Received: 12 April 2022 | Revised: 3 May 2022 | Accepted: 9 May 2022

DOI: 10.1111/myc.13470

ORIGINAL ARTICLE

mycoses Diagnosis, Therapy and Prophylaxis of Fungal Diseases WILEY

Emergence of *Candida auris* in intensive care units in Algeria

Hanane Zerrouki[1,2,3] | Ahmad Ibrahim[1,2] | Sid-Ahmed Rebiahi[3] | Yamina Elhabiri[3] | Djamel-Eddine Benhaddouche[4] | Theun de Groot[5,6] | Jacques F. Meis[5,6] | Jean-Marc Rolain[1,2] | Fadi Bittar[1,2]

[1]Aix-Marseille Université, IRD, APHM, MEPHI, Marseille, France

[2]IHU-Méditerranée Infection, Marseille, France

[3]Laboratoire de Microbiologie Appliquée à l'Agroalimentaire, au Biomédical et à l'Environnement, Université de Tlemcen, Tlemcen, Algeria

[4]Service d'anesthésie et de réanimation, Centre Hospitalo-Universitaire Tlemcen, Tlemcen, Algeria

[5]Department of Medical Microbiology and Infectious Diseases, Canisius-Wilhelmina Hospital, Nijmegen, The Netherlands

[6]Centre of Expertise in Mycology, Radboudumc/Canisius Wilhelmina Hospital, Nijmegen, The Netherlands

Correspondence
Fadi Bittar, Aix-Marseille Université, IHU-Méditerranée Infection, 13005 Marseille, France.
Email: fadi.bittar@univ-amu.fr

Funding information
This work was supported by the French Government under the Investissements d'avenir (Investments for the Future) program managed by the Agence Nationale de la Recherche (ANR,fr: National Agency for Research), (reference: Méditerranée Infection 10-IAHU-03). This work was supported by Région Provence-Alpes-Côte d'Azur and European funding (FEDER (Fonds européen de développement régional) PRIMMI (Plateformes de Recherche et d'Innovation Mutualisées Méditerranée Infection)).

Abstract

Background: Currently, *Candida auris* is among the most serious emerging pathogens that can be associated with nosocomial infections and outbreaks in intensive care units. Clinicians must be able to identify and manage it quickly.

Objective: Here, we report for the first time in Algeria seven cases of *C. auris* infection or colonisation.

Methods and Results: The strains were isolated from clinical sites including bronchial aspirates ($n = 4$), wound swabs ($n = 1$), urine sample ($n = 1$) and peritoneal fluid ($n = 1$), in patients admitted to the intensive care unit. *Candida auris* was identified both by MALDI-TOF and by sequencing the ITS region and the D1/D2 domain. Antifungal susceptibility testing was performed using the *E*-test method. Non-wildtype susceptibility was observed for five strains against fluconazole, itraconazole, voriconazole and caspofungin. Genotyping showed the presence of four clades (I–IV) in one hospital.

Conclusions: Appropriate antifungal treatments with rapid and accurate microbial identification are the cornerstone for the management and control of *C. auris* infections.

KEYWORDS
Algeria, *Candida auris*, clades (I–IV), emergence, ICU

1 | INTRODUCTION

Candida auris is a recently recognised opportunistic, nosocomial yeast pathogen that was first reported in a patient treated for an ear infection at a Japanese hospital in 2009.[1] The earliest known isolate was retrospectively identified from an archived blood culture sample collected in 1996 in South Korea,[2] and the earliest European isolate dates to 2007 in France.[3] The mortality rate due to *C. auris* infection remains significant, up to 60% depending on the patient's underlying conditions and the therapeutic management of infection.[4] It significantly affects

immunocompromised patients and is associated with many comorbid conditions such as diabetes, pneumonia, organ dysfunction, kidney diseases and malignancies.[5] This yeast can easily cause nosocomial infections and can be transmitted in healthcare settings due to its capacity to persist on inanimate surfaces for weeks,[6] form biofilms,[7] and colonise skin and other anatomical sites.[8] Moreover, it is a thermo-resistant, halotolerant and multidrug-resistant fungus; many studies show that it can grow at temperatures up to 42°C with a salinity tolerance of up to 10%.[6,9] In addition, *C. auris* strains may show high resistance levels to several clinically used antifungal agents such as fluconazole, amphotericin B and echinocandins.[10,11] Diagnosis and treatment of this newly described, multi-resistant species remains a challenge, especially in developing countries.[9,12] Recently, new molecular and phenotypic techniques to identify *C. auris* have been developed.[13,14] Despite this, the identification and detection of this yeast still presents difficulties in many countries and research laboratories, especially those using commercial methods that misidentify *C. auris*, such as VITEK, BD Phoenix, API20C-AUX, MicroScan and Chromagar *Candida* culture medium.[15]

Since its emergence, *C. auris* has been identified in invasive infections and nosocomial outbreaks reported from various countries across six continents.[5] Whole-genome sequencing has divided *C. auris* isolates in five distinct clonal lineages, commonly referred to as clade I (South Asian), clade II (East Asian), clade III (African), clade IV (South American) and clade V (Iranian).[16] Clades I and III are the most widespread, with numerous reported cases and a broad geographic distribution.[17] To date, *C. auris* is poorly documented in Africa and has only been reported in Egypt,[18] Kenya,[19,20] Nigeria,[21] South Africa[5] and Sudan,[22] with the prevalence of clades I, III and IV.[16,23] In Algeria, *C. tropicalis* has been the most prevalent isolate from candidemia[24] with no published data on *C. auris*. Here, we describe a series of *C. auris* infection and colonisation at a hospital in Tlemcen, Algeria, with clade distribution and antifungal susceptibility profiles.

2 | MATERIALS AND METHODS

2.1 | Ethical issues

All rules of confidentiality and ethics as prescribed in the Helsinki Declaration have been respected. Informed consent is not required given that the patients' samples were not collected for research purposes but were already ordered by medical doctors to be processed as part of standard laboratory practice (i.e., for routine diagnostic testing). Only residual samples were used for this study. Patient data were collected by the medical staff and were anonymised before further use. The Local Ethics Committee of Tlemcen University approved this survey study.

2.2 | Sample collection, strain characterisation and antifungal susceptibility tests

For microbiological diagnostic purposes, 87 samples including bronchial aspirates ($n = 20$), peritoneal fluid ($n = 4$), urine ($n = 23$), wounds and bedsore swabs ($n = 40$) were collected from the intensive care unit at the University Hospital of Tlemcen in Algeria between 1 October 2017 and 1 June 2019. Firstly, to search for *C. auris* strains, each sample was enriched in Sabouraud liquid medium (OxoidTM, Dardilly, France) for 3 days at 37°C. For DNA extraction, we then used, for each enrichment broth, the EZ1 biorobot (Qiagen BioRobot EZ1) with the EZ1 DNA tissue kit (EZ1 DNA Qiagen). Subsequently, for each DNA sample, a specific real-time PCR test for *C. auris* detection was performed, exactly as described by Ibrahim et al.[14]

In addition, 100 µl of each sample was cultured on CHROMID® Candida (bioMérieux) and SCA (Specific *C. auris*) medium[13] and then incubated at 37°C for 48 h. For microbiological identification, each isolated colony was identified using Matrix-Assisted Laser Desorption/Ionisation Time of Flight Mass Spectrometry (MALDI-TOF-MS) (Microflex™; Bruker Daltonik, Bremen, Germany) as described by L'Ollivier et al.[25]

To be more specific, we performed an additional molecular test on each colony identified as *C. auris*. DNA was extracted, and PCR amplifications of the ITS region and the D1/D2 domain were carried out to confirm its identity.[26] This was followed by Sanger sequencing of the obtained amplicons. The sequences obtained from all tested strains were analysed by NCBI BLASTn against the nr database and deposited in GenBank with the following numbers: OM403669 to OM403675 for the ITS region and OM434430 to OM434436 for the D1/D2 domain. The strains were also submitted to the CSUR collection (Collection de Souches de l'Unite des Rickettsies) with the following numbers: L0048 to L0054.

Antifungal susceptibility tests were carried out using the E-test method on RPMI 1640–2% glucose agar (bioMérieux, Marcy-l'Etoile, France) according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines. Nine antifungal agents were tested, including amphotericin B, fluconazole, isavuconazole, itraconazole, posaconazole, voriconazole, anidulafungin, caspofungin and micafungin (bioMérieux) and incubated for 24 h at 37°C. The susceptibility breakpoints were used as suggested previously[27] and those proposed by the US Centers for Disease Control and Prevention (CDC) in October 2017 and modified in April 2019 (http://www.cdc.gov/fungal/candida-auris/c-auris-antifungal.html accessed on 05/09/2021).

2.3 | Molecular fingerprinting of C. auris isolates

The genotypic relationship between the seven *C. auris* isolates from Algeria and those obtained from other geographical locations, including the major *C. auris* clades, was determined by 12-loci-based short tandem repeat (STR) typing, which was performed as previously described.[28] The phylogenetic relationship between *C. auris* isolates was analysed using the BioNumerics v.7.6.1 software (Applied Maths), by employing the unweighted pair group method with arithmetic mean averages (UPGMA).

TABLE 1 Summary of demographic and clinical data of patients with *Candida auris* colonisation/infections

Strain	Sex/Age Hospitalisation date	Cause of admission to ICU	Co-morbidity	Duration of ICU stay	Antimicrobial treatment	Site of *C. auris* isolation
L0048	M/52 years - 01/09/2017	Head trauma: Meningeal haemorrhage + cerebral oedema	Dialysis	330 days	Broad-spectrum antibiotics/ Amphotericin B	Urine
L0049	M/30 years - 26/05/2017	Multiple trauma: Discomfort + chest pulmonary contusion	/	112 days	Broad-spectrum antibiotics/ Amphotericin B	Bronchial aspiration
L0050	F/76 years - 04/08/2018	Postoperative peritonitis	Diabetes insipidus Dyslipidaemia/Heart disease	2 days	Broad-spectrum antibiotics	Peritoneal fluid
L0051	M/67 years - 26/07/2019	Polytrauma: operated for intraparenchymal haematoma	Diabetes	19 days	Broad-spectrum antibiotics/ Fluconazole	Wound swabs
L0052	M/55 years - 08/08/2019	Haemorrhagic stroke + ventricular flood	Diabetes	277 days	Broad-spectrum antibiotics/ Fluconazole/Caspofungin	Bronchial aspiration
L0053	M/50 years - 02/08/2019	Postoperative respiratory failure: Pituitary Adenoma Surgery	Pituitary adenoma/Diabetes/Heart disease	9 days	Broad-spectrum antibiotics/ Fluconazole	Bronchial aspiration
L0054	F/72 years - 14/01/2018	Pneumothorax disease	Arterial hypertension	15 days	Broad-spectrum antibiotics	Bronchial aspiration

3 | RESULTS

3.1 | Detection of *Candida auris* strains

All seven samples were positive for the *C. auris* specific GPI-encoding gene, as tested by real-time PCR. Moreover, cultures on the SCA medium were suggestive of *C. auris* and pink colonies were observed on the CHROMagar Candida medium. According to the MALDI-TOF-MS identification, all these colonies belong to *C. auris*, with score >2.0. In addition to the MALDI-TOF-MS results, PCR and Sanger sequencing of the ITS region and D1/D2 domains of each isolated *C. auris* were performed and all sequences belong to *C. auris* species according to the BLASTn NCBI database.

Positive samples were obtained from bronchial aspirates ($n = 4$), urine ($n = 1$), peritoneal fluid ($n = 1$) and wound swabs ($n = 1$). Of the seven patients, five were male and the mean age was 57 (ranging from 30 to 76 years). The mean duration of stay in the ICU was 109 days (ranging from 2 to 330 days). Of these patients, four underwent recent surgery and all patients had indwelling devices including central venous catheters, arterial catheters, nasopharyngeal tubes and urinary catheters. All seven patients received mechanical ventilation and broad-spectrum antibiotics. Antifungal drugs including amphotericin B, fluconazole and caspofungin were prescribed for five of the patients. Here, Table 1 shows the demographic and clinical characteristics of patients. It is important to note that, in addition to the *C. auris* strains, we cultured different *Candida* species such as *C. albicans*, *C. glabrata*, *C. parapsilosis*, *C. rugosa* and *C. tropicalis*.

All isolates had a similar susceptibility profile, being wildtype susceptible to isavuconazole. Posaconazole, micafungin and anidulafungin exhibited reduced susceptibility, while non-wildtype susceptibility was observed against itraconazole (MICs ranging from 0.09 to 6 μg/ml) and voriconazole (MICs ranging from 0.064 to 32 μg/ml). Five strains showed high MICs of fluconazole (>256 μg/ml). Only one strain was found with high amphotericin MIC (12 μg/ml) and another with caspofungin (MIC > 32 μg/ml). Table 2 presents the MIC values of the *C. auris* isolates.

3.2 | Fingerprinting of *Candida auris* isolates by STR typing

DNA fingerprinting with STR analysis of seven isolates from seven patients showed that there were *C. auris* isolates from the four clades involved. Three patients had genetically identical isolates involving the South American clade IV, with genotype 9 (L0049, L0050 and L0051 isolates). Similarly, two patients also had a similar genotype 35 in the South African clade III (L0052 and L0053 isolates). Patients L0048 (clade II) and L0054 (clade 1) both had a single genotype (Figure 1).

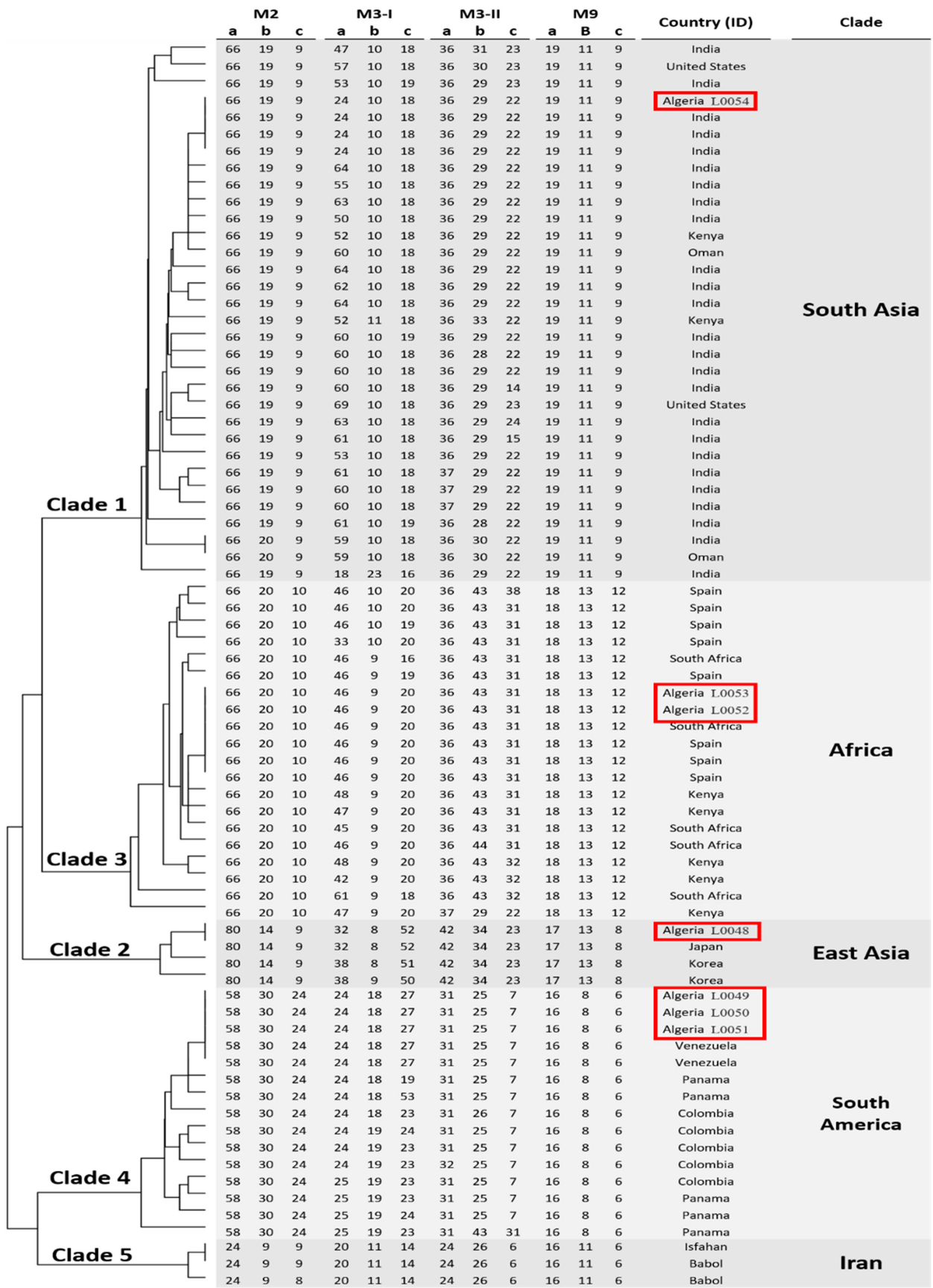
4 | DISCUSSION

Candida auris is an emerging multidrug-resistant yeast that has caused nosocomial outbreaks in multiple countries.[29] In 2016, the

TABLE 2 Antifungal susceptibility testing of *Candida auris* isolates

Stains	Fluconazole	Itraconazole	Voriconazole	Posaconazole	Isavuconazole	Amphotericin B	Caspofungin	Micafungin	Anidulafungin
Breakpoint (μg/ml)[A]	≥32	N/A[B]	N/A[B]	N/A[B]	N/A[B]	≥2	≥2	≥4	≥4
L0048	6	0.09	0.094	0.023	0.023	0.125	0.19	0.094	0.012
L0049	>256	4	6	0.5	0.38	0.5	>32	0.38	0.38
L0050	6	0.19	0.064	0.032	0.032	0.125	0.19	0.012	0.023
L0051	>256	6	12	0.38	0.75	0.75	0.75	0.75	0.38
L0052	>256	2	4	0.094	0.064	0.19	0.38	0.5	0.38
L0053	>256	2	4	0.094	0.125	0.38	1	0.5	0.094
L0054	>256	3	>32	0.25	0.38	12	0.38	0.5	0.5

Note: The minimal inhibitory concentrations (MIC) values (μg/ml) were recorded after 24 h of incubation. A: Proposed Breakpoints (CDC, April 2019), B: Fluconazole susceptibility is used as a surrogate of second-generation triazole susceptibility testing, as recommended by the CDC (April 2019).



M2			M3-I			M3-II			M9			Country (ID)	Clade
a	b	c	a	b	c	a	b	c	a	B	c		
66	19	9	47	10	18	36	31	23	19	11	9	India	South Asia
66	19	9	57	10	18	36	30	23	19	11	9	United States	
66	19	9	53	10	19	36	29	23	19	11	9	India	
66	19	9	24	10	18	36	29	22	19	11	9	Algeria L0054	
66	19	9	24	10	18	36	29	22	19	11	9	India	
66	19	9	24	10	18	36	29	22	19	11	9	India	
66	19	9	24	10	18	36	29	22	19	11	9	India	
66	19	9	64	10	18	36	29	22	19	11	9	India	
66	19	9	55	10	18	36	29	22	19	11	9	India	
66	19	9	63	10	18	36	29	22	19	11	9	India	
66	19	9	50	10	18	36	29	22	19	11	9	India	
66	19	9	52	10	18	36	29	22	19	11	9	Kenya	
66	19	9	60	10	18	36	29	22	19	11	9	Oman	
66	19	9	64	10	18	36	29	22	19	11	9	India	
66	19	9	62	10	18	36	29	22	19	11	9	India	
66	19	9	64	10	18	36	29	22	19	11	9	India	
66	19	9	52	11	18	36	33	22	19	11	9	Kenya	
66	19	9	60	10	19	36	29	22	19	11	9	India	
66	19	9	60	10	18	36	28	22	19	11	9	India	
66	19	9	60	10	18	36	29	22	19	11	9	India	
66	19	9	60	10	18	36	29	14	19	11	9	India	
66	19	9	69	10	18	36	29	23	19	11	9	United States	
66	19	9	63	10	18	36	29	24	19	11	9	India	
66	19	9	61	10	18	36	29	15	19	11	9	India	
66	19	9	53	10	18	36	29	22	19	11	9	India	
66	19	9	61	10	18	37	29	22	19	11	9	India	
66	19	9	60	10	18	37	29	22	19	11	9	India	
66	19	9	60	10	18	37	29	22	19	11	9	India	
66	19	9	61	10	19	36	28	22	19	11	9	India	
66	20	9	59	10	18	36	30	22	19	11	9	India	
66	20	9	59	10	18	36	30	22	19	11	9	Oman	
66	19	9	18	23	16	36	29	22	19	11	9	India	
66	20	10	46	10	20	36	43	38	18	13	12	Spain	Africa
66	20	10	46	10	20	36	43	31	18	13	12	Spain	
66	20	10	46	10	19	36	43	31	18	13	12	Spain	
66	20	10	33	10	20	36	43	31	18	13	12	Spain	
66	20	10	46	9	16	36	43	31	18	13	12	South Africa	
66	20	10	46	9	19	36	43	31	18	13	12	Spain	
66	20	10	46	9	20	36	43	31	18	13	12	Algeria L0053	
66	20	10	46	9	20	36	43	31	18	13	12	Algeria L0052	
66	20	10	46	9	20	36	43	31	18	13	12	South Africa	
66	20	10	46	9	20	36	43	31	18	13	12	Spain	
66	20	10	46	9	20	36	43	31	18	13	12	Spain	
66	20	10	46	9	20	36	43	31	18	13	12	Spain	
66	20	10	48	9	20	36	43	31	18	13	12	Kenya	
66	20	10	47	9	20	36	43	31	18	13	12	Kenya	
66	20	10	45	9	20	36	43	31	18	13	12	South Africa	
66	20	10	46	9	20	36	44	31	18	13	12	South Africa	
66	20	10	48	9	20	36	43	32	18	13	12	Kenya	
66	20	10	42	9	20	36	43	32	18	13	12	Kenya	
66	20	10	61	9	18	36	43	32	18	13	12	South Africa	
66	20	10	47	9	20	37	29	22	18	13	12	Kenya	
80	14	9	32	8	52	42	34	23	17	13	8	Algeria L0048	East Asia
80	14	9	32	8	52	42	34	23	17	13	8	Japan	
80	14	9	38	8	51	42	34	23	17	13	8	Korea	
80	14	9	38	9	50	42	34	23	17	13	8	Korea	
58	30	24	24	18	27	31	25	7	16	8	6	Algeria L0049	South America
58	30	24	24	18	27	31	25	7	16	8	6	Algeria L0050	
58	30	24	24	18	27	31	25	7	16	8	6	Algeria L0051	
58	30	24	24	18	27	31	25	7	16	8	6	Venezuela	
58	30	24	24	18	27	31	25	7	16	8	6	Venezuela	
58	30	24	24	18	19	31	25	7	16	8	6	Panama	
58	30	24	24	18	53	31	25	7	16	8	6	Panama	
58	30	24	24	18	23	31	26	7	16	8	6	Colombia	
58	30	24	24	19	24	31	25	7	16	8	6	Colombia	
58	30	24	24	19	23	31	25	7	16	8	6	Colombia	
58	30	24	24	19	23	32	25	7	16	8	6	Colombia	
58	30	24	25	19	23	31	25	7	16	8	6	Colombia	
58	30	24	25	19	23	31	25	7	16	8	6	Panama	
58	30	24	25	19	24	31	25	7	16	8	6	Panama	
58	30	24	25	19	23	31	43	31	16	8	6	Panama	
24	9	9	20	11	14	24	26	6	16	11	6	Isfahan	Iran
24	9	9	20	11	14	24	26	6	16	11	6	Babol	
24	9	8	20	11	14	24	26	6	16	11	6	Babol	

FIGURE 1 UPGMA dendrogram of STR of seven *Candida auris* isolates from this study and 67 strains originating from various countries and clades. The Algerian isolates clustered in clade I with isolates from India, in clade II with isolates from East Asia, in clade III with isolates from South Africa and in clade IV with isolates from South America

Centre for Disease Control and Prevention (CDC) issued a clinical alert on the international emergence of *C. auris* infections and released recommendations for disinfection and treatment.[2] In this study, we report the first isolation of *C. auris* in Algeria consisting of different clades and antifungal susceptibility.

Candida auris can colonise multiple sites on the body.[30] In the intensive care unit, the massive use of broad-spectrum antibiotics and antifungals has resulted in the commensal microflora elimination and provided favourable ground for the proliferation of this pathogen.[31] In addition, prolonged stay in the ICU and indwelling devices can predispose patients to the transmission of this yeast through caregivers, the environment and patients themselves.[32] We isolated *C. auris* strains from seven patients that spent variable periods of time in the ICU. None of these patients had a recent travel history and all were previously hospitalised in the same university hospital. The infected/colonised patients in this study had similar risk factors as reported in other studies, including immunosuppression, ICU admission, diabetes, dialysis, broad-spectrum antibiotic therapy, recent surgery, and urinary and central venous catheters.[31]

Biochemical methods and phenotypic commercial identification kits often confuse *C. auris* with other yeasts. Laboratories in developing countries which lack molecular identification techniques fail to identify *C. auris*, leading to potentially inappropriate treatment.[29] We previously developed a SCA medium for the selective isolation of *C. auris* yeasts[13] and a RT-PCR system for the specific and rapid detection of this pathogen directly from clinical and environmental samples.[14] This helped with the fast, precise, and low-cost diagnosis of *C. auris* strains, improving infection management and epidemiological surveillance in our healthcare facility. The real prevalence of *C. auris* across the African continent is still unknown due to the limited availability of accurate diagnostic tools. So far, *C. auris* infection/colonisation has only been reported in five African countries, namely Egypt,[18] Kenya,[19,20] Nigeria,[21] South Africa[33] and Sudan.[22]

Candida auris infections are among the most reported nosocomial infections worldwide, and there are no accurate criteria to distinguish colonisation from infection in *C. auris* cases.[34] We recovered *C. auris* from different human sites, including wounds, urine, peritoneal fluid and bronchial aspirations, which is rarely described. Most described strains are isolated from the blood and the ear canal.[33] It is essential to highlight that the presence of *C. auris* in bronchial aspirations, wounds and urine was often interpreted as colonisation rather than infection.[33,35]

The collection of *C. auris* strains had non-wildtype susceptibility to fluconazole, itraconazole, voriconazole, with low MICs to posaconazole, isavuconazole, micafungin and anidulafungin. One isolate (clade I) was resistant to amphotericin B (MIC 12 µg/ml). Moreover, MICs of antifungal drugs varied among cases and geographical locations, but many studies have described *C. auris* as a multidrug-resistant yeast.[36,37] It is interesting to note that three clade IV isolates from three patients (L0049, L0050, L0051) were genotypically the same, but included one with low fluconazole MIC. Genotyping suggests cross-infection between patients L0049-L0051 and patients L0052-L0053.

Although there are no susceptibility breakpoints for *C. auris* strains,[38] echinocandins are the first-line treatment.[39] However, antifungal susceptibility testing is still recommended for the optimal management of infections and outbreaks.[40] We reported for the first time an outbreak of *C. auris* in Algeria. Different epidemiological studies have previously reported the presence of different *C. auris* clades in a single country, such as the presence of four different clades (I, II, III and IV) in the United States[41] and Canada,[42] three clades (I, III and IV) in South Africa,[16] and two clades (I and III) in Germany[43] and Iran (clades I and V),[44] which shows the dissemination of *C. auris* clades between countries (except for the fifth clade). Only in Kenya were *C. auris* isolates from two clades (I and III) reported simultaneously in the same hospital.[23] It is important to note that this is the first report of four different clades of *C. auris* in a single hospital, which has never been described before, especially since the patients reported no recent travel history. Therefore, it would be prudent to routinely test the clade origin of future *C. auris* isolates to trace this yeast in the African continent.

AUTHOR CONTRIBUTIONS

Conceptualisation: J.F.M., J.-M.R. and F.B.; methodology: H.Z., A.I. and T. d.-G.; data collection: S.-A.R., Y.E. and D.-E.B.; writing original draft preparation: H.Z., A.I., J.F.M. and F.B.; writing review and editing: J.F.M., J.-M.R. and F.B.; supervision: J.F.M., J.-M.R. and F.B. All authors have read and agreed to the published version of the manuscript.

ACKNOWLEDGEMENTS

None.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are openly available in GenBank at https://www.ncbi.nlm.nih.gov/genbank/, reference number OM403669 to OM403675 and OM434430 to OM434436.

ORCID

Fadi Bittar https://orcid.org/0000-0003-4052-344X

REFERENCES

1. Satoh K, Makimura K, Hasumi Y, Nishiyama Y, Uchida K, Yamaguchi H. *Candida auris* sp. nov., a novel ascomycetous yeast isolated from the external ear canal of an inpatient in a Japanese hospital. *Microbiol Immunol*. 2009;53:41-44.
2. Du H, Bing J, Hu T, Ennis CL, Nobile CJ, Huang G. *Candida auris*: epidemiology, biology, antifungal resistance, and virulence. *PLoS Pathog*. 2020;16(10):e1008921.
3. Desnos-Ollivier M, Fekkar A, Bretagne S. Earliest case of *Candida auris* infection imported in 2007 in Europe from India prior to the 2009 description in Japan. *J Med Mycol*. 2021;31(3):101139.
4. de Jong AW, Hagen F. Attack, defend and persist: how the fungal pathogen *Candida auris* was able to emerge globally in healthcare environments. *Mycopathologia*. 2019;184(3):353-365.

5. Osei Sekyere J. *Candida auris*: A systematic review and meta-analysis of current updates on an emerging multidrug-resistant pathogen. *Microbiology*. 2018;7(4):e00578.
6. Welsh RM, Bentz ML, Shams A, et al. Survival, persistence, and isolation of the emerging multidrug-resistant pathogenic yeast *Candida auris* on a plastic health care surface. *J Clin Microbiol*. 2017;55:2996-3005.
7. Kean R, Ramage G. Combined antifungal resistance and biofilm tolerance: the global threat of *Candida auris*. *mSphere*. 2019;4(4):e00458-19.
8. Alfouzan W, Ahmad S, Dhar R, et al. Molecular epidemiology of *Candida auris* outbreak in a major secondary-care hospital in Kuwait. *J Fungi*. 2020;6(4):307.
9. Jeffery-Smith A, Taori SK, Schelenz S, et al. *Candida auris*: a review of the literature. *Clin Microbiol Rev*. 2017;31(1):e00029-e00017.
10. Rudramurthy SM, Chakrabarti A, Paul RA, et al. *Candida auris* candidaemia in Indian ICUs: analysis of risk factors. *J Antimicrob Chemother*. 2017;72(6):1794-1801.
11. Tsay S, Welsh RM, Adams EH, et al. Notes from the field: ongoing transmission of *Candida auris* in health care facilities — United States, June 2016–may 2017. *MMWR Morb Mortal Wkly Rep*. 2017;66(19):514-515.
12. Nett JE. *Candida auris*: an emerging pathogen "incognito"? *PLoS Pathog*. 2019;15(4):e1007638.
13. Ibrahim A, Peyclit L, Abdallah R, et al. Sca medium: a new culture medium for the isolation of all *Candida auris* clades. *J. Fungi*. 2021;7(6):433.
14. Ibrahim A, Baron SA, Yousfi H, et al. Development and standardization of a specific real-time PCR assay for the rapid detection of *Candida auris*. *Eur J Clin Microbiol Infect Dis*. 2021;40(7):1547-1551.
15. Kathuria S, Singh PK, Sharma C, et al. Multidrug-resistant *Candida auris* misidentified as *Candida haemulonii*: characterization by matrix-assisted laser desorption ionization-time of flight mass spectrometry and DNA sequencing and its antifungal susceptibility profile variability by vitek 2, CLSI broth microdilution, and Etest method. *J Clin Microbiol*. 2015;53(6):1823-1830.
16. Naicker SD, Maphanga TG, Chow NA, et al. Clade distribution of *Candida auris* in South Africa using whole genome sequencing of clinical and environmental isolates. *Emerg Microbes Infect*. 2021;10(1):1300-1308.
17. Chen J, Tian S, Han X, et al. Is the superbug fungus really so scary? A systematic review and meta-analysis of global epidemiology and mortality of *Candida auris*. *BMC Infect Dis*. 2020;20(1):827.
18. Khairat, S.M.; Anany, M.G.; Ashmawy, M.M.; Farouk Ahmed Hussein, A. Setting a protocol for identification and detecting the prevalence of *Candida auris* in tertiary Egyptian hospitals using the cdc steps. *Open Access Maced. J Med Sci*. 2021, 9(A):397-402.
19. Adam RD, Revathi G, Okinda N, et al. Analysis of *Candida auris* fungemia at a single facility in Kenya. *Int J Infect Dis*. 2019;85:182-187.
20. Heath CH, Dyer JR, Pang S, Coombs GW, Gardam DJ. *Candida auris* sternal osteomyelitis in a man from Kenya visiting Australia, 2015. *Emerg Infect Dis*. 2019;25(1):192-194.
21. Agbalaya O, Adeleke G, Ettu AW, Oladele R. Investigating the emergence of *Candida auris* in a resource limited setting in West Africa. *Int J Infect Dis*. 2022;116:S103-S104.
22. Badri AM. First detection of emergent fungal pathogen *Candida auris* in Khartoum state, Sudan. *Am J Biomed Sci Res*. 2019;6(1):4-7.
23. Chow NA, Muñoz JF, Gade L, et al. Tracing the evolutionary history and global expansion of *Candida auris* using population genomic analyses. *MBio*. 2020;11(2):e03364-19.
24. Megri Y, Arastehfar A, Boekhout T, et al. *Candida tropicalis* is the most prevalent yeast species causing candidemia in Algeria: the urgent need for antifungal stewardship and infection control measures. *Antimicrob Resist Infect Control*. 2020;9(1):50.
25. L'Ollivier C, Cassagne C, Normand AC, et al. A MALDI-TOF MS procedure for clinical dermatophyte species identification in the routine laboratory. *Med Mycol*. 2013;51(7):713-720.
26. Cassagne C, Normand AC, Bonzon L, et al. Routine identification and mixed species detection in 6,192 clinical yeast isolates. *Med Mycol*. 2016;54(3):256-265.
27. Kordalewska M, Perlin DS. Identification of drug resistant *Candida auris*. *Front Microbiol*. 1918;2019:10.
28. de Groot T, Puts Y, Berrio I, Chowdhary A, Meis JF. Development of *Candida auris* short tandem repeat typing and its application to a global collection of isolates. *MBio*. 2020;11(1):e02971-19.
29. Chowdhary A, Sharma C, Meis JF. Candida auris: A rapidly emerging cause of hospital-acquired multidrug-resistant fungal infections globally. *PLoS Pathog*. 2017;13(5):e1006290.
30. Proctor DM, Dangana T, Sexton DJ, et al. Integrated genomic, epidemiologic investigation of *Candida auris* skin colonization in a skilled nursing facility. *Nat Med*. 2021;27(8):1401-1409.
31. Bidaud AL, Chowdhary A, Dannaoui E. *Candida auris*: an emerging drug resistant yeast – A mini-review. *J Mycol Med*. 2018;28(3):568-573.
32. Biswal M, Rudramurthy SM, Jain N, et al. Controlling a possible outbreak of *Candida auris* infection: lessons learnt from multiple interventions. *J Hosp Infect*. 2017;97(4):363-370.
33. Govender NP, Magobo RE, Mpembe R, et al. *Candida auris* in South Africa, 2012–2016. *Emerg Infect Dis*. 2018;24(11):2036-2040.
34. Jung J, Kim MJ, Kim JY, et al. *Candida auris* colonization or infection of the ear: A single-center study in South Korea from 2016 to 2018. *Med Mycol*. 2020;58(1):124-127.
35. Vallabhaneni S, Kallen A, Tsay S, et al. Investigation of the first seven reported cases of *Candida auris*, a globally emerging invasive, multidrug-resistant fungus - United States, may 2013–august 2016. *Am J Transplant*. 2017;17(1):296-299.
36. Lockhart SR, Etienne KA, Vallabhaneni S, et al. Simultaneous emergence of multidrug-resistant *Candida auris* on 3 continents confirmed by whole-genome sequencing and epidemiological analyses. *Clin Infect Dis*. 2017;64(2):134-140.
37. Chakrabarti A, Singh S. Multidrug-resistant *Candida auris*: an epidemiological review. *Expert Rev Anti Infect Ther*. 2020;18(6):551-562.
38. Ninan MM, Sahni RD, Chacko B, Balaji V, Michael JS. *Candida auris*: clinical profile, diagnostic challenge and susceptibility pattern: experience from a tertiary-care Centre in South India. *J Glob Antimicrob Resist*. 2020;21:181-185.
39. Cândido E d S, Affonseca F, Cardoso MH, Franco OL. Echinocandins as biotechnological tools for treating *Candida auris* infections. *J. Fungi*. 2020;6(3):185.
40. Lepak AJ, Zhao M, Berkow EL, Lockhart SR, Andes DR. Pharmacodynamic optimization for treatment of invasive *Candida auris* infection. *Antimicrob Agents Chemother*. 2017;61(8):e00791-17.
41. Chow NA, Gade L, Tsay SV, et al. Multiple introductions and subsequent transmission of multi-drug-resistant *Candida auris* in the USA: a molecular epidemiological survey. *Lancet Infect Dis*. 2018;18(12):1377-1384.
42. Eckbo EJ, Wong T, Bharat A, et al. First reported outbreak of the emerging pathogen *Candida auris* in Canada. *Am J Infect Control*. 2021;49(6):804-807.
43. Hamprecht A, Barber AE, Mellinghoff SC, et al. *Candida auris* in Germany and previous exposure to foreign healthcare. *Emerg Infect Dis*. 2019;25(9):1763-1765.
44. Mirhendi H, Charsizadeh A, Aboutalebian S, et al. South Asian (clade I) *Candida auris* meningitis in a paediatric patient in Iran with a review of the literature. *Mycoses*. 2022;65(2):134-139.

How to cite this article: Zerrouki H, Ibrahim A, Rebiahi S-A, et al. Emergence of *Candida auris* in intensive care units in Algeria. *Mycoses*. 2022;65:753-759. doi: 10.1111/myc.13470