Prevalence of *Aspergillus* section *Fumigati* in portuguese slaughterhouses: a fungal and mycotoxin concern

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Introduction

Within the *Aspergillus* genus, *Aspergillus fumigatus* species is one of the most ubiquitous saprophytic fungi and is considered the species with higher clinical relevance [1, 2].

The fungi belonging to the *Fumigati* section are the most common cause of invasive aspergillosis and a major source of infection related mortality in immunocompromised patients[3]. One of the most abundant metabolites produced by *Aspergillus fumigatus* is the metabolite gliotoxin, which exhibits a diverse array of biologic effects on the immune system[4].

Further, environments contaminated with *A. fumigatus* may be the cause or enhance respiratory problems in the workers of those specific settings. These species produce specific allergens and mycotoxins that could cause respiratory disorders.

Aim of study

The aim of the present work was to determine the prevalence of *Aspergillus* section *Fumigati* by cultural and molecular methods in poultry; swine and bovine; and large animal (bovine and horses) slaughterhouses.

Materials and Methods

Eighteen air and 18 surface samples were collected and subject to further macro and microscopic observations.

Quantitative PCR (qPCR) amplification of genes from *A. fumigatus* complex were performed.

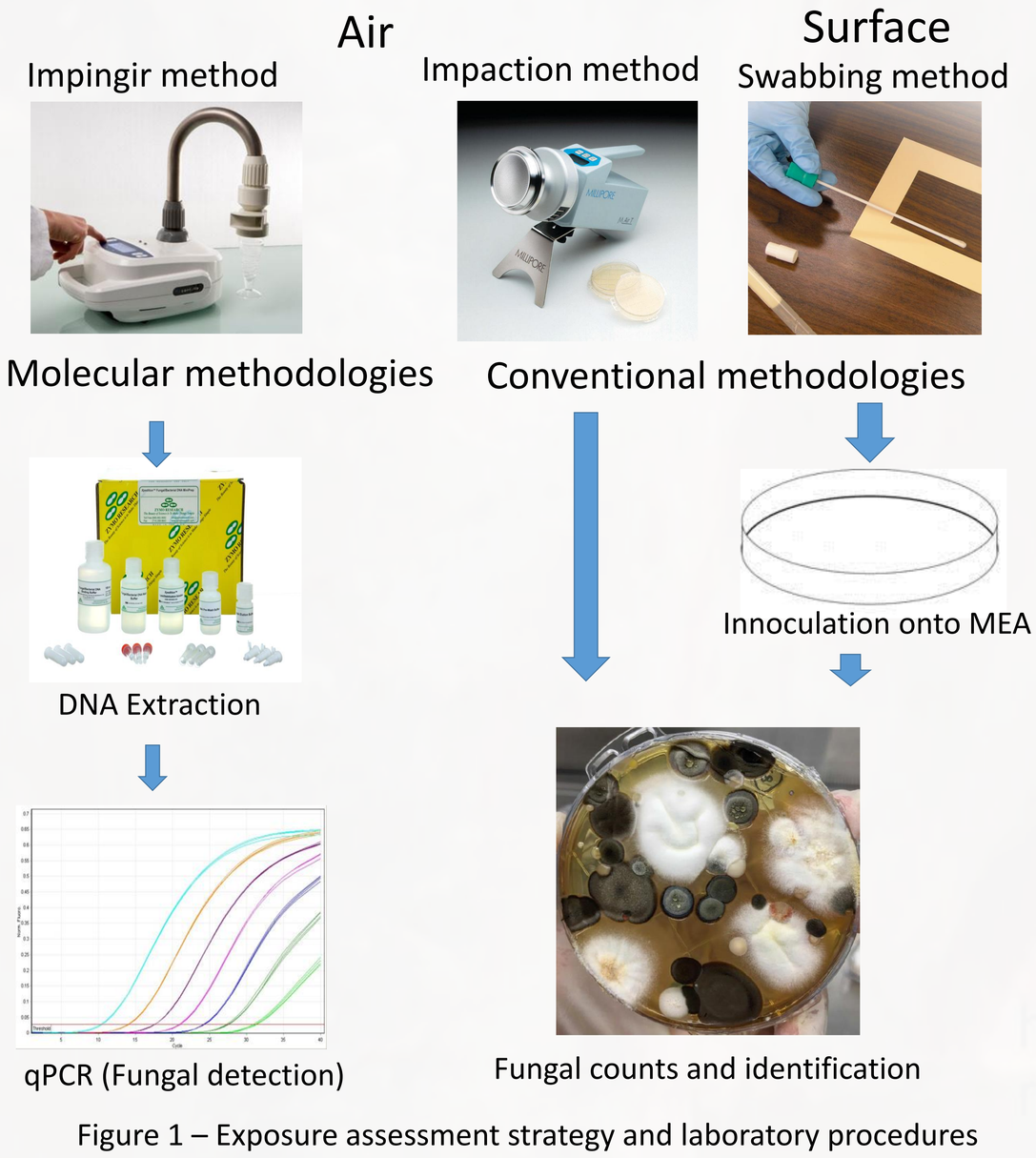

Figure 1 – Exposure assessment strategy and laboratory procedures

Results and discussion

Through conventional methods, isolates from *Aspergillus* section *Fumigati* were found only in Stacker, Bleeding and Evisceration air collected from the Poultry Slaughterhouse, and in air from the Gut Room collected in the Bovine Slaughterhouse.

Table 1 - Conventional and molecular detection and quantification of isolates belonging to *A. fumigatus* complex in the three slaughterhouses; n.d. - not detected.

Poultry slaughterhouse (PS)	Air (CFU/m³)*	Surfaces (CFU/m²)*	Real Time PCR (Ct – Cycle threshold)
Birds hanging	-	-	n. d.
Reception	-	-	n. d.
Stacker	10	-	35.7
Bleeding	30	-	35.92
Evisceration	10	-	36.53
Cutting	-	-	n.d.
Swine and bovine slaughterhouse (SBS)	**Air (CFU/m³)***	**Surfaces (CFU/m²)***	**Real Time PCR (Ct – Cycle threshold)**
Gut room swine	-	-	33.91
Gut room bovine	10	-	n. d.
Bleeding swine	-	-	33.53
Cutting swine	-	-	33.61
Bleeding bovine	-	-	n.d.
Cutting bovine			35.89
Large animal slaughterhouse (LAS)	**Air (CFU/m³)***	**Surfaces (CFU/m²)***	**Real Time PCR (Ct – Cycle threshold)**
Bovine line	-	-	n.d.
Paws room	-	-	35.85
Heads room	-	-	n. d.
Gut room	-	-	n.d.
Expedition	-	-	34.47

Molecular tools amplified successfully DNA in six more sampling sites where the presence of this fungal species was not identified by conventional methods.

Conclusions

- *A. fumigatus* complex presence in slaughterhouses strongly indicates harmful fungal contamination;
- Conventional and molecular tools should be used as a combined strategy to ensure a proper characterization of fungal occupational exposure;
- Interactions between mycotoxins and fungi in slaughterhouses should be considered since *Aspergillus fumigatus* detection pinpoint to exposure to gliotoxin and other possible mycotoxins.

References

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