High prevalence of triazole resistance in *Aspergillus fumigatus*, especially mediated by TR/L98H, in a French cohort of patients with cystic fibrosis

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Objectives: Triazole resistance in *Aspergillus fumigatus* due to a single azole resistance mechanism (TR/L98H) is increasingly reported in European countries. Data from patients with cystic fibrosis (CF) are limited. Our study aimed to investigate the prevalence and molecular mechanisms of azole resistance in *A. fumigatus* in a cohort of patients with CF.

Methods: Eighty-five *A. fumigatus* isolates from 50 CF patients, collected between January 2010 and April 2011, were retrospectively analysed for azole resistance using agar plates containing 4 mg/L itraconazole. MICs of itraconazole, voriconazole and posaconazole were determined according to EUCAST methodology for each isolate able to grow on this medium. Species identification was performed by sequencing of the \( b\)-tubulin gene. Sequencing analysis of the \( cyp51A \) gene and its promoter region was conducted.

Results: Nine isolates (four patients, 8% prevalence) were able to grow on itraconazole-containing agar plates. Itraconazole resistance was confirmed by EUCAST methodology (MICs \( \geq 2 \) mg/L). All isolates had mutations in the \( cyp51A \) gene at residues previously involved in azole resistance: L98H (n = 5), M220T (n = 4) and G54R (n = 1). One patient had three genetically distinct azole-resistant isolates identified during the study. The isolates with L98H that were recovered from three patients (6% prevalence) also had the 34 bp tandem repeat in the promoter region of \( cyp51A \) (TR/L98H) and displayed multiazole resistance.

Conclusions: We report an 8% prevalence of itraconazole resistance in CF patients in our centre, mostly driven by TR/L98H (6%). Our data confirm that TR/L98H occurs in France and can be highly prevalent in CF patients.

Keywords: \( cyp51A \) mutations, multi-azole resistance, *A. fumigatus*, CFTR

Introduction

*Aspergillus fumigatus* is widespread in the environment and is the main *Aspergillus* species responsible for human diseases in both immunocompromised and immunocompetent hosts. Inherently resistant to fluconazole, *A. fumigatus* is usually susceptible to the other triazole antifungal drugs, such as itraconazole, voriconazole or posaconazole, and voriconazole is the first-line therapy for invasive aspergillosis. Since the first two published cases in 1997, an ever-growing number of studies focusing on acquired azole resistance in both clinical and environmental *A. fumigatus* isolates suggest that azole resistance is increasing.1,3 Azole resistance mainly results from substitutions in lanosterol 14\( \alpha \)-demethylase (encoded by the \( cyp51A \) gene).6 In the Netherlands, the main mechanism involves a 34 bp tandem repeat in the promoter region of the \( cyp51A \) gene along with a leucine to histidine substitution at residue 98 (also referred to as TR/L98H), which confers multiazole resistance.3 The main hypothesis explaining why TR/L98H is found in >90% of *A. fumigatus* azole-resistant isolates from the Netherlands relies on the widespread use of azole compounds in agriculture.5,6 Outside the Netherlands, isolates with...
TR/L98H have been reported in most European countries, including Belgium, Denmark, the UK and Spain, and recently outside Europe, e.g. in India, suggesting a global spread of this resistance mechanism.\textsuperscript{2,5,7–9} Although TR/L98H has also been recently reported in France, there are limited data regarding its prevalence in this country.\textsuperscript{10,11} Here, we present the results of a 16 month retrospective study to determine the frequency and molecular mechanisms of azole resistance in a cohort of patients with cystic fibrosis (CF).

**Patients and methods**

One hundred and forty-two sputum and bronchial aspiration samples (mean number of samples per patient = 2.8; 1–18 samples per patient) from 50 CF patients (mean age = 21 years; 5–46 years of age) admitted to the Pneumology Department of Nantes University Hospital (France) during January 2010 to April 2011 were analysed retrospectively. Ninety-seven of the 142 (68.3%) samples were positive for A. fumigatus. Twenty-six patients (52%) had several positive samples (two to six samples). Eighty-five of the 97 isolates (12 unavailable for analysis) were included in this study.

Azole resistance was screened by subculturing each isolate on agar plates containing 4 mg/L itraconazole. Plates were prepared in-house and contained RPMI 1640 medium (Sigma–Aldrich, Saint-Quentin-en-Yvelines, France) supplemented with 2% α-glucose (Sigma–Aldrich) buffered with 3-(N-morpholino)propanesulfonic acid (MOPS; 0.165 M final concentration, Sigma–Aldrich) at pH 7.0 and 1.5% Bacto agar (Difco, Pont de Claix, France). Briefly, fresh conidia from a 7-day-old culture on Sabouraud dextrose agar slants with chloramphenicol (bioMérieux, Marcy l’Étoile, France) were suspended in sterile water at a turbidity equivalent to that of a 0.5 McFarland standard. Plates were inoculated by dipping a sterile swab into the inoculum suspension and swabbing the entire agar surface. Plates were then incubated at 35°C for 72 h. Two Aspergillus ustus isolates were included as positive controls in each set of experiments. Itraconazole resistance was evaluated by Etest\textsuperscript{8} (AB Biodisk, bioMérieux, France) for each isolate that was able to grow on azole-containing agar plates. MICs of itraconazole, voriconazole and posaconazole were therefore determined by the reference microdilution method according to EUCAST (CNRMA, Institut Pasteur, Paris, France).\textsuperscript{12} Isolates with MICs > 2 mg/L were considered resistant to itraconazole\textsuperscript{13} and voriconazole,\textsuperscript{4} and isolates with MICs > 0.25 mg/L were considered resistant to posaconazole.\textsuperscript{14}

Species identification of itraconazole-resistant isolates was performed by amplification and sequencing of the β-tubulin gene.\textsuperscript{15} Each of these isolates was further subjected to the amplification and sequencing of the cyp51A gene, as described previously,\textsuperscript{10} and of a 234 bp region of its promoter using the primers AFTR-F (5’-TAATGGAGCACCCCATG-3’) and AFTR-R (5’-GGTTGACACTGAGGGA-3’). Nucleotide sequences were compared with the reference sequence of the A. fumigatus azole-susceptible strain CM-237 (GenBank accession number AF338659). Genotyping of the itraconazole-resistant isolates was performed using four microsatellite markers with a global discriminatory power of 0.994, as described previously.\textsuperscript{16} Briefly, amplification was carried out in a 20 μL reaction mixture containing 1.5 mM MgCl\textsubscript{2}, 50 mM KCl, 10 mM Tris-HCl (pH 8.3), 0.1 mM each dNTP, 0.1 μM each primer (Sigma, Paris, France) and 1 U of AmpliTaq Gold Taq DNA polymerase (Applied Biosystems, Meylan, France). After an initial denaturation step at 94°C for 5 min, samples were amplified by 30 cycles of denaturation at 94°C for 30 s, annealing at 59°C for 30 s and elongation at 72°C for 30 s, and then a final extension at 72°C for 30 min. Next, 2 μL of the PCR product was mixed with 13 μL of HiDi Formamide (Applied Biosystems) containing 0.5 μL of 6-carboxy-X-rhodamine-labelled Genefluor 625 size standard (Eurx, Gdansk, Poland). Capillary electrophoresis was performed using the ABI Prism 3730XL sequencer and allele sizes were calculated with GeneMapper software (version 4; Applied Biosystems). Since the four microsatellite markers consist of dinucleotide repeats, the alleles were considered to be different when a 2 bp difference was observed.

**Results and discussion**

Nine of the 85 isolates (four patients, 8% global prevalence) were able to grow on itraconazole-containing agar (Table 1). Sequencing of the β-tubulin gene confirmed that these isolates were A. fumigatus sensu stricto. Each isolate also had high MICs by Etest.\textsuperscript{8} Itraconazole resistance was confirmed using EUCAST methodology, with all isolates having MICs > 2 mg/L. Distinct patterns of antifungal susceptibility were observed for voriconazole and posaconazole (Table 1). Importantly, five out of the nine isolates, coming from three patients (Patients 1, 2 and 3, Table 1), displayed multiazole resistance (resistance to itraconazole, voriconazole and posaconazole). Previous exposure to mould-active azoles (mostly itraconazole) was recorded for each of these patients.

To provide further insight into the mechanisms responsible for azole resistance in these isolates, we amplified the cyp51A coding sequence and its promoter. The nine itraconazole-resistant isolates displayed mutations in the cyp51A gene at residues previously linked to azole resistance: L98H (n = 5), M220T (n = 4) and G54R (n = 1) (Table 1). All isolates with L98H also displayed the 34 bp tandem repeat (TR/L98H) and were identified from their environment on antifungal plates in terms of azole activity (MIC > 0.25 mg/L).

Overall, whereas the acquisition of TR/L98H in Patients 1, 2 and 3 can hardly be excluded from having arisen from long-term azole therapy (as none of these patients was ‘azole naive’), the main hypothesis is that these patients were contaminated by A. fumigatus itraconazole-resistant isolates from their environment.\textsuperscript{5} This hypothesis is supported by microsatellite typing data, as Patients 1, 2 and 3 displayed almost identical TR/L98H genotypes (Table 1). In stark contrast, other isolates (including itraconazole-susceptible isolates from these patients) had completely different genotypes (Table 1).

One interesting finding is the description of Patient 1, who was colonized for 11 months by a unique itraconazole-resistant A. fumigatus isolate with TR/L98H upon genotyping. Such chronic colonization by a multiazole-resistant isolate in the course of CF, also reported in another study,\textsuperscript{8} must be considered in antifungal management strategies after lung transplantation. However, our study also illustrates that colonization of the respiratory tract by A. fumigatus in the course of CF is a complex and dynamic process, as illustrated here by: (i) the recovery of multiple azole-resistant isolates from a single patient (Patient 3); and (ii) the recovery of itraconazole-susceptible isolates before (Patient 4) or after the recovery of itraconazole-resistant isolates (Patient 3).

In previous studies, the prevalence of itraconazole resistance was < 1%, 4.5% and 4.6% in Portugal,\textsuperscript{17} Denmark\textsuperscript{5} and France.
of itraconazole resistance in *A. fumigatus* have been missed. Limitation of our study as some non-susceptible isolates could have been missed.

Variation from 0.01% to 9.4%.10,18

Indeed, azole resistance has been shown to be lower but highly variable in patients with haematological malignancies, with prevalence rates varying from centre to centre and probably also according to the underlying diseases.18

As already shown, itraconazole-containing plates are easy to use in a routine mycology laboratory, offering the possibility of screening large collections of clinical strains at low cost.8

However, the use of a concentration of 4 mg/L itraconazole, which has also been reported by others8,9,18 but is above the susceptibility breakpoint for *A. fumigatus* (<1 mg/L),13 might be a limitation of our study as some non-susceptible isolates could have been missed.

In summary, the present study highlights a high prevalence of itraconazole resistance in *A. fumigatus*, mostly driven by TR/L98H, in CF patients at our centre. From a more global perspective, nationwide and multicentre surveys involving medical centres responsible for the management of patients at high risk of invasive aspergillosis, such as those with CF, are urgently needed to evaluate the burden of azole resistance in *A. fumigatus*.

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**Transparency declarations**

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**References**


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