

PHENOTYPICAL AND METAGENOMIC ANALYSIS OF FEEDCOMPOUND FOR LONG-TERM SWINE PRODUCTIVE CYCLE

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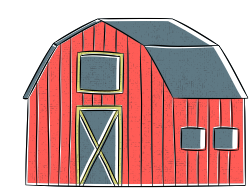
*both 1st authors

Introduction

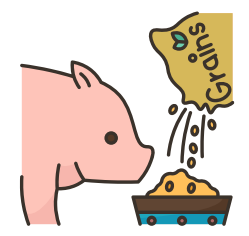
Compound feed (CF) for farmed animals may be contaminated by micro-organisms or pharmacologically active substances resulting from cross-contamination during production, transport and storage. These contaminations can put both animal and public health at risk.

Objective: exploratory assessment of the metagenome of feed supplied to pigs between birth and slaughter on a full-cycle intensive pig farm.

Materials & Methods



1 intensive pig holding – complete cycle



4 CF samples at different phases of the cycle:

- F1 – sows in lactation (maternity)
- F2 – initiation
- F3 – rearing
- F4 – finishing



Bacteriological isolations: Commensal *E. coli* and ESBL, *Salmonella* spp. and *Enterococcus* spp.

Antibiotic susceptibility testing (AST)

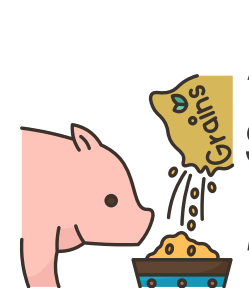
Research antibiotic residues

Metagenomic shotgun (Nanopore sequencing):

metagenoma sequencing, antimicrobial resistance genes (ARGs), virulence factors

Results

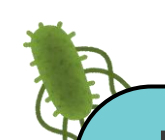
Bacteriological isolations and TSA



E. coli commensal + all samples

Salmonella spp. & *E. coli* ESBL – all samples

Enterococcus faecium + F2



Phenotype

multiresistant
(cloranfenicol, sulfametoxazol and tetracycline)

Complete

Susceptibility

Antibiotic Residues

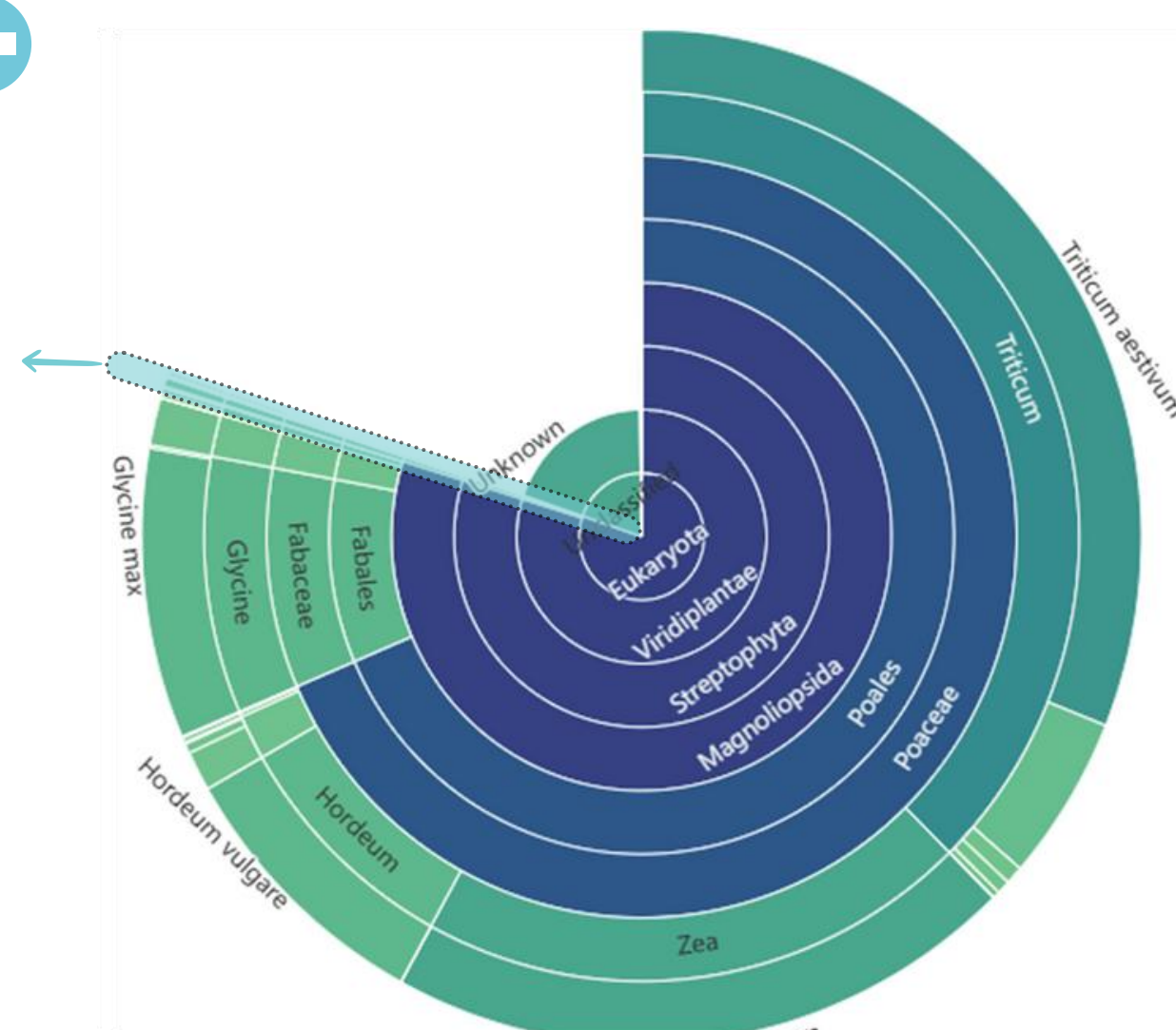


Not detected

Metagenome

Sequenced species:

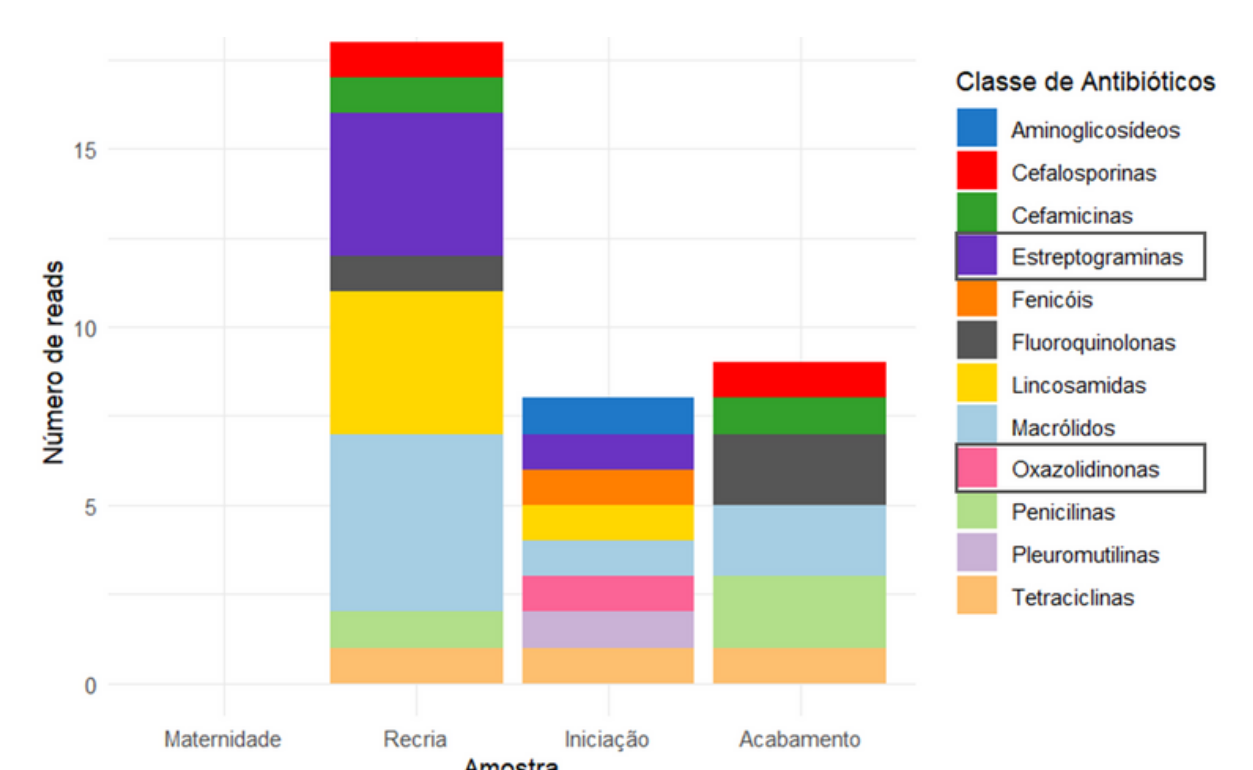
- 120 spp. bacteria
- 25 spp. fungi
- 2 spp. virus
- 2 spp. insects



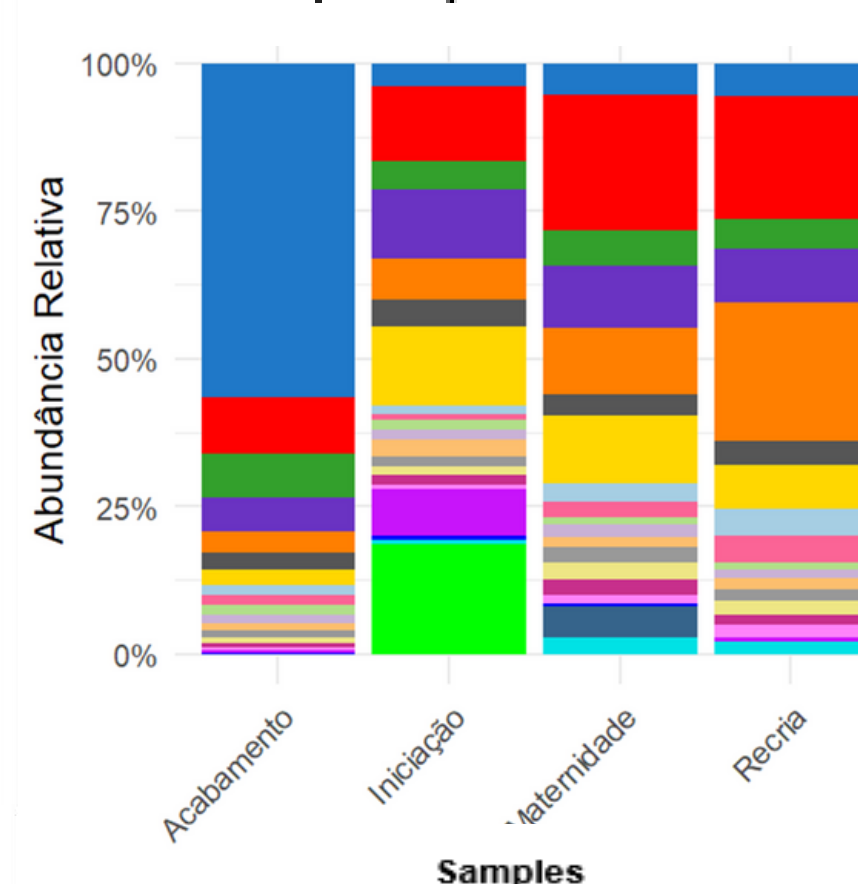
Sequenced species (F1)

GRA

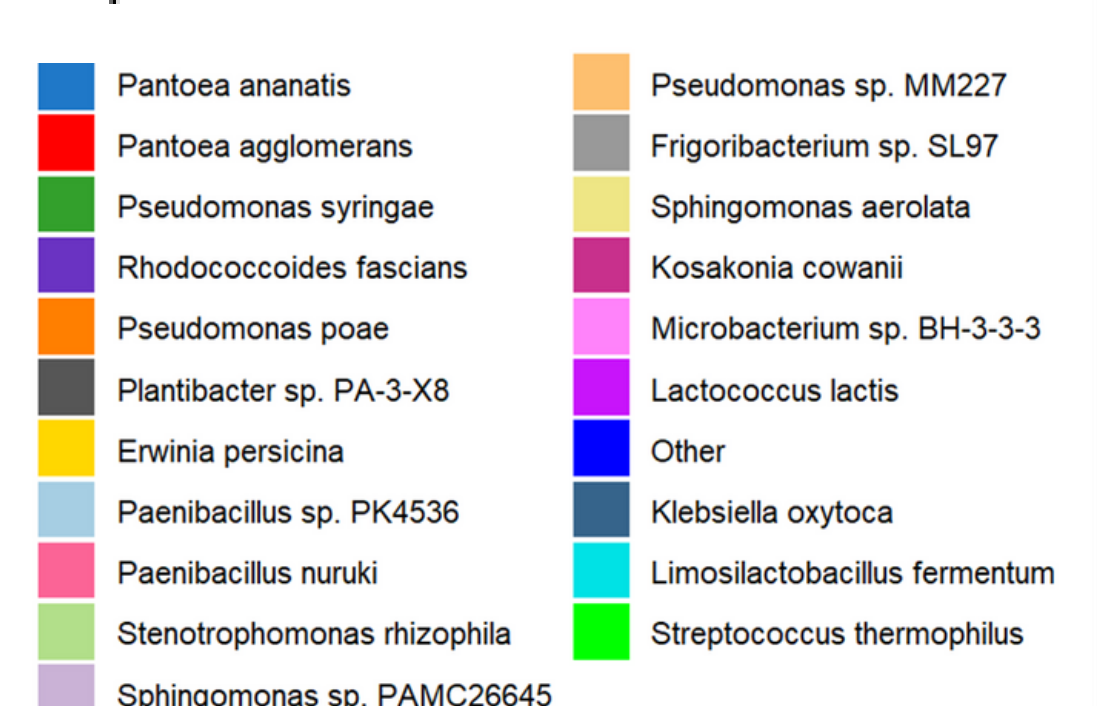
AMR genes present in pig rations



Top 20 Species - Bacteria



Species



Conclusion

The application of an integrated approach of phenotypic study with the metagenomic analysis of food, can contribute to the prevention of health and productive problems, through the timely characterization of the metabiome, the detection of pathogens, antimicrobial resistance and virulence factors present in food sources.