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# From the farm to the fork: fungal occupational exposure in the swine meat supply chain

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# Introduction

Aim of study

Feed production, swine and slaughterhouses were already reported as occupational environments with high fungal contamination [1,2]. This condition can ultimately lead to the development of several health conditions [3].

## Swine feed unit

- **Air:** Most prevalent were *Cladosporium* sp. (54.6%) and *Alternaria* sp. (35.8%).
- Surface: Mucor sp., Rhyzopus sp., Alternaria sp.

#### Swine units

Unit 1: 80.6% of the isolates in air belonged to

Cladosporium sp., followed by Aspergillus ochraceus complex and Fusarium graminearum complex (each 3.7%). In the **surfaces**, countless colonies of *Mucor* sp. and *Rhyzopus* sp. were detected.

This study aimed to characterize the occupational exposure to fungal burden in three different settings: swine feed unit, swine units and slaughterhouse.

## Materials and Methods

Air samples were collected through an impaction method onto malt extract agar (MEA) supplemented with chloramphenicol (0.05%), alongside with surface swabs. Outdoor samples were also performed to be used as reference. All the collected samples were incubated at 27°C for 5 to 7 days. In addition, we collected air samples using the impinger method in order to perform real-time quantitative PCR (qPCR) amplification of genes from *Aspergillus* sections

**Unit 2:** *Cladosporium s*p. (52.7%), *A. ochraceus* complex (23.7%) and *Penicillium* sp. (11.9%) were present in the **air**. *Scopulariopsis candida, Penicillium* sp. and *Rhyzopus* sp. were detected in **surfaces**.

#### Slaughterhouse

- Air: Cladosporium sp. (48.2%), Penicillium sp. (31.8%) and Aureobasidium sp. (10.6%).
- Surface: Cladosporium sp. (50%) followed by Penicillium sp. and Phoma sp.

#### Molecular tools

# Results and Discussion

Circumdati, Flavi and Fumigati.



Figure 1 – Fungal load found in the different settings assessed in air samples (CFU/m<sup>3</sup>).

# SURFACES (CFU/ $m^2$ )



qPCR analysis successfully amplified DNA from the **A**. *fumigatus* complex in 10 out of 20 sampling sites where the presence of this fungal species was not identified by culture

based-methods.

## Conclusions

Although swine units showed the highest fungal load, in
all the 3 settings fungal species with toxigenic potential
were present.

Is important to consider interactions between fungi and mycotoxins in the risk assessment process. The molecular tools applied permitted to target selected fungal indicators, allowing a more precise

characterization of the fungal burden.



Figure 2 – Fungal load found in the different settings assessed in surface samples (CFU/m<sup>2</sup>).

References

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