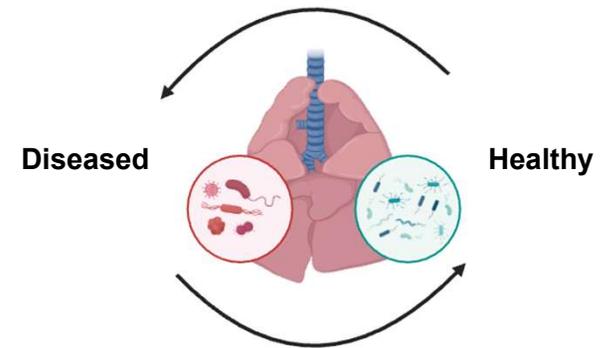
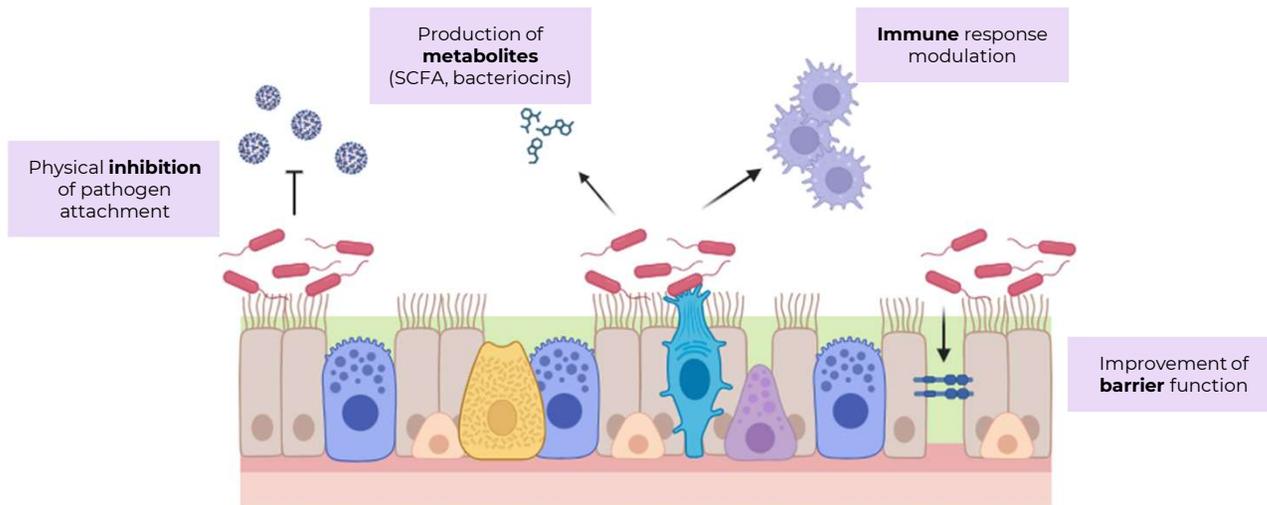
Viral-bacterial interactions?

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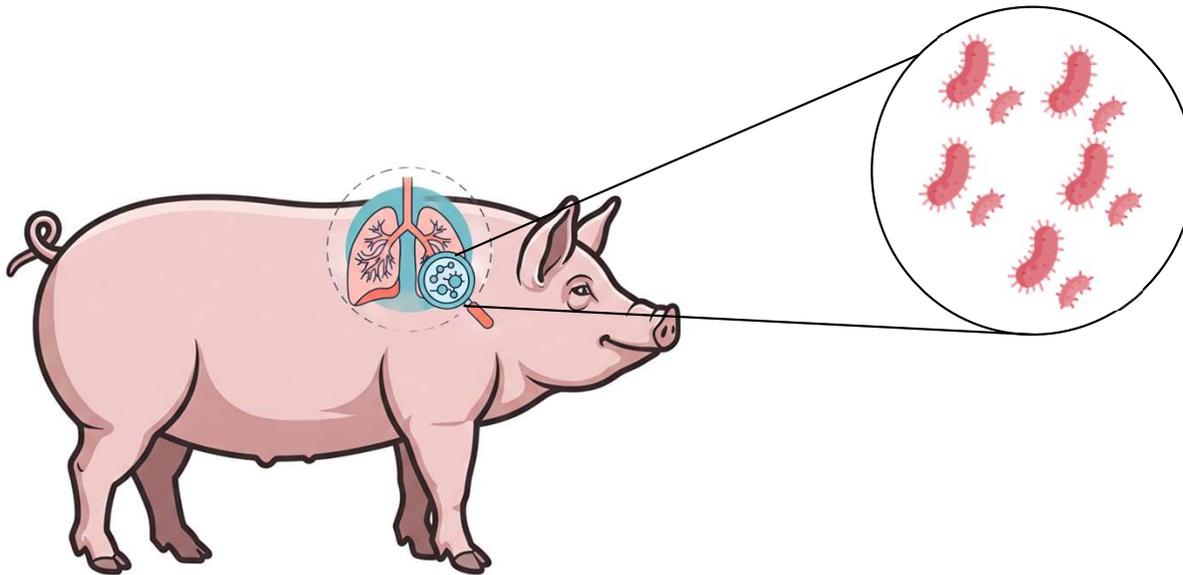
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Respiratory microbiome → Bacteria commonly present in the respiratory system



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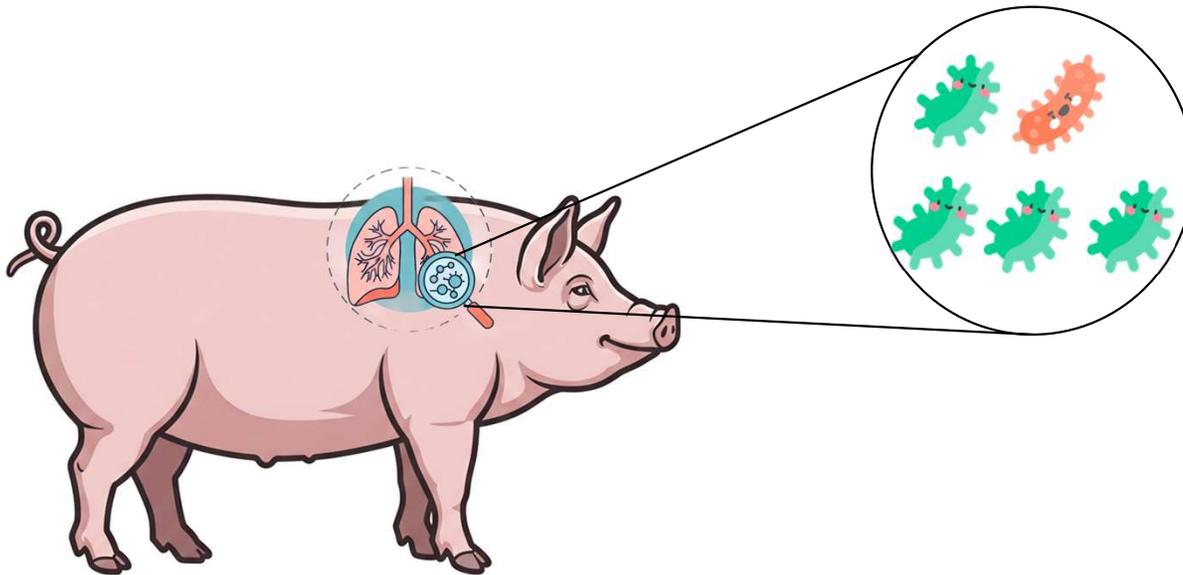
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What is the actual role of the lower respiratory tract microbiome in respiratory diseases in finisher pigs?

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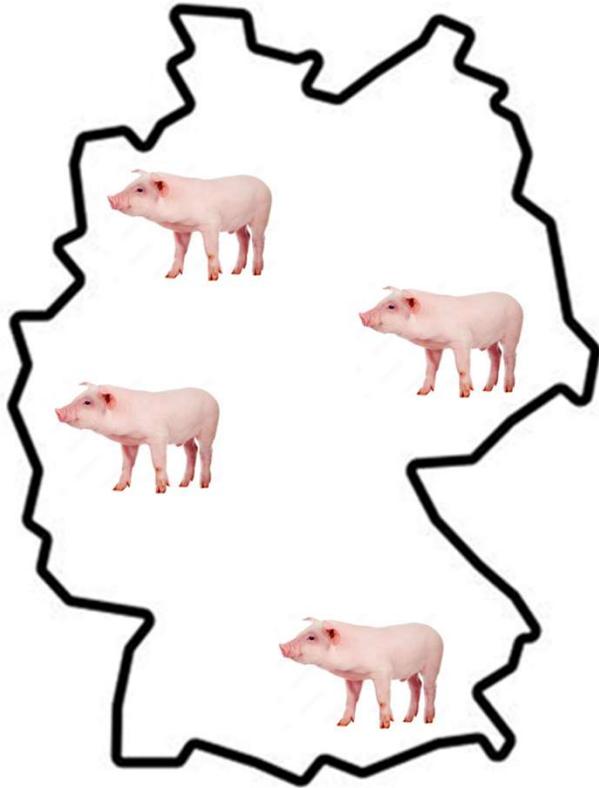


What is the actual role of the lower respiratory tract microbiome in respiratory diseases in finisher pigs?



Importance of distinguishing 'good' bacteria from 'bad' bacteria

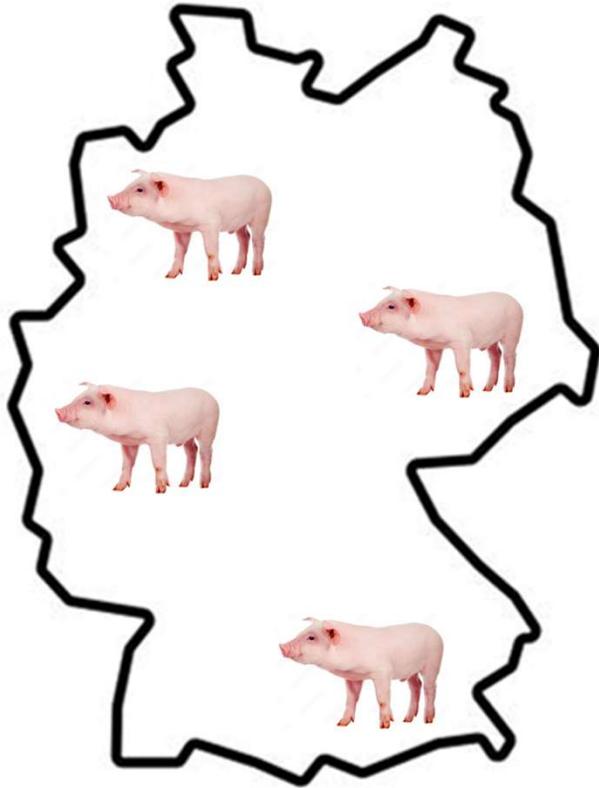
Experimental setup & Methods



- 15 German farms  
- Winter period (November 23 - March 24)
- 15 pigs sampled in each farm
- Tracheo-bronchial swabs (TBS)
- Pigs aged 3-5 months old with respiratory symptoms

Paper soon to be released > Panattoni et al., 2025

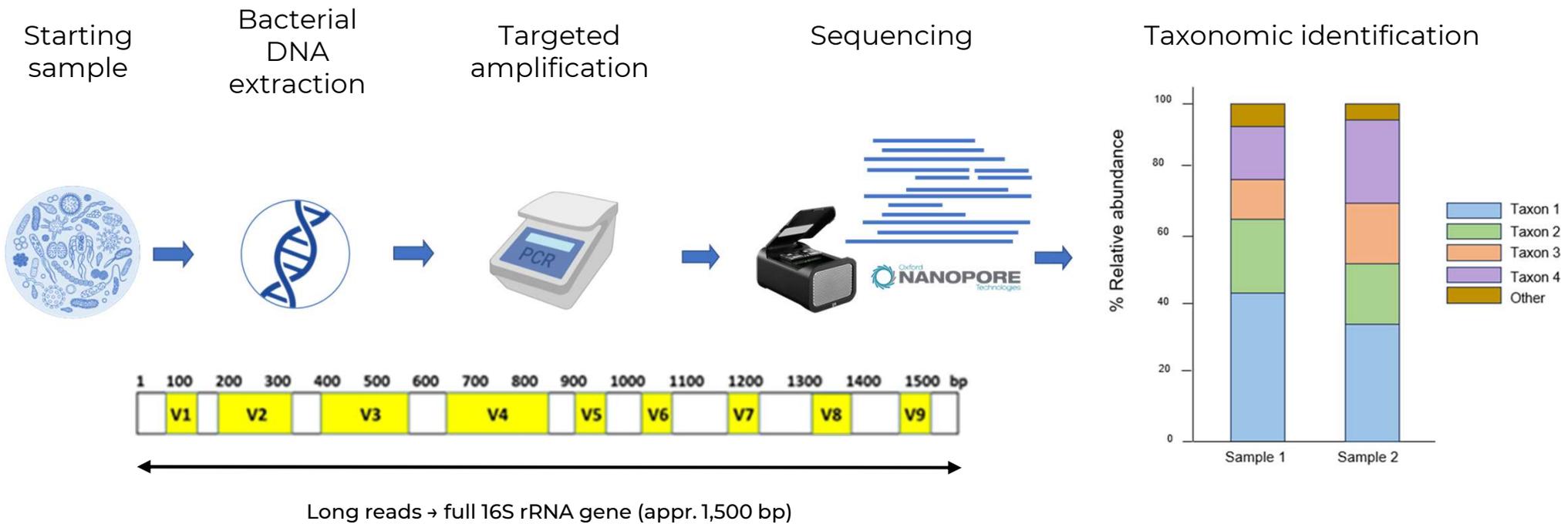
Experimental setup & Methods



- PathoSense **diagnostic assay**
 - ↳ Detection of viral infections
- Full-length **16S rRNA** gene sequencing
 - ↳ Bacterial profile characterization
- **Shotgun** metagenomics
 - ↳ Functional characterization (e.g., **virulence factors** detection)

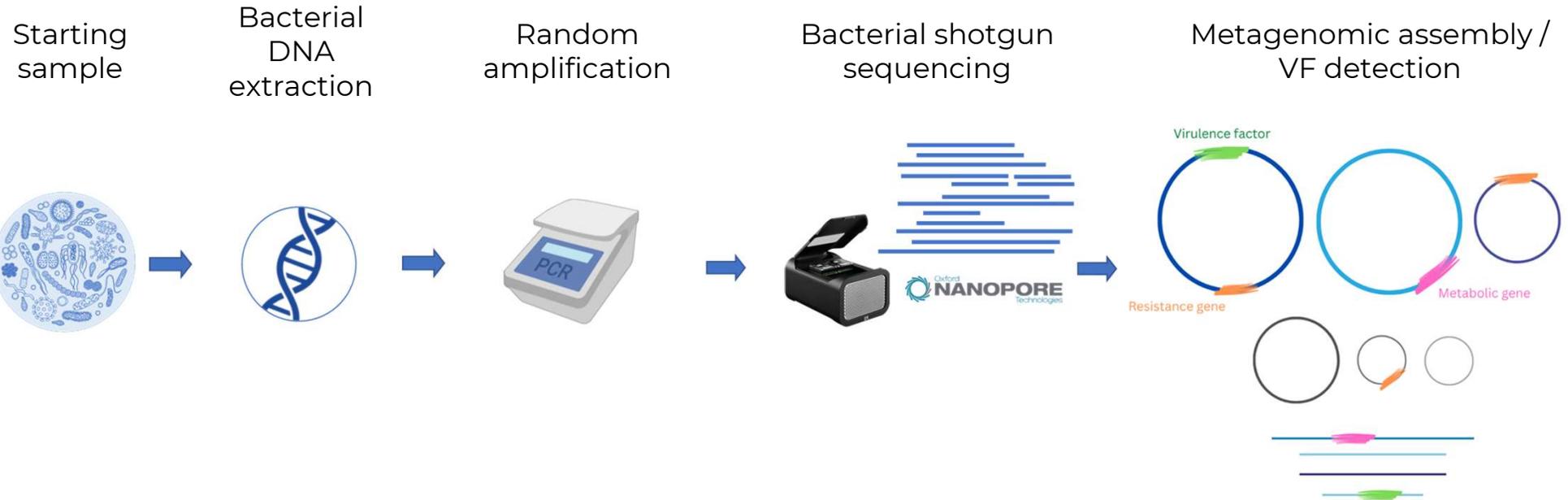
Experimental setup & Methods

Full-length 16S rRNA gene sequencing



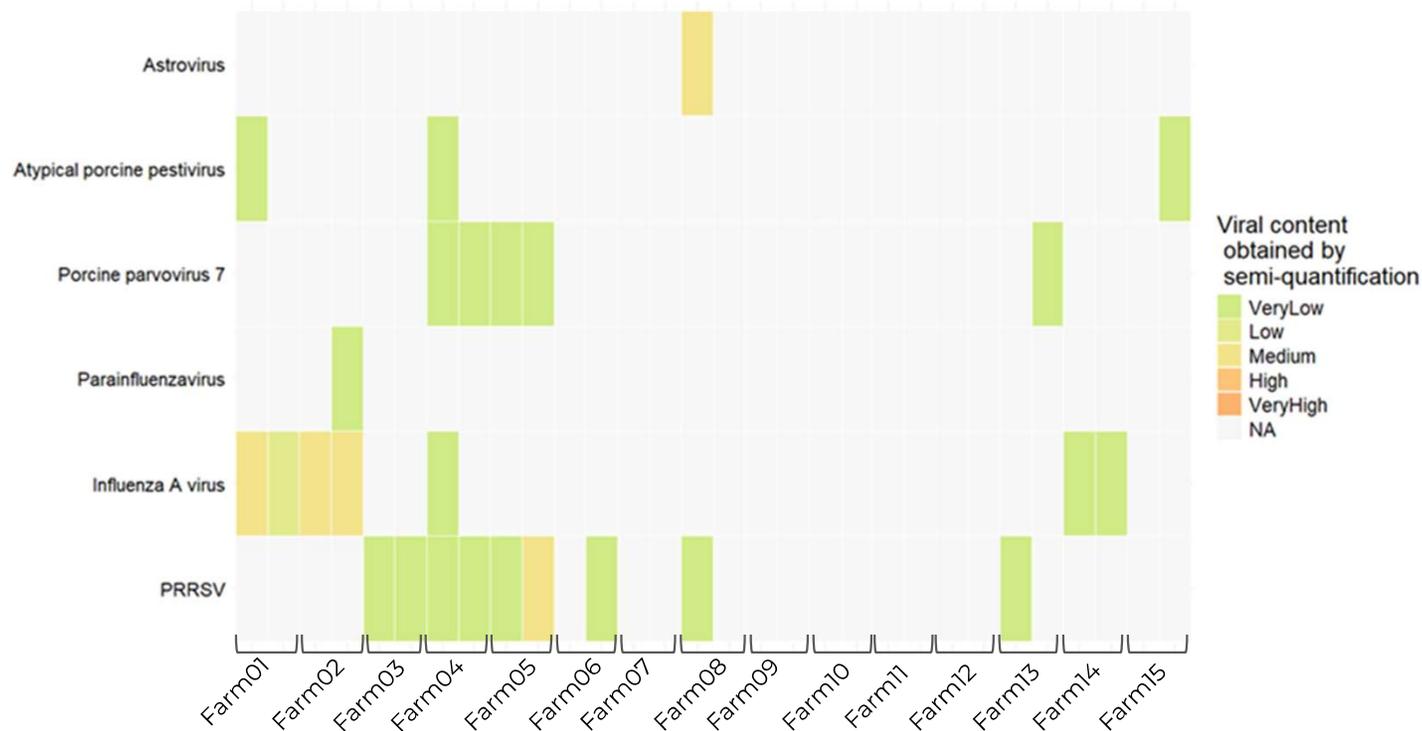
Experimental setup & Methods

Shotgun metagenomics



No pre-selection!

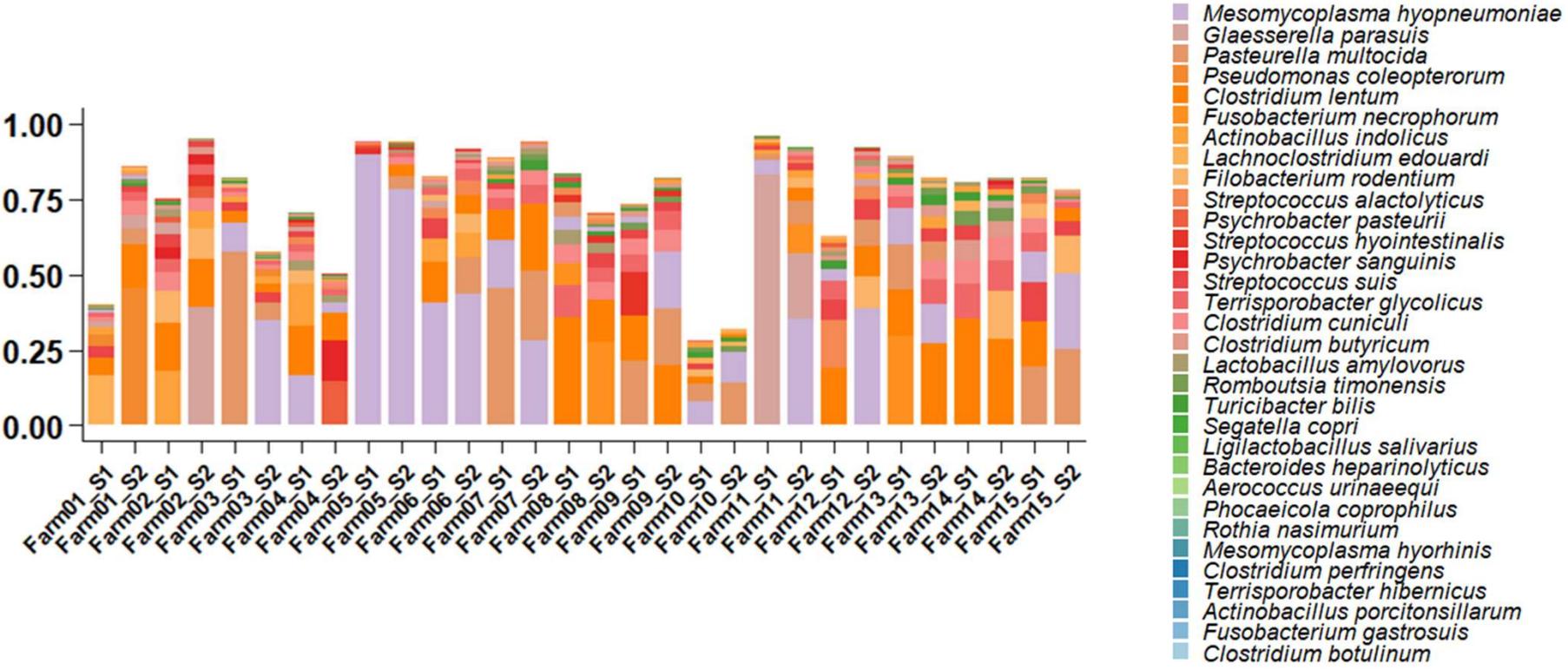
PathoSense diagnostic assay: highest prevalence of PRRSV and Influenza A



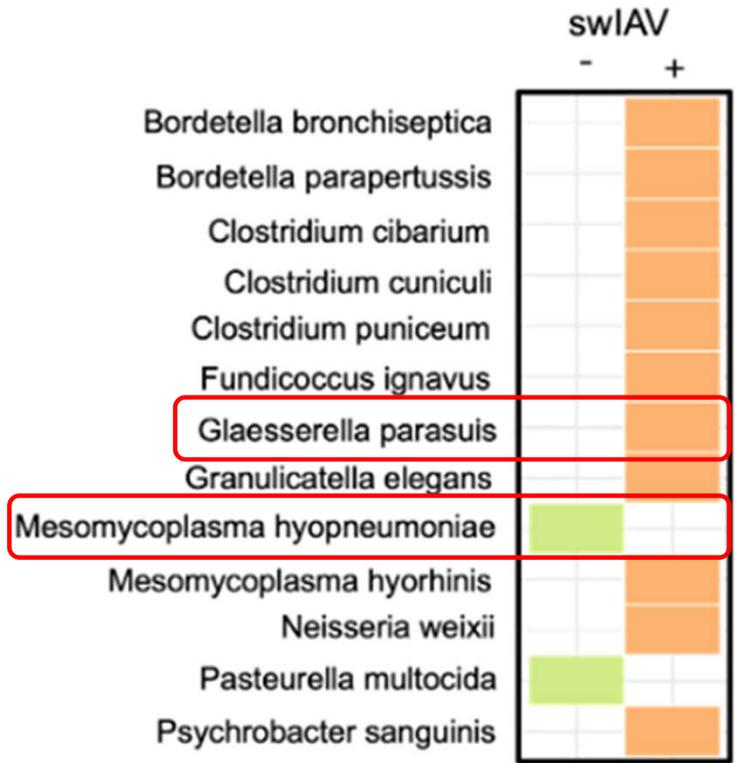
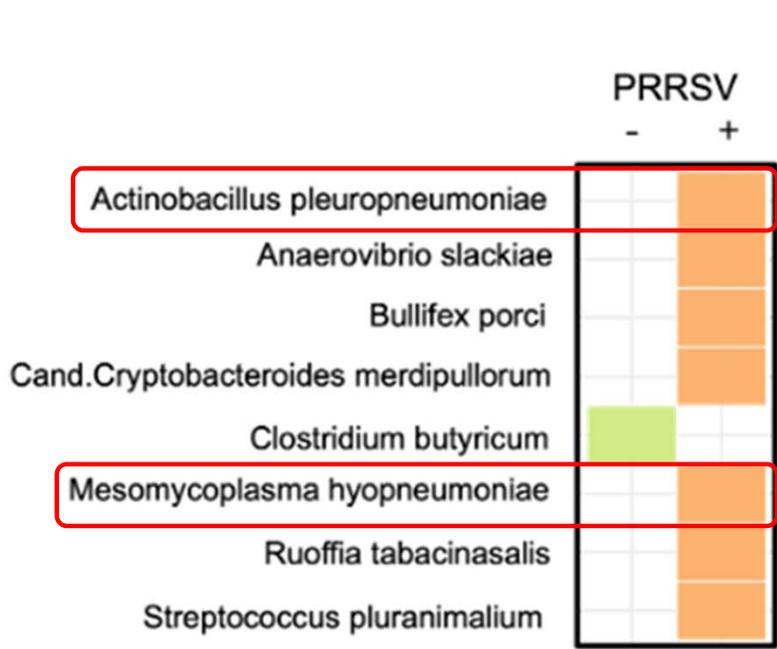
19 out of 30 samples (~**63%**) presented **both a viral and bacterial infection** going on

Abundances are indicated from very high to very low based on a semi-quantification method

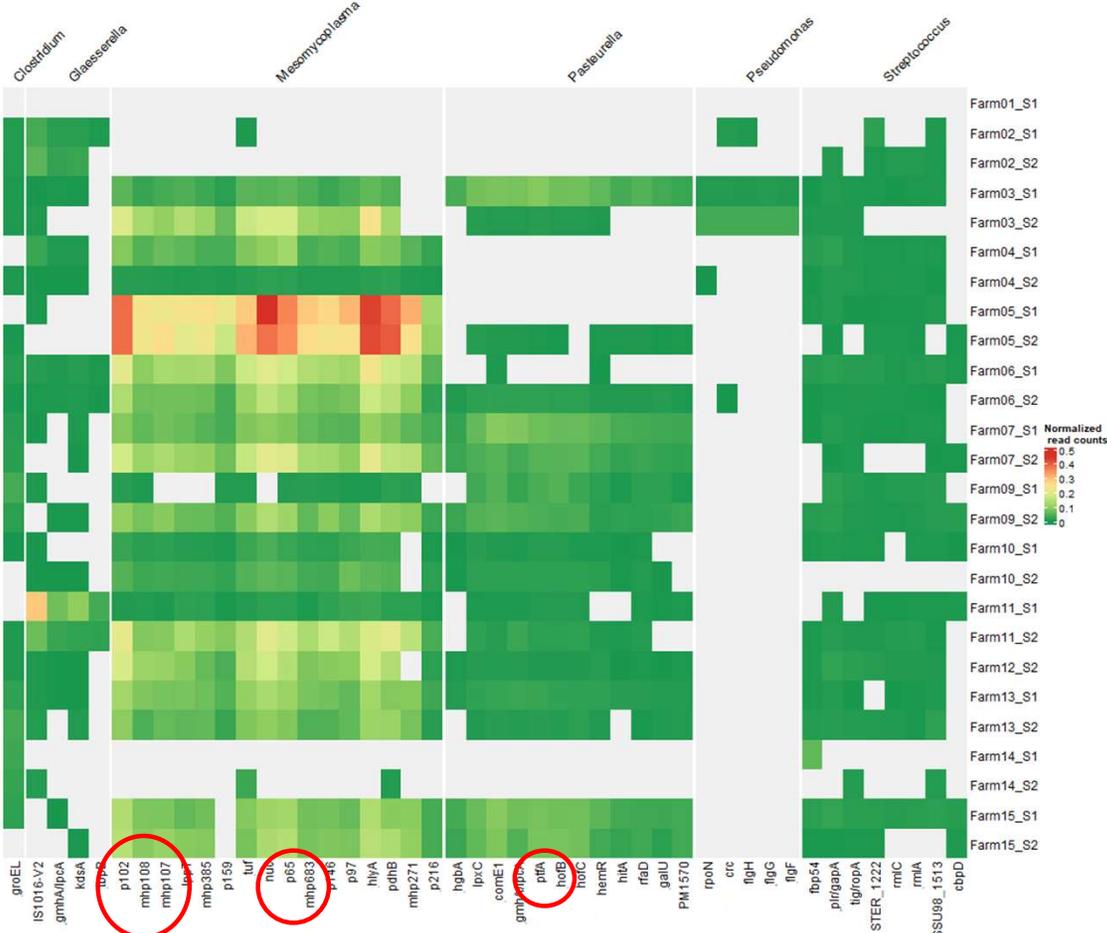
Bacterial opportunistic pathogens dominate the lower airways' microbiome of sick finisher pigs



Viral-bacterial co-infections are widespread in the lower respiratory tract of diseased pigs



Virulence factors are detected in respiratory samples through untargeted and culture free detection

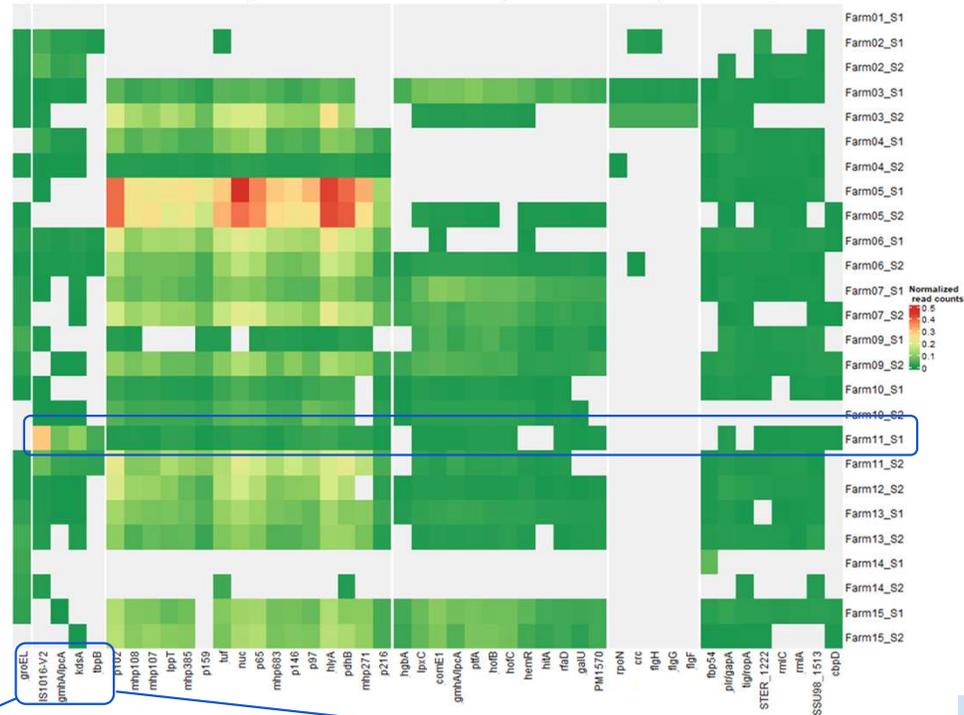


Technical advancement

- low bacterial load
- high host material
- difficult to lyse mucus

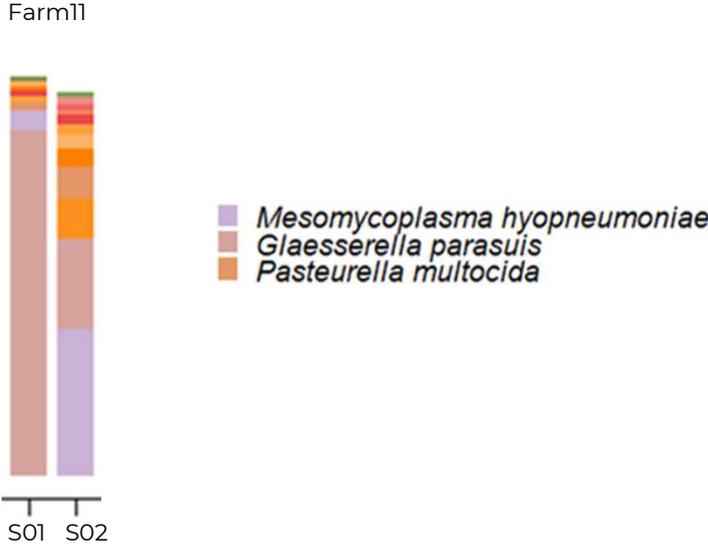
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Glaesserella



IS1016-V2: insertion-like gene flanking capsulation cluster
 kdsA: endotoxin-related

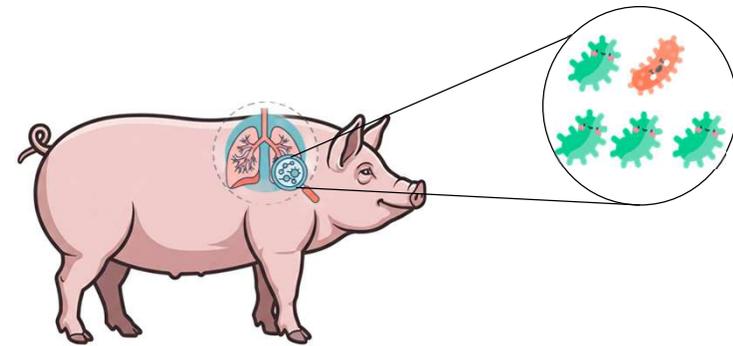
Highest load detected in Farm11 - S01



Are these virulence factors contributing to the high relative bacterial abundance?

Final considerations

- More research needs to be done to understand which virulence factors can be discriminating in a disease state
- Appropriate **detection of virulence factors** can improve the currently available diagnostics tools



Acknowledgements

Thanks to all the study collaborators:

Ilke De Boeck

Stijn Wittouck

Pauline Deffner

Kathrin Lillie- Jaschniski

Julia Stadler

Sarah Lebeer

Sebastiaan Theuns



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Thank you for your attention!