

41 FEED PRODUCTION, SWINE AND SLAUGHTERHOUSE: WHERE IS THE HIGHEST OCCUPATIONAL EXPOSURE TO *ASPERGILLUS* SPP. IN THIS PRODUCTION LINE?

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Purpose:

This study intended to characterize fungal contamination in two swine farms, in one feed production unit, and also in one swine slaughterhouse. We aimed to identify where the highest occupational exposure to *Aspergillus* spp. was detected during the production line.

Methods:

Twenty two air and 22 surfaces samples were collected from the four units through impaction and swabbing methods, respectively. After laboratory processing and incubation of the collected samples, quantitative and qualitative results were obtained, with the identification of the isolated fungal species. For molecular analysis, 300L of air were also collected from each same sampling site using the impinger method. Real Time PCR (RT-PCR) was done to perform the molecular detection of the *Aspergillus* sections *Circumdati*, *Fumigati* and *Flavi* (only the toxigenic strains).

Results:

Eleven species of filamentous fungi were identified in air samples from the feed production unit, with a total of 1666 isolates. None *Aspergillus* species was isolated. Seven species of filamentous fungi were found from the slaughterhouse, with a total of 810 isolates and only 10 isolates from the *Aspergillus fumigatus* complex (section *Fumigati*) were isolated. Twelve species were found in the air from one of the analyzed swine farms with a total of 3080 isolates. *Aspergillus* genus showed low prevalence (6.5%), being the sections *Candidi*, *Circumdati* and *Terrei* the ones isolated. Regarding the other assessed swine farm, 15 fungal species were identified, in a total of 5080 isolates. *Aspergillus* genus presented the higher prevalence (15.7%). Among this genus, *Eurotium herbariorum* (section *Restricti*) was the most prevalent (45.0%). *Fumigati* and *Circumdati* sections were also isolated.

Regarding the results obtained from molecular methods, *A. fumigatus* complex was detected in 10 sampling sites where this species-complex was not isolated by conventional methods: 2 in feed production, 4 in slaughterhouse and 2 in each swine farm assessed.

Conclusion:

Cultural methods showed that swine farms were the settings with the highest fungal load, presenting also the highest number of isolates belonging to *Aspergillus* spp., and more diversified number of species-complexes. The applied molecular tools enabled to target selected fungal indicators of higher occupational risk, belonging to the same genus, allowing a more accurate characterization on occupational exposure to *Aspergillus*.

Conventional and molecular methods showed to be complementary methodologies and should always be applied together in occupational environments with high fungal load in order to ensure the best possible characterization of fungal burden in a given sampling source.