



La ciencia al servicio de la vida

Detection of CYP51A mutations in airborne *Aspergillus* spp.



isolates from intrahospital environments.

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INTRODUCTION

Aerobiological studies have found an increasing number of Aspergillus spores in intrahospital environments¹. There is a gap in knowledge on drug-susceptibility in Aspergillus circulating intrahospital environments². In this work, we evaluated the CYP51A genome alterations and isolates susceptibility to antifungal drugs.

OBJETIVE

determinate CYP51A gene mutations 10 antifungal susceptibility and in clinical environmental and Aspergillus intrahospital fumigatus isolates from environments in Medellin, Colombia.



Sampling

Genomic ID

Susceptibility test



CONCLUSIONS

RESULTS

40 Aspergillus section Fumigati isolates: 25 intrahospital, 12 clinical and 3 outdoor environments.

Figure 1. Morphological characterization of Aspergillus section *fumigatus* isolates. Culture in Sabouraud Dextrose Agar; SDA, Malta Extract Agar; MEA and Czapek Yeast Agar; CYA and Potato Dextrose Agar; PDA. The images are representative of 40 isolates.

A. fumigatus	Gene ∆nucleotide/ aminoacid		Susceptibility profile			
Isolate code	cyp51_A	cyp51_B	VCZ	ITZ	PCZ	AmE
MHA1	A1147G N248K	NA	S	S	S	R
MHA43	A1147G N248K	NA	S	S	S	S
MHA59	NA	NA	S	S	S	R
MHA71	A1147G N248K	NA	S	S	S	S
MHA73	A1147G N248K	NA	S	S	S	S
MHA77	A1147G N248K	NA	S	S	S	S
MHA78	T1167A I242V	NA	S	S	S	S
MHA79	T1167A I242V	NA	S	S	S	S
MHA80	A1147G N248K	NA	S	S	S	S
MHA81	T1167A I242V	NA	S	S	S	S
MHA13	A1147G N248K	NA	S	S	S	S
MHA2	NA	NA	S	S	S	R

Identification of *A. fumigatus* at species was achieved through whole level genome sequence.

Described mutations had been related resistance to voriconazole, with itraconazole and had not been tested with posaconazole. In this work, Isolates presenting non-synonymous mutations were susceptible to all tested azoles with breakpoints >1 mg/L.

N248K³ Mutation previously was described only in isolates from clinical samples. Mutation 1242V⁴ was found in clinical and environmental samples from agricultural lands. Here we described SNPs isolates from these in

Figure 3. Antifungal susceptibility profile of cyp51A mutant isolates.

Figure 2. Phylogenetic tree based on combined data set of ITS, BenA, CaM and RPB2 sequences showing the relationship of Aspergillus section Fumigati. The probability values and bootstrap percentages of the maximum likelihood analysis are represented at the branches. A. clavati was used as outgroup. Isolates from this study are colored in green (susceptible) and red (resistance).

Figure 4. CMA14 clinical isolate, antifungal susceptibility profile showed resistance to VCZ.

intrahospital environments.

Amphotericin resistance В was observed in 4 isolates from intrahospital environments.

This work is the first one describing mutations and elucidating its role in the drug-resistance of airborne Aspergillus fumigatus in Medellín, Colombia.

BIBLIOGRAPHY

1. G. Morris, et al. Sampling of Aspergillus spores in air. Journal of Hospital Infection. 2000; 44:2.Pag 81-92.

2. Burks C, et al. Azole-resistant Aspergillus fumigatus in the environment: Identifying key reservoirs and hotspots of antifungal resistance. PLOS Pathogens 2021;17(7): e1009711.

3. Chen P, et al. Uncovering New Mutations Conferring Azole Resistance in the Aspergillus fumigatus cyp51A Gene. Front Microbiol. 2020;10:3127.

4. Etienne KA, Berkow EL, Gade L, et al. Genomic Diversity of Azole-Resistant Aspergillus fumigatus in the United States. *mBio*. 2021;12(4):e0180321. doi:10.1128/mBio.01803-21

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