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

Viegas C.1, 2, Pacifico C.1, Faria T.1, Quintal Gomes A.1, 2, Viegas S.1, 2

1 Environment and Health RD - Lisbon School of Health Technology - Polytechnic Institute of Lisbon, 2 Campus de Belas in Saúde Pública, Escola Nacional de Saúde Pública; 3 Institute of Molecular Medicine, Faculty of Medicine of Lisbon

For further information please contact: carla.viegas@esttesi.ip.pt

Introduction

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].

Aim of study

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 Circumdati, Flavi and Fumigati.

Results and Discussion

![AIR (CFU/m³)](image1)

Figure 1 - Fungal load found in the different settings assessed in air samples (CFU/m³).

![SURFACES (CFU/m²)](image2)

Figure 2 – Fungal load found in the different settings assessed in surface samples (CFU/m²).

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.
- **Unit 2**: Cladosporium sp. (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

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.
- It 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.

References