session en partenariat avec la SF2H – jeudi 18 juin 2026

« Pathogènes hautement résistants : prévenir ET guérir »

Candidozyma (syn. *Candida*) *auris* et autres menaces fongiques émergentes

guillaume.desoubeaux@univ-tours.fr

27es JNI 2026 PARIS
et la région Ile de France — Palais des Congrès

Journées Nationales d'Infectiologie
du jeudi 18 juin au samedi 20 juin 2026
Journée Nationale de Formation des Paramédicaux en Infectiologie
Vendredi 19 juin 2026

Orateur : Guillaume Desoubeaux PU-PH Tours

président de la société française de mycologie médicale (SFMM)

☑ **Je déclare les liens d'intérêt potentiels suivants 2014-2025** (* rapport direct avec la présente intervention)

- *Intérêts financiers* aucun
- *Liens durables ou permanents* SFMM
- *Interventions ponctuelles* Gilead*, Pfizer, Mundipharma (conférences invitées), ANRS, HAS, SpF, Minist. Transition Ecolologique (expertise), Mylan-Viatris* (étude industrielle)
- *Intérêts indirects* aucun

Le buzz médiatique (presse grand public)

biologiste365

Candida auris : Les causes d'une épidémie émergente

The New York Times

A Mysterious Infection, Spanning the Globe in a Climate of Secrecy

The rise of Candida auris embodies a serious and growing public health threat: drug-resistant germs.

franceinfo:

Candida auris, le "champignon tueur des hôpitaux", mérite-t-il vraiment son terrifiant surnom ?

NATIONAL GEOGRAPHIC

Candida auris, le supergerme qui inquiète les hôpitaux assaillis par le coronavirus

The Washington Post

By Lena H. Sun

Deadly fungal infection that doctors have been fearing now reported in U.S.

USA TODAY NEWS

This superbug is a 'serious global health threat you need to know about Candida auris

JORGE L. ORTIZ | USA TODAY

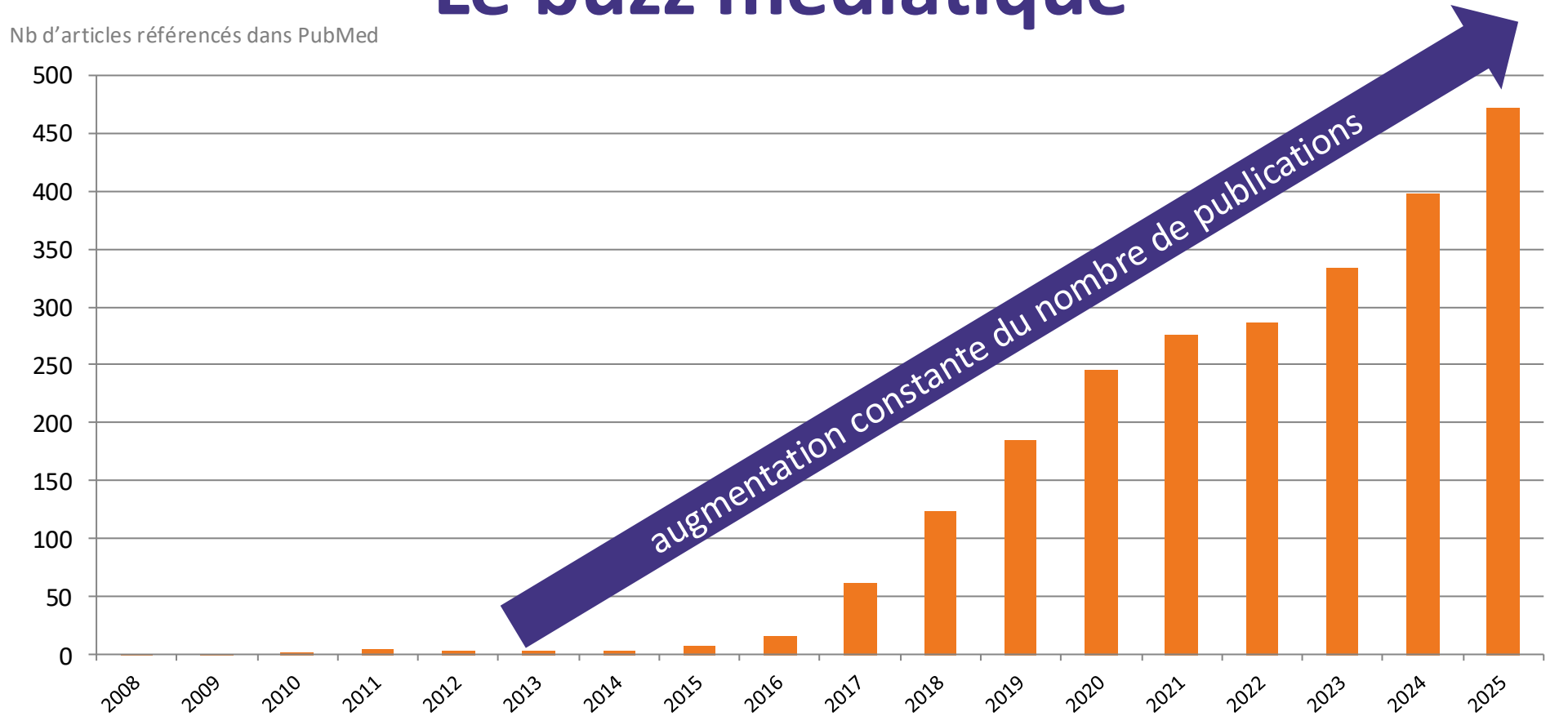
the U.S. and abroad in recent years, with 617 confirmed cases domestically and more than 20 other countries reporting multiple

Candida auris : doit-on craindre la propagation en France de ce "champignon tueur" ?

LCI

Le buzz médiatique (presse spécialisée)

Le buzz médiatique



R E P U B L I Q U E D E S C H A M P I G N O N S

NATIONAL IDENTITE CARTE NO. : 20241213 — Nationalité fongique

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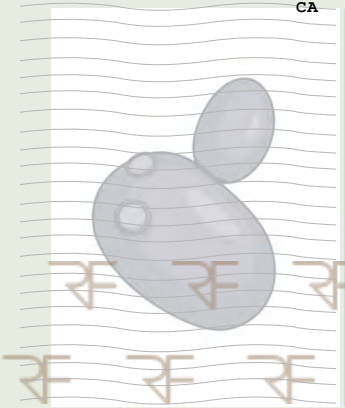


Nom de famille **Metschnikowiaceae**

Espèce ***Candidozyma* (ex-*Candida*) *auris***

Proche parent ***Candidozyma haemuli*** (ex-*C. haemulonii*)

1ère description **2009**

Adresse **partout dans le monde**

Taille **2,5 à 5 µm** (diamètre de la levure)

Signature *Candida auris*

1ère description

IDFUNGCANDIDAAURIS<<<<<<<<<<<<37000

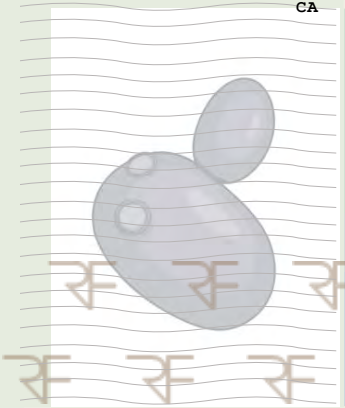
20221006AURIS<<<<<1863172A9

proche du complexe *haemuli*

Sarma S, Upadhyay S. Infect Drug Resist. 2017; **10** : 155-65
Eyre DW, *et al. N Engl J Med.* 2018; **379** : 1322-31
Bougnoux ME *et al. Antimicrob Resist Infect Control.* 2018 ; **27** (7) :45
Desoubeaux G *et al. J Mycol Med.* 2022 ; **32** (2) : 101248
Desoubeaux G *et al. J Mycol Med.* 2018 ; **28** (2) : 407-10

R E P U B L I Q U E D E S C H A M P I G N O N S

NATIONAL IDENTITE CARTE NO. : 20241213 — Nationalité fongique



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IDFUNGCANDIDAAURIS<<<<<<<<<<<<37000

20221006AURIS<<<<<1863172A9

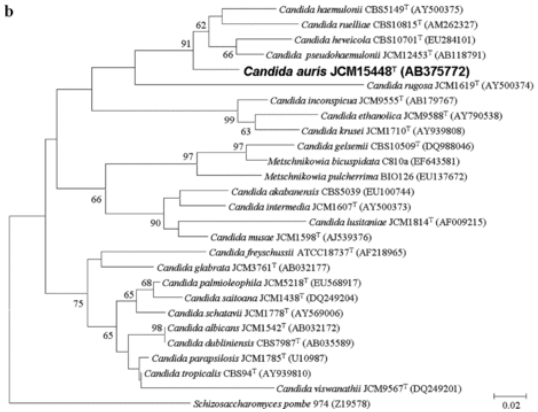


Table 3. WHO fungal priority pathogens list

Critical group	High group	Medium group
Cryptococcus neoformans	*Nakaseomyces glabrata (Candida glabrata)*	*Scedosporium spp.*
Candida auris	*Histoplasma spp.*	*Lomentospora prolificans*
Aspergillus fumigatus	Eumycetoma causative agents	*Coccidioides spp.*
Candida albicans	Mucorales	*Pichia kudriavzeveii (Candida krusei)*
	Fusarium spp.	*Cryptococcus gattii*
	Candida tropicalis	*Talaromyces marneffei*
	Candida parapsilosis	*Pneumocystis jirovecii*
		Paracoccidioides spp.

https://www.who.int/publications/i/item/9789240060241

Sarma S, Upadhyay S. Infect Drug Resist. 2017; **10** : 155-65
Eyre DW, *et al. N Engl J Med.* 2018; **379** : 1322-31
Bougnoux ME *et al. Antimicrob Resist Infect Control.* 2018 ; **27** (7) :45
Desoubeaux G *et al. J Mycol Med.* 2022 ; **32** (2) : 101248
Desoubeaux G *et al. J Mycol Med.* 2018 ; **28** (2) : 407-10

Des propriétés hors norme

TABLE 1 Growth results for panel of *Candida* isolates[a] (Table view)

	Growth by strain and type of medium[b]				
	SAB			YNB	
Candida species (location of collection)	Dextrose	Dulcitol	Mannitol	Dulcitol	Mannitol
C. auris (South Asia)	+	+	+	+	+
C. auris (Africa)	+	+	+	+	+
C. auris (South America)	+	+	+	+	+
C. auris (East Asia)	+	+	+	+	+
C. glabrata	+	–	–	–	–
C. albicans	–	–	–	–	–
C. doubushaemulonii	–	–	–	–	–
C. haemulonii	–	–	–	–	–
C. parapsilosis	–	–	–	–	–
C. tropicalis	–	NA[c]	NA	NA	NA

[a] Isolates incubated at 40°C with shaking at 250 rpm in a Sabouraud broth or yeast nitrogen base with either dextrose, dulcitol, or mannitol as the added carbon source.
[b] SAB, Sabouraud broth; YNB, yeast nitrogen base. All media contained 10% NaCl (wt/vol).
[c] NA, not available.

Thermotolérance

températures ≤ 40-42°C

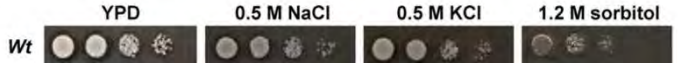
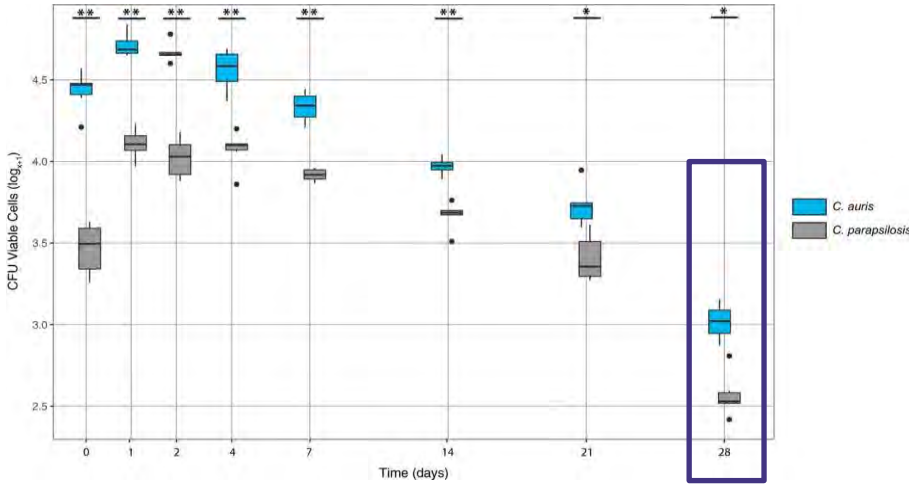


FIG 4 Stress-protective roles of *C. auris* Hog1. (A) Hog1 is required for resistance to diverse stresses. Exponentially growing cells were spotted in serial dilutions onto YPD agar plates containing the indicated additives and incubated for 24 or 48 h at 30°C.

Halotolérance

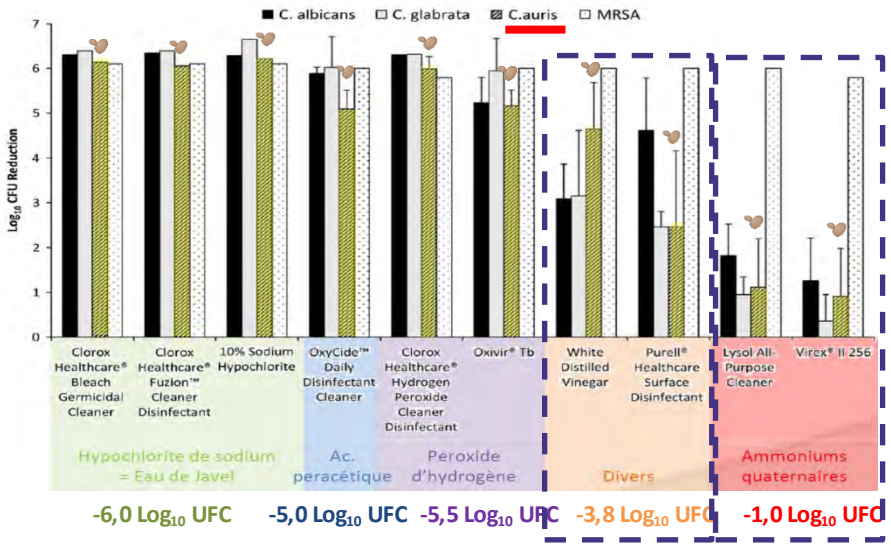


Persistance importante sur les surfaces

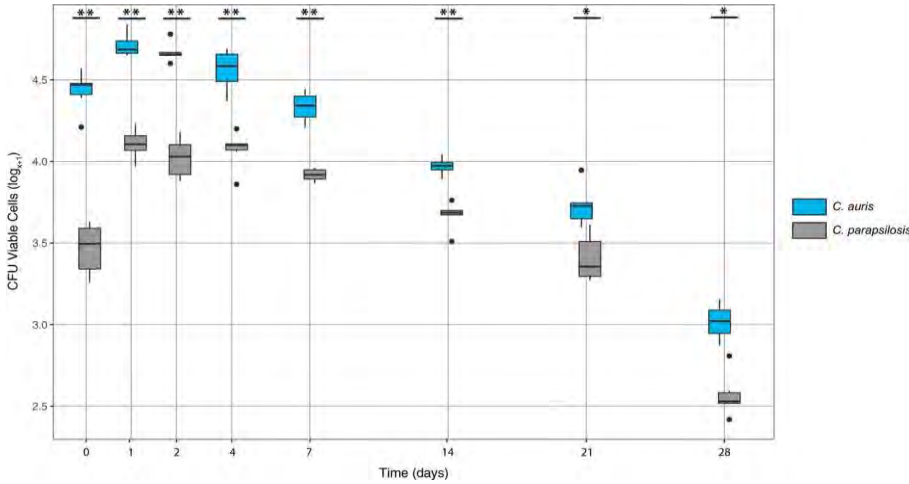
3,0 Log_{10} UFC *C. auris vs.* 2,6 Log_{10} UFC *C. parapsilosis*

Welsh RM *et al. J Clin Microbiol* 2017 ; **55** : 2996–3005

Des propriétés hors norme



Moindre sensibilité à certains désinfectants



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3,0 Log_{10} UFC *C. auris vs.* 2,6 Log_{10} UFC *C. parapsilosis*

Cadnum JL *et al. Infect Control Hosp Epidemiol* 2017 ; **38** :1240–3
Chesnay A *et al. J Mycol Med.* 2021 ; **31** (4) : 101173

Welsh RM *et al. J Clin Microbiol* 2017 ; **55** : 2996–3005

Des propriétés hors norme

TABLE 2 *Candida auris* antifungal MIC ranges determined by the CLSI broth microdilution reference method

Drug	Tentative[a] resistance breakpoints	MIC range (μg/ml)[b] MIC	MIC_{50}	MIC_{90}
Fluconazole	≥32	0.12 to ≥64	≥64	≥64
Voriconazole	NA	0.032 to 16	0.5 to 2	2 to 8
Itraconazole	NA	0.032 to 2	0.06 to 0.5	0.25 to 1
Posaconazole	NA	0.015 to 16	0.016 to 0.5	0.125 to 2
Isavuconazole	NA	0.015 to 4	0.125 to 0.25	0.5 to 2
Anidulafungin	≥4	0.015 to 16	0.125 to 0.5	0.5 to 1
Caspofungin	≥2	0.03 to 16	0.25 to 1	1 to 2
Micafungin	≥4	0.015 to 8	0.125 to 0.25	0.25 to 2
Amphotericin	≥2	0.06 to 8	0.5 to 1	2 to 4

[a]Tentative breakpoints proposed by the CDC (https://www.cdc.gov/fungal/diseases/candidiasis/recommendations.html). NA, the CDC has recommended using fluconazole as a surrogate.
[b]MIC ranges were compiled from the references 12, 21, 24, and 37. The total number of isolates is 355.

Table 4. Distribution of *C. auris* isolates exhibiting MDR and cross-resistance to azoles

Resistance type	Number of isolates (%)
MDR	
azoles + 5-FC	48 (14)
azoles + AMB	26 (7)
azoles + echinocandins[a]	7 (2)
azoles + AMB + 5-FC	4
azoles + echinocandins + 5-FC	2
azoles + AMB + echinocandins	1
Multi-azole resistance	
FLC + VRC	39 (11)
pan-azole[a]	14 (4)
FLC + ITC	6 (1.7)

> 25 % multi résistance

AMB, amphotericin B (≥2 mg/L); 5-FC, 5-flucytosine (≥32 mg/L); FLU, fluconazole (≥32 mg/L); VRC (≥2 mg/L), voriconazole; ITC (≥2 mg/L), itraconazole (≥2 mg/L); ISA, isavuconazole (≥2 mg/L); POS, posaconazole (≥2 mg/L).
[a]Includes only micafungin and anidulafungin (≥8 mg/L).
[b]FLC + VRC + ISA + POS ($n = 5$), FLC + VRC + ISA ($n = 3$), FLC + ITC + VRC ($n = 2$), FLC + ITC + VRC + ISA ($n = 2$), FLC + ITC + VRC + ISA + POS ($n = 1$), FLC + ITC + ISA + POS ($n = 1$).

Résistance aux antifongiques

- ≥90 % au fluconazole
- x3 aux échinocandines entre 2019 et 21
- 16 % à la 5-FC pour les isolats asiatiques

Lyman M *et al. Ann Int Med.* 2023 ; 176 (4) : 489-95

Spivak ES, Hanson KE. *J Clin Microbiol.* 2018 ; **56** (2) :e01588-17

Division of foodborne, waterborne, and environmental Ddseases, Centers for Diseases control and Prevention. Recommandations for identification of *Candia auris*. 2017

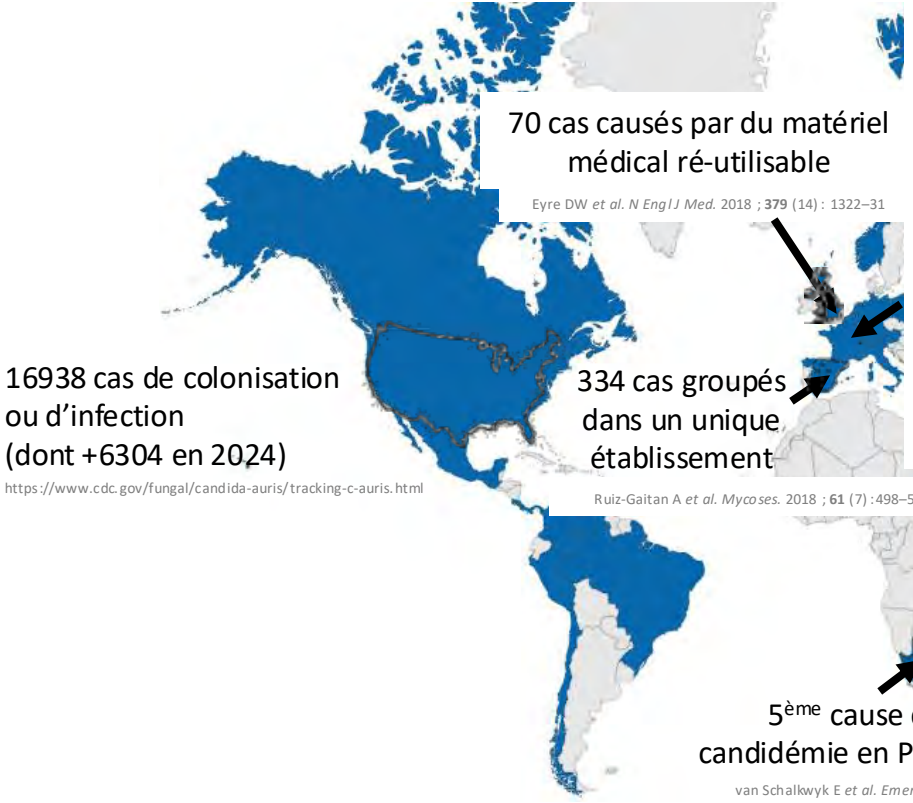
Arendrup M.C, *et al. Antimicrob Agents Chemother.* 2017 ; **61** (6) :e00485-17

Forsberg K, *et al. Med Mycol.* 2019 ; **57** (1) : 1-12

Chowdhary A *et al. J Antimicrob Chemother.* 2018 ; **73** (4) :891–9

Quelle est la situation épidémiologique actuelle de *C. auris* ?

Distribution mondiale



16938 cas de colonisation ou d'infection (dont +6304 en 2024)

https://www.cdc.gov/fungal/candida-auris/tracking-c-auris.html

70 cas causés par du matériel médical ré-utilisable

Eyre DW *et al. N Engl J Med.* 2018 ; **379** (14) : 1322–31

334 cas groupés dans un unique établissement

Ruiz-Gaitan A *et al. Mycoses.* 2018 ; **61** (7) : 498–505

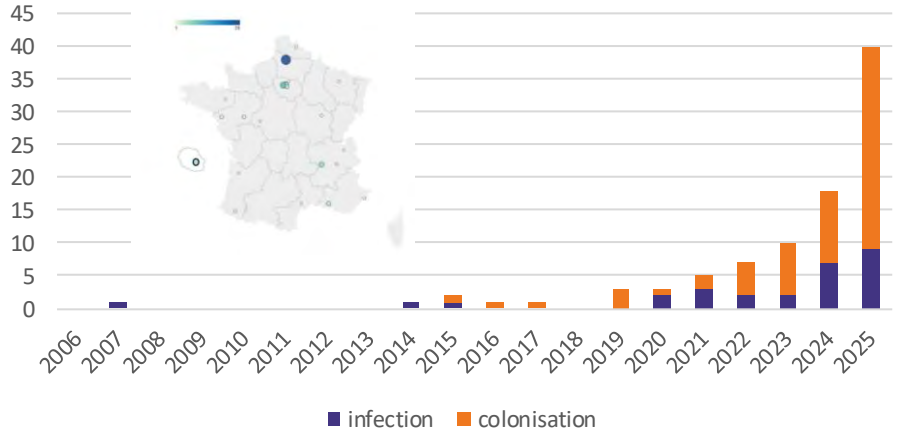
5ème cause de candidémie en Pédiatrie

van Schalkwyk E *et al. Emerg Infect Dis.* 2019 ; **25** (9) : 1698–707

60% des candidémies dans un service de Réa

Chowdhary A *et al. Emerg Infect Dis.* 2020 ; **26** (11) : 2694–6

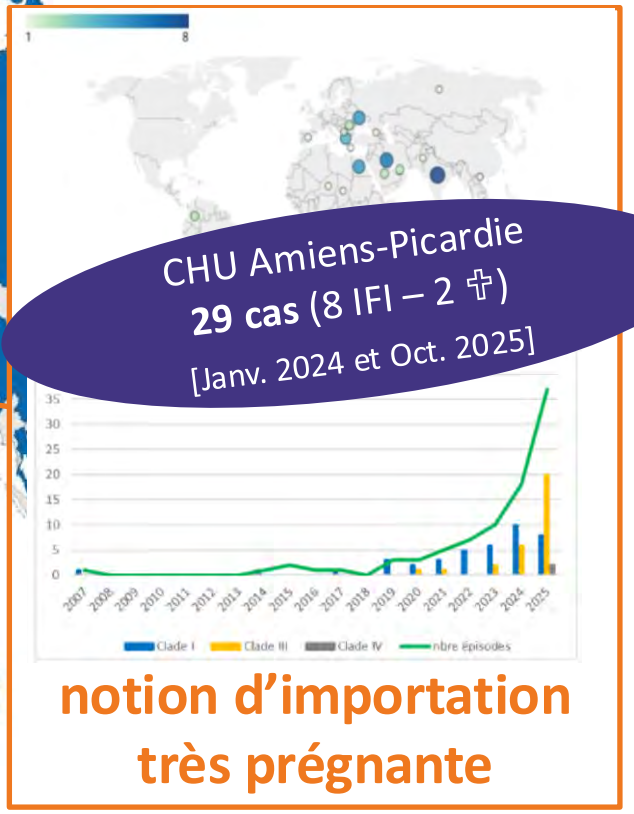
Nb de cas répertoriés au CNRMA de l'Institut Pasteur de Paris (F. Lanternier et A. Alanio)



arrêté en Décembre 2024

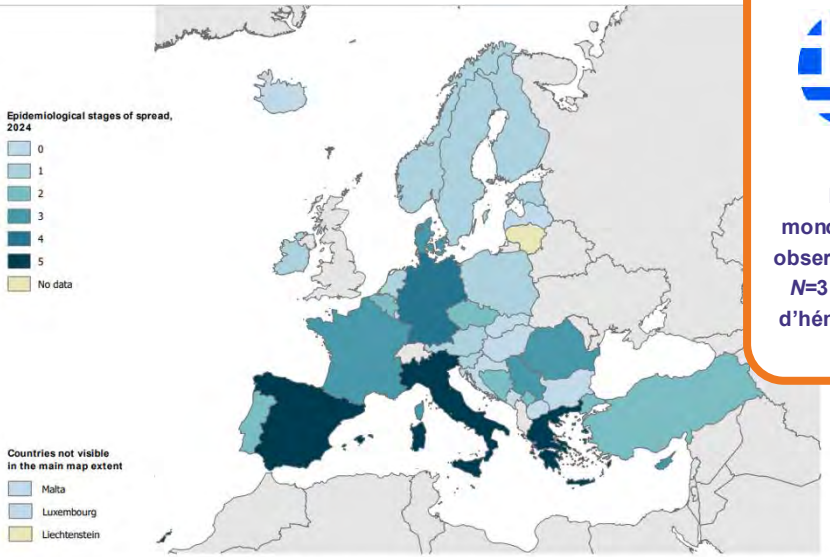
https://www.cdc.gov/fungal/candida-auris/tracking-c-auris.html

Distribution mondiale



Données du CNRMA, Institu Pasteur de Paris
Plachouras D *et al. Euro Surveill*. 2020 ; **25** (12) : pii=2000240

Distribution mondiale

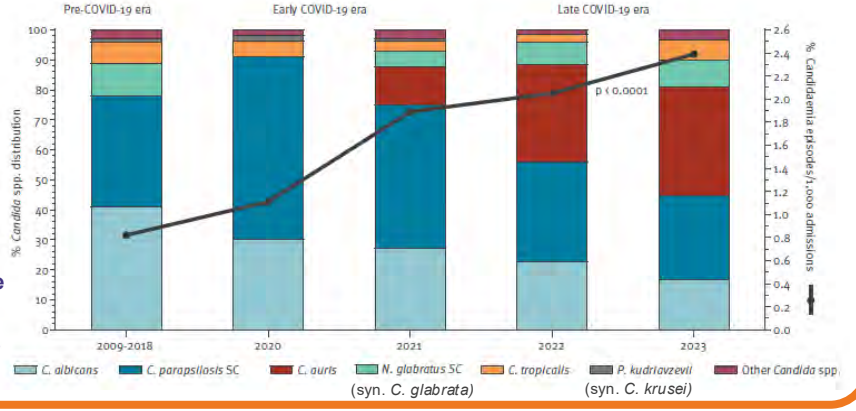


[a]*Epidemiological stages of* C. auris *spread are defined as: Stage 0: No cases of* C. auris *infection or colonisation have been detected. Stage 1: Only imported cases of* C. auris *have been detected. Stage 2: Only sporadic cases of* C. auris *that were locally acquired or of unknown origin have been detected. Stage 3: Sporadic outbreaks of* C. auris *have occurred without or with only limited inter-facility spread. Stage 4: Multiple outbreaks of* C. auris *with verified or plausible inter-facility spread have occurred. Stage 5:* C. auris *is endemic in parts of the country (regional spread).* [b]*Denmark has reported only one outbreak of two cases in 2021.* [c]*Data are included for the EU enlargement countries Bosnia and Herzegovina, Kosovo, Montenegro, North Macedonia, Serbia and Türkiye.*

ECDC 2024

Situation épidémiologique en Grèce

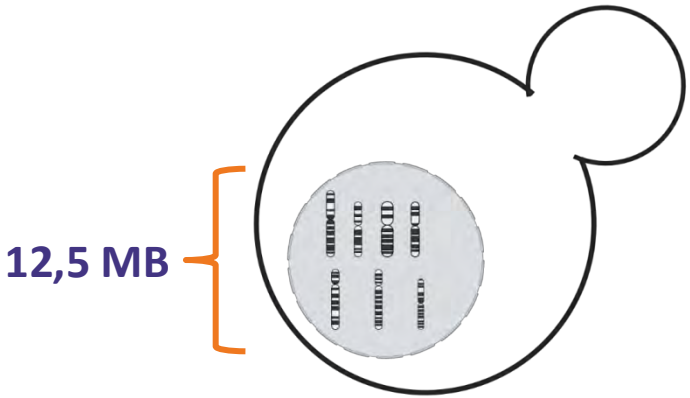
Étude monocentrique observationnelle *N*=365 isolats d'hémocultures



Siopi M *et al. Euro Surveill.* 2024

☞ **déjà devenu endémique dans certains pays européens**

Typage moléculaire et circulation des souches



génome haploïde

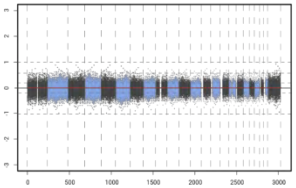
(cinq à sept chromosomes)

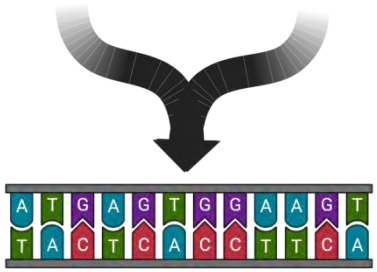
PFGE

électrophorèse en champ pulsé

WGS

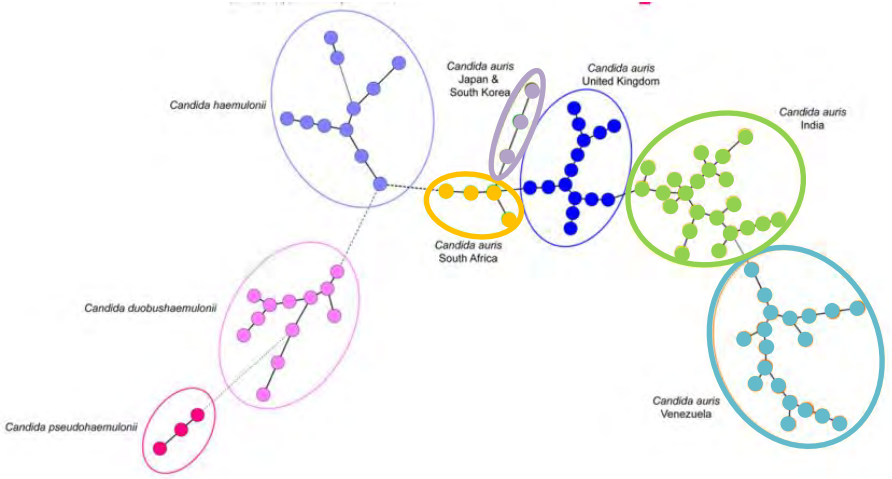
séquençage du génome entier





Sarma S, Upadhyay S. *Infect Drug Resist.* 2017 ; **10** : 155-165
Eyre DW, *et al. N Engl J Med.* 2018 ; **379** : 1322-31
Bougnoux ME *et al. Antimicrob Resist Infect Control.* 2018 **27** (7) : 45

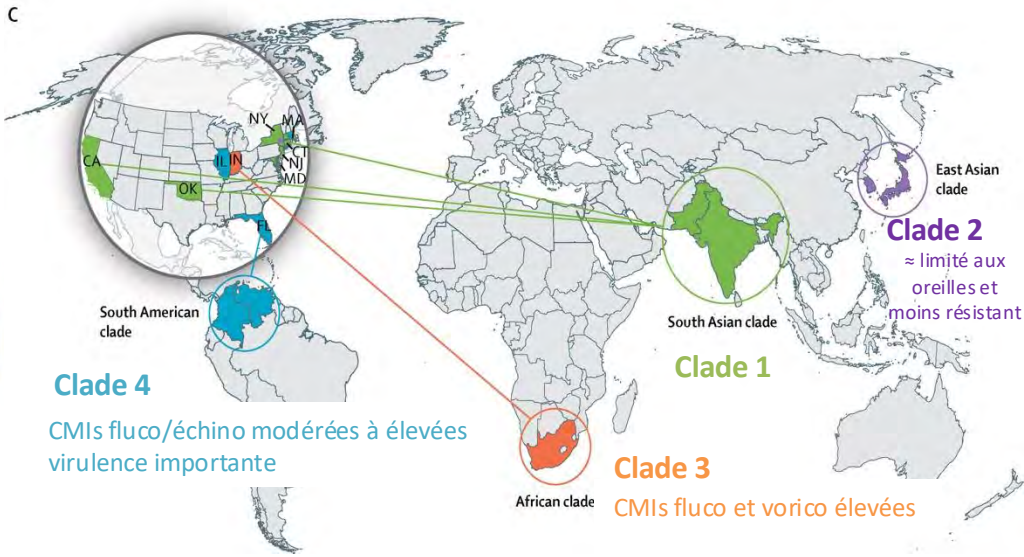
Typage moléculaire et circulation des souches



Schelenz S *et al. Antimicrob Resist and Infect Control*. 2016 ; **5**: 35

diversité faible entre isolats d'une même origine

(1-100 SNPs)



+ 2 autres clades récents

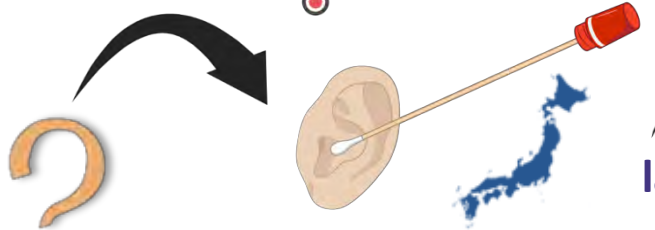
Chow NA *et al. Lancet Infect Dis.* 2018 ; **18** : 1377–84
Szekely A *et al. J Clin Microbiol*. 2019 ; **57** (5) : e02055-18

D'où vient *Candidozyma* (syn. *Candida*) *auris* ?

La question originelle

l'adaptation à l'Homme

37 °C



la dispersion mondiale

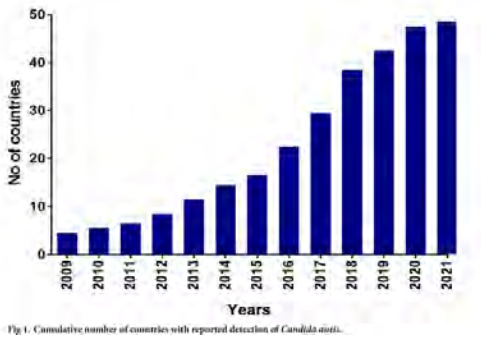


Fig 1. Cumulative number of countries with reported detection of *Candida auris*.

les origines

2008

1 patient ♂ 70 ans

2025

> 45 pays

$13x10^6$ porteurs ou infectés

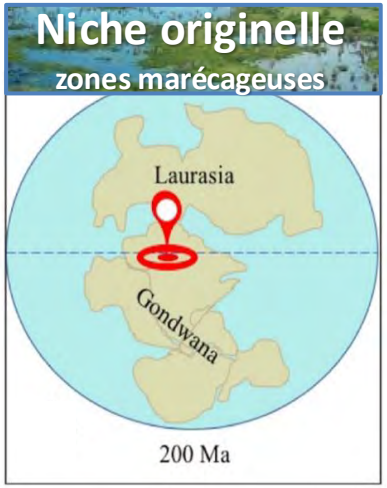
$1,5x10^6$ ✞

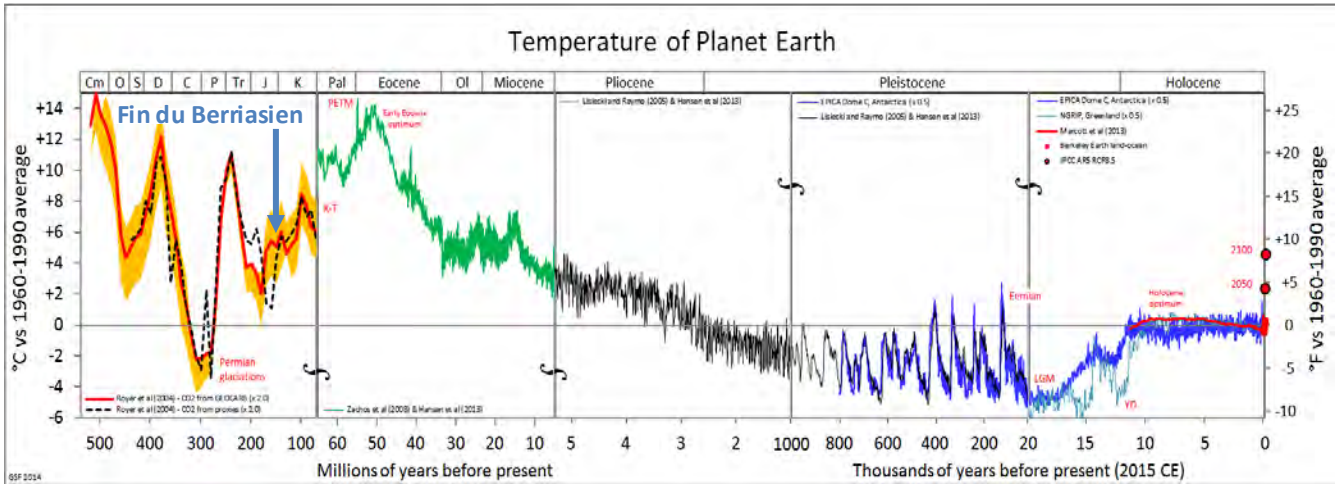
Akinbobola AB *et al. PLoS Pathog*. 2023 ; **19** (4) :e1011268

Comment *Candidozyma* (syn. *Candida*) *auris* a-t-elle émergé ~ simultanément de sites géographiquement distants ?

Qu'est-ce qui a dirigé l'apparition de la virulence de *Candidozyma* (syn. *Candida*) *auris* pour l'Homme ?

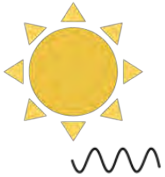
Hypothèse du changement climatique et de la dérive des continents





Bornman JF *et al. Photochem Photobiol Sci.* 2019 ; **18** : 681–716
Chybowska AD *et al. Front Genet.* 2020 ; **11** : 354
Osborn HF. *Proc Natl Acad Sci U S A.* 1929 ; **15** : 691–695

sélection positive

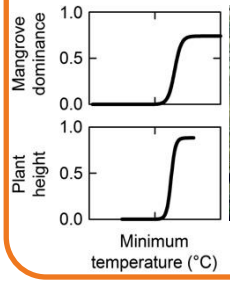


hyperexpression de Hsp90

mutations *uv*-induites

⊕

⇗ réservoir environnemental



densification végétale

⊕

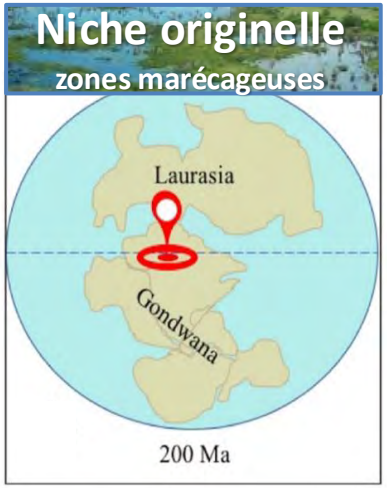
colonisation d'hôtes

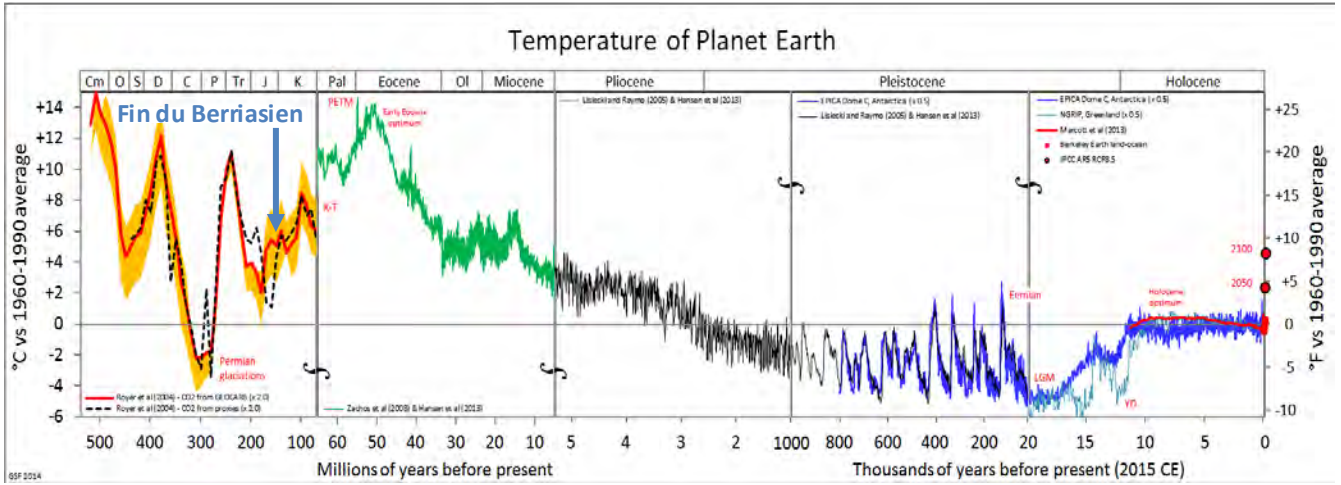
extinction massive de diverses espèces ectothermes

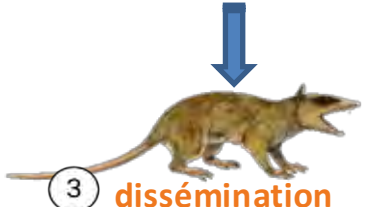
Eomaia sp.

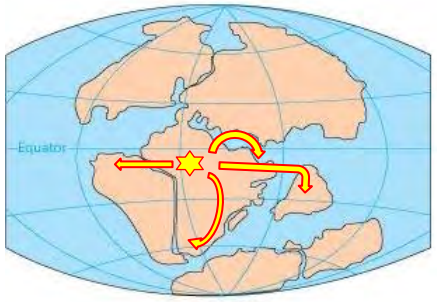
Sinodelphys sp.

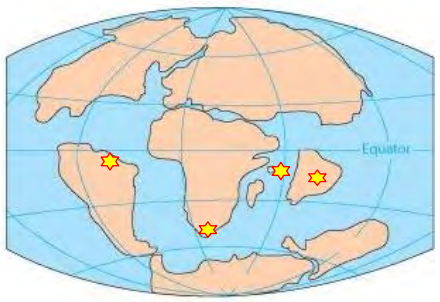
Hypothèse du changement climatique et de la dérive des continents

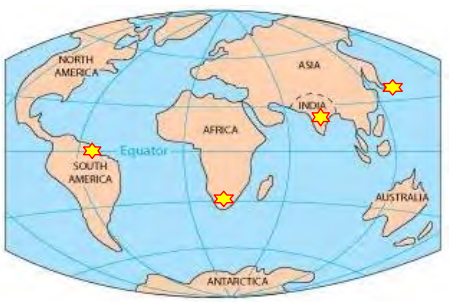






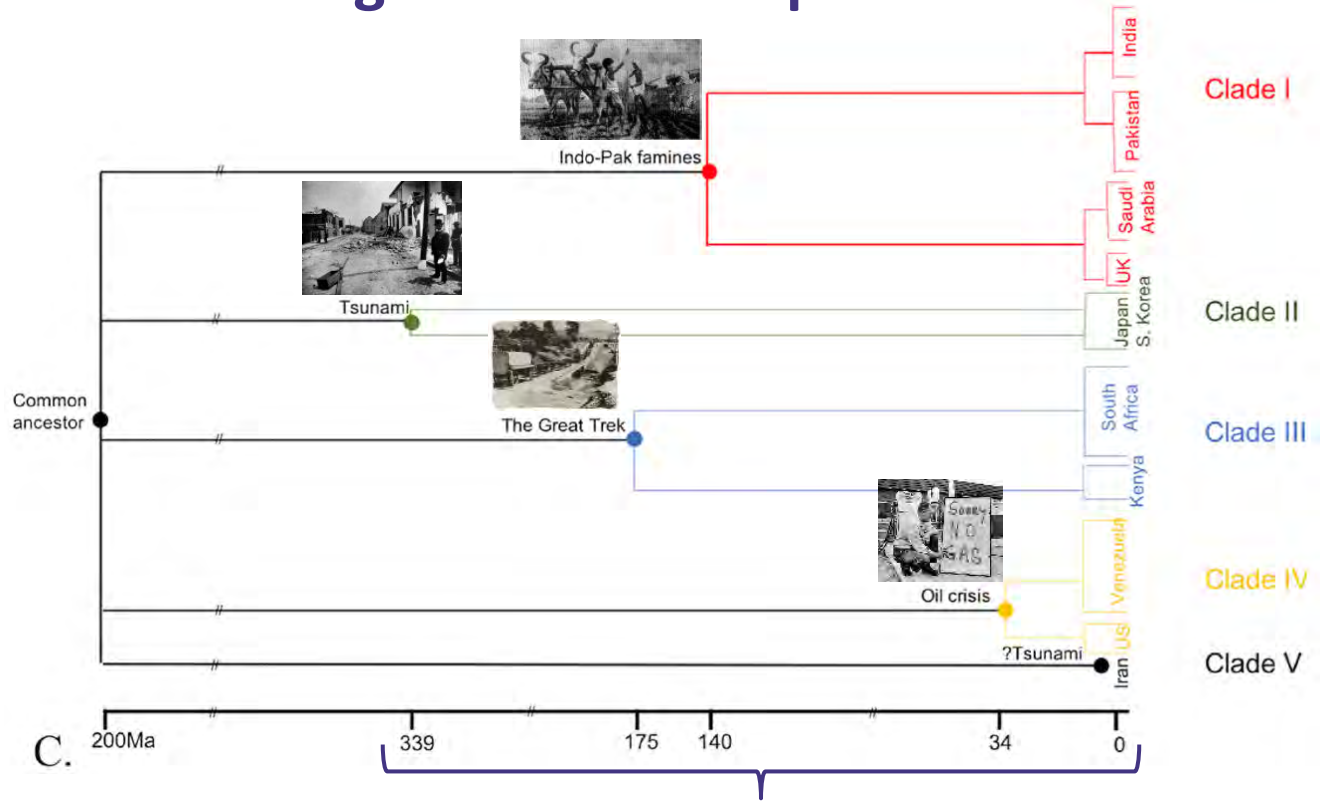






Sharma M et Chakrabartia A *mBio.* 2020 ; **11** (6) : e02102-20

Hypothèse du changement climatique et de la dérive des continents

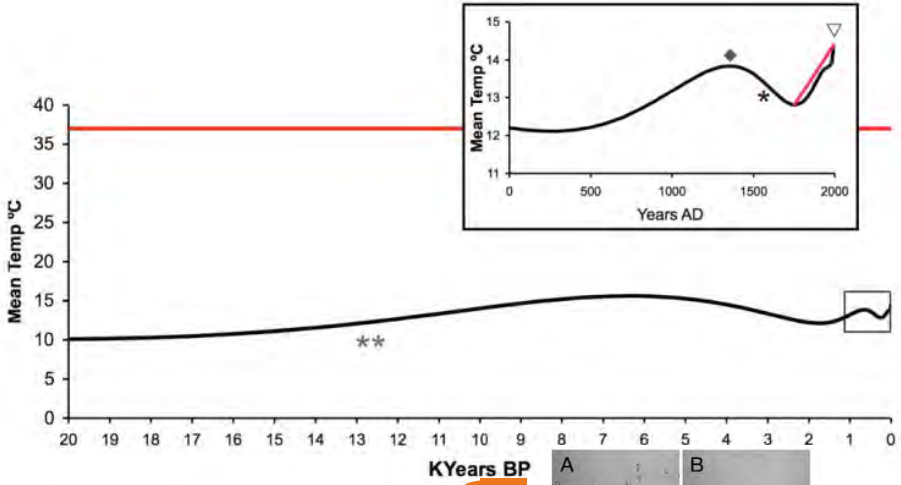


apparition dans l'environnement humain en parallèle de la survenue de phénomènes naturels ou sociétaux

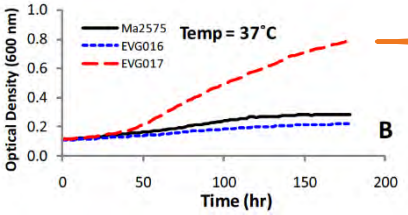
17ème siècle → fin 80'
mi-90' → 2022

période initiale de rapprochement avec l'Homme
émergence massive suite à une capacité d'adaptation plus récemment induite ?

Sharma M et Chakrabartia A *mBio.* 2020 ; **11** (6) : e02102-20



Modèle de *Metarhizium anisopliae*
(22 cycles de 22 à 38°C pendant [13h-394h])



induction *in vitro* de thermotolérance à 37°C

Figure 2
Growth curves at 36.5°C (A) and 37°C (B) of wild-type and temperature adapted *M. anisopliae* isolates. Growth experiments were performed using a high-throughput Bioscreen C plate reader and are the averages of at least 30 independent growth curves each for three independent batches of fungal conidia (>90 cultures).

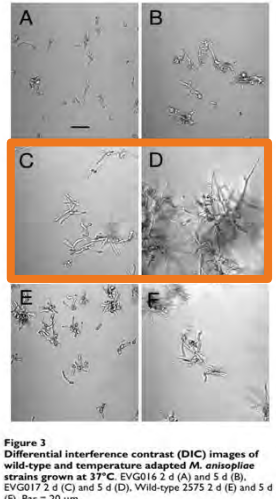
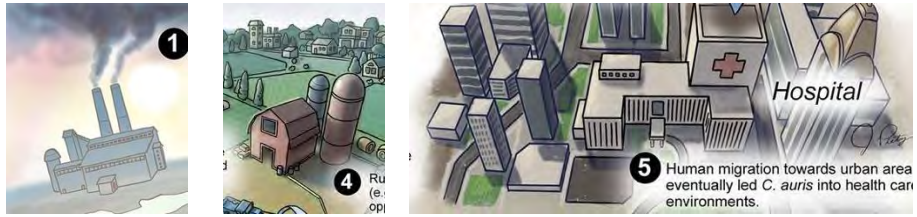
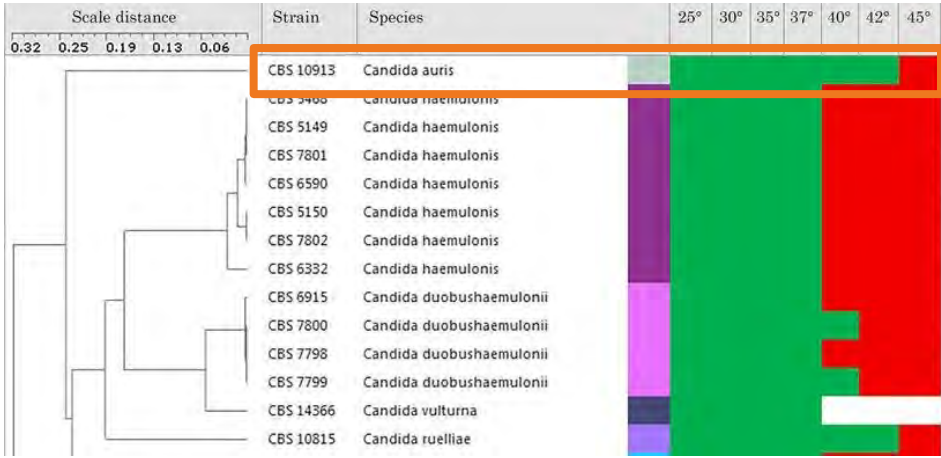


Figure 3
Differential interference contrast (DIC) images of wild-type and temperature adapted *M. anisopliae* strains grown at 37°C. EVG016 2 d (A) and 5 d (B), EVG017 2 d (C) and 5 d (D), Wild-type 2575 2 d (E) and 5 d

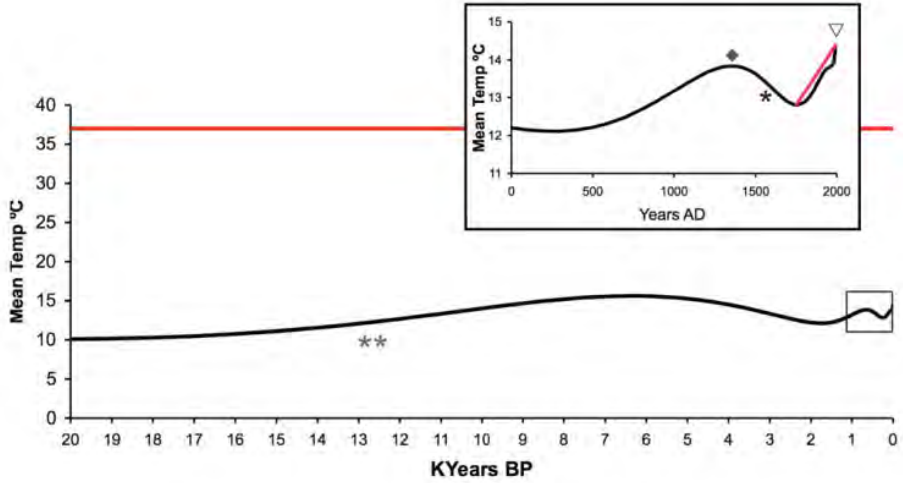
induction d'une thermotolérance XXL

37 °C





de Crecy E *et al. BMC Biotechnol.* 2009 ; **9** : 74



Fungal Biology 128 (2024) 1638–1641

Contents lists available at ScienceDirect

Fungal Biology

journal homepage: www.elsevier.com/locate/funbio

British Mycological Society promoting fungal science

Review

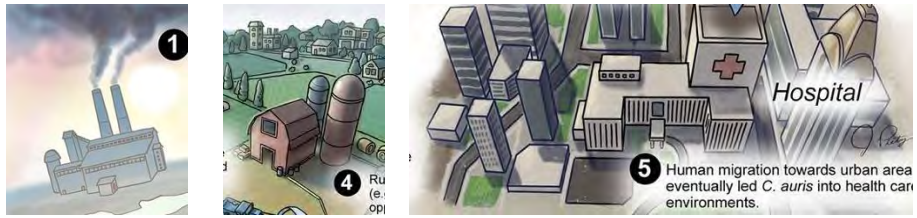
Fungal thermotolerance revisited and why climate change is unlikely to be supercharging pathogenic fungi (yet)

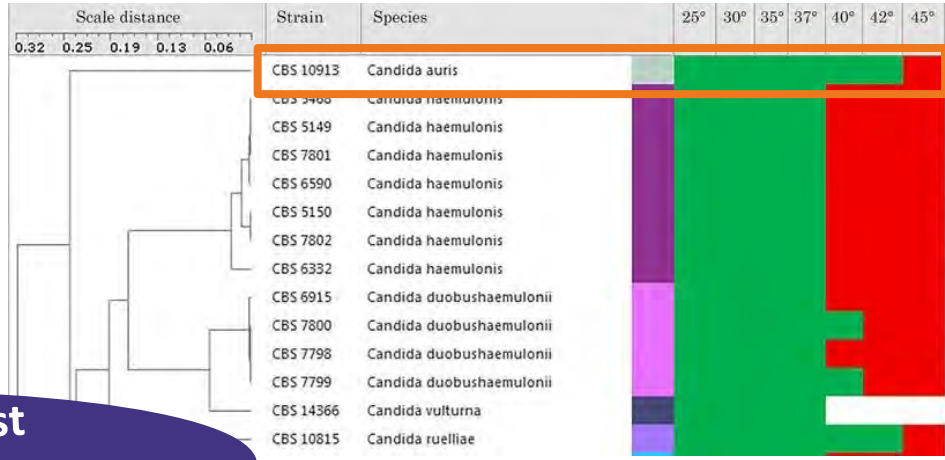
Nicholas P. Money

Western Program and Departm

induction d'une thermotolérance XXL

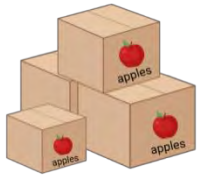
37 °C





le dérèglement climatique n'est vraisemblablement pas le seul responsable

Facteurs additionnels au dérèglement climatique



fruits stockés et traités

fruits frais ± traités

TABLE 2 Spectrum of yeast species from the surfaces of 62 apples and detection of fungicides

Slot no. of apples[a]	Date of collection	Apple variety	No. of apples positive for *C. auris*/total apples screened (no. of *C. auris* colonies)
1	16 March 2020	Red Delicious	2/5 (*n* = 3)
2	15 April 2020	Royal Gala	1/9 (*n* = 5)
3	4 June 2021	Royal Gala	1/3 (*n* = 2)
4	26 July 2021	Royal Gala	1/5 (*n* = 1)
5	26 July 2021	Red Delicious	1/5 (*n* = 2)
6	26 July 2021	Royal Gala	1/5 (*n* = 2)
7	26 July 2021	Red Delicious	1/5 (*n* = 1)
8	26 July 2021	Red Delicious	0/5
9	3 September 2021	Red Delicious	0/5
10	3 September 2021	Red Delicious	0/5
11	7 September 2021	Red Delicious	0/5
12	21 September 2021	Red Delicious	0/5

[a]Slot no. 1 to 8 represent apples purchased from local vendors (nonseasonal stored apples), slot no. 9 to 12 repres
India, slot no. 9 to 10, from orchards used nonorganic farming, and slot no. 11 to 12 used organic farming.
[b]Demethylation inhibitor (DMI) triazoles.
[c]Negative for specific category of fungicide.

13 %

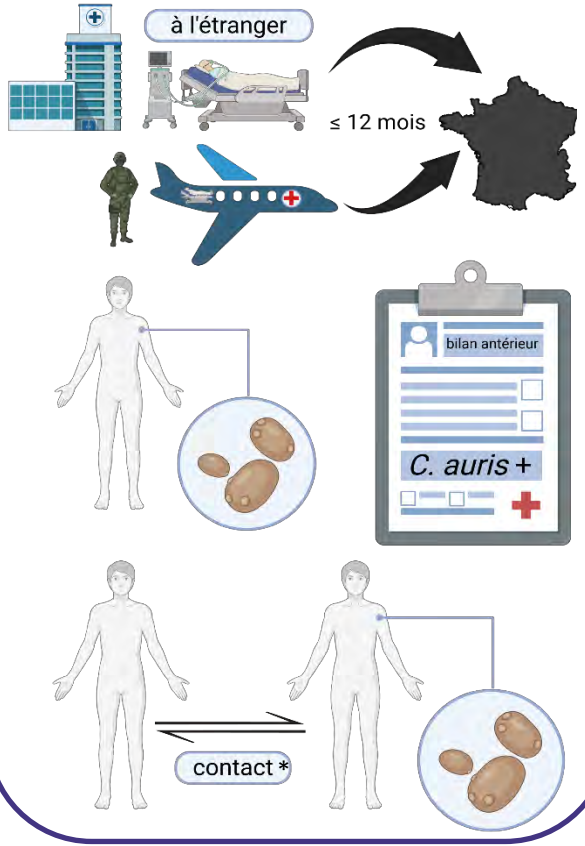
nouvelle route de transmission ?
chemin pour la sélection de résistance(s) ?

FIG 2 Maximum-likelihood phylogenetic tree of 60 *C. auris* strains was constructed by using RAxML v8.0.25. Included in the tree are 16 *C. auris* strains from surfaces of apples (CasSA), 13 environmental strains from Andaman Islands, India, and 30 Indian clinical strains along with reference strain, B8441. The tree was constructed based on the 1,281 shared SNPs among the 59 strains. Branches with bootstrap support over 75% of 100 bootstrap iterations are labeled with red markers. CasSA were highlighted in red and clustered in 5 subclusters (A to E).

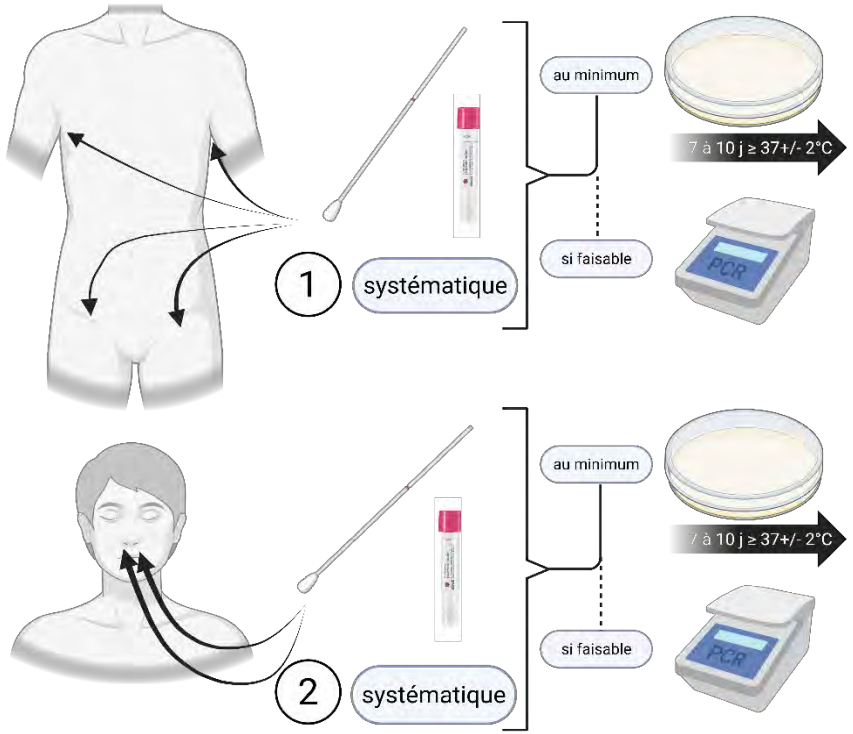
souches des fruits = proches de celles cliniques

Dans quel contexte rechercher *C. auris* et comment empêcher sa propagation ?

Population-cible

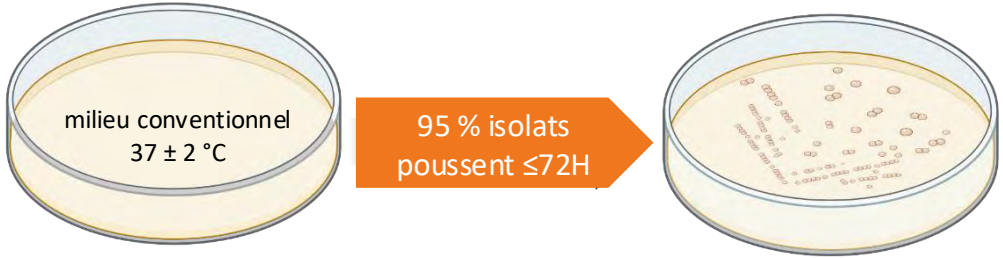


Stratégie de dépistage et prélèvements



*risque moyen : PCC pas mise en œuvre dans le service à l'arrivée du cas ou installation dans une chambre occupée par un cas sans bionettoyage renforcé ou avec prélèvements environnementaux positifs
*risque élevé : contexte épidémique

Recherche conventionnelle



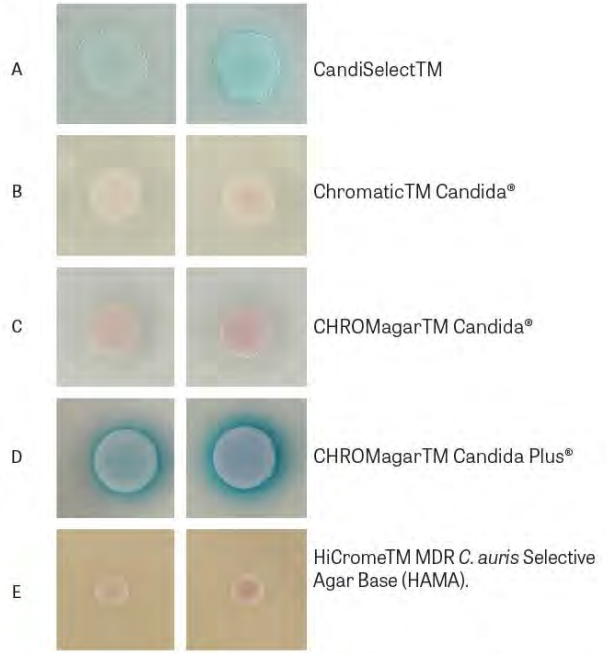
Conditions de culture idéale

- ≥ 35°C et jusqu'à 42°C
- sous agitation 250 rpm
- pendant 10 jours
- milieu enrichi en sel 10%

pas toujours faisable

Welsh *et al. J Clin Microbiol*. 2019

aspect de *C. auris* sur géloses chromogènes

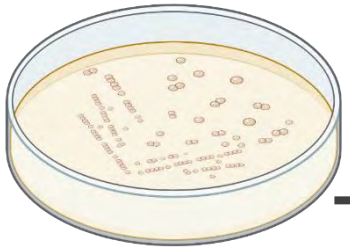


Les milieux ont été incubés 48 heures à 35°C ou à 42°C pour la gélose HA-MA.

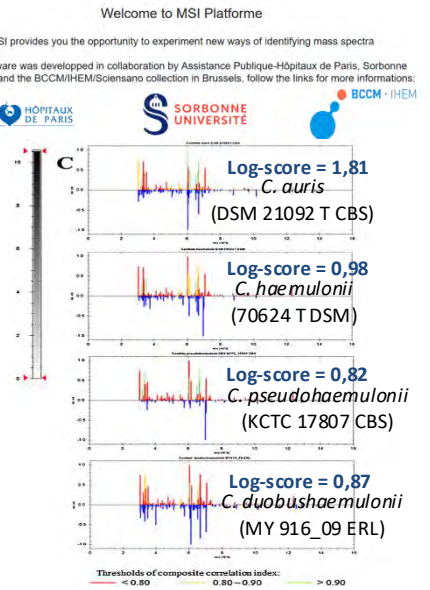
Alanio A *et al. Hygiènes*. 2023 ; **31** (6)

Recherche conventionnelle

95 % isolats poussent ≤72H

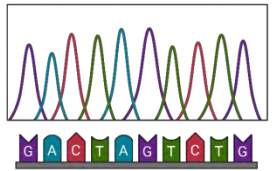


confirmation obligatoire



spectrométrie de masse MALDI-TOF

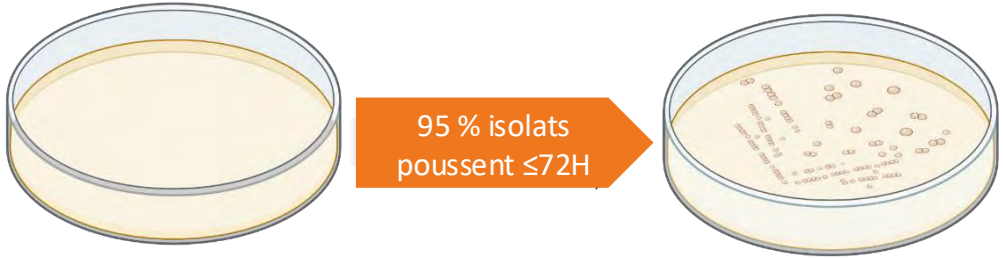
adressage de la souche



séquençage ADN Sanger

Recherche conventionnelle

EUCAST European Committee on Antimicrobial Susceptibility Testing



⇨ **réaliser des tests *in vitro* de susceptibilité aux antifongiques**

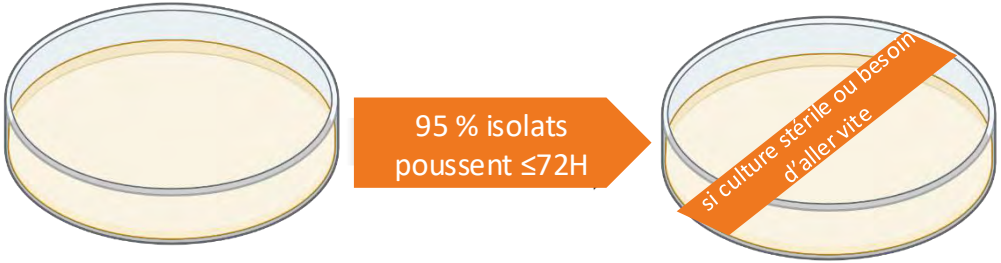
± traçage épidémiologique

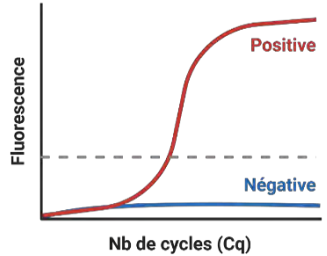
European Committee on Antimicrobial Susceptibility Testing

Breakpoint tables for interpretation of MICs for antifungal agents

Antifungal agent	*Candida auris*	
	S ≤	R >
Amphotericin B	0.001[1]	2
Anidulafungin	0.25	0.25
Caspofungin	IE	IE
Fluconazole	Note[3]	Note[3]
Isavuconazole	IE	IE
Itraconazole	IE	IE
Micafungin	0.25	0.25
Posaconazole	IE	IE
Rezafungin[7]	IE	IE
Voriconazole	IE	IE

Approche moléculaire en complément





RT-PCRq

solutions « maison » ou commerciales

Tableau I – Kits commerciaux de PCR pour l'identification de *C. auris*, leur technique et performances.

Kit	Technique	Prélèvement	Performances	Référence
AurisID® (Olm Diagnostics, Newcastle Upon Tyne, Royaume-Uni)	Avec sondes et amorces (28S *ribosomal gene region*) Résultats en 45 minutes	À partir d'une colonie suspecte en culture et tous types de prélèvements	Limite de détection : 1 copie par réaction Faux positifs possibles	[21]
Fungiplex® RUO (Bruker, Billerica, MA, États-Unis)	Avec sondes et amorces (*mating locus alpha**) Résultats en 2 heures		Limite de détection : 9 copies par réaction Pas de faux positif	[21]
CanAur Monodose dtec-qPCR Test (Genetic PCR Solution, Orihuela, Espagne)	Résultats en 45 minutes		100% de Se et Sp Limite de détection : 1 copie par réaction	[22]
Candida auris kit BD Max™ System (BioGX, Birmingham, AL, États-Unis)	Avec sondes et amorces (ITS 1/2)		100% de Se et Sp	[23]

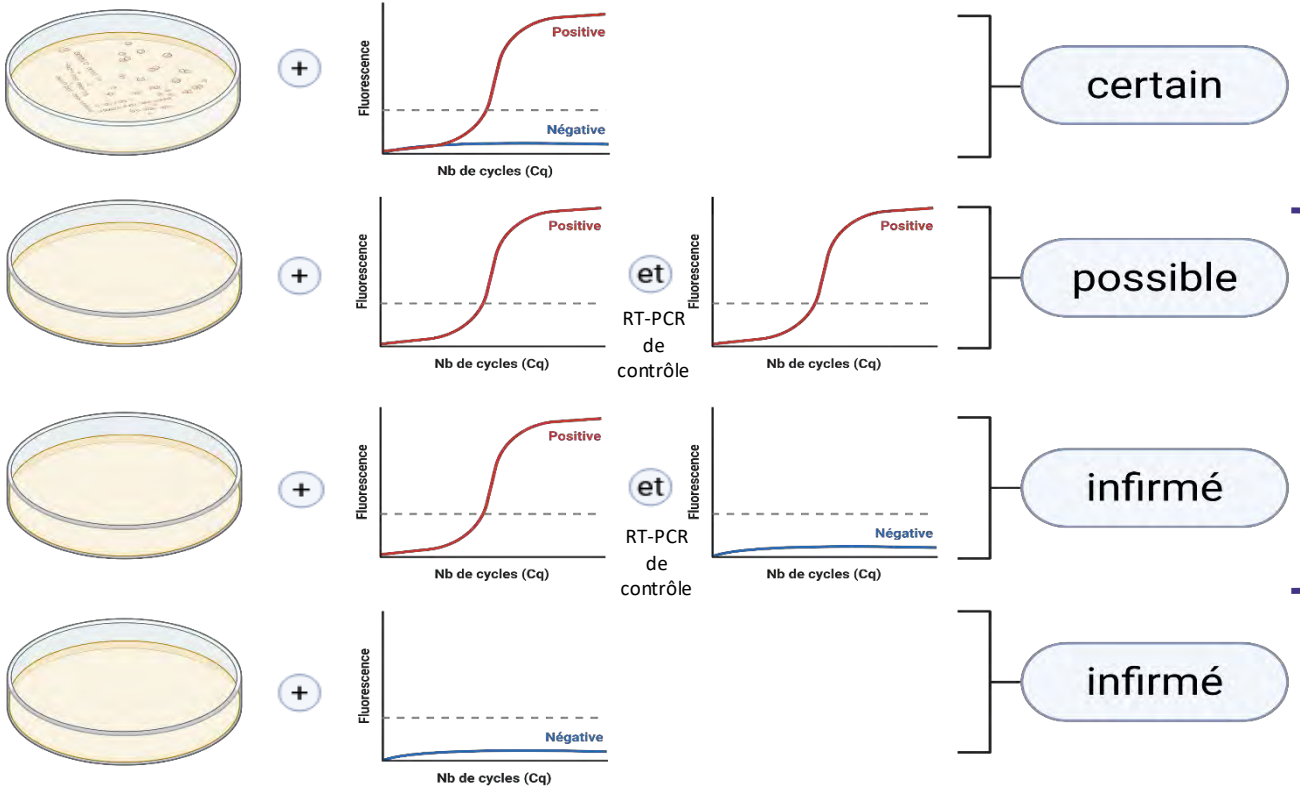
ITS : *internal transcribed spacer* ; RUO : *research use only* ; Se : sensibilité ; Sp : spécificité.

⚠

⇨ pas vraiment de supériorité de l'une par rapport aux autres

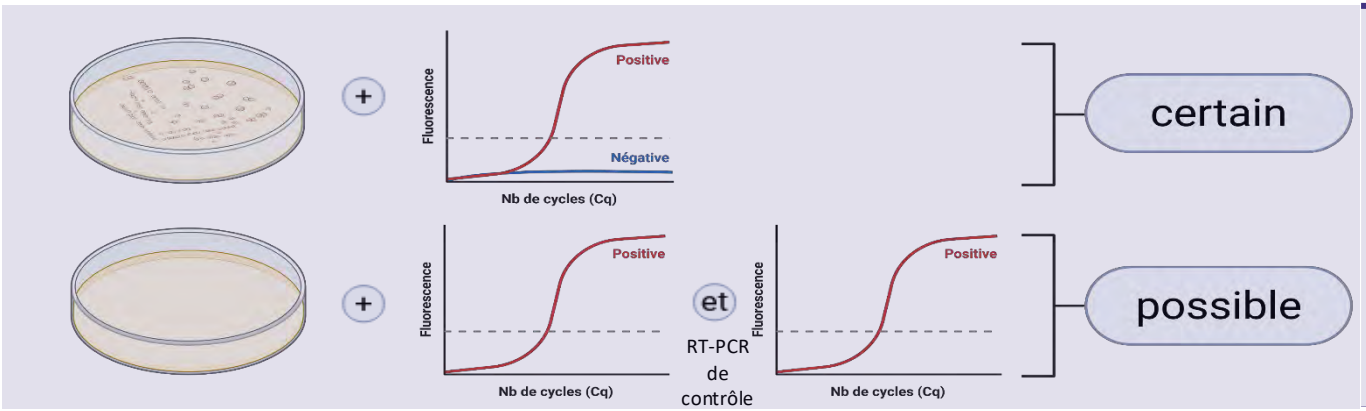
Alanio A *et al. Hygiènes.* 2023 ; **31** (6)

Interprétation des résultats mycologiques

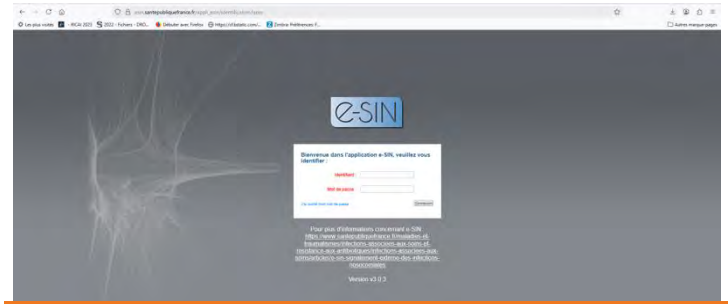


penser à élargir les sites de prélèvement (rectal, gorge, urines, …) **et renouveler au moins deux fois**

Interprétation des résultats mycologiques

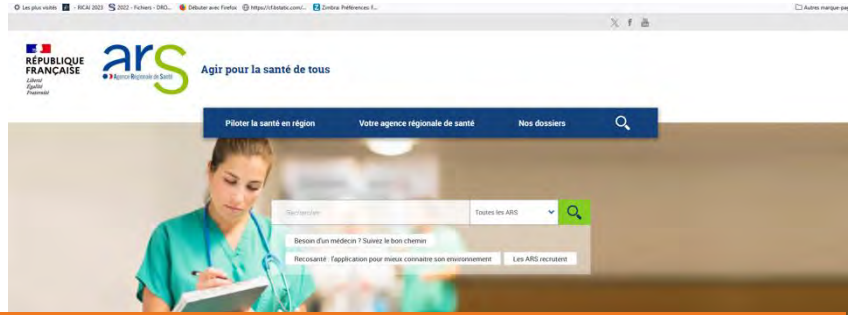


prévenir EPRI
+
service clinique hébergeur



Santé publique France

Réseau des CPias

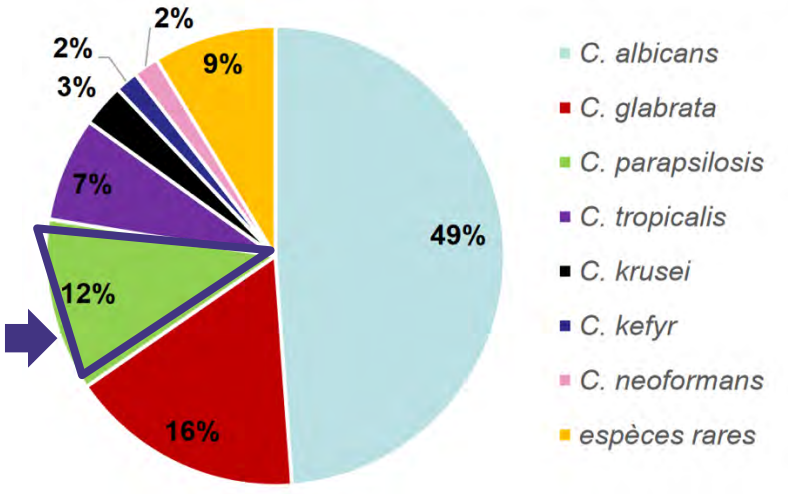


+ notification aux autorités

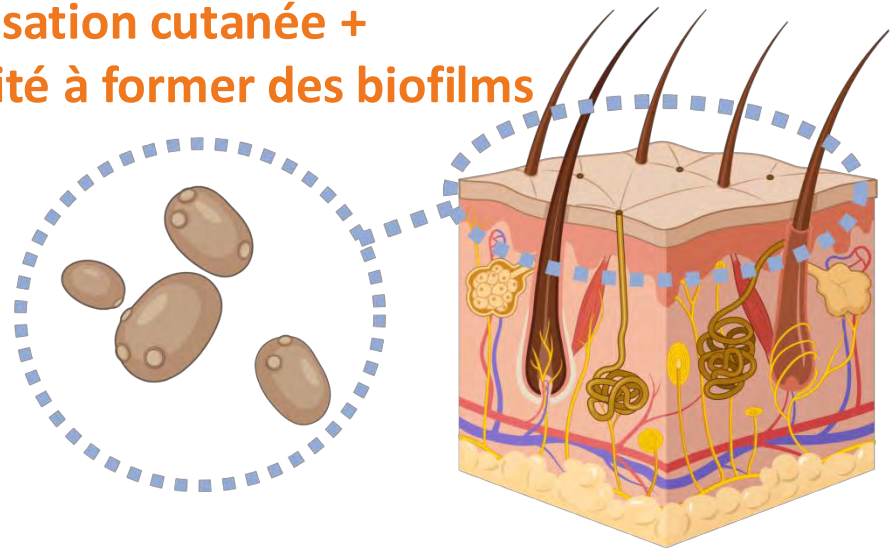
D'autres situations comparables d'émergence de pathogènes fongiques multi-résistants ?

Cas particulier de *Candida parapsilosis*

Distribution des espèces responsables de fongémies en France (RESSIF 2012-2018)



colonisation cutanée +
capacité à former des biofilms



Bretagne S *et al*. *mBio.* 2022 ; **13** (3) :e0092022
Données du CNRMA de l'Institut Pasteur de Paris

Données historiques de susceptibilité aux antifongiques

Rapport d'activités 2021
CNR des Mycoses Invasives et Antifongiques

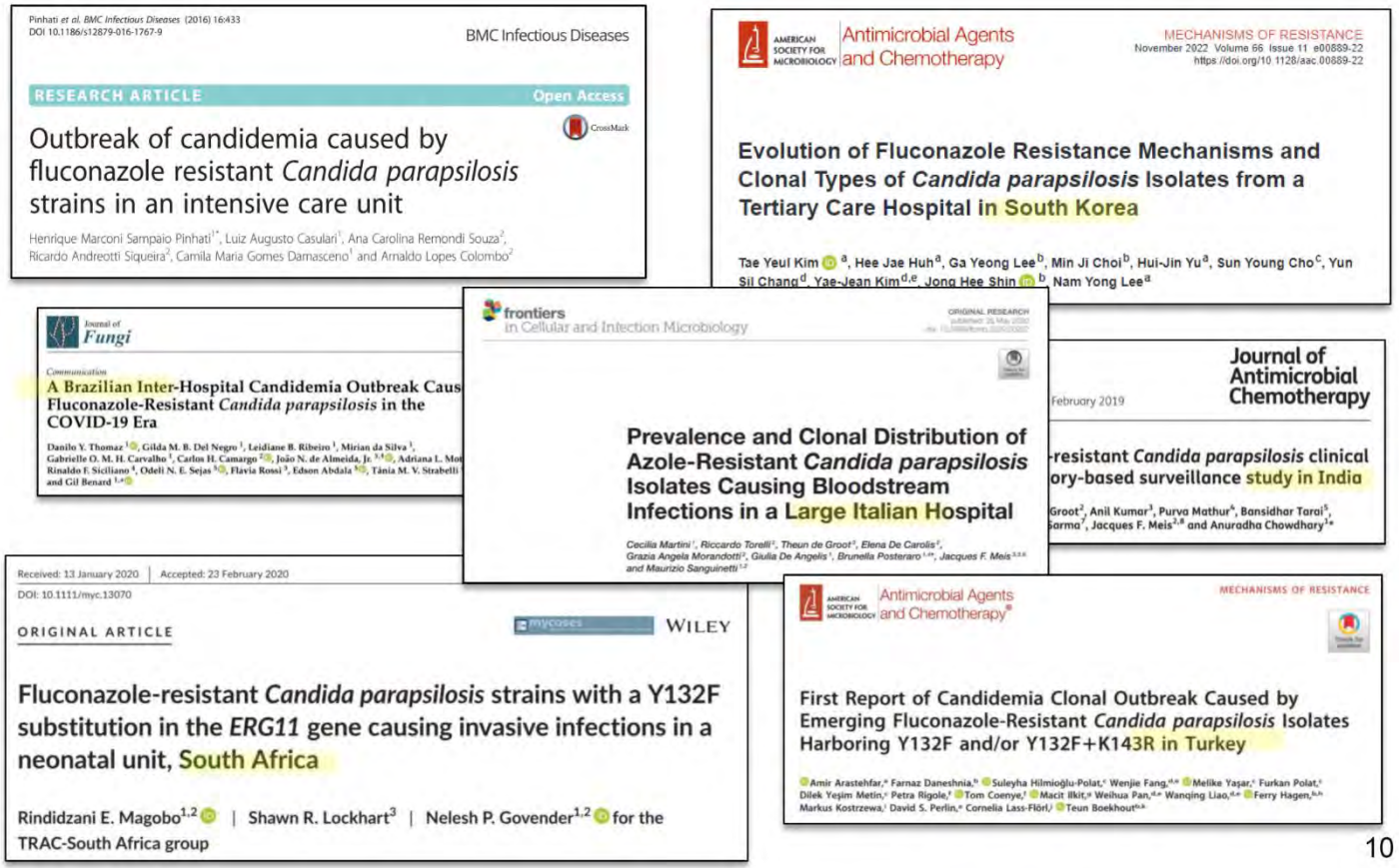
Institut Pasteur

Espèces étudiées		CMI50 / CMI90 mg/L					
Nom d'usage en clinique (nbre d'isolats testés)	Nom actuel	AMB	5-FC	Fluco	Vori	Posa	Caspo**
C. albicans (n=3454)		0.06/0.12	≤0.12/0.5	0.25/0.5	≤0.01/≤0.01	≤0.01/0.06	0.03/0.06
C. dubliniensis (n=149)		≤0.014/0.03	≤0.12/≤0.12	≤0.12/0.25	≤0.01/≤0.01	0.03/0.06	0.015/0.03
C. glabrata (n=1348)		0.12/0.25	≤0.12/≤0.12	16/64	0.25/1	0.5/2	0.06/0.12
C. nivariensis (n=16)		0.12/0.25	0.5/1	2/4	0.06/0.12	0.12/0.25	0.03/0.12
C. parapsilosis (n=867)		0.06/0.12	≤0.12/0.25	0.5/2	≤0.01/0.06	0.06/0.12	0.25/1
C. orthopsilosis (n=62)		0.03/0.06	≤0.12/≤0.12	0.5/8	0.03/1	0.06/0.12	0.06/0.25
C. metapsilosis (n=50)		0.06/0.12	≤0.12/≤0.12	1/2	0.03/0.06	0.03/0.12	0.06/0.25
C. tropicalis (n=668)		0.06/0.12	≤0.12/32	0.5/4	0.03/0.25	0.06/0.25	0.03/0.06
C. krusei (n=360)	*Pichia kudriavzevii*	0.12/0.25	2/4	32/64	0.25/0.5	0.12/0.25	0.12/0.25
C. inconspicua (n=49)	*Pichia cactophila*	0.12/0.25	2/4	16/32	0.12/0.25	0.12/0.12	0.03/0.06
C. kefyr (n=177)	*Kluyveromyces marxianus*	0.06/0.12	0.5/8	0.25/1	≤0.01/≤0.01	0.06/0.12	0.015/0.03

☑ habituellement sensible aux azolés

☒ CMIs naturellement plus élevées aux échinocandines

Multiplication des épidémies clonales à *C. parapsilosis* fluco-résistant



Pinhati et al. BMC Infectious Diseases (2016) 16:433
DOI 10.1186/s12879-016-1767-9

BMC Infectious Diseases

RESEARCH ARTICLE Open Access

Outbreak of candidemia caused by fluconazole resistant *Candida parapsilosis* strains in an intensive care unit

Henrique Marconi Sampaio Pinhati[1*], Luiz Augusto Casulari[1], Ana Carolina Remondi Souza[2], Ricardo Andreotti Siqueira[2], Camila Maria Gomes Damasceno[1] and Arnaldo Lopes Colombo[2]

AMERICAN SOCIETY FOR MICROBIOLOGY | Antimicrobial Agents and Chemotherapy

MECHANISMS OF RESISTANCE
November 2022 Volume 66 Issue 11 e00889-22
https://doi.org/10.1128/aac.00889-22

Evolution of Fluconazole Resistance Mechanisms and Clonal Types of *Candida parapsilosis* Isolates from a Tertiary Care Hospital in South Korea

Tae Yeul Kim[a], Hee Jae Huh[a], Ga Yeong Lee[b], Min Ji Choi[b], Hui-Jin Yu[a], Sun Young Cho[c], Yun Sil Chang[d], Yae-Jean Kim[d,e], Jong Hee Shin[b], Nam Yong Lee[a]

Journal of Fungi

Communication

A Brazilian Inter-Hospital Candidemia Outbreak Caus... Fluconazole-Resistant *Candida parapsilosis* in the COVID-19 Era

Danilo Y. Thomaz[1], Gilda M. B. Del Negro[1], Leidiane B. Ribeiro[1], Mirian da Silva[1], Gabrielle O. M. H. Carvalho[1], Carlos H. Camargo[2], João N. de Almeida, Jr.[3,4], Adriana L. Mot... Rinaldo F. Siciliano[4], Odeli N. E. Sejas[5], Flavia Rossi[3], Edson Abdala[5], Tânia M. V. Strabelli... and Gil Benard[1,*]

frontiers in Cellular and Infection Microbiology

ORIGINAL RESEARCH

Prevalence and Clonal Distribution of Azole-Resistant *Candida parapsilosis* Isolates Causing Bloodstream Infections in a Large Italian Hospital

Cecilia Martini[1], Riccardo Torelli[1,2], Theun de Groot[3], Elena De Carolis[1], Grazia Angela Morandotti[1], Giulia De Angelis[1], Brunella Posteraro[1,4*], Jacques F. Meis[3,5,6] and Maurizio Sanguinetti[1,2]

Journal of Antimicrobial Chemotherapy

February 2019

...resistant *Candida parapsilosis* clinical ...ory-based surveillance study in India

...Groot[3], Anil Kumar[3], Purva Mathur[4], Bansidhar Tarai[5], ...arma[3], Jacques F. Meis[2,6] and Anuradha Chowdhary[1*]

Received: 13 January 2020 | Accepted: 23 February 2020

DOI: 10.1111/myc.13070

ORIGINAL ARTICLE

mycoses | WILEY

Fluconazole-resistant *Candida parapsilosis* strains with a Y132F substitution in the *ERG11* gene causing invasive infections in a neonatal unit, South Africa

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AMERICAN SOCIETY FOR MICROBIOLOGY | Antimicrobial Agents and Chemotherapy

MECHANISMS OF RESISTANCE

First Report of Candidemia Clonal Outbreak Caused by Emerging Fluconazole-Resistant *Candida parapsilosis* Isolates Harboring Y132F and/or Y132F+K143R in Turkey

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Multiplication des épidémies clonales à *C. parapsilosis* fluco-résistant

Madrid, 16 hôpitaux, 2019-21

(*n* = 354)

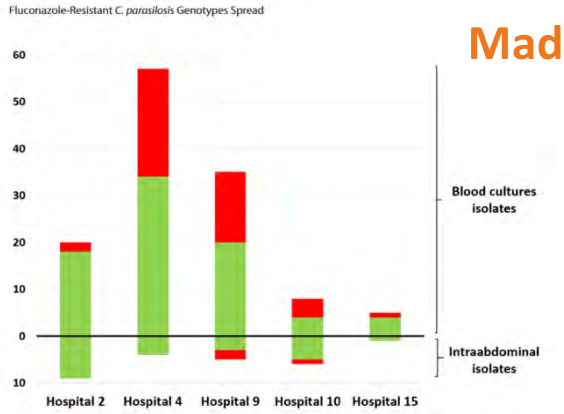


FIG 1 Hospitals in which fluconazole-resistant isolates were detected. The number of fluconazole-resistant isolates (red) and fluconazole-susceptible isolates (green) grouped by clinical source (blood cultures or intraabdominal samples) are shown.

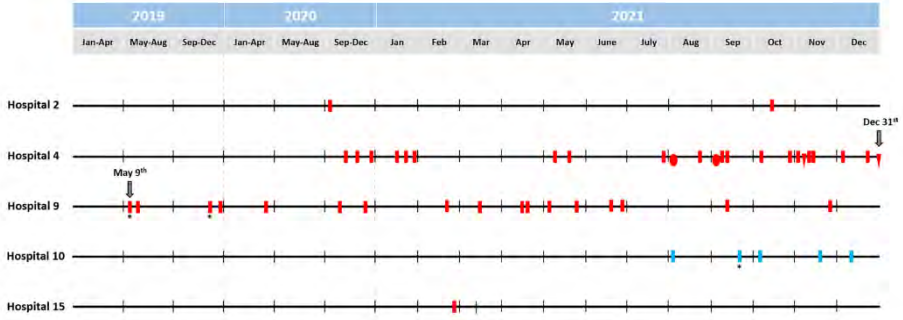


FIG 2 Timeline of the detection of fluconazole-resistant *C. parapsilosis* isolates over time at each of the five affected hospitals (represented in different lines). Colored symbols refer to a fluconazole-resistant *C. parapsilosis* isolate from blood cultures otherwise indicated by an asterisk that represents isolates from intraabdominal samples. Red indicates isolates within the clonal complex (CP-451, bar; CP-673, oval; and CP-674, triangle) of genotypes harboring the Y132F substitution. Blue indicates isolates within the CP-675 genotype harboring the G458S substitution. Arrows indicate the first or last time when resistant isolates were detected.

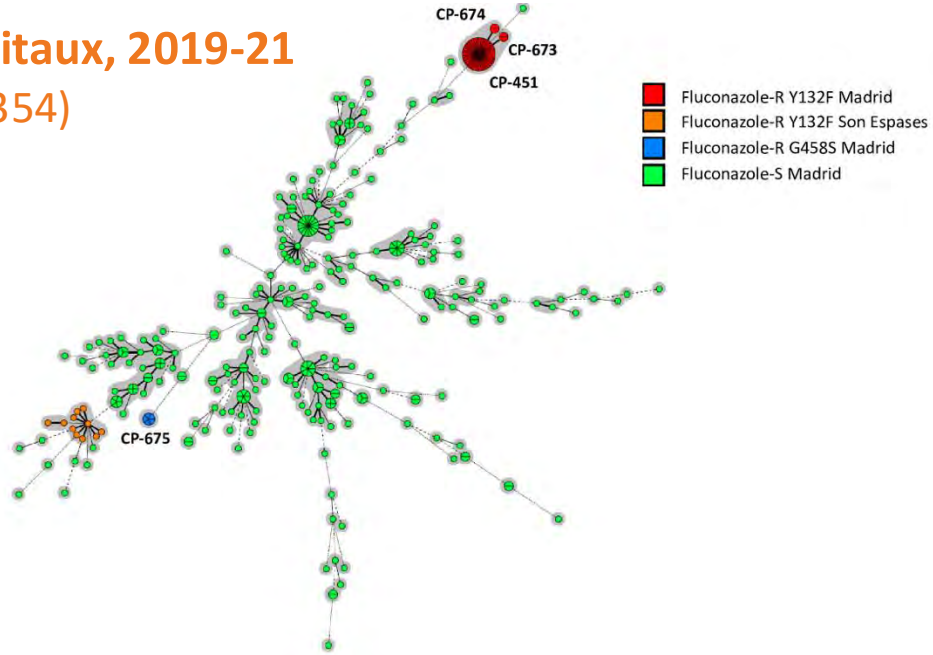


FIG 3 Minimum spanning tree showing the *C. parapsilosis* fluconazole-resistant isolates harboring the Y132F substitution (isolates from hospitals in Madrid [red], isolates from Son Espases hospital [orange]), the G458S substitution (blue); and fluconazole-susceptible isolates (green). Circles represent different genotypes and the circle size of the number of isolates belonging to the same genotype. Connecting lines between the circles show profile similarities. The solid bold line indicates differences in only 1 marker, the solid line indicates differences in 2 markers, the dashed line indicates differences in 3 markers, and the dotted line indicates differences in 4 or more markers. R, resistant; S, susceptible. CP-673 and CP-674 genotypes differ from CP-451 at markers B and CP6 microsatellite markers.

13,6% FLU-R dont 90% portent la mutation Y132F

└ 39/43 = même complexe clonal mais hôpitaux ≠

Díaz-García J *et al. Antimicrob Agents Chemother.* 2022 ; **66** (8) : e0071022

Multiplication des épidémies clonales à *C. parapsilosis* fluco-résistant

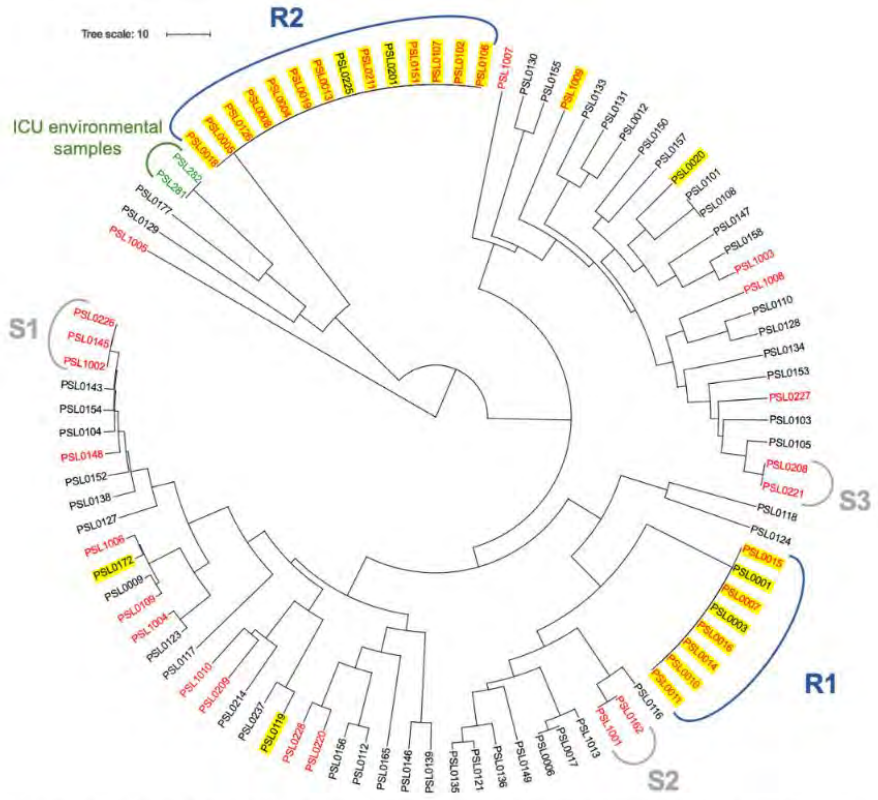


FIG 1 UPGMA (unweighted pair group method with arithmetic mean) dendrogram of 93 *Candida parapsilosis* isolates typed by microsatellite approach. Fluconazole-resistant isolates ($n = 26$) are highlighted in yellow. Isolates from a single intensive care unit are in red. R1 and R2 represent 2 clusters of fluconazole-resistant isolates responsible for 2 outbreaks in 4 and 10 patients, respectively. S1 to S3 represent clusters of susceptible isolates.

Paris, Pitié-Salpêtrière 2012-19 (n = 283)

TABLE 3 Data for 78 patients who developed an invasive infection due to *Candida parapsilosis*[b]

Characteristic	Invasive infections due to fluconazole-susceptible isolates	Invasive infections due to fluconazole-resistant isolates	*P* value
No. of patients	67	11	
Mean age (median [IQR]) (yrs)	59.4 (62 [51–72])	59.6 (65 [56–65.5])	0.78
Sex (no. male/no. female)	52/15	9/2	1
Clinical presentation [no. (%)]			
Candidemia	55 (82.1)	9/11 (81.8)	1
Mediastinitis	3 (4.5)	2/11 (18.2)	0.14
Others	9 (13.4)	0	0.34
Hospital ward [no. (%)]			
ICU	34 (50.7)	10 (90.9)	**0.019**
Non-ICU	22 (32.8)	0	**0.028**
Chirurgical unit	11 (16.4)	1 (9.1)	1
Immunosuppression [no. (%)][a]	25/60 (41.7)	3/11 (27.3)	0.5
Presence of catheter and/or external devices [no. (%)]	46/53 (86.8)	11/11 (100)	0.34
Recent chirurgical intervention (last 30 days) [no. (%)]	42/57 (73.7)	10/11 (90.9)	0.44
Broad-spectrum antibiotic therapy [no. (%)]	40/50 (80)	10/10 (100)	0.19
Preexposition to antifungal drugs (last 3 mo) [no. (%)]	8/47 (17)	2/10 (20)	1
Targeted antifungal therapy [no. (%)]	36/39 (92.3	8/10 (80)	0.27
Echinocandin based	12/36 (33.3)	5/8 (62.5)	0.22
Fluconazole based	21/36 (58.3)	1/8 (12.5)	**0.046**
Other	3/36 (8.3)	2/8 (25)	0.22
All-cause mortality [no. (%)]			
All patients			
Day 30	15/67 (22.4)	5/11 (45.5)	0.082
Day 90	19/64 (29.7)	6/11 (54.5)	0.12
ICU patients			
Day 30	9/34 (26.5)	4/10 (40)	0.40
Day 90	11/31 (35.5)	5/10 (50)	0.46

[a]Immunocompromised conditions include solid organ transplantation, HIV infection, neutropenia (<500 cells/μl), long-term corticosteroid therapy (>3 weeks), malignancies, and allogeneic hematopoietic stem cell transplantation.
[b]Comparison between susceptible and fluconazole-resistant isolates. Statistically significant values are in bold. ICU, intensive care unit; IQR, interquartile range.

9,2% FLU-R avec mutation Y132F ++

Fekkar A *et al. AntimicrobAgents Chemother.* 2023 ; **95** (5) : e02036-20

Multiplication des épidémies clonales à *C. parapsilosis* fluco-résistant

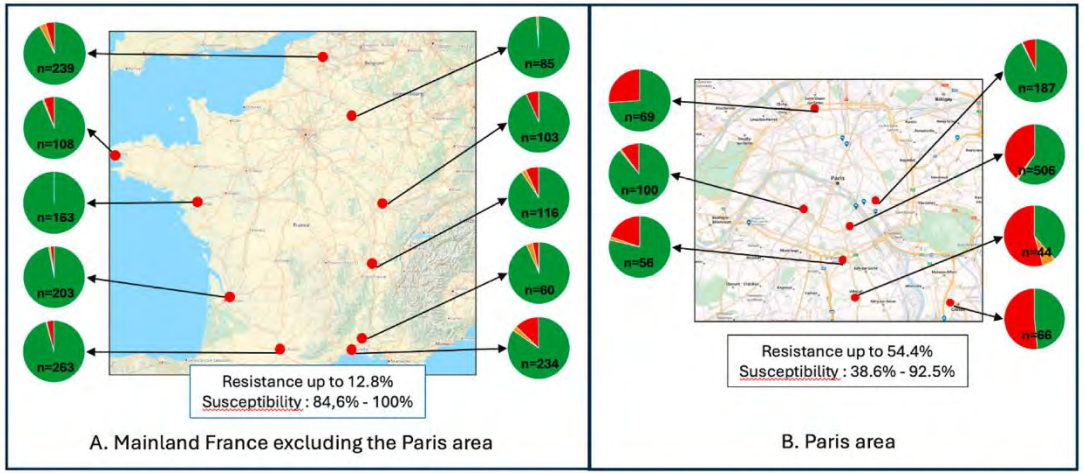
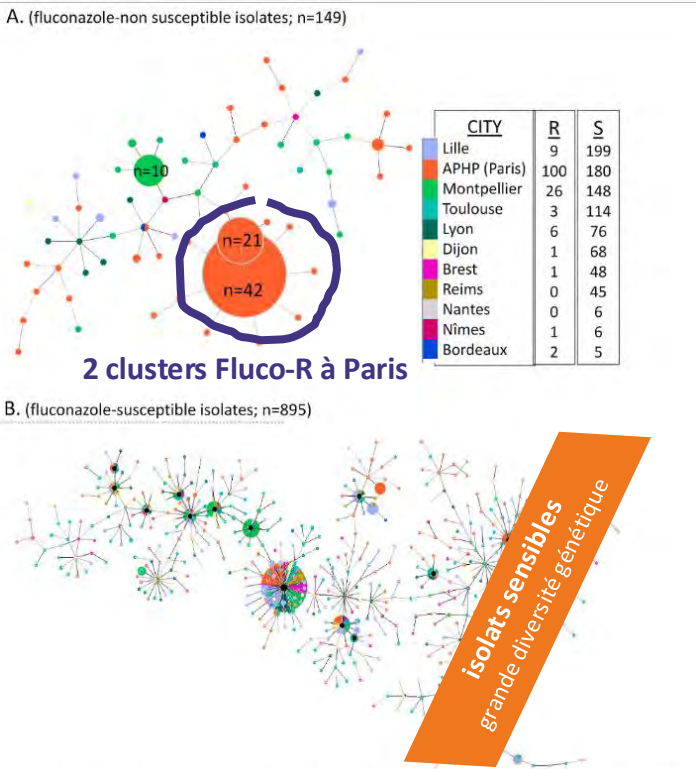


Fig. 2. Distribution of *Candida parapsilosis* isolates collected from 15 medical mycology laboratories (17 hospital) in France between May 2022 and February 2024, according to their susceptibility to fluconazole as determined by Etest®. Green: susceptible isolates (MIC ≤2 mg/L); orange: intermediate susceptibility (MIC = 4 mg/L); red: resistant isolates (MIC >4 mg/L). A: mainland France excluding the Paris region. B: Paris region.

- 15 centres hospitaliers français
- Mai 2022 – Février 2024
- 2602 isolats *C. parapsilosis* (*n*=1830 patients)

☞ 15,1 % résistants

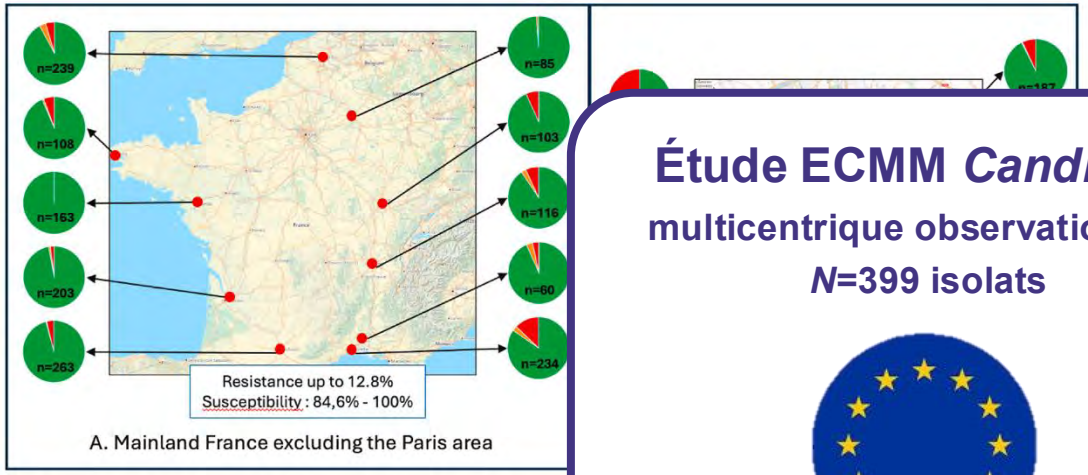


CITY	R	S
Lille	9	199
APHP (Paris)	100	180
Montpellier	26	148
Toulouse	3	114
Lyon	6	76
Dijon	1	68
Brest	1	48
Reims	0	45
Nantes	0	6
Nîmes	1	6
Bordeaux	2	5

Fig. 4. Minimum spanning tree showing the analysis of the genotypic diversity determined by microsatellite method for 1,044 isolates of *Candida parapsilosis* collected in 15 French mycology laboratories according to their susceptibility to fluconazole.
A. Distribution of the fluconazole non-susceptible isolates (resistant or intermediate; n = 149). Two resistant clones circulating in several hospitals in the Paris area were observed in 34.2% (63/184) of patients harboring non-susceptible isolates. Another resistant clone was found in the city of Montpellier in 42.5% (10/22) of the patient.
B. Distribution of the fluconazole susceptible isolates (n = 895). Genetic diversity was higher among susceptible isolates, although several profiles circulating in different hospitals were observed and especially one circulating between 11 hospitals and representing 4.9% (44/895) of the patients carrying a susceptible isolate.

Fekkar A *et al. New Microbes New infect.* 2026 ; **71** : 101738

Multiplication des épidémies clonales à *C. parapsilosis* fluco-résistant



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Étude ECMM *Candida* III

multicentrique observationnelle

***N*=399 isolats**

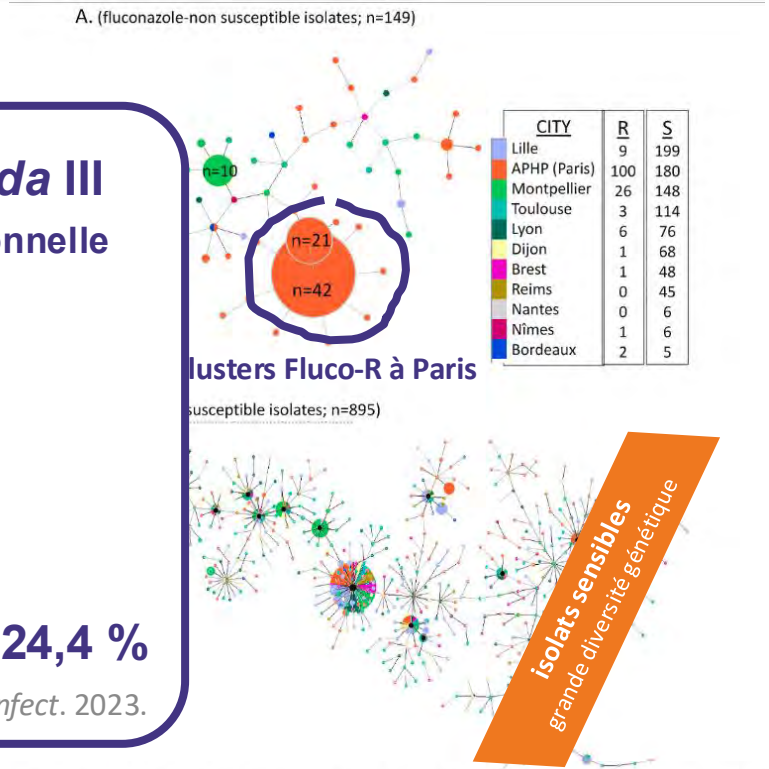
Proportion Fluco-R = 24,4 %

Arendrup M *et al. J Infect*. 2023.

- 15 centres hospitaliers fr
- Mai 2022 – Février 2024
- 2602 isolats *C. parapsilosis* (*n*=1850 patients)

☞ **15,1 % résistants**

Fekkar A *et al. New Microbes New infect.* 2026 ; **71** : 101738



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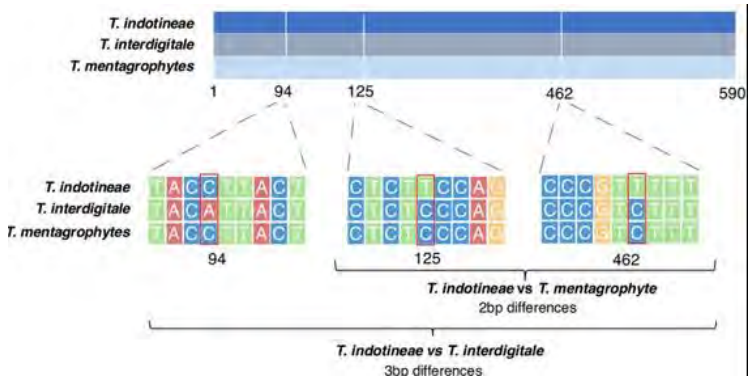
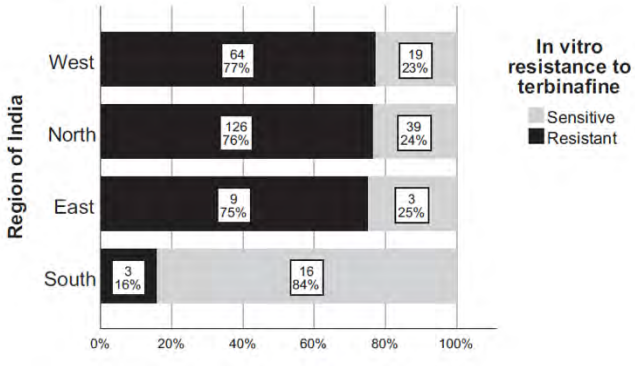
Arrivée de *Trichophyton indotinae* (ex- T. *mentagrophytes* génotype VIII)

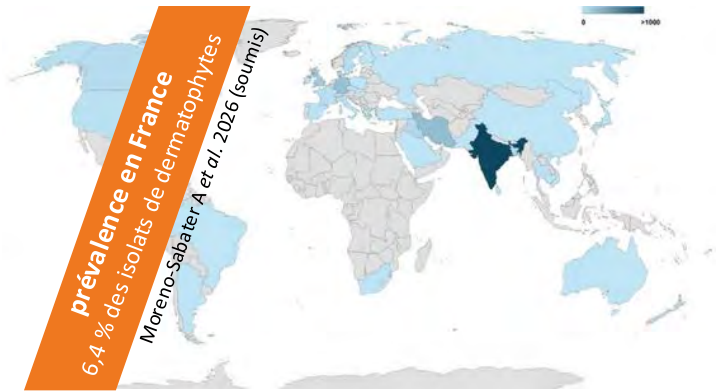
Verma SB *et al. Indian J Dermatol Venereol Leprol*. 2021 ; **87** (2) : 154-75



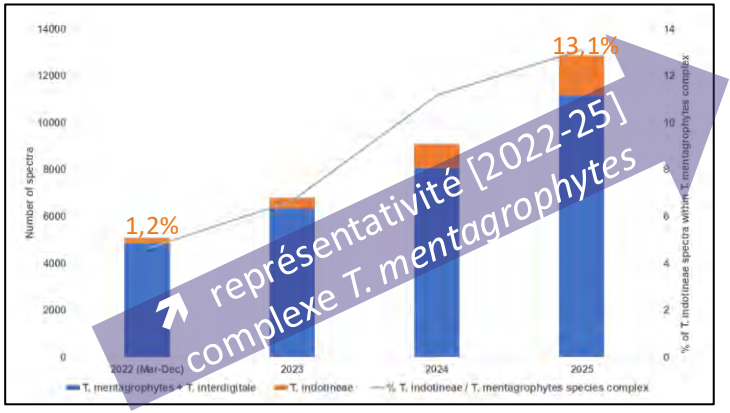
Gupta Ak *et al. J Eur Acad Dermatol Venereol.* 2026 ; **40** (1) : 29-45



Ebert T *et al. Mycoses*. 2020 ; 63 (7) : 717-28



Ortiz B *et al. Mycoses.* 2026 ; **69** (4) : e70170



Jabet A *et al* and Fekkar A. *Emerg Infect Dis* 2026 *in press.* 2026

L'exemple symbolique d'*Aspergillus fumigatus*

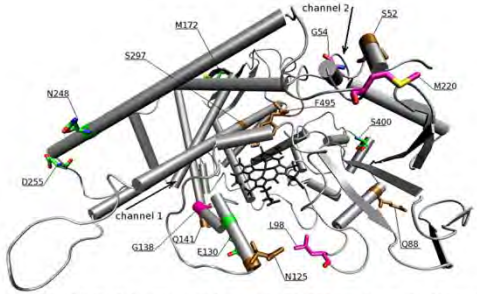


FIG. 2. Mapping of mutations found in the *A. fumigatus cyp51A* gene in the CYP51A homology model. The two ligand access channels are indicated by arrows. The heme cofactor is black. Mutations correlated with azole resistance are purple, and mutations correlated with an azole-susceptible profile are green. Mutations additionally found in azole-resistant strains are brown.

Snelders E *et al. Antimicrob Agents Chemother.* 2010 ; **54** (6) : 2425-30

prévalence pour les souches cliniques
= 9,2 % en France

rapport CNRMA 2025

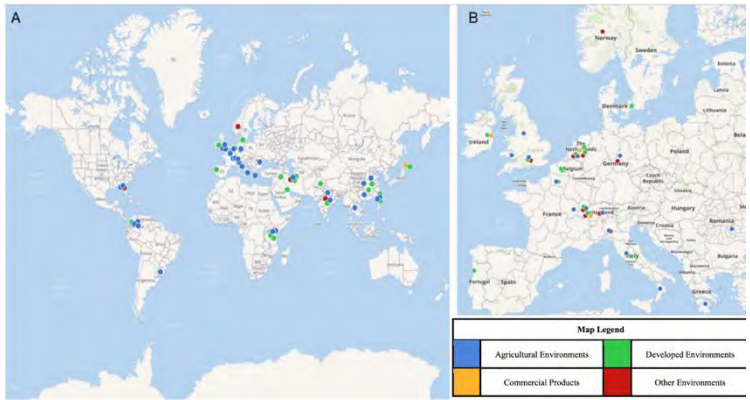
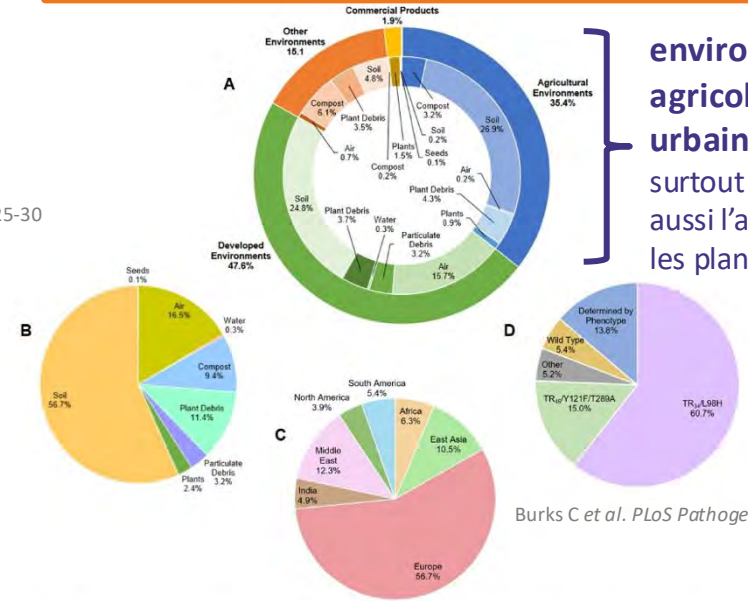


Fig 1. Azole-resistant *Aspergillus fumigatus* in the environment detected throughout **(A)** the world and **(B)** in Europe. The figure legend indicates different environmental settings from which resistant isolates were recovered. The digital map that includes additional environmental data, *cyp51A* alleles, and links to the published articles for each isolate can be found at https://maphub.net/cburks817/AfumMap. The base layer of the map can be found at https://maphub.net/map.



environnements agricoles mais aussi urbains
surtout dans le sol, mais aussi l'air, le compost et les plantes

Burks C *et al. PLoS Pathogens.* 2021 ; **17** (7) : e1009711

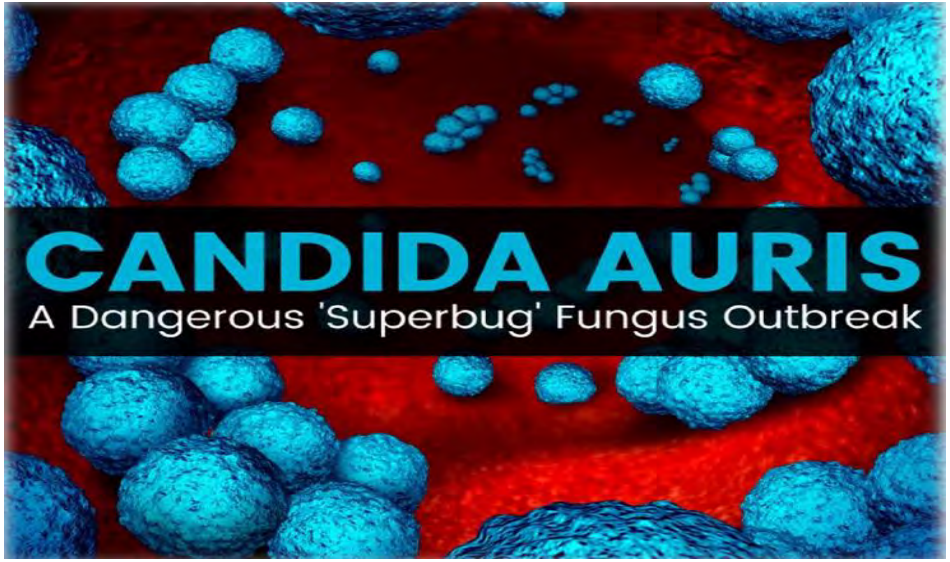
Fig 2. Frequency of azole-resistant *Aspergillus fumigatus* isolates detected in the environment by **(A)** environmental setting and substrate sampled, **(B)** substrate sampled across all environmental settings, **(C)** geographic region, and **(D)** *cyp51A* allele ("Other" includes less frequently detected *cyp51A* alleles and "Determined by Phenotype" includes resistant isolates that were not analyzed for *cyp51A* polymorphisms (S1 Table)).

L'exemple symbolique d'*Aspergillus fumigatus*

projet SporeWatch

Des actions de recherche et de prévention en cours dans le territoire …

WANTED



grandes capacités d'adaptation !!

profite de ≠ facteurs favorisant sa dissémination

- **durée d'hospitalisation prolongée**
- **patients lourds**
- **réalité du quotidien**
  - difficultés RH
  - impossibilité de fermer les services
  - possible méconnaissance

et peut-être bientôt d'autres micromycètes émergents (très) résistants…

ex. : *Trichosporon austroamericanum* (72 IFI en chir cardio-thoracique depuis 2015 dans 14 hôpitaux)

A consulter sans modération …

SF2H
Prévention du Risque Infectieux

Société française d'Hygiène Hospitalière

INSTITUT Pasteur

Centre National de Référence
Mycoses Invasives et Antifongiques

SFMM
Société Française de Mycologie Médicale

Société Française de Mycologie Médicale

Avis relatif à la conduite à tenir devant un cas de colonisation ou d'infection à *Candidozyma auris*

27/04/2026

Cet avis élaboré sur la base des connaissances disponible… …ation, est susceptible d'évoluer en fonction des nouvelles données.

Participants au gr…

Coordination : FOURNIER Sandra
Membres :
Centre national de référence des mycoses invasi… …ALANIO Alexandre, DESNOS-OLLIVIER Marie, LANTERNIER Fanny
Société française de mycologie médicale : BO… …OUBEAUX Guillaume
Société française d'hygiène hospitalière … …SSIER Pierre, DANANCHÉ Cédric, DECOUSSER Jean-Winoc, FLORENTIN A… …andra, JANVIER Frédéric, LOCHER Gwenaelle, MELLON Guillaume

G… …re

BROCHART Julie, COPPRY Maïder, DA… …ARD Juliette, JOLIVET Sarah, KAMUS Laure, KEITA-PERSE Olivia, KERNEIS Solen… …MARKIEWICZ-MASSY Amélie, ORY Jérôme, ROMANO-BERTRAND Sara, SOUYR…

MERCI !!