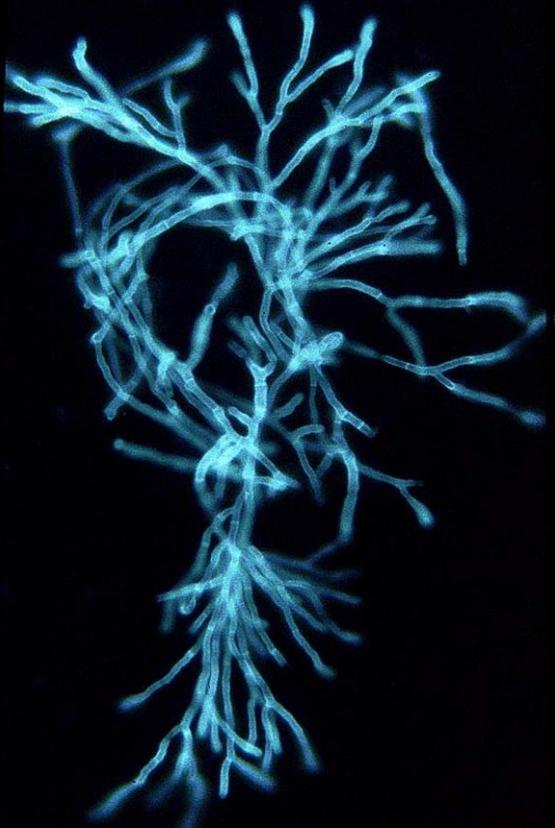


Resistenzentwicklung bei *Candida* und *Aspergillus* - ein klinisches Problem?

PEG-Jahrestagung 2018, Wien



Dr. Oliver Bader

Resistenzentwicklung bei *Candida* und *Aspergillus* - ein klinisches Problem?

Candida auris

Ausbrüche azolresistenter Stämme

Candida glabrata

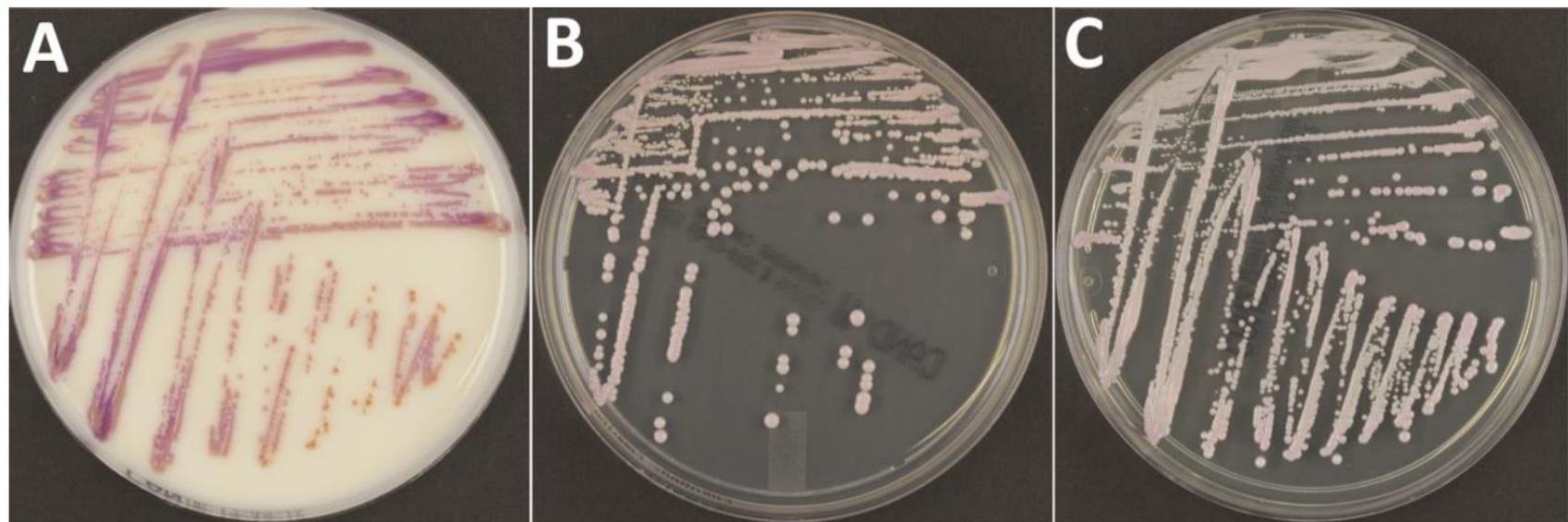
Vermehrtes Auftreten von Isolaten mit erhöhten Echinocandin MHKs

Aspergillus fumigatus

Pandemisches Auftreten azolresistenter Isolate

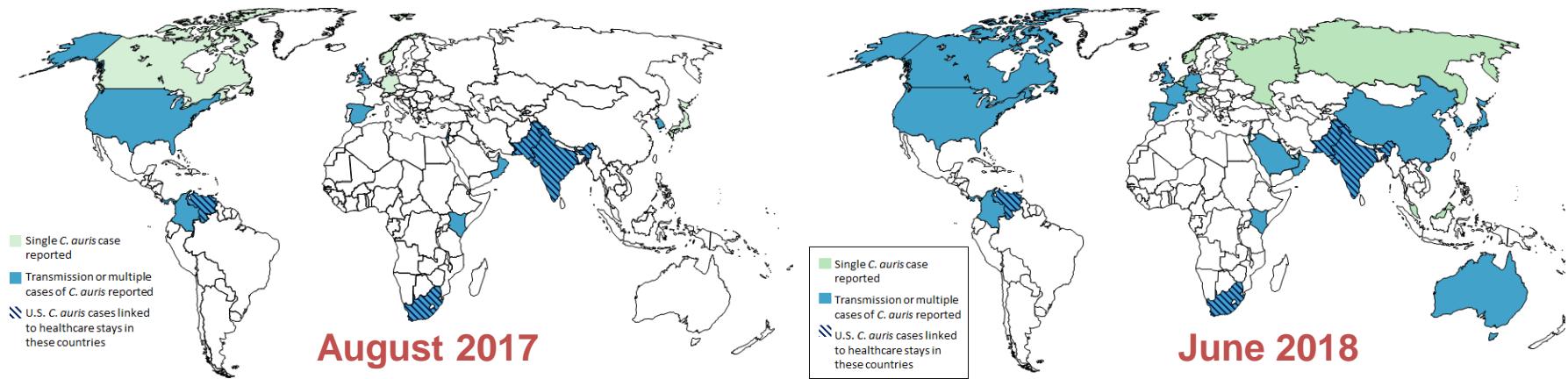
Candida auris

- Emerging yeast, first described in Japan 2009
- Nosocomial transmission
- Multidrug resistant
- Rapid dissemination worldwide
- Difficult to identify

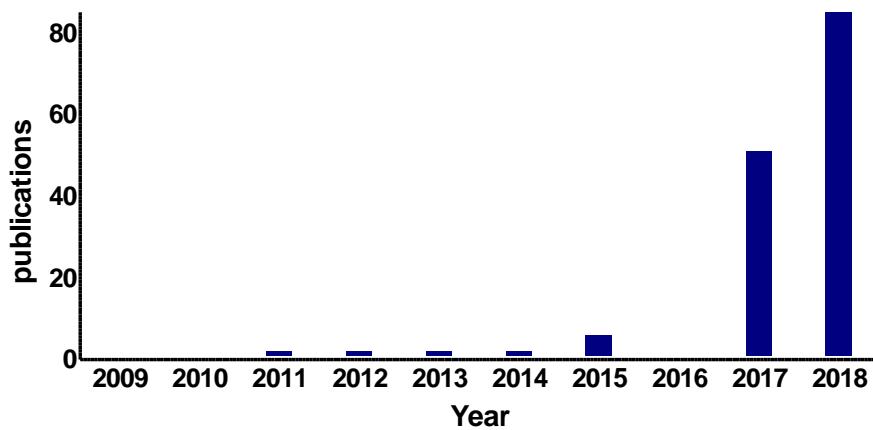


Technical Appendix Figure. *Candida auris* colonies from an otherwise healthy patient in Austria after 48 hours at 37°C on various chromogenic media: A) Brilliance Candida Agar; B) CHROMagar Candida; C) Candida ID.

global dissemination



source: US gov't, CDC (<https://www.cdc.gov/fungal/diseases/candidiasis/tracking-c-auris.html#world>)



Reported cases in DE / AT

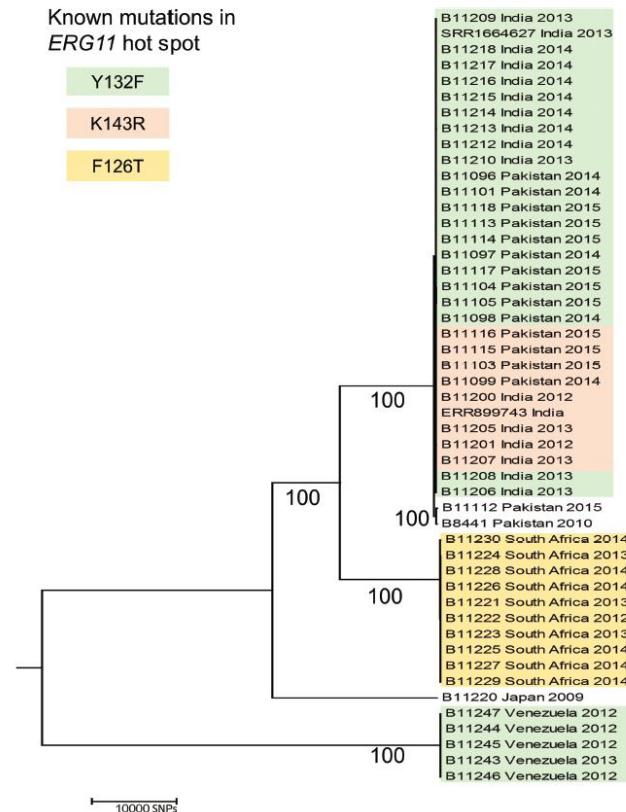
Date	City	clinical background	reference
11/2015	Stuttgart	prosthetic joint infection	Unpublished cases data courtesy of Oliver Kurzai (HKI Jena) and Axel Hamprecht (Uni Cologne)
12/2015	Nuremberg	SIRS	
06/2017	Cologne	intracranial hemorrhage	
07/2017	Munich	neurological disorder	
08/2017	Munich	polytrauma	
11/2017	Aachen	gunshot wound	
12/2017	Regensburg	tetraplegia	
01/2018	Vienna	otitis	Pekard-Amenitsch (2018) EID 24(8): 1596–1597

MICs for fluconazole high, but low for amphotericin B
Favourable outcome in all cases
Positive travel history in nearly all cases → imported pathogens

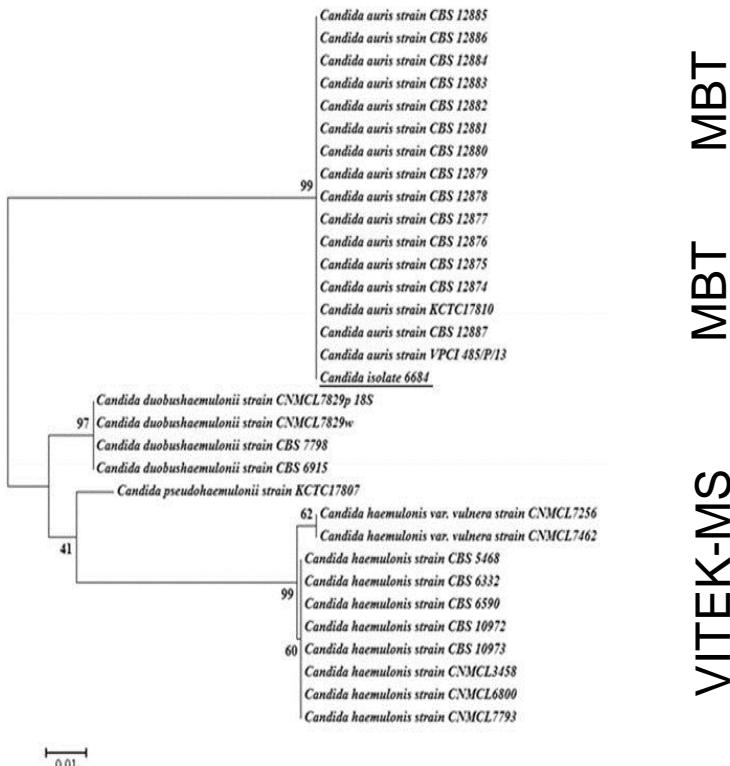
C. auris clades

There are at least 3 different lineages of *C. auris*, with geographically biased distribution

→ Epidemiology still unclear !



... is now contained in major MALDI-TOF databases

MBT
VITEK-MS

Matrix-assisted laser desorption ionization time-of-flight mass spectrometry for the rapid identification of yeasts causing bloodstream infections

A. K. Ghosh, S. Paul, P. Sood, S. M. Rudramurthy, A. Rajbanshi, T. J. Jillwin and A. Chakrabarti
Department of Medical Microbiology, Postgraduate Institute of Medical Education and Research (PGIMER), Chandigarh, India

Ghosh et al, CMI 2015

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

Shallu Kathuria,^a Pradeep K. Singh,^a Cheshta Sharma,^a Anupam Prakash,^a Aradhana Masih,^a Anil Kumar,^b Jacques F. Meis,^{c,d} Anuradha Chowdhary^a
Department of Medical Mycology, Vallabhbhai Patel Chest Institute, University of Delhi, Delhi, India;^a Department of Microbiology, Amrita Institute of Medical Sciences & Research Centre, Kochi, Kerala, India;^b Department of Medical Microbiology and Infectious Diseases, Canisius-Wilhelmina Hospital, Nijmegen, The Netherlands;^c Department of Medical Microbiology, Radboudumc, Nijmegen, The Netherlands

Kathuria et al, JCM 2015

Identification and typing of the emerging pathogen *Candida auris* by matrix-assisted laser desorption ionisation time of flight mass spectrometry

Victoria Girard,¹ Sandrine Mailler,¹ Marion Chetry,¹ Céline Vidal,² Géraldine Durand,¹ Alex van Belkum,¹ Arnaldo L. Colombo,³ Ferry Hagen,⁴ Jacques F. Meis^{4,5} and Anuradha Chowdhary⁶

¹R&D Microbiology, bioMérieux, La Balme les Grottes, France, ²R&D Biomathematics, bioMérieux, Grenoble, France, ³Laboratório Especial de Micologia, Escola Paulista de Medicina, UNIFESP, São Paulo, Brazil, ⁴Department of Medical Microbiology and Infectious Diseases, Canisius Wilhelmina Hospital, Nijmegen, The Netherlands, ⁵Department of Medical Microbiology, Radboud University Medical Center, Nijmegen, The Netherlands and ⁶Department of Medical Mycology, Vallabhbhai Patel Chest Institute, University of Delhi, Delhi, India

Girard et al, Mycoses 2016

C. auris contained in DB: MBT ✓; VITEK-MS RUO ✓; VITEK-IVD: end 2017

Candida glabrata

Rising incidence in echinocandin resistance?

Echinocandin resistance rates

US: (Perlin, Ann N Y Acad Sci 2015)

Echinocandin resistance of 8.0–9.3% was reported in a recent SENTRY program among 1669 bloodstream isolates (BSI) of *C. glabrata*. Similarly, over a 10-year period, echinocandin resistance in *C. glabrata* rose from 2–3% to > 13%.

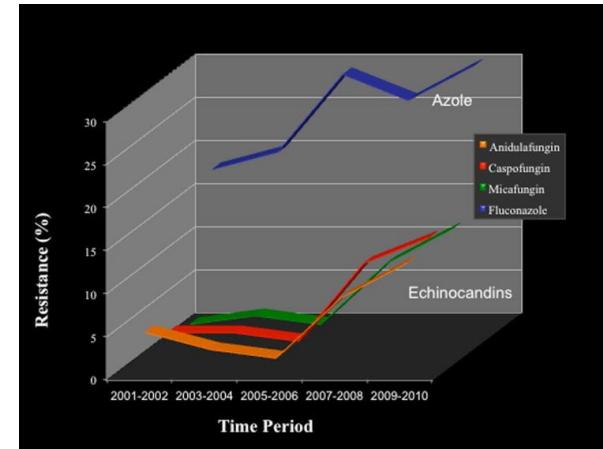
Italy: (Mencarini, Infection 2018)

Between 2005 and 2015, increased use of echinocandins, but only one *Candida glabrata* isolate was resistant to caspofungin (1.9%) while 30% of *C. glabrata* were resistant to fluconazole.

China: (Hou, AAC 2018)

Among 158 *Candida glabrata* bloodstream isolates 8.9% were FLZ^R, 1.9% echinocandin-cross^R.

→ Echinocandin resistance rates in *C. glabrata* vary from 2% to 15%, depending on geography and host population.



Echinocandin resistance

Echinocaninds inhibit fungal glucan synthases, encoded by “fks” genes

Where most yeast only have a single gene, *C. glabrata* has two!

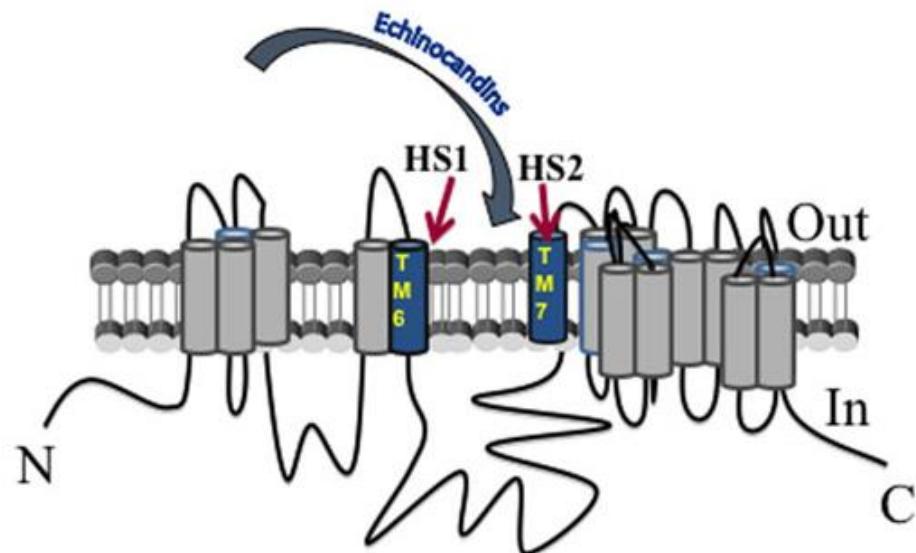


Table 1 Overview of Fks hot spot sequences and amino acid sequence positions resulting in echinocandin resistance

Species	Fks1p				Fks2p	
	Hot spot 1	Hot spot 2		Hot spot 1	Hot spot 2	
<i>C. albicans</i>	641	F LTL S LRDP	1357	D W IIRR R YTL		
<i>C. dubliniensis</i>	641	FLTL S LRDP	1357	DWIRRYYTL		
<i>C. glabrata</i>	625	F L I L S LRDP	1340	D W VRRYYTL	659	F L I L S LRDP
						1374 D W IIRR R YTL

CgFKS mutations seen in Germany

2016/17 @ NRZMyk:

- 41 isolates with ANI^R
- 12 isolates FLU^R, ANI^R with limited remaining treatment options
- 80% with ANI > 0,125 harbour FKS mutations, but only 20% of those with ANI = 0.125

mutation	gene	# isolates
S663P	<i>FKS2</i>	4
F659Y	<i>FKS2</i>	2
F659del	<i>FKS2</i>	2
D666N	<i>FKS2</i>	1
D666Y	<i>FKS2</i>	1
L630Q	<i>FKS1</i>	1
none	-	9

Wagener et al, Der Mikrobiologe 2018

Walther and Kurzai, poster@DMYKG2018 (Innsbruck)

Fitness cost?

- close association exists between drug exposure and the emergence of resistance.
- *FKS*-mediated resistance is directly linked to prior, prolonged, and/or repeated drug exposure.
- chromosomal instability is rapidly observed following exposure to azoles or echinocandins
- cellular stress increases genetic diversity by altering genome integrity

Evolution of MICs and genetic alteration of six related sequentially isolated *Candida glabrata* responsible for invasive infection in a solid organ transplant recipient receiving multiple antifungal therapy

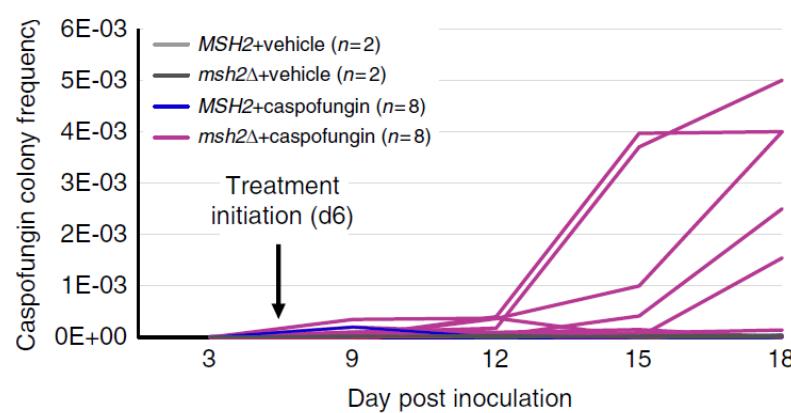
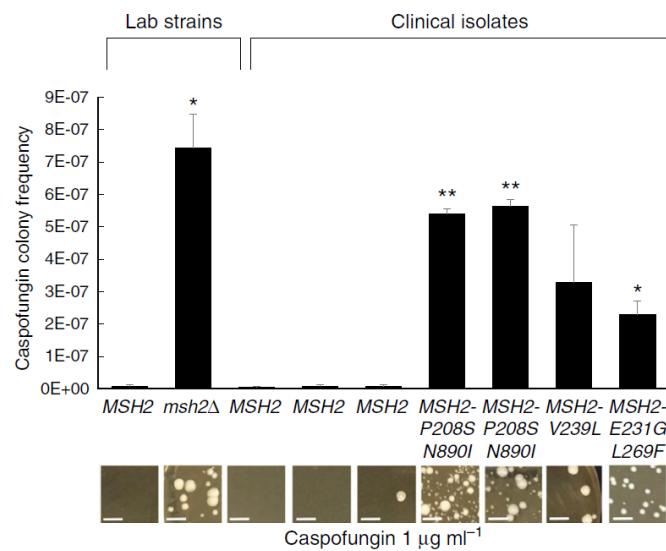
Characteristic	Isolate no.					
	1	2	3	4	5	6
Postoperative day	8	25	97	104	108	119
Source of sample	Blood culture	Liver abscess	Blood culture	Blood culture	Blood culture	Blood culture
Antifungal drug administered at time of sampling (number of days from start of treatment)	Fluconazole (8)	Voriconazole (15)	Micafungin ^a (7) and caspofungin (4)	Liposomal amphotericin B (7)	Liposomal amphotericin B (11)	Liposomal amphotericin B (22)
Determination of MICs (mg/L) by EUCAST method	Amphotericin B Fluconazole Itraconazole Voriconazole Posaconazole Caspofungin Micafungin	1 8 1 0.125 0.5 0.25 <0.03	1 >64 >16 4 >8 0.5 <0.03	1 >64 >16 4 >8 >16 2	1 >64 >16 4 >8 >16 1	1 >64 >16 8 >8 0.5 <0.03
Molecular analysis of genes related to antifungal resistance	<i>FKS1</i> (HS1, HS2, HS3) <i>FKS2</i> <i>FKS3</i>	WT HS1 HS2 WT	WT WT WT WT	WT S663P WT WT	WT S663P WT WT	WT WT WT WT

EUCAST, European Committee on Antimicrobial Susceptibility Testing; HS, hot spot; MIC, minimum inhibitory concentration; WT, wild type.

^a Last dose of micafungin was administrated the day before blood was sampled for culture.

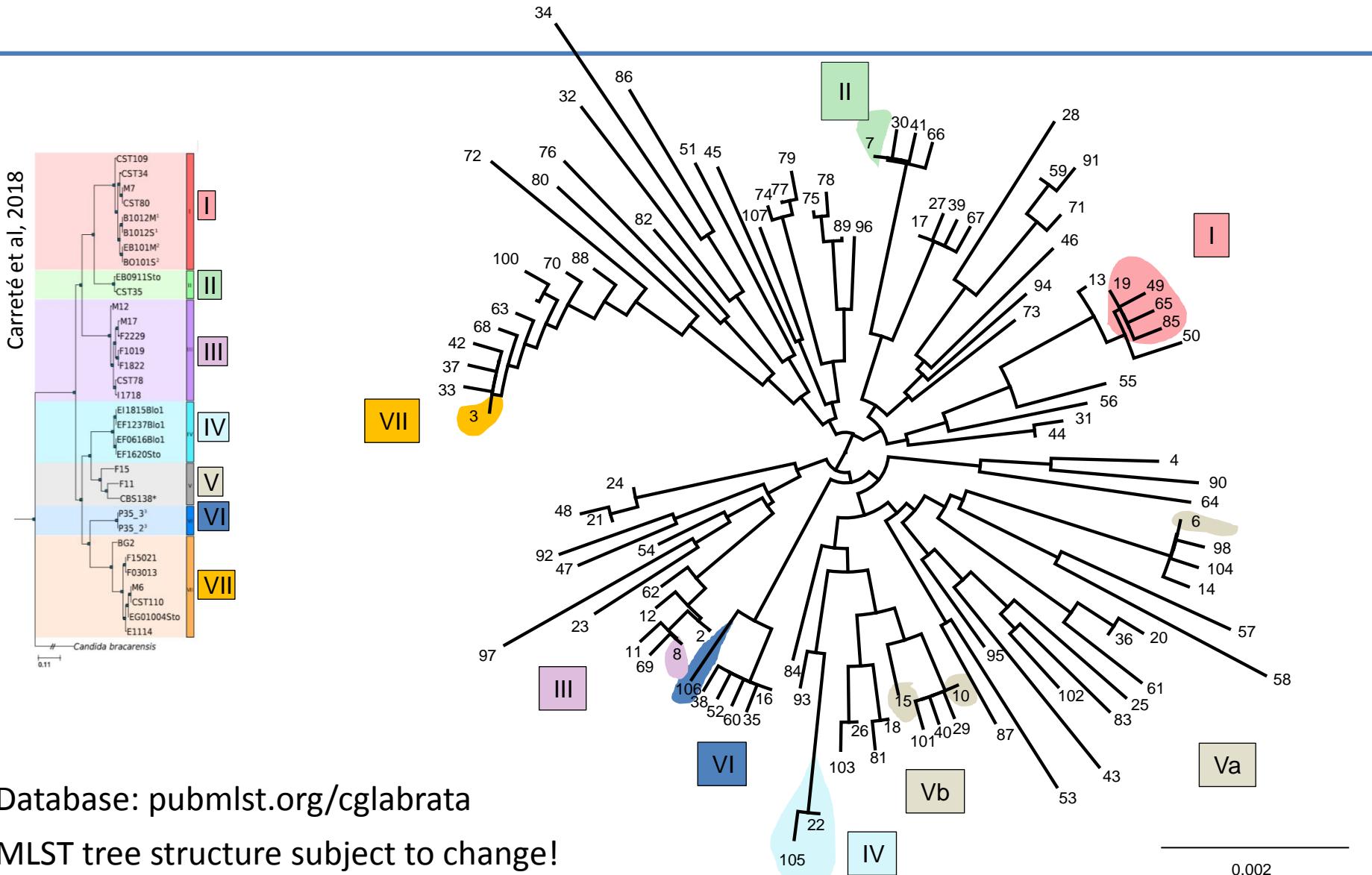
DNA mismatch repair

55% of all *C. glabrata* isolates (susceptible and resistant) recovered from patients contain mutations within the MMR gene *MSH2*. Strains with specific *msh2* mutations exhibit a higher frequency of emergence of resistance *in vitro*, and deletion of *MSH2* causes elevated propensity to breakthrough antifungal treatment in a mouse model of gastrointestinal (GI) colonization.

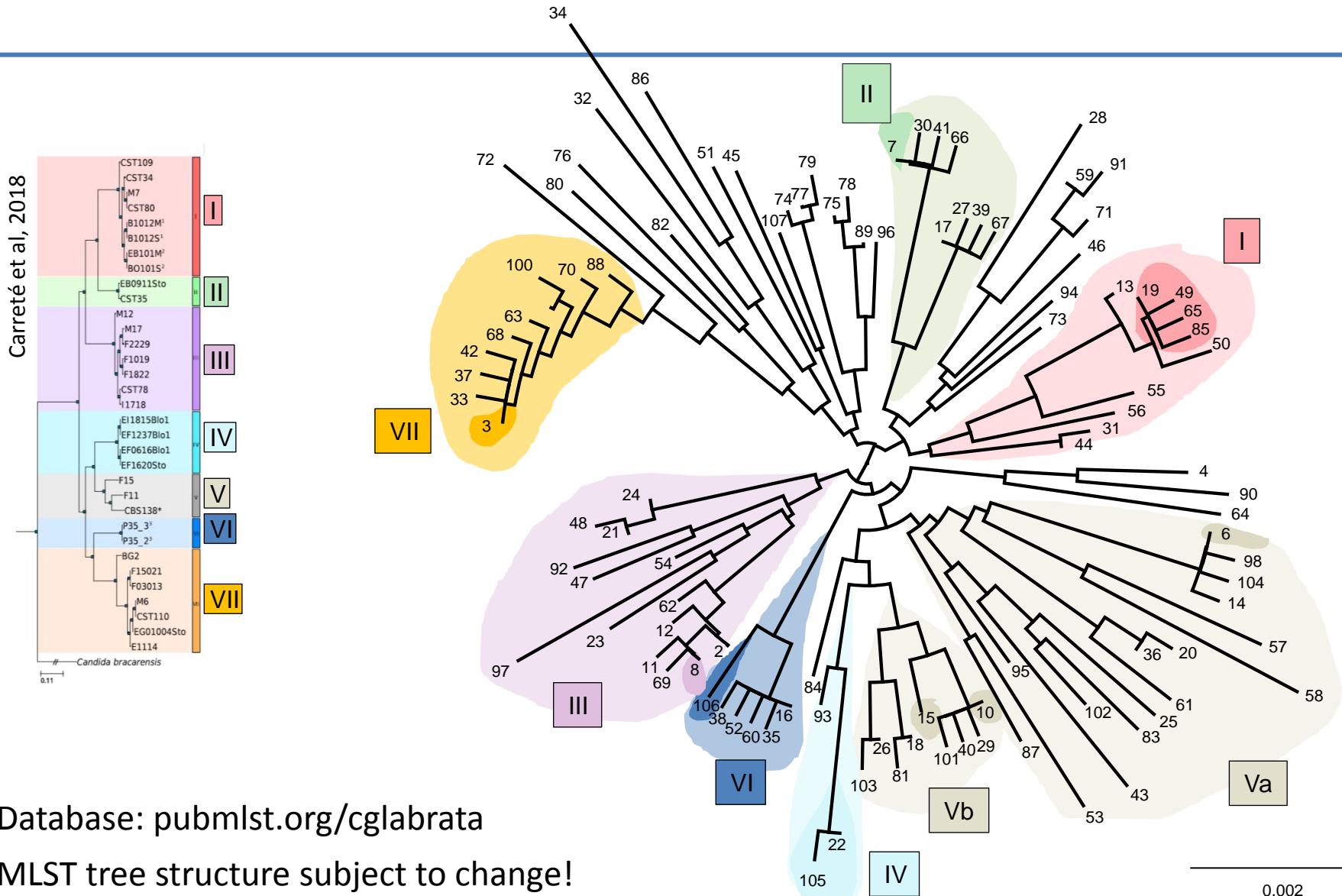


Mouse	Day	<i>fks</i> mutation (nucleotide change)
Δ-1	9	Fks1-625delF (1875_1877delCTT)
Δ-1	12	Fks1-S629P (t1885c)
Δ-1	18	Fks1-S629P (t1885c)
Δ-1	21	Fks1-S629P (t1885c)
Δ-2	18	Fks1-S629P (t1885c)
Δ-3	18	Fks1-S629P (t1885c)
Δ-6	15	Fks1-S629P (t1885c)
Δ-6	18	Fks1-S629P (t1885c)
Δ-6	21	Fks1-S629P (t1885c)

C. glabrata population structure

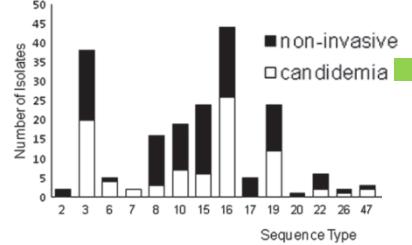


C. glabrata population structure

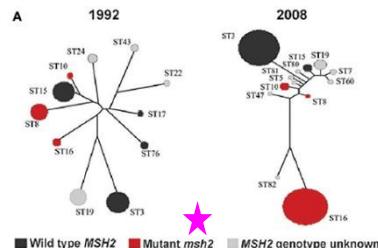


C. glabrata population structure

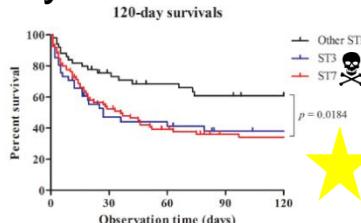
Lott et al 2012



Healey et al 2016

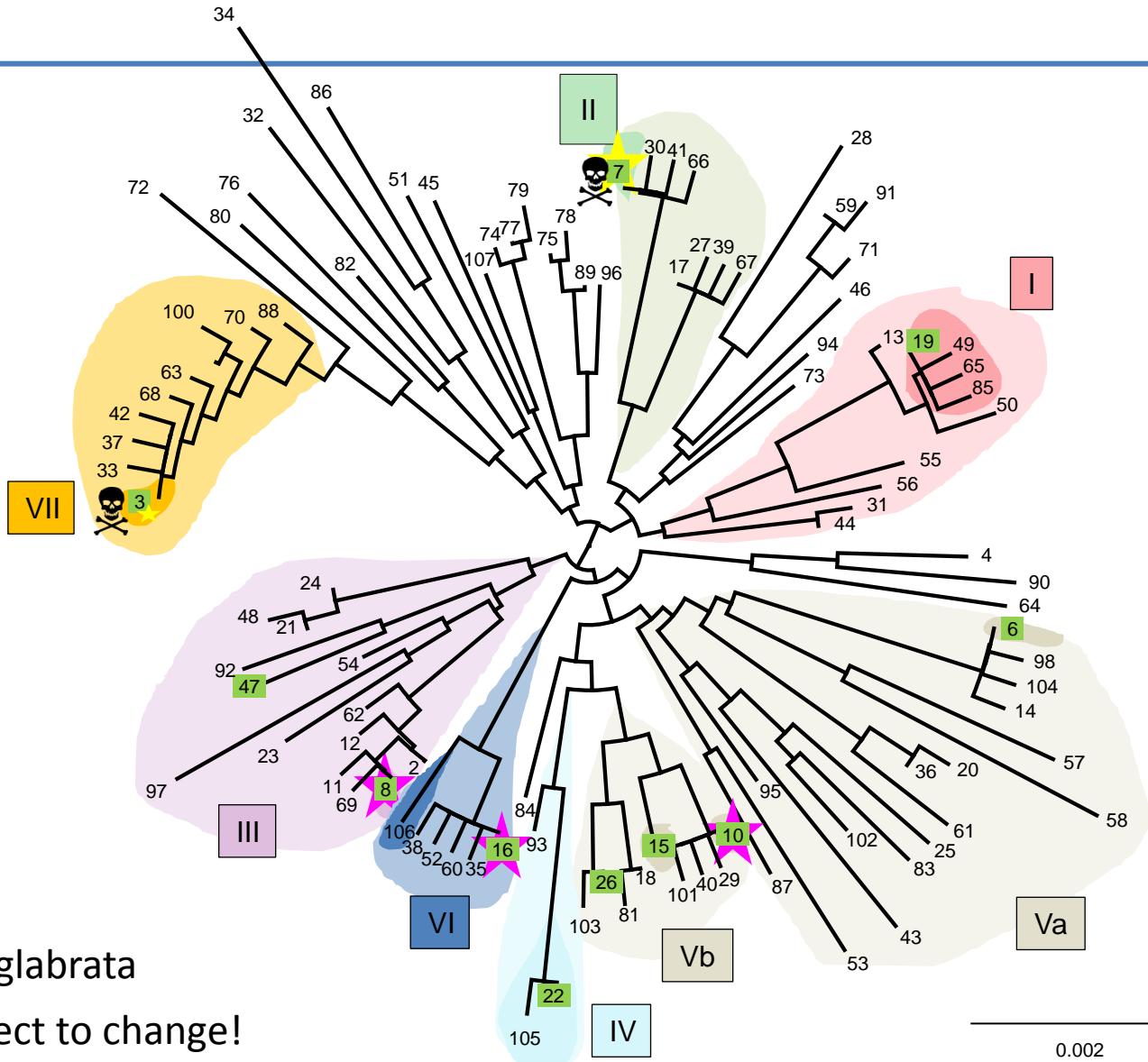


Byun et al 2018



Database: pubmlst.org/cglabratat

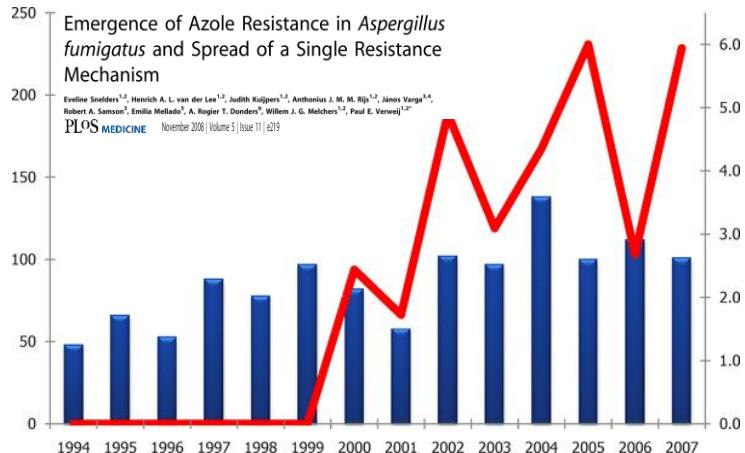
MLST tree structure subject to change!



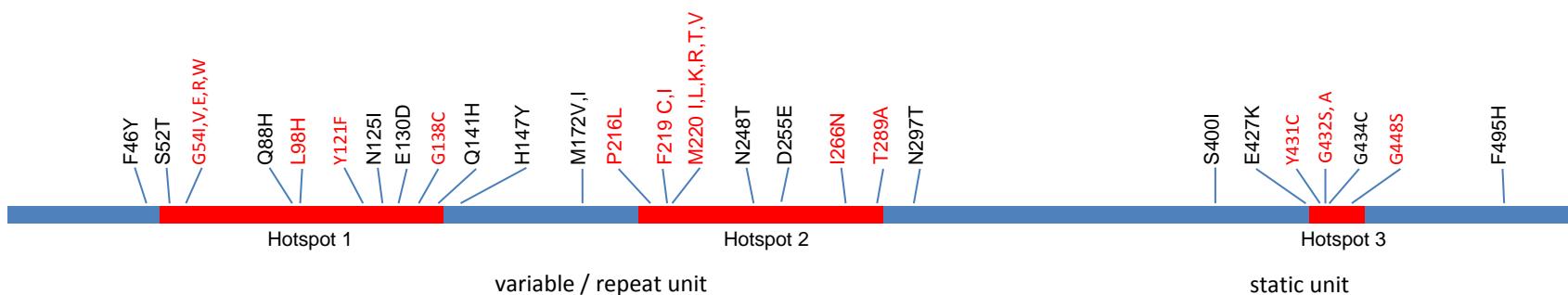
Aspergillus fumigatus

Global spread of azole resistant lineages

Mechanisms of azole resistance: Cyp51A

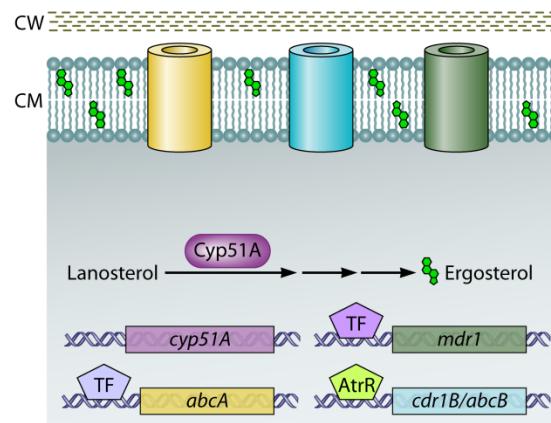
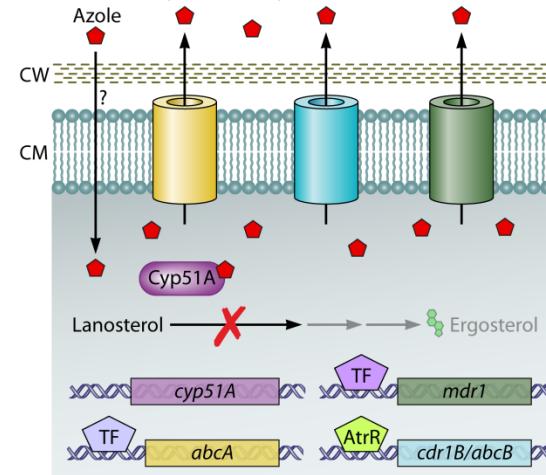
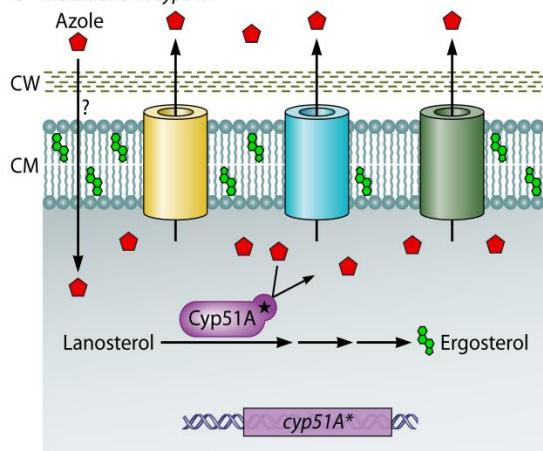
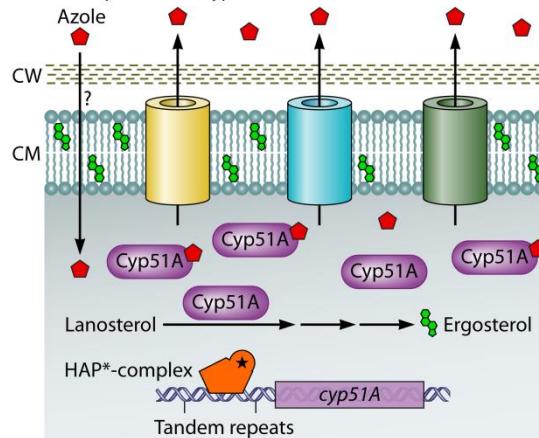
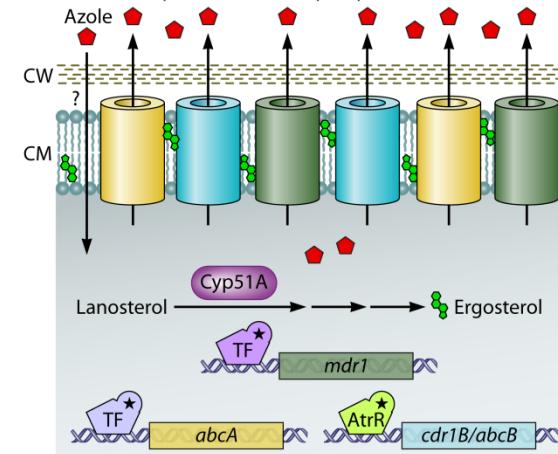


“pandemic” alleles:
 $\text{TR}_{34}/\text{L98H}$
 $\text{TR}_{46}/\text{Y121F/T289A}$



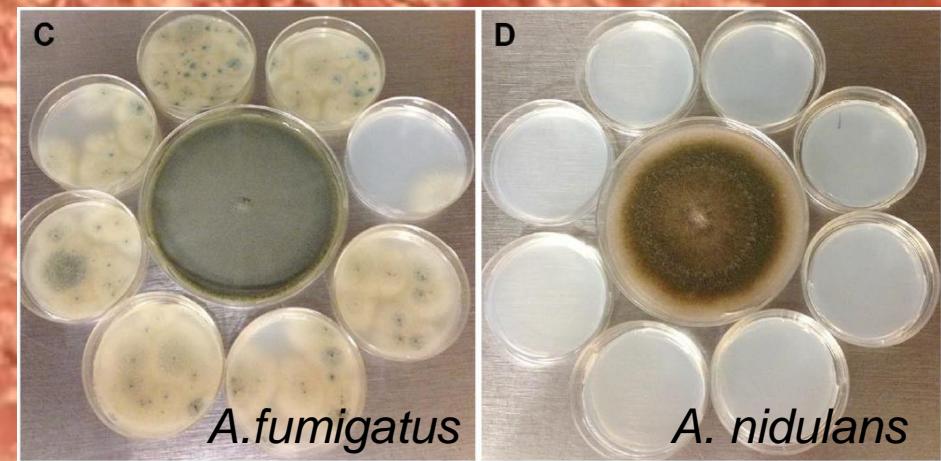
A. fish	gcagcattaccc CAGGG-TGTCTC -----TA-----	GAGTCACGCGGTCCGGATGTGTGCTGAGCCGAAT GAGAGTTGCCTAA tact
A. oerl	gcagcattaccc CAGGG-TGTCTGTCTAGGTA -----	GAATCACGCGGTCCGGATGTGTGCTGAGCCGAAT GAGAGTTGCCTAA tact
A. fu wt	gcagcaccactt CAGAGTTGTC -----TA-----	GAATCACGCGGTCCGGATGTGTGCTGAGCCGAAT GAAAGTTGCCTAA tact
A. fu TR ₃₄	gcagcaccactt CAGAGTTGTC -----TA GAATCACGCGGTCCGGATGTGTGCTGAGCCGAAT	GAATCACGCGGTCCGGATGTGTGCTGAGCCGAAT GAAAGTTGCCTAA tact
A. fu TR ₄₆	gcagcaccactt CAGAGTTGTC -----TAGA ATCACGCGGTCCGGATGTGTGCTGAGCCGAAT GAAAGTTGCCTAA tact	GTCTAGAATCACGCGGTCCGGATGTGTGCTGAGCCGAAT GAAAGTTGCCTAA tact
A. fu TR ₅₃	gcagcaccactt CAGAGTTGTC -----TAGA ATCACGCGGTCCGGATGTGTGCTGAGCCGAAT GAAAGTTGCCTAA tact	GTCTAGAATCACGCGGTCCGGATGTGTGCTGAGCCGAAT GAAAGTTGCCTAA tact

Aazole resistance mechanisms in A.f.

A Normal susceptible cell in absence of azoles**B** Normal susceptible cell in presence of azoles**C** Mutations in *cyp51A***D** Overexpression of *cyp51A***E** Increased expression of efflux pumps

Current working hypothesis

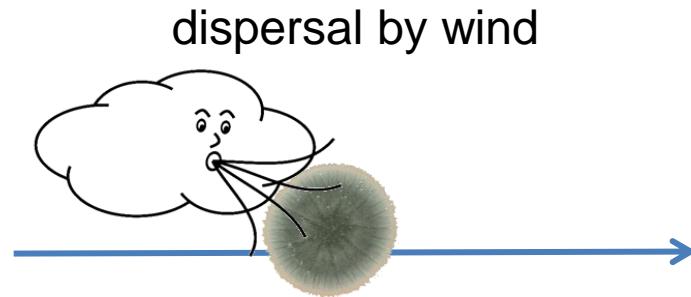
A. fumigatus is one of the best-adapted fungi to dispersal, and its conidia are found world-wide incl. the upper atmosphere, and both polar regions



Current working hypothesis



Unintentional induction of resistance in
A. fumigatus
e.g. TR₃₄/L98H
or TR₄₆/Y121F/T289A
(G54?)



selection over
susceptible strains
through agricultural azoles?

- presence in hosts
- opportunistic infection
- (selection through azole prophylaxis ???)
- not only humans but also wild animals!

conidia also travel the land route...

Intercountry Transfer of Triazole-Resistant *Aspergillus fumigatus* on Plant Bulbs

¹Department of Clinical Microbiology, Trinity College Dublin, Ireland; ²Department of Medical Microbiology and Infectious Diseases, Canisius Wilhelmina Hospital, and ³Centre of Expertise in Mycology, Radboud University Medical Center/Canisius Wilhelmina Hospital, Nijmegen, The Netherlands

Katie Dunne,¹ Ferry Hagen,^{2,3} Niamh Pomeroy,¹ Jacques F. Meis,^{2,3} and Thomas R. Rogers¹

Sample No. ^a	Date of Sample	Type of Sample	Origin	No. of Triazole-Resistant/ <i>A. fumigatus</i> Colonies/Plant Bulb Pack	MIC, mg/L ^b			Resistance Mechanism
					Itraconazole (ECV = 1) [9]	Voriconazole (ECV = 1) [9]	Posaconazole (ECV = 0.5) [9]	
P1	Jan 2016	Double mixed tulip bulbs (30 ^c)	Lisse, the Netherlands	1/5	0.5	>8	0.5	TR ₄₆ /Y121F/T289A
P2, P3	Jan 2016	Bastogne tulip bulbs (6 ^c)	Lisse, the Netherlands	2/3	1	4	1	TR ₄₆ /Y121F/T289A
					8	>8	0.5	TR ₃₄ /L98H
P4	Jan 2016	Triumph tulip bulbs (6 ^c)	Breezand, the Netherlands	1/4	8	4	0.5	TR ₃₄ /L98H
P5, P6	Jan 2016	Narcissus bulbs (8 ^c)	Breezand, the Netherlands	2/5	0.5	>8	1	TR ₄₆ /Y121F/T289A
					8	4	0.5	TR ₃₄ /L98H
P7	Jan 2016	Tall Triumph mixed tulip bulbs (10 ^c)	The Netherlands (region not specified)	1/2	1	>8	1	TR ₄₆ /Y121F/T289A
D6	Feb 2016	Soil (2 g)	Hospital campus, Dublin, Ireland	...	8	4	0.5	TR ₃₄ /L98H

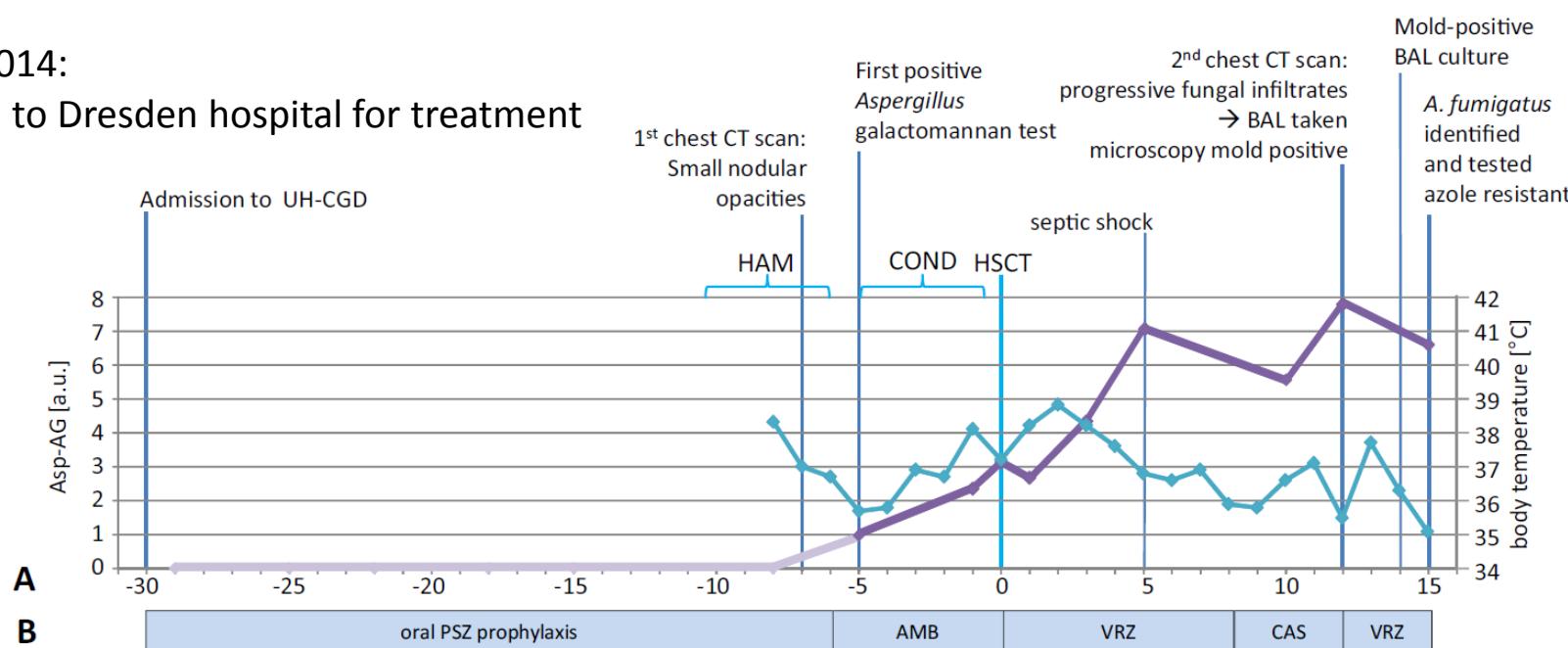
AML Case

Up to June 2014:

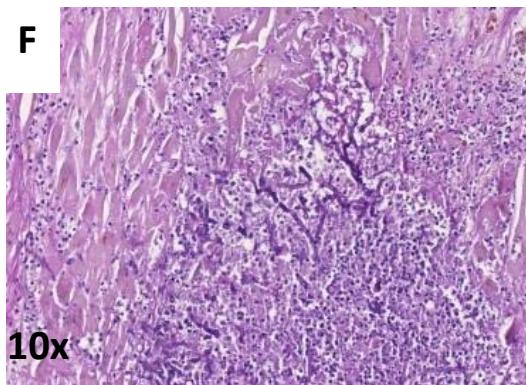
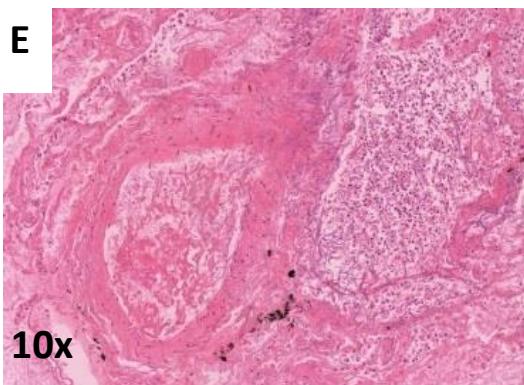
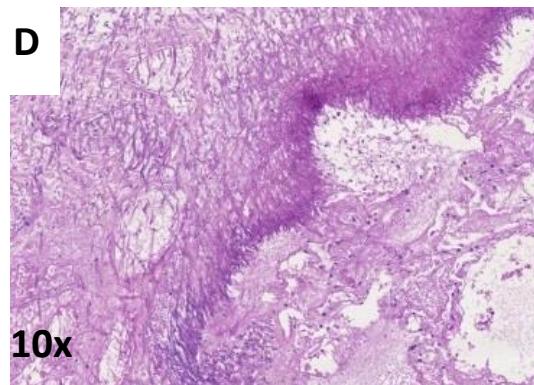
- 71-year old male patient
- treated in a general hospital for AML with adverse-risk cytogenetic features.
- received induction chemotherapy and oral posaconazole for antifungal prophylaxis
- Eventually, a new bone marrow aspirate revealed residual AML
- because of progressive AML, decitabine therapy was initiated

In August 2014:

- referred to Dresden hospital for treatment



AML Case



- (C) multiple fungal lesions on the surface of the lung,
- (D) fungal abscess in lung parenchyma (PAS reaction),
- (E) vascular invasive growth and detection of dichotomously branched and septated fungi in the lumen of a lung vessel
- (F) fungal septipyemic focus in the anterior wall of the heart with surrounding granulocytic reaction (PAS reaction)

AML Case

antifungal susceptibility testing of the culture isolate (BAL)

Antifungal agent	E-test		EUCAST borth microdilution		
	MIC	interpretation	MIC	breakpoints	Interpretation
posaconazole	0.5	resistant	0.5	S <= 0.12; R > 0.25	resistant
itraconazole	2	sensitive	1	S <= 1; R > 2	sensitive
voriconazole	>32	resistant	> 32	S <= 1; R > 2	resistant
amphotericin B	0.25	sensitive	< 0.125	S <= 1; R > 2	sensitive

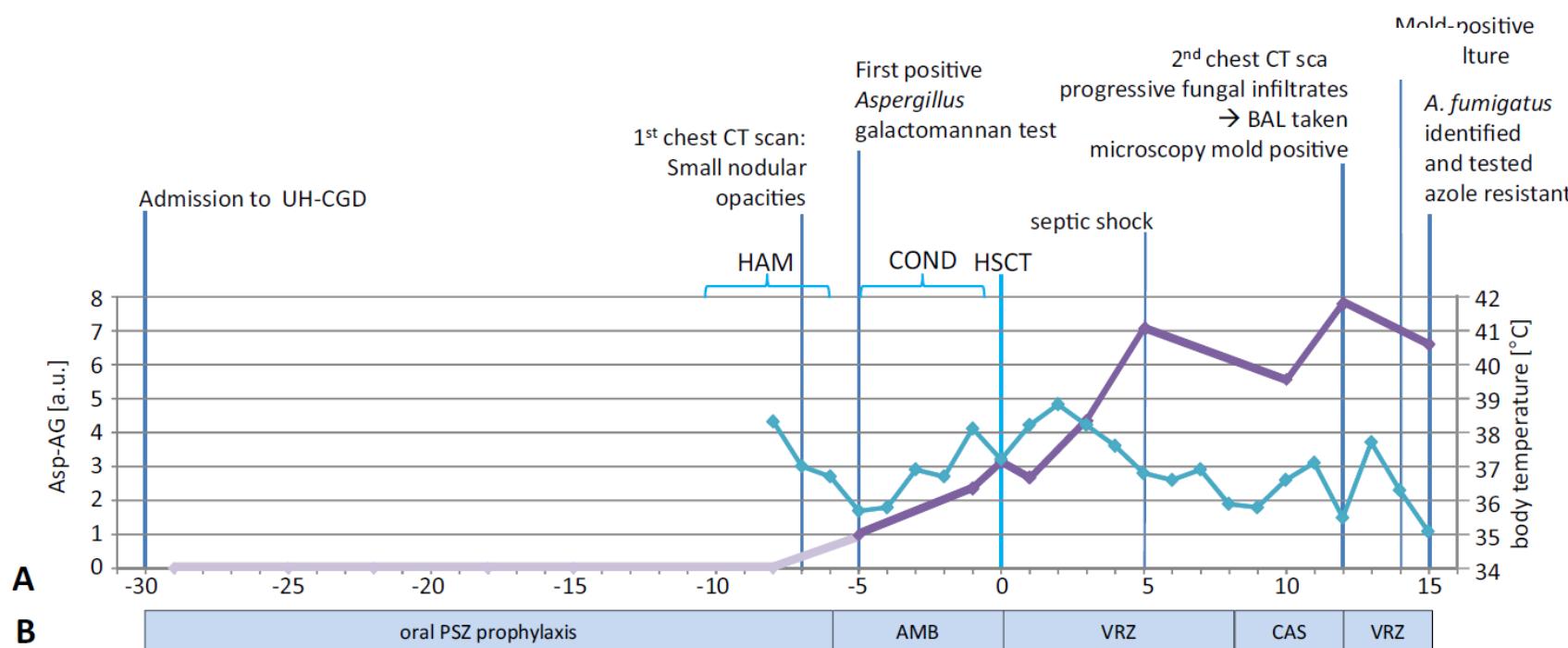
MIC = minimal inhibitory concentration [μ g/ml]

EUCAST = European Committee on Antimicrobial Susceptibility Testing

AML Case

PSZ and VRZ ineffective in this patient

Strain with PSZ^R and VRZ^R strain with TR₄₆/Y121F/M172/T289A cyp51A mutation



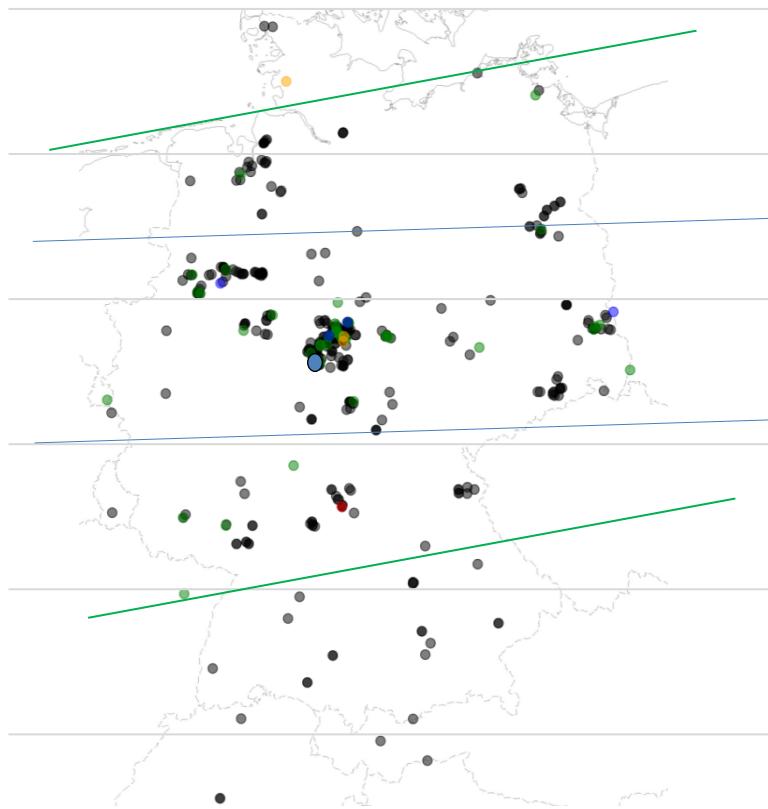
Reported isolates in Germany

clinical

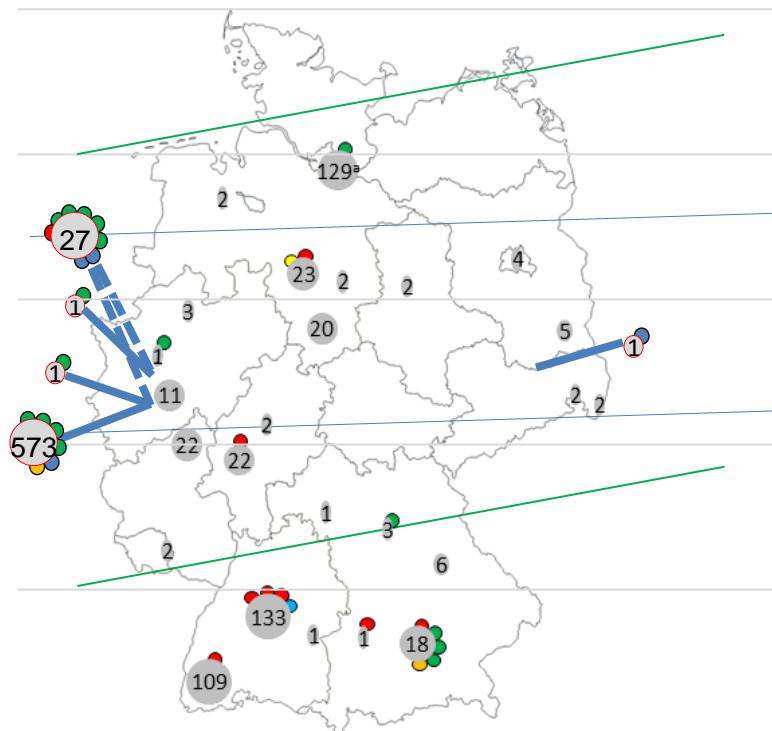
NRZ data 201719 isolates, 2/3 with mutations in CYP51A
(Walther, Kurzai, Poster@DMYKG2018)**35 reported clinical isolates****NRZ data 2017**19 isolates, 2/3 with mutations in CYP51A
(Walther, Kurzai, Poster@DMYKG2018)

North-South imbalance ?

environmental
isolates



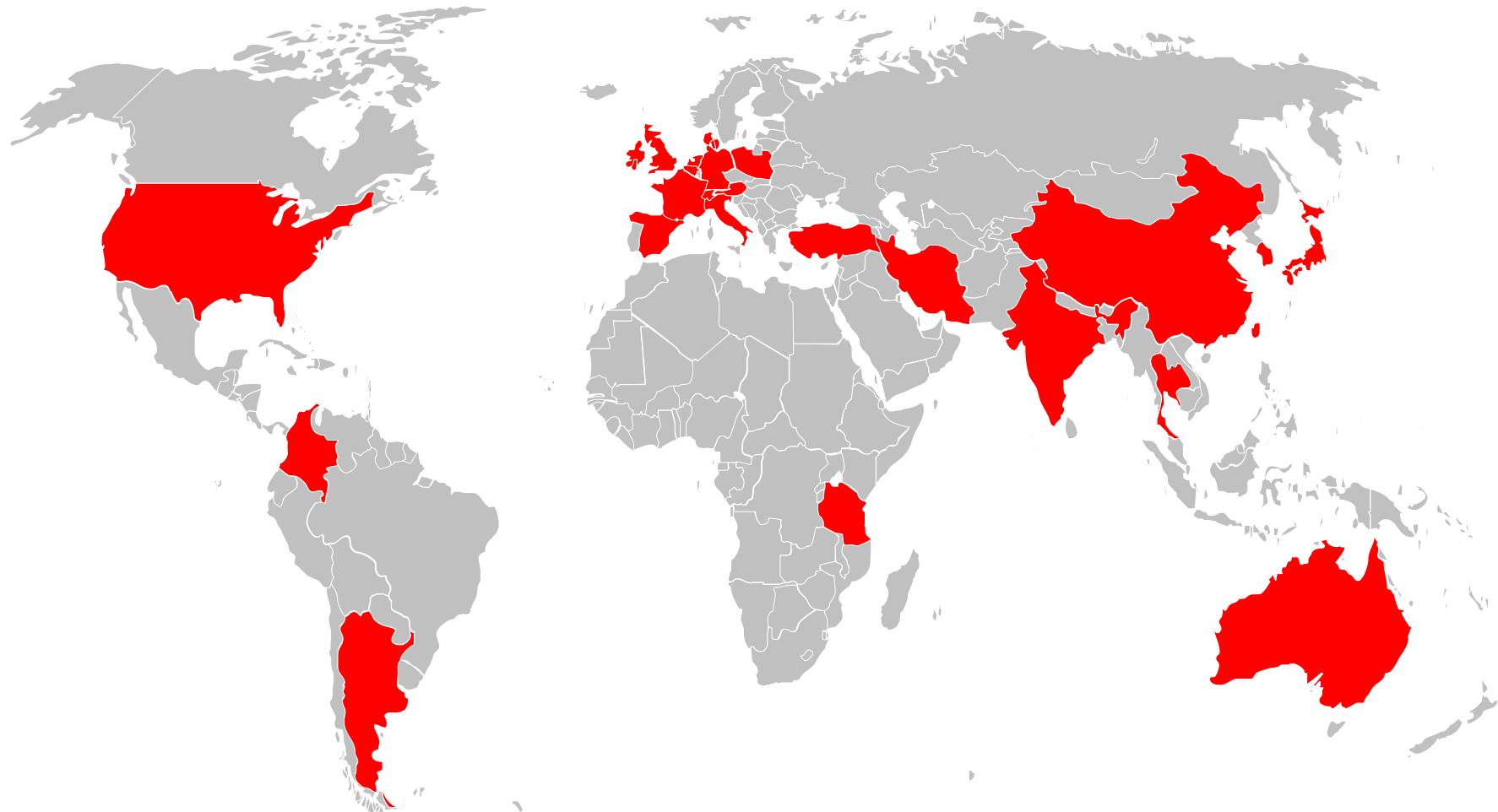
clinical isolates



Legend:

- n.d. (grey dot)
- none (red dot)
- G54E/R (blue dot)
- G54W (yellow dot)
- TR/L98H (green dot)
- M220I/V/T (orange dot)
- F219C (cyan dot)
- TR₄₆/Y121F/(M172I)/T289A (dark blue dot)

ARAf findings by country



→ if people look for ARAf, they will find it !

No fitness cost associated with ARAf

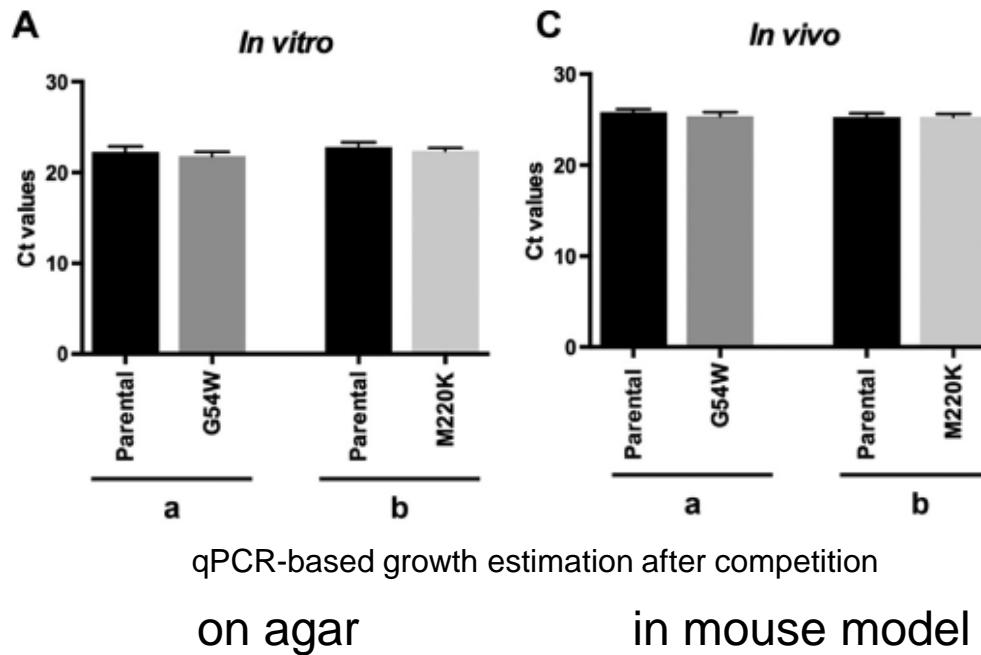
Fitness Studies of Azole-Resistant Strains of *Aspergillus fumigatus*

Isabel Valsecchi,^a Emilia Mellado,^b Rémi Beau,^a Shriya Raj,^a Jean-Paul Latgé^a

Unité des Aspergillus, Institut Pasteur, Paris, France^a; Mycology Reference Laboratory, Instituto de Salud Carlos III, Madrid, Spain^b

Antimicrobial Agents and Chemotherapy

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“International expert opinion”

(in the absence of clinical guidelines)

International expert opinion on the management of infection caused by azole-resistant *Aspergillus fumigatus*

Paul E. Verweij^{a,*}, Michelle Ananda-Rajah^b, David Andes^c, Maiken C. Arendrup^d,
Roger J. Brüggemann^e, Anuradha Chowdhary^f, Oliver A. Cornely^g, David W. Denning^h,
Andreas H. Grollⁱ, Koichi Izumikawa^j, Bart Jan Kullberg^k, Katrien Lagrou^l,
Johan Maertens^m, Jacques F. Meis^{a,n}, Pippa Newton^h, Iain Page^h,
Seyedmojtaba Seyedmousavi^a, Donald C. Sheppard^o, Claudio Viscoli^p, Adilia Warris^q,
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Verweij et al, (2015) Drug Res Updates 21:30-40

- microbiological diagnostics critical to guiding therapy
- if azole resistant isolates are obtained,
 - the underlying mechanism should be identified for epidemiological reasons,
 - but neither therapy initiation/modification nor MIC determination delayed
- 2-10% environmental prevalence → alternative therapies must be considered
- 10 % environmental prevalence → definitely re-evaluate azole therapy
- at least 5 independent colonies should tested for AST

culture

cave: susceptible / resistant – mixed cultures !!! → screening agar

J Antimicrob Chemother 2015; 70: 412–415
doi:10.1093/jac/dku410 Advance Access publication 17 October 2014

**Journal of
Antimicrobial
Chemotherapy**

CORRESPONDENCE

Voriconazole-Susceptible and Voriconazole-Resistant *Aspergillus fumigatus* Coinfection

To the Editor:

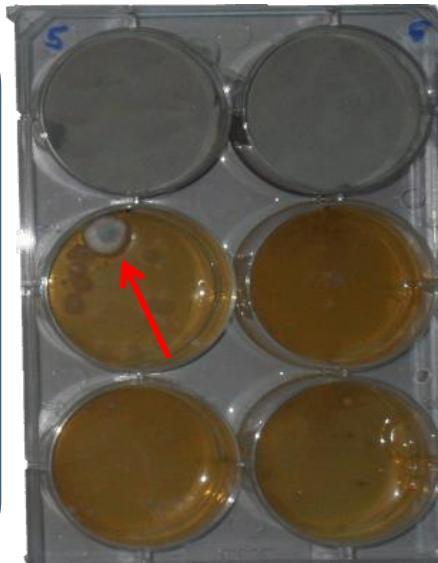
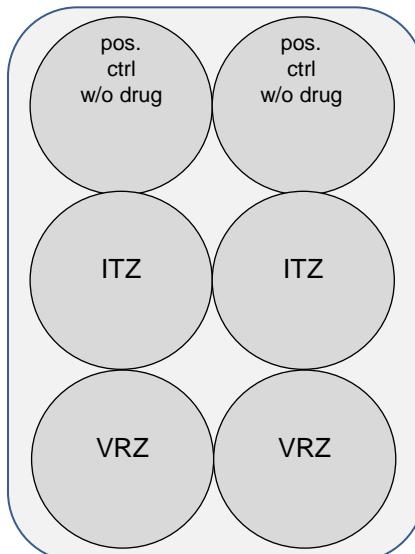
Azole resistance is an increasing problem in *Aspergillus fumigatus* infection (1). Two mutations, TR₃₄/L98H and TR₄₆/Y121F/T289A, are frequently recovered from isolates of patients with azole-resistant invasive aspergillosis and are believed to originate from the environment (2, 3). In regions with these environmental mutations, azole-resistant *Aspergillus* diseases may develop in patients not previously treated with azoles, and mortality rates are very high (4–6). We review the clinical course of three patients with proven invasive aspergillosis resulting from voriconazole-susceptible and voriconazole-resistant *A. fumigatus* strains. We hypothesized that in regions with TR₃₄/L98H and TR₄₆/Y121F/T289A environmental mutations, individual pulmonary lesions may arise from *A. fumigatus* strains with different azole resistance profiles.

unit because of pulmonary deterioration requiring mechanical ventilation. The BAL showed heavy growth of *A. fumigatus*. Resistance screening of four colonies indicated voriconazole-susceptible infection, and voriconazole was added to the regimen. Ten days after voriconazole was started, routine follow-up bronchial aspirate yielded a voriconazole-resistant *A. fumigatus* colony (Table 1). Because the patient was improving clinically with adequate voriconazole plasma levels, voriconazole was continued. However, a bronchial aspirate taken on day 13 showed heavy growth of voriconazole-resistant *A. fumigatus*. Despite continued clinical improvement, amikacin was added. Almost 2 weeks after intubation, ventilator support could be withdrawn, and immunosuppressive drugs were reintroduced. A follow-up computed tomography scan of the thorax showed cavity formation in the right upper lobe lesion and multiple nodular lesions. The patient suddenly died after having received voriconazole and amikacin combination therapy for 34 days. At autopsy, multiple pulmonary fungal lesions were found, as well as one fungal lesion in the kidney transplant. *A. fumigatus* colonies cultured from the cavitating

Concomitant occurrence of itraconazole-resistant and -susceptible strains of *Aspergillus fumigatus* in routine cultures

Ahmad et al, 2015 JAC 70:412-415

Kolwijk et al, 2016
Am J Respir Crit Care Med 193



large-scale screening



Clinical Microbiology
Reviews®

Molecular Tools for the Detection and Deduction of Azole Antifungal Drug Resistance Phenotypes in *Aspergillus* Species

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- molecular mechanisms
- a scheme to screen large scale collections
- tools to locally analyse sequencing data

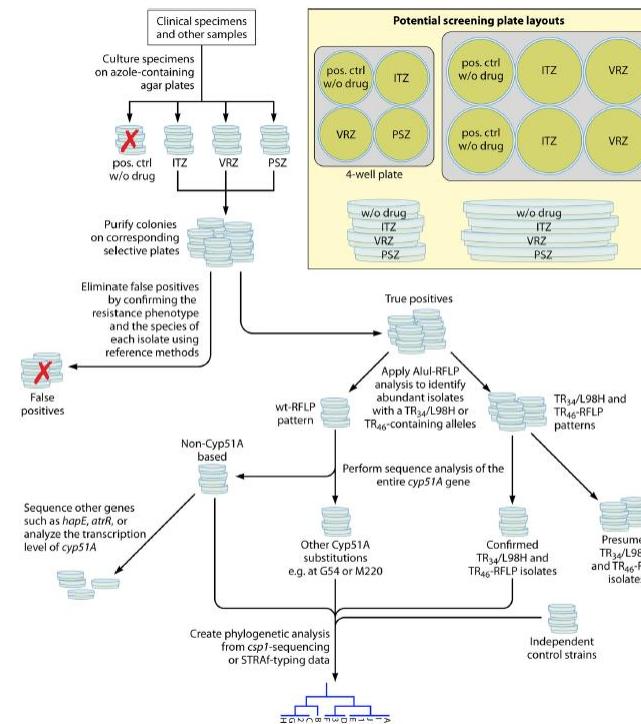


FIG 3 Potential sampling workflow for ARAF screening studies. No standardized scheme for conducting screening studies is established yet, but combining several approaches proposed in the literature gives rise to an efficient workflow that eliminates false-positive results and yields robust numbers on the prevalence and phylogenetic cohesion of resistant isolates.

Take-home messages

- *Candida auris* is a globally emerging, fluconazole resistant species associated to (nosocomial?) outbreaks
- Echinocandin resistance is emerging in *Candida glabrata*
- Potentially tied to hypermutability phenotype (*MSH2*), already present in parts of the *C. glabrata* population
- Spread of azole resistance in *A. fumigatus* is not an academic, but a clinical problem.
- It is not restricted to The Netherlands, but of global concern
- Environmental screening makes sense to estimate the prevalence in local clinics / wards

Acknowledgement

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Contributions of strains:

J. Steinmann (Nürnberg), A. Hamprecht (Köln), S. Rößler (Dresden)



Bundesministerium
für Gesundheit



 **MSD**
(Posaconazol)

Multiplex -PCR approach

(AsperGenious Assay, PathoNostics, NL)

The screenshot shows the PathoNostics website with a header menu: PATHO/NOSTICS, home, compact, products, news, contact. Below the header is a decorative graphic of blue and white circular patterns. The main content area features a product image of a white box labeled 'PATHONOSTICS AsperGenius' and text describing the AsperGenius assay as a multiplex Real Time PCR assay for the detection of *Aspergillus fumigatus* and identification of azole resistance markers. It highlights a rapid diagnosis of azole resistance within 2.5 hours. The page also includes sections for Overview, Products (listing species and resistance multiplexes), Diagnostic Specimens (BAL samples from hematology and intensive care), Quality (validation on clinical samples, CE-IVD marked), Features & benefits (direct detection on clinical samples, triazole resistance mutations, 3.5 hours diagnosis, IAC included, positive/negative control, interpretation software available), Targets (A. fumigatus, A. terreus, A. spec.), Species multiplex (A. fumigatus, A. terreus, A. spec., Internal Amplification Control), and Resistance multiplex (L98H, T284A, Y121F).

company statement: multi-platform RT-PCR
Detects *A. fumigatus*, *A. terreus*, *A. spec.* from BAL samples
From *A. fumigatus*: L98H, TR34, T289A, Y121F

Analytical and Clinical Evaluation of the PathoNostics AsperGenius Assay for Detection of Invasive Aspergillosis and Resistance to Azole Antifungal Drugs during Testing of Serum Samples

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The commercially developed PathoNostics AsperGenius species assay is a multiplex real-time PCR capable of detecting aspergillosis and genetic markers associated with azole resistance. The assay is validated for testing bronchoalveolar lavage fluids, replacing the requirement for culture and benefiting patient management. Application of this assay to less invasive, easily obtainable samples (e.g., serum) might be advantageous. The aim of this study was to determine the analytical and clinical performance of the AsperGenius species and resistance assays for testing serum samples. For the analytical evaluations, serum samples were spiked with various concentrations of *Aspergillus* genomic DNA for extraction, following international recommendations. For the clinical study, 124 DNA extracts from 14 proven/probable invasive aspergillosis (IA) cases, 2 possible IA cases, and 33 controls were tested. The resistance assay was performed on *Aspergillus fumigatus* PCR-positive samples when a sufficient fungal burden was evident. The limits of detection of the species and resistance assays for *A. fumigatus* DNA were 10 and ≥ 75 genomes/sample, respectively. Nonreproducible detection at lower burdens was achievable for all markers. With a positivity threshold of 39 cycles, the sensitivity and specificity of the species assay were 78.6% and 100%, respectively. For 7 IA cases, at least one genetic region potentially associated with azole resistance was successfully amplified, although no resistance markers were detected in this small cohort. The AsperGenius assay provides good clinical performance with the added ability to detect azole resistance directly from noninvasive samples. While the available burden will limit application, it remains a significant advancement in the diagnosis and management of aspergillosis.

White, Posso, Barnes (2015) JCM 53:2155-21

Multiplex -PCR approach

(AsperGenius Assay, PathoNostics, NL)

PATHO/NOSTICS

home compact products news contact

AsperGenius®: a multiplex Real Time PCR assay for the detection of *Aspergillus fumigatus* and identification of azole resistance markers

Overview

AsperGenius® is a multiplex real-time PCR assay developed by PathoNostics to rapidly diagnose *Aspergillus* infections and simultaneously identifies azole resistance. Within 2.5 hours, detection and characterization is accomplished in lower respiratory tract samples of *Aspergillus* infected patients. AsperGenius® allows for timely, targeted antifungal treatment resulting in reduced toxic side effects and improved treatment outcome in these patients.

The AsperGenius® multiplex PCR assay is suitable for real-time PCR instruments using melting curve analysis and has been validated on LightCycler 480 (Roche), Rotor-Gene 6000 (Corbett) and Rotor-Gene Q (QIAGEN).

Products

- AsperGenius® Species multiplex (PN-001)
 - 50 reactions
 - Detection and differentiation of *Aspergillus* species
- AsperGenius® Resistance multiplex (PN-002)
 - 50 reactions
 - Detection and differentiation of *Aspergillus* species
 - Identification of 4 azole resistance markers in *Aspergillus fumigatus*

Targets

Species multiplex

- *Aspergillus fumigatus*
- *Aspergillus terreus*
- *Aspergillus specia*
- Internal Amplification Control (IAC)

Resistance multiplex

- L98H
- Tandem repeat 3H
- T289A
- Y121F

Diagnostic Specimens

- Bronchoalveolar lavage (BAL) samples from hematology patients
- Bronchoalveolar lavage (BAL) samples from intensive care unit patients

Quality

- Validated on fungal cultures
- Validated on clinical samples (BAL)
- CE-IVD marked

Features & benefits

- Direct detection on clinical samples
- Identification of the most prevalent triazole resistance mutations
- Diagnosis within 2.5 hours after nucleic acid extraction
- Internal Amplification Control (IAC) included
- Positive control included
- Interpretation software available

company statement: multi-platform RT-PCR
Detects *A. fumigatus*, *A. terreus*, *A. spec.* from BAL samples
From *A. fumigatus*: L98H, TR34, T289A, Y121F

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J Antimicrob Chemother
doi:10.1093/jac/dkw323**Journal of
Antimicrobial
Chemotherapy**

PCR-based detection of *Aspergillus fumigatus* Cyp51A mutations on bronchoalveolar lavage: a multicentre validation of the AsperGenius assay® in 201 patients with haematological disease suspected for invasive aspergillosis

G. M. Chong^{1*}, M. T. van der Beek², P. A. von dem Borne³, J. Boelens⁴, E. Steel⁵, G. A. Kampinga⁶, L. F. R. Span⁷, K. Lagrou⁸, J. A. Maertens⁹, G. J. H. Dingemans¹⁰, G. R. Gaaijteaan¹⁰, D. W. E. van Tegelen¹⁰, J. Cornelissen¹¹, A. G. Vonk¹² and B. J. A. Rijnders¹

Results: Two hundred and one patients each contributed one BAL sample, of which 88 were positive controls and 113 were negative controls. The optimal cycle threshold cut-off value for the *Aspergillus* species PCR was <38. With this cut-off, the PCR was positive in 74/88 positive controls. The sensitivity, specificity, positive predictive value and negative predictive value were 84%, 80%, 76% and 87%, respectively. 32/74 BAL samples were culture negative. Azole treatment failure was observed in 6/8 patients with a RAM compared with 12/45 patients without RAMs ($P=0.01$). Six week mortality was 2.7 times higher in patients with RAMs (50.0% versus 18.6%; $P=0.07$).

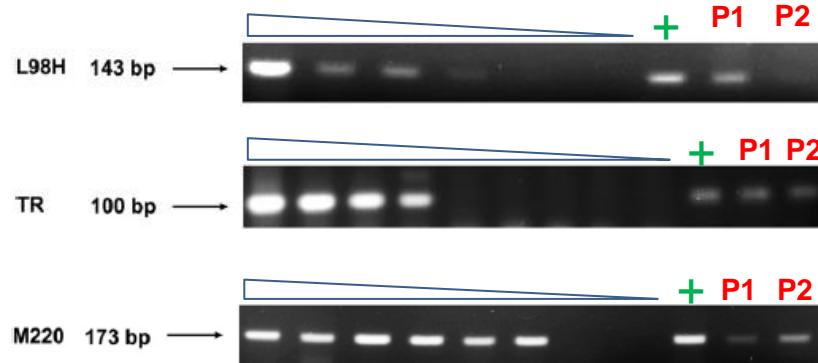
nested-PCR approach / AML case

(Spieß & Buchheidt; Mannheim)

Development of Novel PCR Assays To Detect Azole Resistance-Mediating Mutations of the *Aspergillus fumigatus cyp51A* Gene in Primary Clinical Samples from Neutropenic Patients

Birgit Spieß,^a Wolfgang Selfarth,^a Natalia Merker,^a Susan J. Howard,^b Mark Reinwald,^a Anne Dietz,^c Wolf-Karsten Hofmann,^a and Dieter Buchheidt^a

Spiess et al. (2012) AAC 56:3309-10



```

CypA-TR-S1
AGCAAGGGAGAAAGGAAAGAACACTCTGAATAATTACACTGTCTCCCTAGAAAAAAACTCATGAGTGA
CypA-TR-S_A
GGAGAAAGGAAAGAACACTCTGAATAATTACACTGTCTCCCTAGAAAAAAACTCATGAGTGA
34bp tandem repeat
ATAATCGCAGCACCACTTCAGAGTTGTCTGAATCAGCGGTCGGATGTTGCTGAGGCCAATGAAAGT
CypA-TR-AS_A
TGCTCTAAATTACTAAGGTGTAGTCCAGCATACATACACCCTAACTCATACTACGGTAGGTAGATCTACT
CypA-TR-AS1
TACCTATGAACCTATATTTGTTAGGTAGGTGAATATAAAATACAGCATGGAACATGTTTCTTATTAGCTGG
TCTCTCATTCGGCTCTGGCTTAAGGCTTAAGGAACATGGAACAGAACGCCAATGGTCTTCTTGTCTTCCATTTC
TCCTATTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG
+ 1 cds →
AAATGGTGTAGTCCAGCATACATACACCCTAACTCATACTACGGTAGGTAGATCTACT
TGTCTTATCAATTATCTTCGGCTTTGGAAACGAACAGAACGCCAATGGTCTTCTTGTCTTCCATTGGTCTTCCATT
CTGGTAGTACCATAGTTACGGGATTGATCCCTACAGGTCTTCTTGTCTGAGAAAAGGCCAAGTC
TCAAGATTGTAGTTGACATTCACTCTGGGCAATTGCTGAGATTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG
CypA-L98H-S_A
GATATCTTCACTTTACTGTGGGTCAAAACACCAGCTCTGGCGCTCAGGGAAAGAGTTA
L98H SNP: T to A (base 364)
TTCTCAACGGCAAGGCTCAAGGATGTCATCGGAAGAGGTCTATAGTCATTGACGACCCCCGTTTCGG
CypA-L98H-AS_A
ATCGGACGTGGTATGATGTCCCAATTCCAAAGCTGATGGAGCAGAAAAGTCATCAAGTACGGCTTG
ACTCAGTCTGGCTTAGAGTCTCATGTGCCACTATTGAGAAGGGAGTTTGACTATCTGCGCAGTCAC
CGAACATTCAAGGCTGTCGGCCGGATGGACATCTCTGCGCAATGGCTGAGATTACCATTTACCGC
CypA-M220-S_A
TGCTCGAGCCCTCAAGGCCAGGAAGTCGTCCTCAAACTCACGGCTGAGTCGCTGACCTCTATCATGAC
M220 SNP (base 731)
CTGGACAAGGGCTTACTCCCATAATTATGTCACCGTGGGCCCATGCGCATAACAAGAACGGAG
CypA-M220-AS_A
ATGCTGCTCATGCGCATGAGGTCAATCTACGTTGACATCATCAATCAGCGCCGCTTGACGGTGACAA

```

sequencing!

Amplification of specific *cyp51A* fragments from autopsy material (lung, heart) of the patient shown at this talk's beginning

→ confirms TR₄₆, Y121F, and T289A (region with M172 not covered)

Rößler S, Bader O, et al., AAC 2017