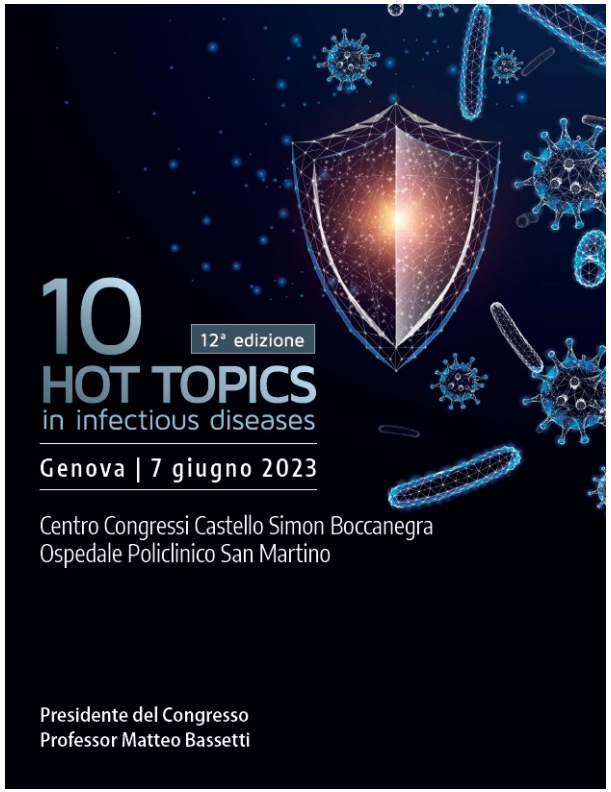

Candida auris: un nemico di tutti gli ospedali?

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OSPEDALE POLICLINICO SAN MARTINO
Sistema Sanitario Regione Liguria
Istituto di Ricovero e Cura a Carattere Scientifico

Disclosures

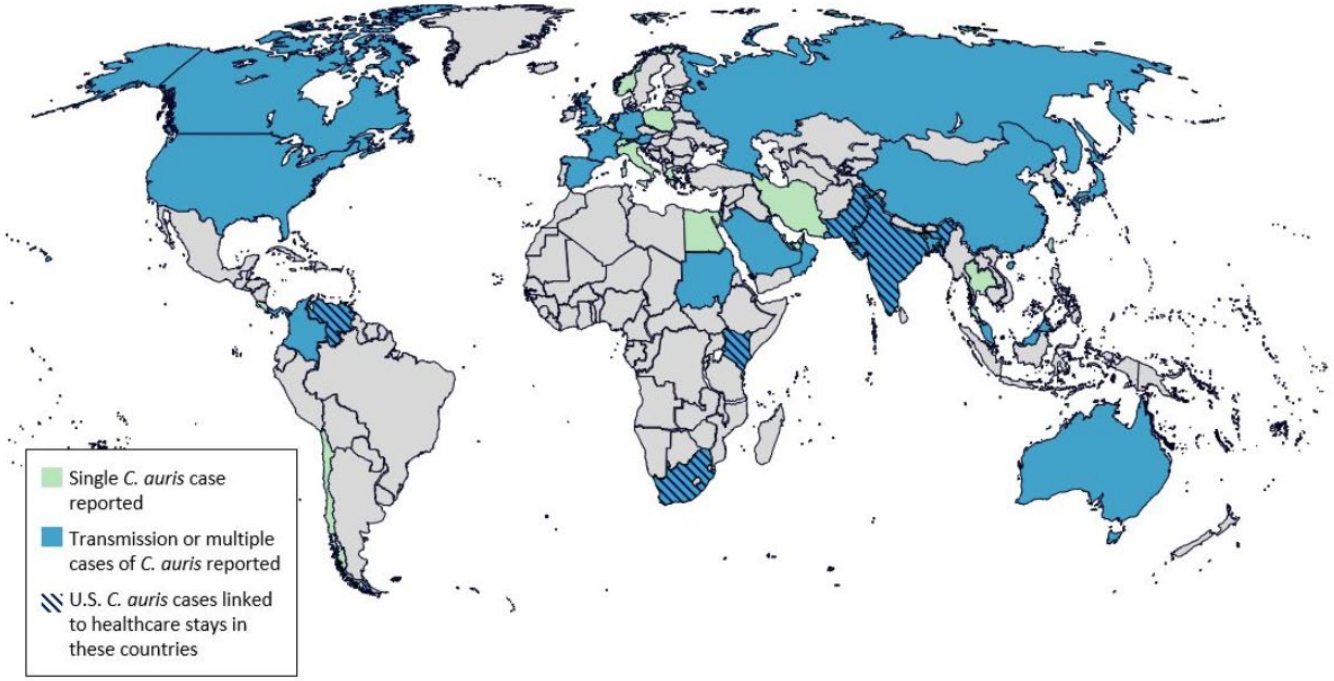
Lecture fees and board meeting fees from:

- Gilead
- Janssen
- MSD
- Mundipharma
- Pfizer

None related to this presentation

Epidemiology

- First cases reported in 2009 in 2006 isolates
- **1996 - the earliest known occurrence of *C. auris***
- The first known case of *C. auris* infection imported in **2007** in **Europe** from India (prior to the 2009 description in Japan)
- CDC: As of February 15, 2021 this map is no longer being updated given how widespread *C. auris* has become (46 counties)



Cases on July 30th 2020

Forseberg et al. Medical Mycology, 2018; Desnos-Olliviera et al. Journal of Medical Mycology 31, 2021

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

RAPID COMMUNICATION

Increasing number of cases and outbreaks caused by *Candida auris* in the EU/EEA, 2020 to 2021

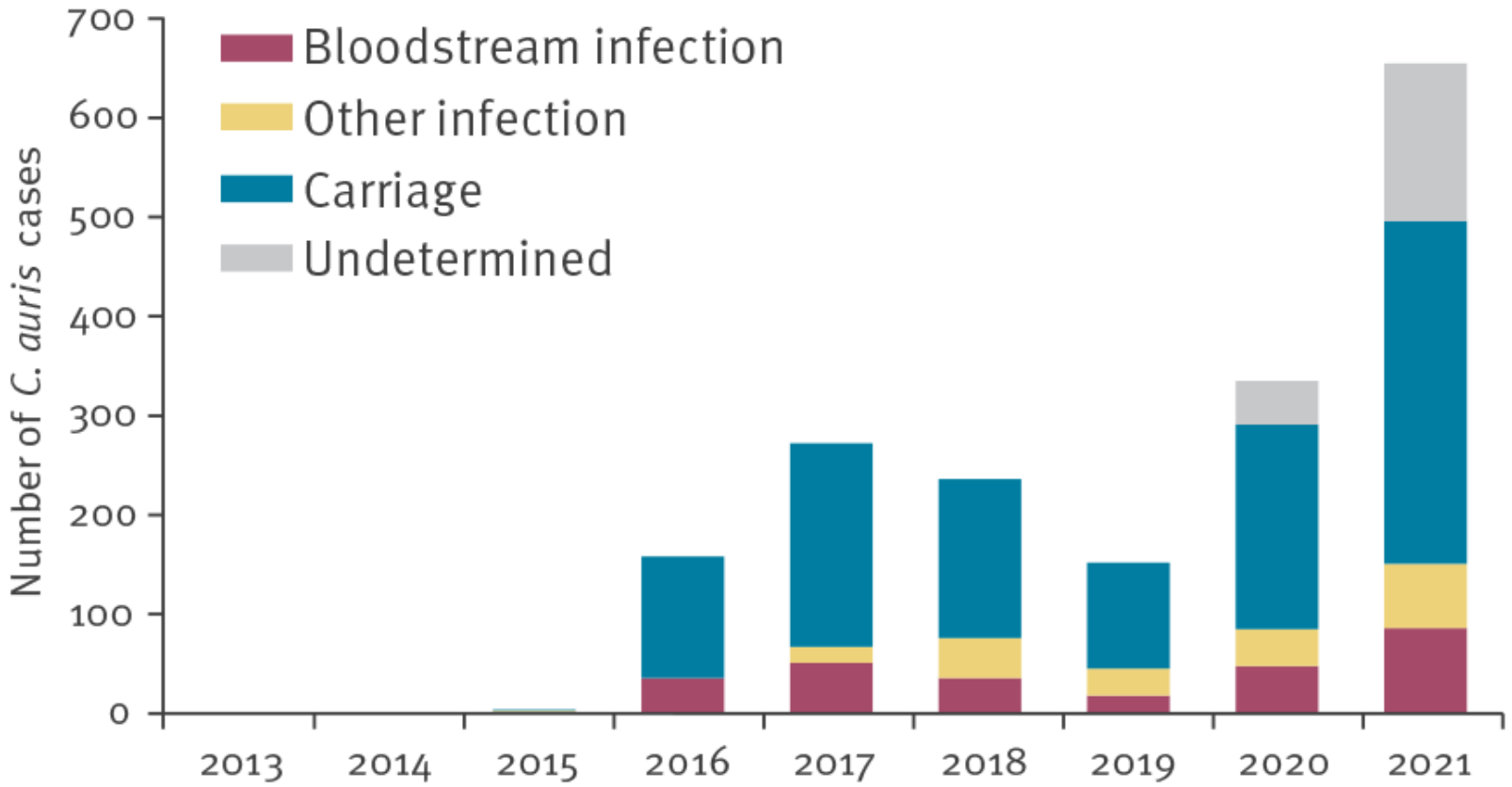
Anke Kohlenberg[1] , Dominique L Monnet[1] , Diamantis Plachouras[1] , *Candida auris* survey collaborative group[2]
1. European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
2. The members of the *Candida auris* survey collaborative group are listed under Collaborators and at the end of the article

Correspondence: Anke Kohlenberg (anke.kohlenberg@ecdc.europa.eu)

Collaborators: The collaborators are listed at the end of the article.

Citation style for this article:
Kohlenberg Anke, Monnet Dominique L, Plachouras Diamantis, Candida auris survey collaborative group. Increasing number of cases and outbreaks caused by Candida auris in the EU/EEA, 2020 to 2021. Euro Surveill. 2022;27(46):pii=2200846. https://doi.org/10.2807/1560-7917.ES.2022.27.46.2200846

Article submitted on 28 Oct 2022 / accepted on 14 Nov 2022 / published on 17 Nov 2022



- 2019 – 2021
- 5 countries (Denmark, France, Germany, Greece and Italy) reported 14 *C. auris* outbreaks, defined as ≥ 2 cases with an epidemiological link
- Total of 327 affected patients

RAPID COMMUNICATION

Increasing number of cases and outbreaks caused by *Candida auris* in the EU/EEA, 2020 to 2021

Anke Kohlenberg[1] , Dominique L Monnet[1] , Diamantis Plachouras[1] , *Candida auris* survey collaborative group[2]
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Article submitted on 28 Oct 2022 / accepted on 14 Nov 2022 / published on 17 Nov 2022

Epidemiological stages of *C. auris*

Stage 0: No cases of C. auris infection or colonisation have been detected.

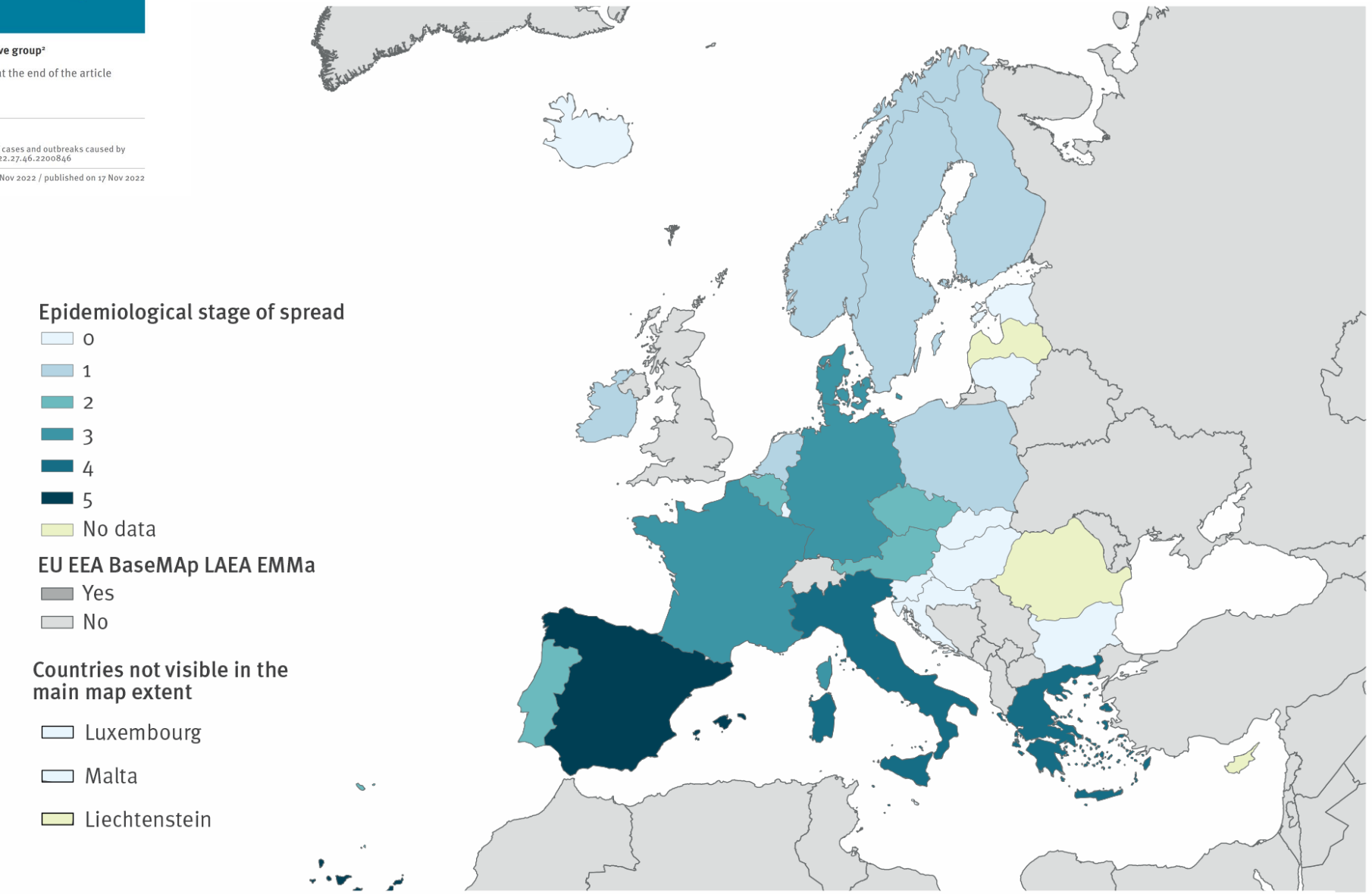
Stage 1: Only imported cases of C. auris have been detected.

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).



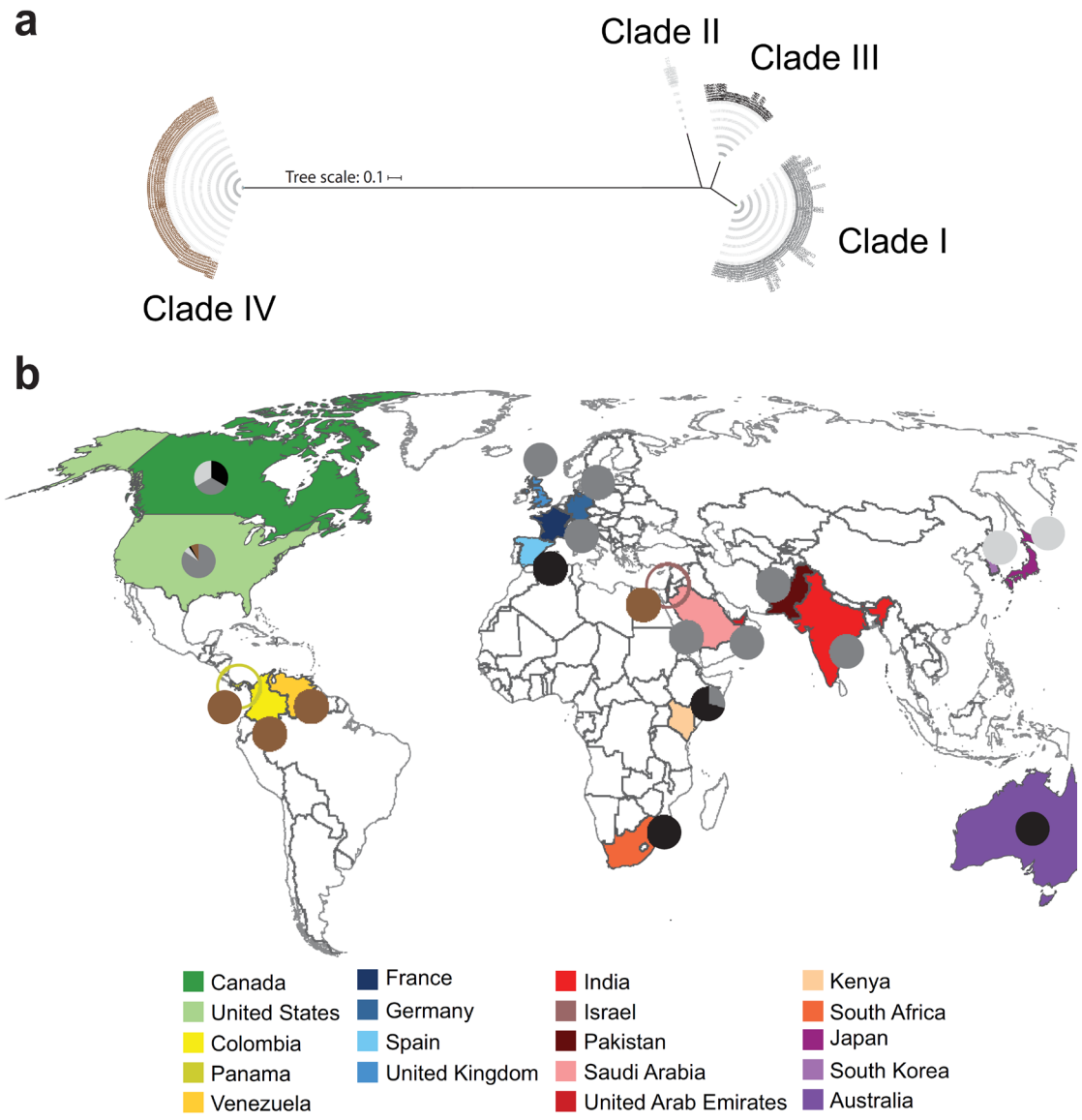
Nov 2021-Dec 2022: 64 Italian cases outside Liguria

Global spread

5 distinct geographical phylogenetic clades documented by WGS

- **Clade I - South Asian**
- Clade II, East Asian
- Clade III, South African
- Clade IV, South American
- Clade V, Iran

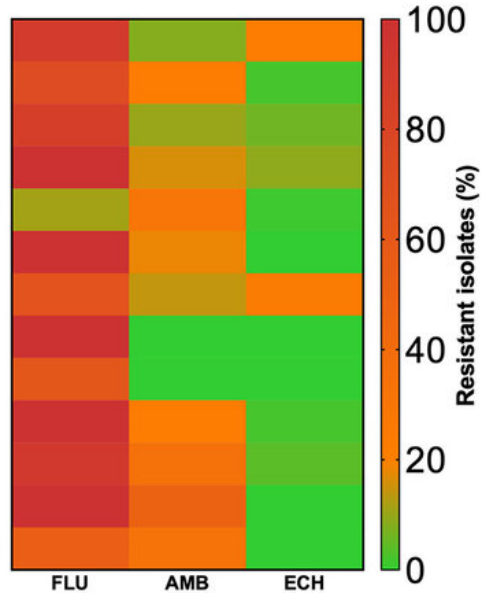
- Multiple introductions of *C. auris* into the US and UK, followed by local transmission

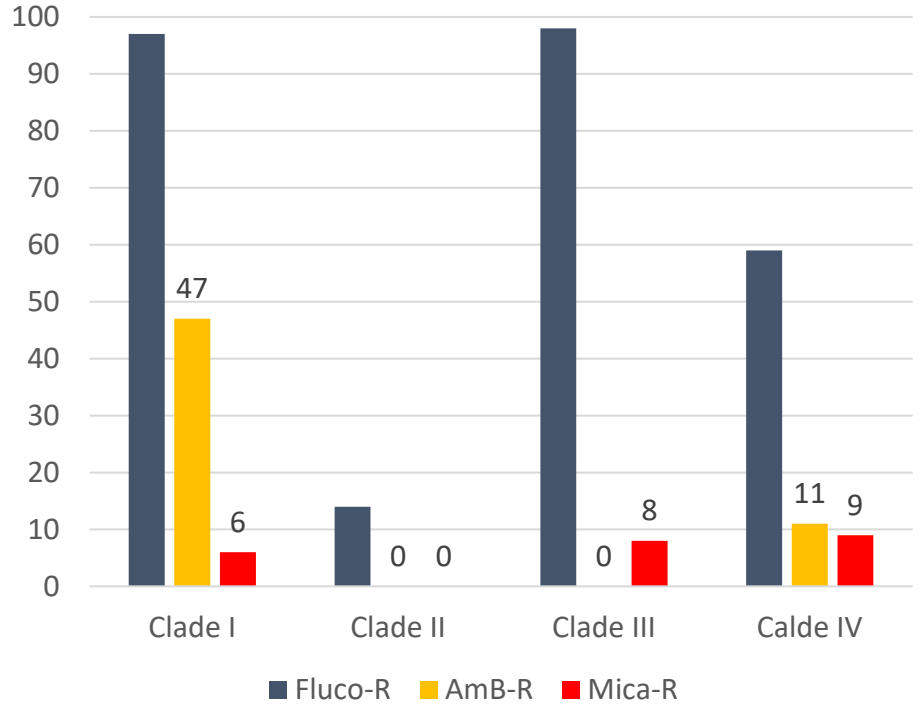


Chow NA, et al. 2020. Tracing the evolutionary history and global expansion of Candida auris using population genomic analyses. mBio 11:e03364-19. https:// doi.org/10.1128/mBio.03364-19; Garcia-Bustos, V. et al. What Do We Know about Candida auris? State of the Art, Knowledge Gaps, and Future Directions. Microorganisms 2021, 9, 2177. https://doi.org/10.3390/ microorganisms9102177

Antifungal resistance rates and clades

Reference	Country (no. of isolates)	Method
(8)	India (350)	CLSI
(39)	United Kingdom[a] (119-128)	CLSI
(72)	India[*] (123)	CLSI
(11)	India (90)	CLSI
(14)	Colombia (87)	CLSI, Etest for AMB
(13)	United Kingdom[#] (73-79)	SYO
(32)	India (74)	CLSI
(10)	Spain (73)	EUCAST
(2)	Korea[#] (61)	CLSI
(9)	Kuwait (56)	Etest
(4)	Multiple[b] (54)	CLSI
(12)	Venezuela (18)	CLSI
(1)	Korea (15)	CLSI, Etest for AMB





Chow NA, et al. 2020. Tracing the evolutionary history and global expansion of Candida auris using population genomic analyses. mBio 11:e03364-19. https:// doi.org/10.1128/mBio.03364-19

A case of in vivo development of high-level AmB resistance **during therapy** was reported and a novel mechanism mutation in the *C. auris* sterol-methyltransferase gene ERG6 was found (Rybak, Barker et al. 2022).

Ryan Kean, Gordon Ramage, Combined Antifungal Resistance and Biofilm Tolerance: the Global Threat of *Candida auris,* mSphere, 2019

Rapid communication

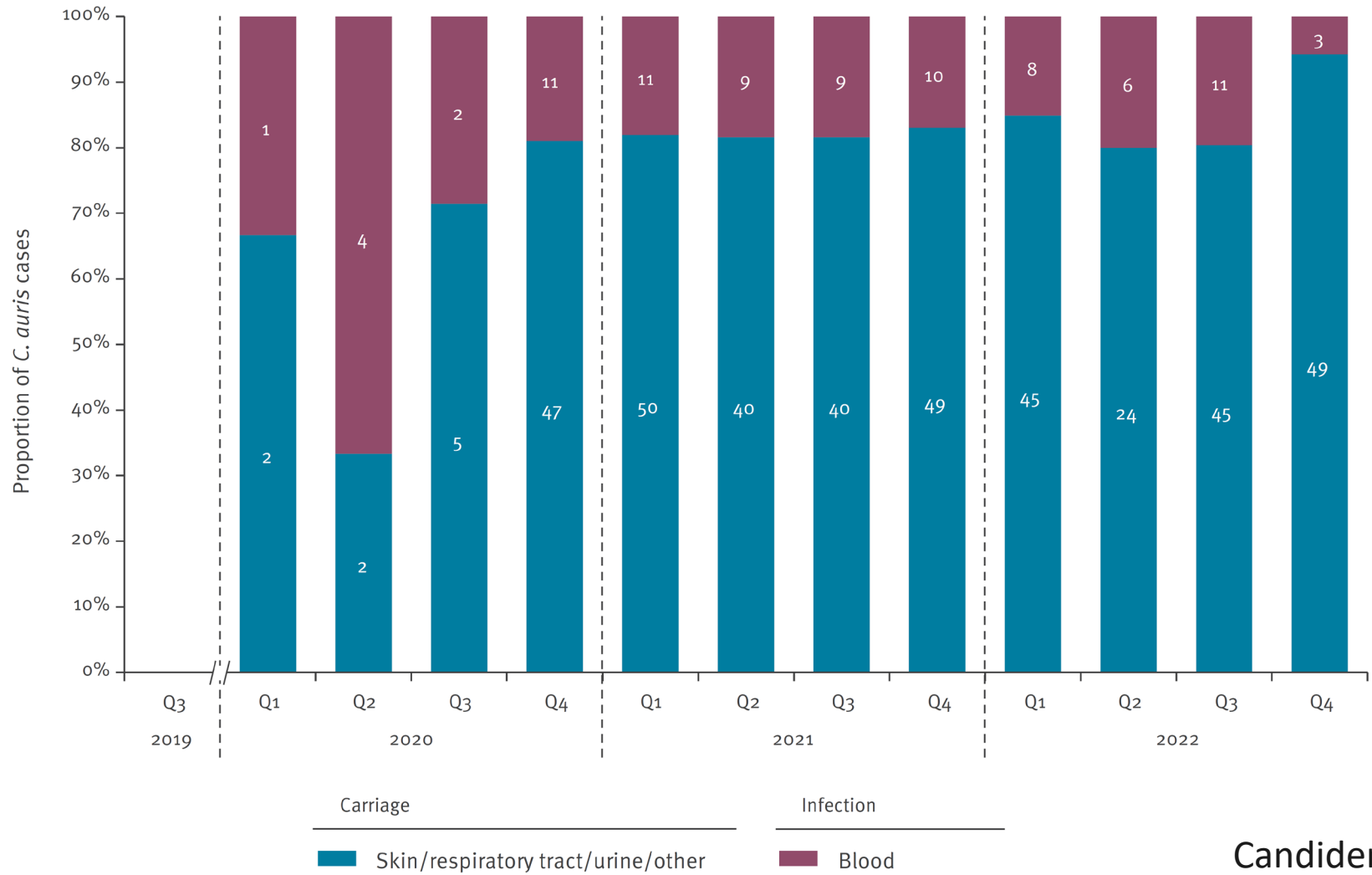
In vivo evolution to echinocandin resistance and increasing clonal heterogeneity in *Candida auris* during a difficult-to-control hospital outbreak, Italy, 2019 to 2022

Giulia Codda[1], Edward Willison[2], Laura Magnasco[3], Paola Morici[2], Daniele Roberto Giacobbe[3,4], Antonella Mencacci[5,6], Daniele Marini[5,6], Malgorzata Mikulska[3,4], Matteo Bassetti[3,4], Anna Marchese[1,2], Vincenzo Di Pilato[1]

- A difficult-to-control outbreak of *Candida auris* is ongoing in a large tertiary care hospital in Liguria, Italy
- July 2019 – December 2022: 503 cases of *C. auris* carriage or infection
- Genomic surveillance identified
  - putative cases that no longer occurred as part of one defined outbreak
  - the emergence of echinocandin (pandrug) resistance following independent selection of *FKS1*S639F and *FKS1*F635Y mutants upon prolonged exposure to caspofungin and/or anidulafungin

Codda G, et al. Euro Surveill. 2023 Apr;28(14).

B. Candidaemia after carriage

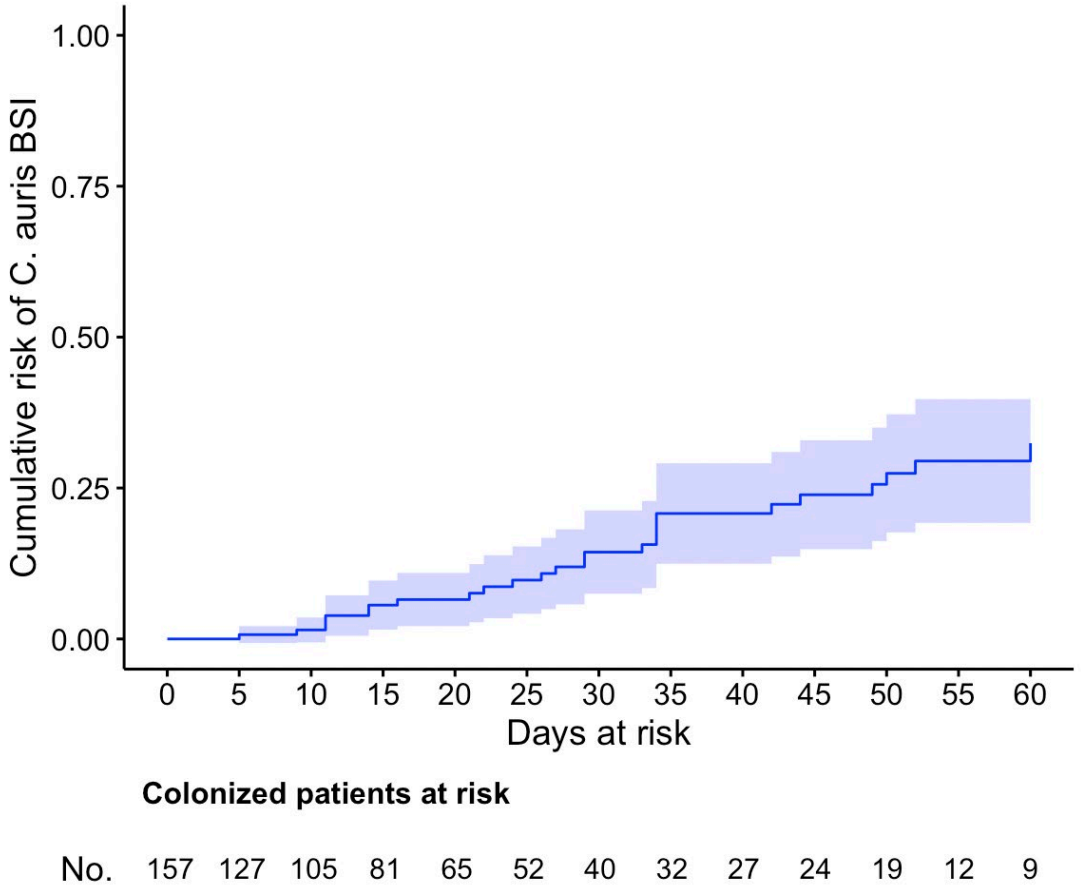


Candidemia
85/483 (17.6%)

Q: calendar quarter; WGS: whole genome sequencing.

Panel B shows the case numbers on the columns.

Risk of *C. auris* candidemia in colonised patients



27/157 (17%) patients developed at least one episode of *C. auris* candidemia, after a median of 29 days (IQR 15–38) from the first detection of colonization

Independent predictors

- Previous ICU stay in days

HR 1.01, 95%CI 1.00–1.03 p=0.075

- CRRT

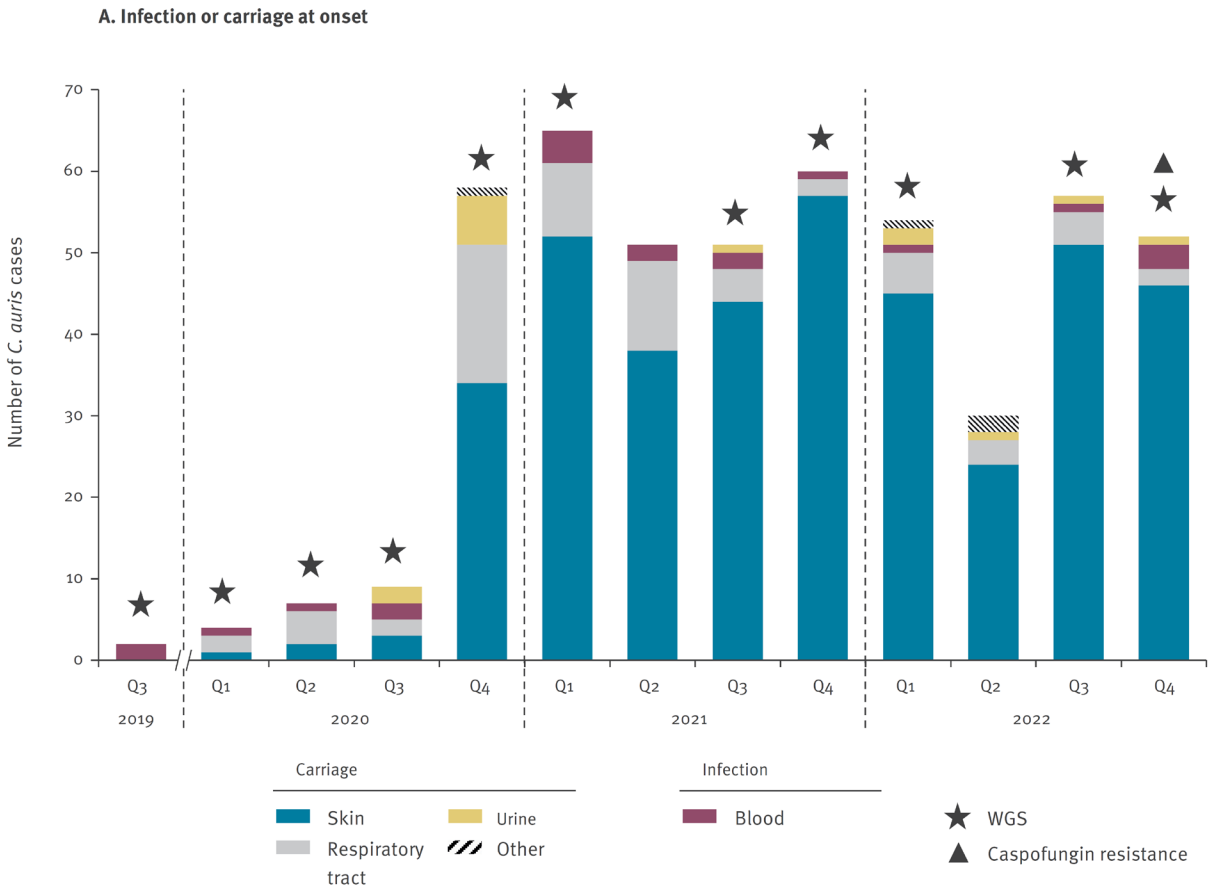
HR 2.23, 95%CI 0.98–5.07 p=0.056

- Multisite colonisation

HR 9.67 , 95%CI 1.30–71.91 p=0.027

Figure 1 legend. Cumulative risk of *Candida auris* candidemia in colonized ICU patients. The risk was estimated by means of the Aalen-Johansen method, with the first occurring *C. auris* candidemia as the event of interest, death as a competing event, and discharge from the ICU as a right-censoring event. ICU, intensive care unit.

Briano et al. Infect Dis Ther (2022) 11:1149–1160



Codda G, et al. Euro Surveill. 2023 Apr;28(14).

WGS investigations on 32 *C. auris* isolates

- 2 isolates resistant to echinocandins,
- 7 isolates from patients with confirmed *C. auris* carriage/infection from samples collected within 0–24h since hospital admission (i.e. suspected epidemiologically unrelated cases)
- 23 isolates representative of the outbreak timespan

- In 18 cases isolates cultured from a different specimen from the same patient were also characterized to allow for pairwise genomic comparison between echinocandin-susceptible and -resistant isolates and between surveillance and clinical isolates (mean separating days: 38 ± 40; median: 23; IQR: 12–64).

How long does it take to get colonised?

Clonal heterogeneity

All clade I (South Asian), subclade Ic

- 18 double isolates (colonization + infection) - uniformly low values of separating SNPs (mean: 4 ± 4; median: 3; IQR: 2–6)

- 7 isolates from patients with *C. auris* carriage/infection from samples collected within 0–24h from hospital admission (i.e. suspected epidemiologically unrelated cases)
  - 5/7 had markedly higher values of separating SNPs: mean: 14 ± 3; median: 13; IQR: 12–16)
  - 4/5 patients had a recent history of contact with the healthcare system or transfer to our institution from other hospitals
  - 2/7 no history of previous hospital, lower SNP difference (mean: 6 ± 4; median: 6; IQR: 4–9)

- Further estimation of the overall clonal heterogeneity excluding the five cases suspected to be epidemiologically unrelated yielded values of separating SNPs (mean: 5 ± 2, median: 5; IQR: 4–7) similar to those previously inferred as baseline genomic diversity (mean: 4 ± 4; median: 3; IQR: 2–6).

Codda G, et al. Euro Surveill. 2023 Apr;28(14).

Table 2

In vitro antifungal susceptibility profiles of the sequential caspofungin-susceptible and resistant Candida auris isolates associated with different FKS1 genotypes, Italy, 2019–2022 (n = 2)

	Patient A		Patient B	
FKS1 genotype	WT	F635Y	WT	S639F
Antifungal agent	MIC			
Caspofungin	0.06	>8	0.25	2
Anidulafungin	0.125	2	0.5	4
Micafungin	0.125	2	0.125	>8
Days to candidaemia from hospital admission	29		95	
Days to candidaemia from first C. auris colonisation	23		74	
Previous echinocandin exposure[a]	Cumulative days			
Anidulafungin	19		23	
Caspofungin	None		58	

MIC: minimum inhibitory concentration; WT: wild type.

[a] Exposure to caspofungin preceded that with anidulafungin in patient B.

MIC range, MIC50, MIC90 values reported as mg/L.

- Prolonged exposure to echinocandins due to intraabdominal candidiasis after abdominal surgery
- Resistant isolates emerged after 19 (Patient A) and 74 (Patient B) days of echinocandin exposure, during anidulafungin therapy
- Both successfully treated with L-AmB + flucytosine (Patient A) and L-AmB (Patient B)

Table 1

In vitro antifungal susceptibility profiles of Candida auris isolates characterised in this study, Italy, 2019–2022 (n = 60)

Antifungal agent	MIC range	MIC50	MIC90	CDC*	ECV
Fluconazole	>256	>256	>256	≥32	
Itraconazole	0.25 to 2	0.5	1	?	
Voriconazole	2 to 4	2	4	?	0.5**/2
Posaconazole	0.25 to 1	0.25	0.5	?	0.25**/1
Isavuconazole	1 to 2	1	2	?	
Caspofungin	0.06 to >8	0.25	0.25	≥ 2	
Anidulafungin	0.125 to 4	0.25	0.5	≥ 4	
Micafungin	0.125 to >8	0.125	0.25	≥ 4	
Amphotericin B	1 to 4	4	4	≥ 2	

MIC: minimum inhibitory concentration.

MIC range, MIC50, MIC90 values reported as mg/L.

*CDC Tentative MIC Breakpoints (with CLSI method)
**Since no CDC tentative breakpoints for other triazoles were proposed, *C. glabrata* epidemiological cutoff values published by the CLSI (ECVs 1 µg/ml for posaconazole and 0.25 µg/ml for voriconazole) were applied in some studies (1,2) and one of them found that 31 tested isolates exhibited high rates of resistance to VRC but susceptibility to PSC (2)

1) Espinel-Ingroff A, et al. Antimicrob Agents Chemother 2014;58:2006–12. doi:10.1128/AAC.02615-13;
2) Ceballos-Garzon A, et al. Int J Antimicrob Agents. 2022 Apr;59(4):106558. doi: 10.1016/j.ijantimicag.2022.106558

Codda G, et al. Euro Surveill. 2023 Apr;28(14).

Antimicrobial Agents and Chemotherapy®

SUSCEPTIBILITY

Antifungal Resistance Trends of *Candida auris* Clinical Isolates in New York and New Jersey from 2016 to 2020

Shannon Kilburn,[a] Gabriel Innes,[b] Monica Quinn,[a] Karen Southwick,[c] Belinda Ostrowsky,[d] Jane A. Greenko,[e] Emily Lutterloh,[a,f] Rebecca Greeley,[b] Reed Magleby,[b] Vishnu Chaturvedi,[a] Sudha Chaturvedi[a,f]

1148

134

TABLE 1 Resistance and non-wild-type antifungals pattern of New York *C. auris* clinical isolates from 2016 through 2020

Year and total no. of isolates			2016 (28)	2017 (141)	2018 (231)	2019 (300)	2020 (448)	
Antifungal	CDC BP	ECV UL-WT	% (n) resistance/non-wild-type					*P* value
FLC	≥ 32	-	100% (28)	100% (141)	100% (231)	100% (300)	99.6% (446)	0.6393
ITC	-	2	0	0	0	0.7% (2)	0.2% (1)	0.666
ISA	-	2	0	7.1% (10)	0.9 (2)	0	9.2% (41)	$4.42e^{-12}$
POS	-	0.5	0	23.4% (33)	13.4% (31)	33% (99)	42.6% (191)	$2.2e^{-16}$
VRC	-	4	7.4% (2)	14.2% (20)	0.9% (2)	4.3% (13)	4.9% (22)	$3.94e^{-6}$
AFG	≥ 4	-	0	1.4% (2)	0.4% (1)	2.3% (7)	4% (18)	0.05707
CAS	≥ 2	-	0	1.4% (2)	0.4% (1)	2.3% (7)	4% (18)	0.05707
MFG	≥ 4	-	0	1.4% (2)	0.9% (2)	1.7% (5)	3.8% (17)	0.1549
AMB	≥ 2	-	82.1% (23)	75.9% (107)	48.1% (111)	45.3% (136)	51.3% (230)	$1.019e^{-9}$
5-FC	-	0.125	7.1% (2)	11.3% (16)	19.4% (31)[a]	-	-	0.0793

[a]160 of 231 *C. auris* isolates were part of testing due to discontinuation of 5-FC Etest strips in 2018.

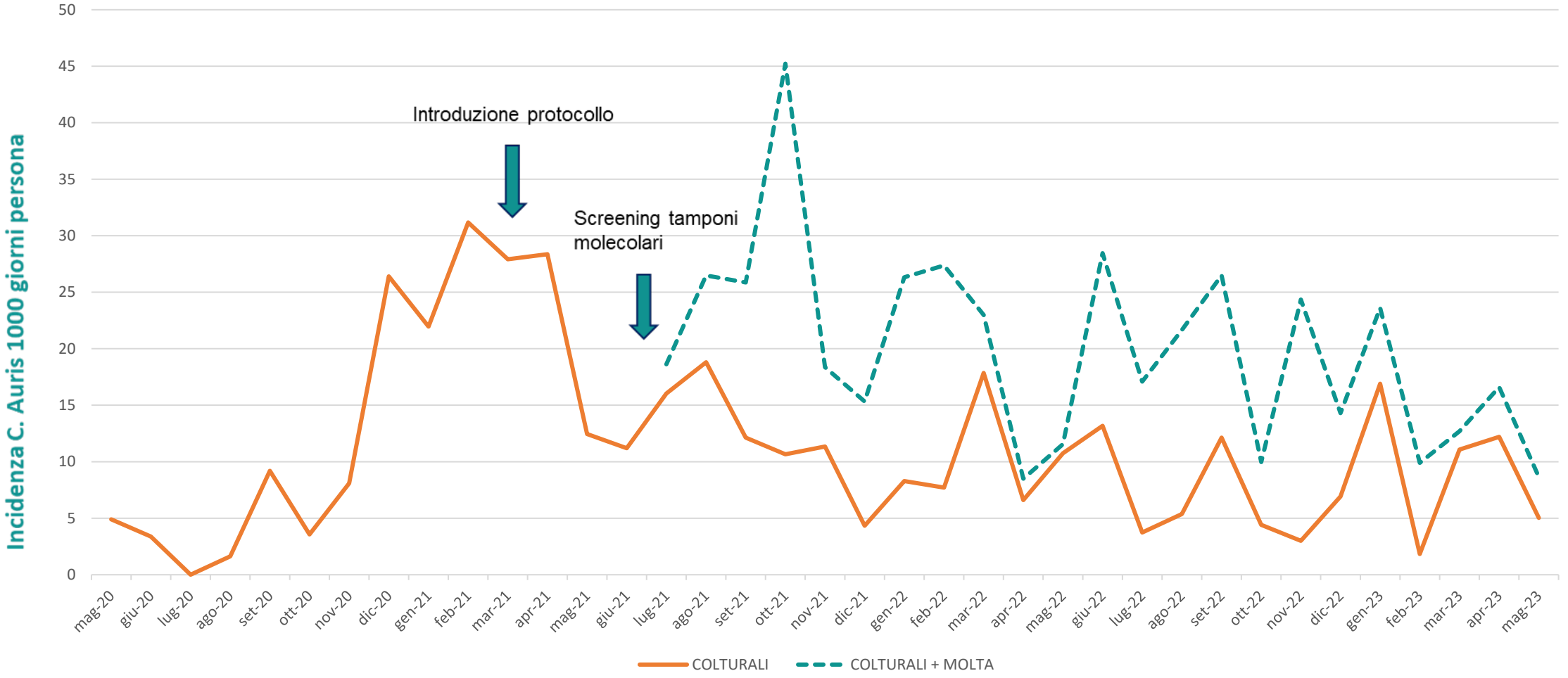
TABLE 2 Resistance and non-wild-type antifungals pattern of New Jersey *C. auris* clinical isolates from 2017 through 2020

Year and total no. of isolates			2017 (12)	2018 (13)	2019 (48)	2020 (61)	
Antifungal	CDC BP	ECV UL-WT	% (n) resistance/non-wild-type				*P* value
FLC	≥ 32	-	100% (12)	100% (13)	100% (48)	100% (61)	1
ITC	-	2	0	7.7% (1)	0	0	0.1852
ISA	-	2	0	7.7% (1)	0	14.8% (9)	0.01613
POS	-	0.5	0	15.4% (2)	18.7% (9)	47.5% (29)	0.0002489
VRC	-	4	8.3% (1)	7.7% (1)	2.1% (1)	4.9% (3)	0.3546
AFG	≥ 4	-	0	0	0	0	1
CAS	≥ 2	-	0	0	0	0	1
MFG	≥ 4	-	0	0	0	0	1
AMB	≥ 2	-	66.7% (8)	46.2% (6)	43.7% (21)	31.1% (19)	0.1108

ECV, epidemiological cutoff value was used to find upper limit of the wild type (UL-WT) values, which helps to identify non-wild-type strains

Espinel-Ingroff A, Turnidge J. The role of epidemiological cutoff values (ECVs/ECOFFs) in antifungal susceptibility testing and interpretation for uncommon yeasts and moulds. Rev Iberoam Micol. 2016 Apr-Jun;33(2):63-75

Incidenza nuovi rilevamenti C. auris presso **singolo reparto Terapia Intensiva e Rianimazione**, IRCCS Ospedale Policlinico San martino Genova, maggio 2020 – maggio 2023



Courtesy of Prof. A Orsi

Caratteristiche nuovi rilevamenti *C. auris* presso **singolo reparto Terapia Intensiva e Rianimazione**, IRCCS Ospedale Policlinico San martino Genova, maggio 2020 – maggio 2023

	PERIODO	
	Maggio 2020-Marzo 2021	**Agosto 2021-Maggio 2023**
Totale pazienti ricoverati in UTI (denominatore)	360	1116
Totale pazienti con *C. auris*	68 (18%)	**257 (23%)**
Candidemia	10 (15%)	44 (17%)
Età mediana (min-max)	61,5 (23-89)	63 (15-88)
Lunghezza mediana ricovero	55	39
COVID-19 co-infezione	35 (10%)	29 (2.6%)
Tempo dalla prima positività al decesso (mediana)	13	21
Decessi	30 (44%)	54 (21%)

Courtesy of Prof. A Orsi

Identificazione precoce dei casi di C. Auris

- Screening con tampone cutaneo (ascella e inguine bilateralmente) all'ingresso nel reparto e una volta alla settimana

Bundle of infection control interventions

1. screening for skin carriage (combined axilla and groin skin swab) at admission to ICU for early identification of possible community-acquired cases;
2. repeated weekly screening for carriage at skin, respiratory (whenever mechanically ventilated) and urine level during the ICU stay until first detection of *C. auris*;
3. implementation of strict contact precautions for colonized patients
4. screening for skin carriage upon when a *C. auris*-negative patient was discharged from the ICU and admitted to a different ward, with preventive contact precautions pending culture results;

Animal models to understand the mechanism of the heightened capacity of *C. auris* to colonize skin compared to other *Candida* species

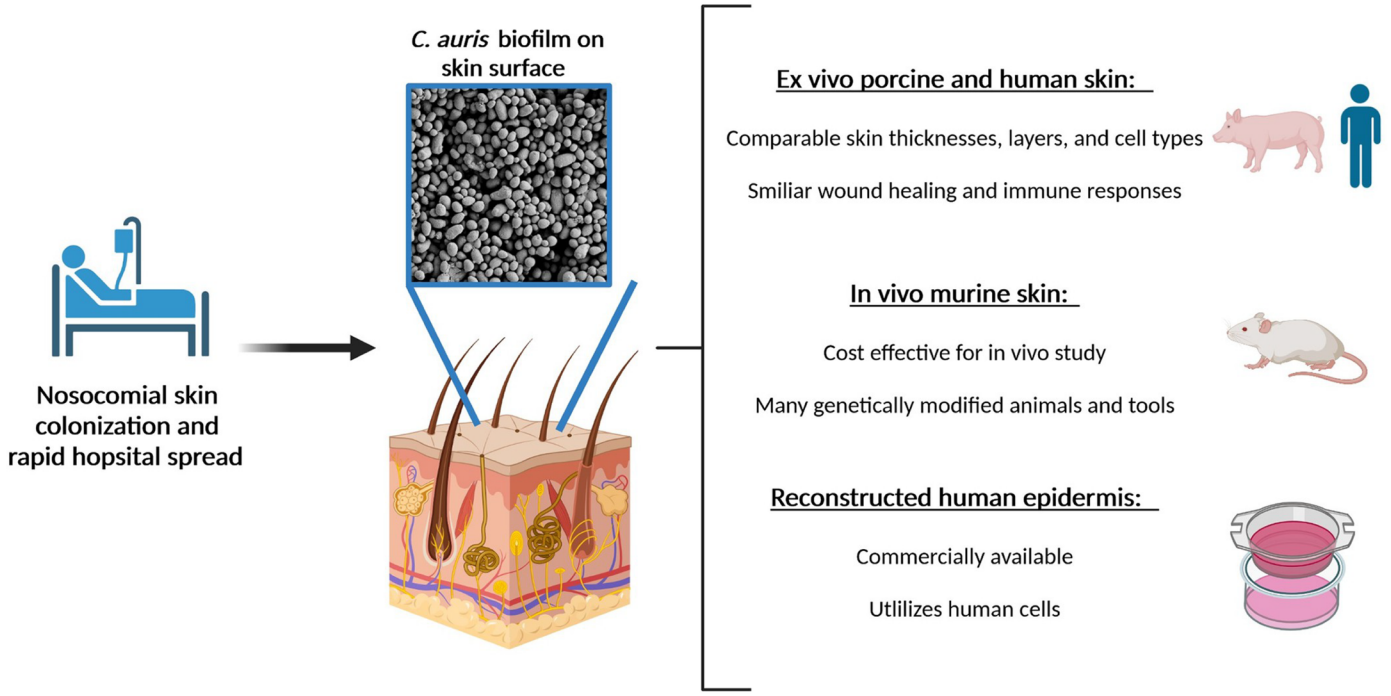


Fig 1. Modeling *C. auris* skin colonization. *C. auris* spreads rapidly in healthcare settings and proliferates on patient skin, leading to severe disease. Skin colonization can be modeled using ex vivo human and porcine skin, in vivo using mice, and with reconstructed human epidermis. Each of these models has its own advantages and limitations. *C. auris* biofilm growth on the surface of ex vivo human skin was imaged by scanning electron microscopy. Created with BioRender.com.

https://doi.org/10.1371/journal.ppat.1010730.g001

- In mouse and porcine skin models, ***C. auris* proliferates to burdens 10- to 100-fold greater than *C. albicans***
- Chlorhexidine treatment of porcine skin with C. auris colonization also reduces fungal burden, but **by a more modest amount** (0.5 log reduction) than in mice (2log)
- This is in contrast to in vitro conditions where similar chlorhexidine treatment leads to a 2 log reduction and typically eliminates in vitro regrowth
- **In both murine and porcine models, *C. auris* appears to reside in deeper tissues, such as the hair follicles**
- While chlorhexidine can reduce the burden of C. auris on skin, it **does not appear to eradicate** the organism, allowing for fungal regrowth and persistent colonization, mirroring clinical observations.

Eix EF, Nett JE (2022) Modeling *Candida auris* skin colonization: Mice, swine, and humans. PLoS Pathog 18(9): e1010730. https://doi.org/10.1371/journal.ppat.1010730

Post-discharge infection control

- Patients who are colonized or infected with *C. auris* should be **isolated until discharge and flagged for at least 1 year after the first negative screening culture**
- NY: Of 45 patients eligible **28 patients were serially negative (62%;** rate 5.1/100 person-months), at a median time from initial *C auris* of **8.6 months (IQR, 5.7–10.8 months)**
- Readmission of a previous *C. auris* -positive patient:
  - place in contact isolation and screened on 3 consecutive days
  - if all 3 screens negative, discontinue isolation but
  - screen weekly as *C. auris* may resurface after antibiotic therapy

Kenters et al. International Journal of Antimicrobial Agents 54 (2019) 400–406

American Journal of Infection Control 000 (2023) 1–5

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journal homepage: www.ajicjournal.org

Major Article

Candida auris admission screening pilot in select units of New York City health care facilities, 2017-2019

Jemma Rowlands MPH [a,*], Elizabeth Dufort MD, MPH [a], Sudha Chaturvedi PhD [b,d], YanChun Zhu MS [b],

ABSTRACT

Background: This pilot project implemented admission screening for *Candida auris* (*C. auris*) using real-time polymerase chain reaction (rt-PCR) in select high-risk units within health care facilities in New York City.

Methods: An admission screening encounter consisted of collecting 2 swabs, to be tested by rt-PCR, and a data collection form for individuals admitted to ventilator units at 2 nursing homes (NHA and NHB), and the ventilator/pulmonary unit, intensive care unit, and cardiac care unit at a hospital (Hospital C) located in New York City from November 2017 to November 2019.

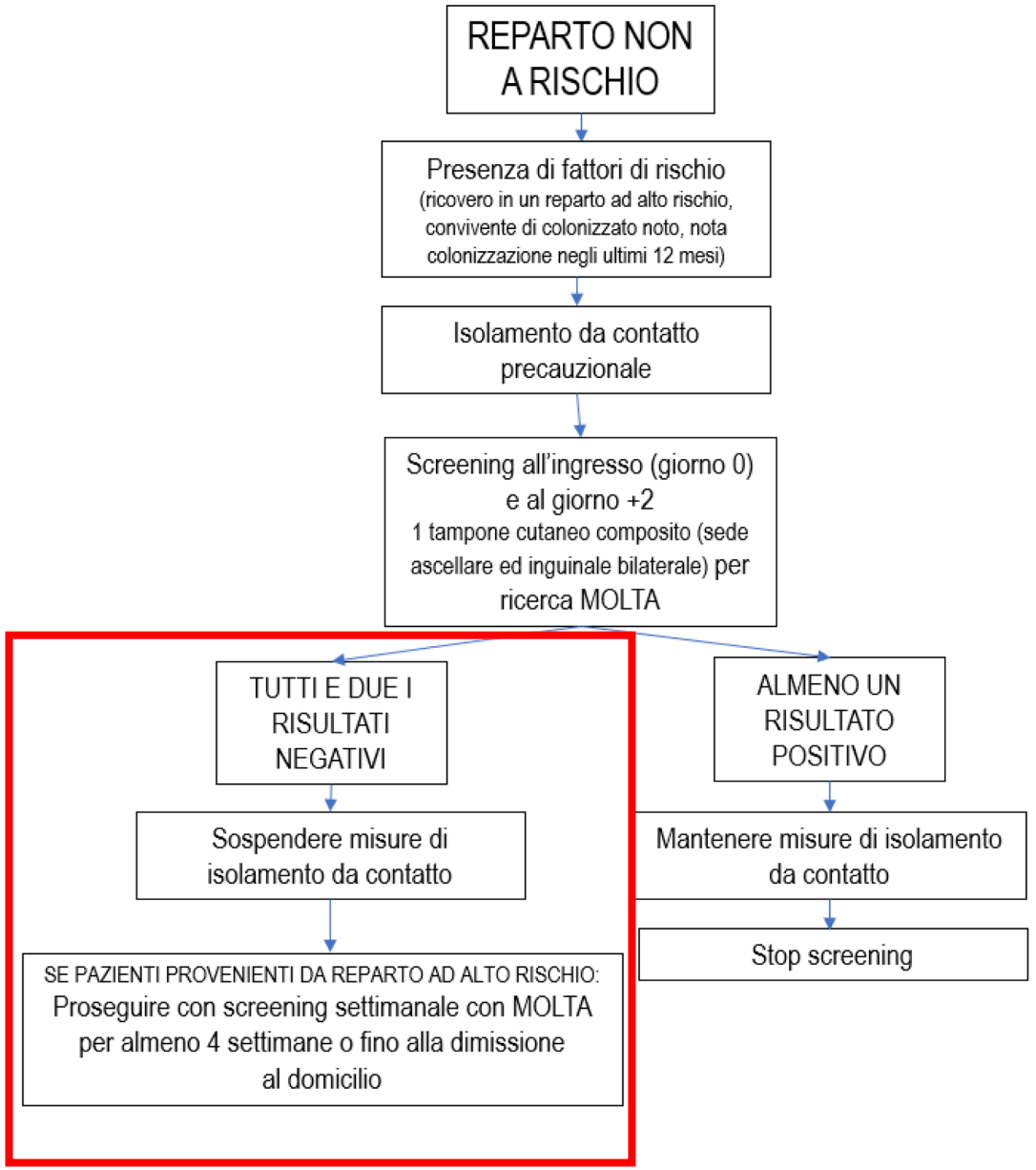
Results: *C. auris* colonization was identified in 6.9% (n = 188/2,726) of admissions to participating units. Rates were higher among admissions to NHA and NHB (20.7% and 22.0%, respectively) than Hospital C (3.6%). Within Hospital C, the ventilator/pulmonary unit had a higher rate (5.7%) than the intensive care unit (3.8%) or cardiac care unit (2.5%).

Discussion: Consistent with prior research, we found that individuals admitted to ventilator units were at higher risk of *C. auris* colonization.

Conclusions: This project demonstrates the utility of admission screening using rt-PCR testing to rapidly identify *C. auris* colonization among admissions to health care facilities so that appropriate transmission-based precautions and control measures can be implemented rapidly to help decrease transmission.

Limiting the damage

Preventing secondary horizontal transmissions outside the endemic settings



2022

NEJM Journal Watch

SUMMARY | INFECTIOUS DISEASES, HOSPITAL MEDICINE, GENERAL MEDICINE

INFORMING PRACTICE

Apr 28, 2023

Candida auris: Coming to a Health Care Facility Near You?

Daniel Kaul, MD

Annals of Internal Medicine

ORIGINAL RESEARCH

Worsening Spread of *Candida auris* in the United States, 2019 to 2021

Meghan Lyman, MD; Kaitlin Forsberg, MPH; D. Joseph Sexton, PhD; Nancy A. Chow, PhD, MS; Shawn R. Lockhart, PhD; Brendan R. Jackson, MD, MPH; and Tom Chiller, MD, MPHTM

Figure 1. Number of clinical and screening *C auris* cases reported to the Centers for Disease Control and Prevention during 2013 to 2021.

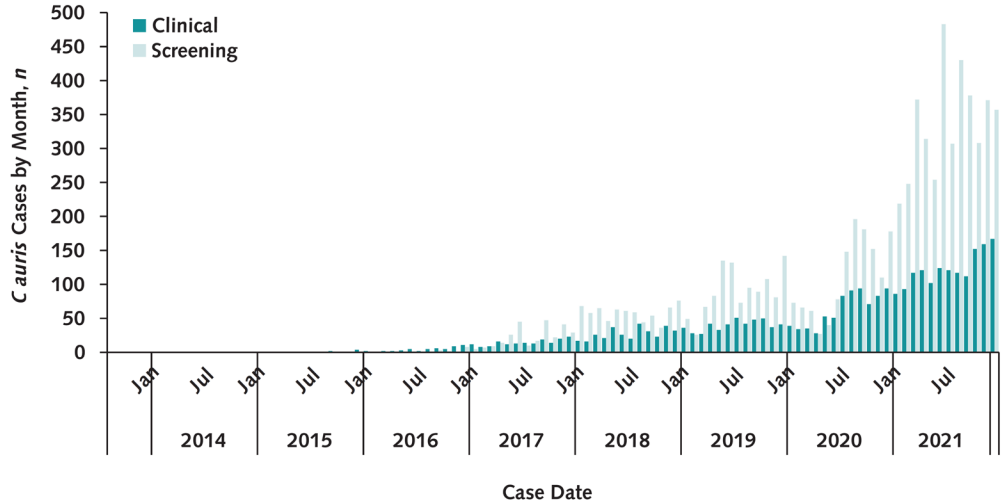


Figure 2. Volume of *C auris* screening through the Antimicrobial Resistance Laboratory Network, 2013 to 2021.

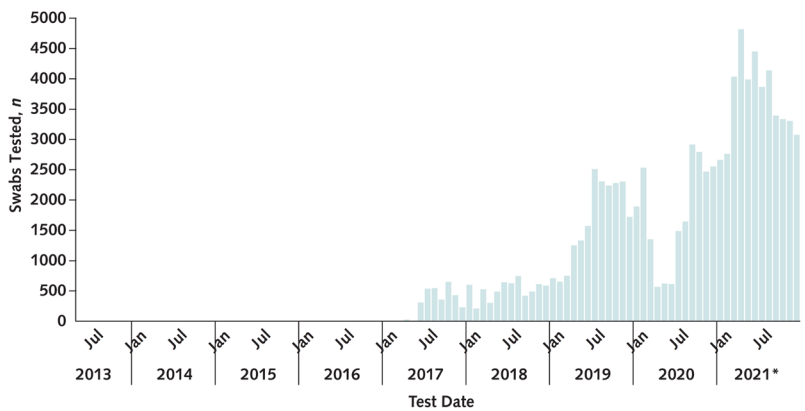
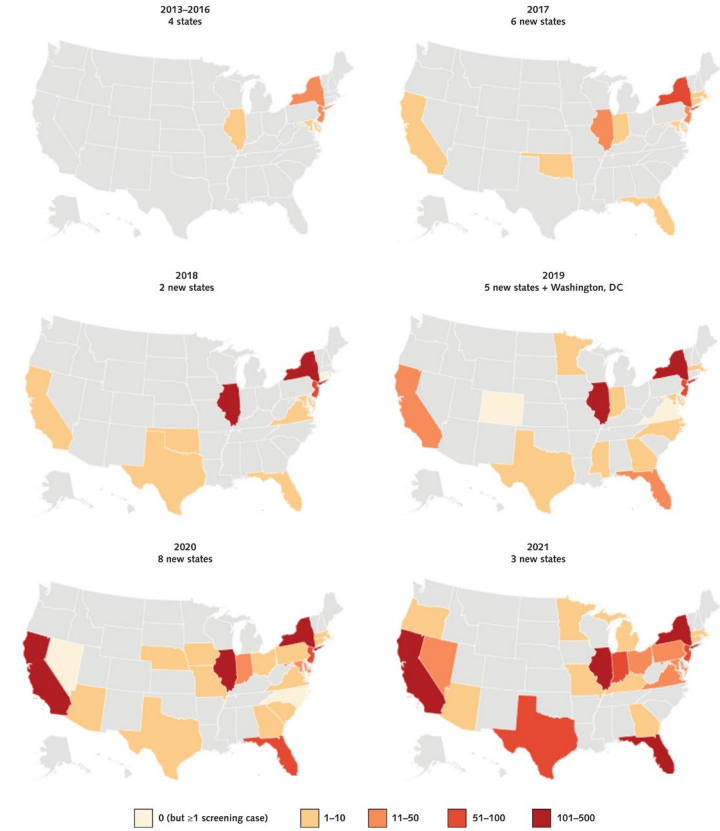
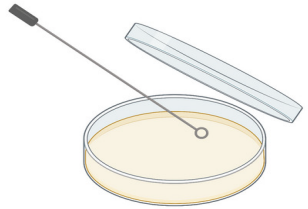


Figure 3. Geographic distribution of clinical *C auris* cases in the United States reported to the Centers for Disease Control and Prevention by state during 2013 to 2021.



- 3270 clinical cases and 7413 screening cases of *C. auris* were reported in the US until 31/12/2021
- Colonization screening volume and screening cases increased
- The number of *C. auris* cases that were resistant to echinocandins in 2021 was about 3 times that in each of the previous 2 years (1.2% in 2020)

Expert recommendations for prevention and management of Candida auris transmission



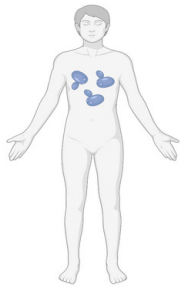
(A) Laboratory

A.1 Identify *C. auris* by MALDI-TOF

A.2 Perform susceptibility testing for all *C. auris* isolates

A.3 Identify all yeasts from high-risk patients to the species level

A.4 Submit all *C. auris* isolates to NRZMyk



(B) Single Patient

B.1 Isolate *C. auris* patient in a single room

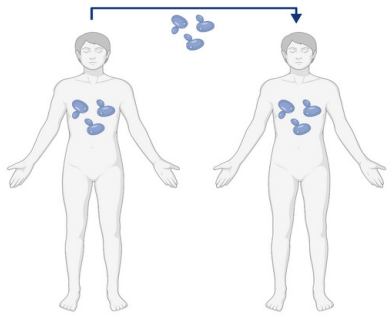
B.2 Ensure appropriate protection equipment, hand hygiene and 1:1 care

B.3 Inform / teach staff about *C. auris*

B.4 Amend disinfectant procedures

B.5 Treat only clinically relevant infection

B.6 Screen close contacts for *C. auris*



(C) Transmission

C.1 Set up a multi-disciplinary outbreak panel

C.2 Set up a work-flow for *C. auris* screening

C.3 Stop admissions of patients

C.4 Separate *C. auris* affected and non-affected patients

C.5 Test all patients in the unit for *C. auris*

C.6 Review and amend hygiene plans

C.7 Analyse potential transmission routes

C.8 Implement rules for de-isolation of patients

C.9 Perform long-term surveillance

Mycoses, Volume: 65, Issue: 6, Pages: 590-598, First published: 19 April 2022, DOI: (10.1111/myc.13445)

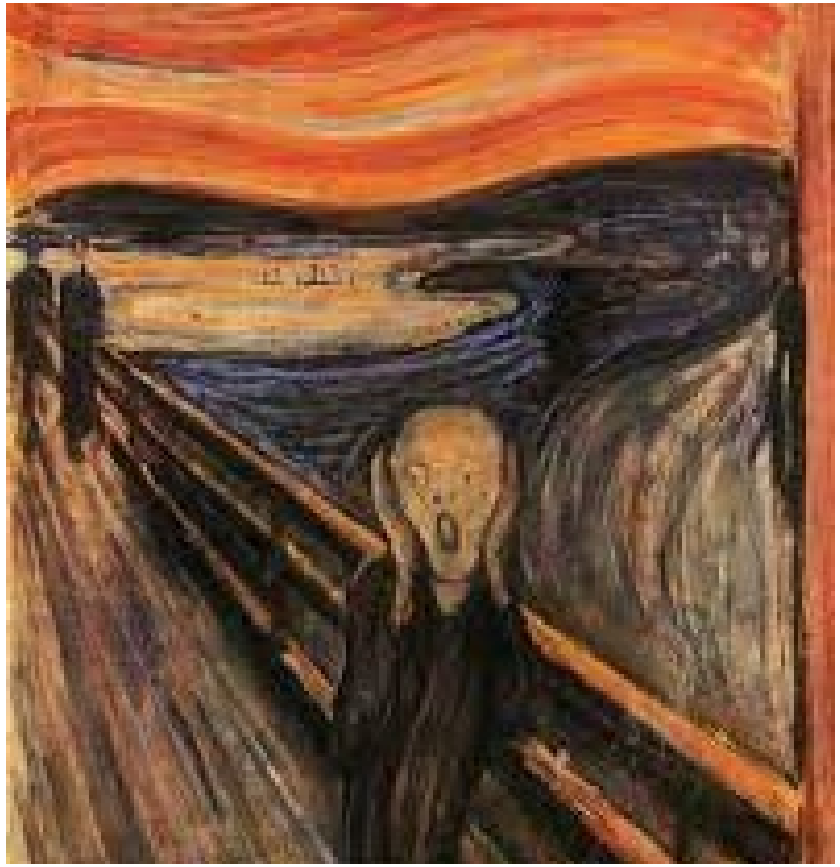
Staff testing

For example, during outbreak control at the Royal Brompton Hospital, London, 5 swabs each (hands, nose, axilla, groin and throat) were taken from 258 individuals as part of a staff screening program.
A total of one transient carrier were identified (positive nasal swab, other materials negative), but the affected person had contact with only one patient and was not a source of dissemination according to epidemiological analyses

Schelenz S, Hagen F, Rhodes JL, et al. First hospital outbreak of the globally emerging *Candida auris* in a European hospital. *Antimicrob Resist Infect Control*. 2016;5:35.

Candida auris: un nemico di tutti gli ospedali? Conclusioni

- Threat which has emerged and is spreading fast
- Different resistance patterns, already MDR but emergence of (pan)resistance have been reported
- Outbreaks best contained if spotted early, but in many places eradication is not an option but limiting its spread is still fundamental




Thank you