FLC-treated or untreated infected flies (P < 0.0001). As POSA is a cell-associated drug, we are conducting *C. auris* phagocytosis assays with Drosophila hemocytes that are co-incubated or not with POSA.

Conclusion. Drosophila is a promising, fast, and inexpensive *in-vivo* model to study pathogenesis and drug activity in *C. auris* candidiasis.

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381. Morphologic Changes Associated With Echinocandin Tolerance Enhance Immunoevasion of *Candida glabrata*

Chenlin Hu, PhD¹; Dimitrios P Kontoyiannis, MD, ScD, PhD² and <u>Nicholas</u> <u>D. Beyda</u>, PharmD, BCPS^{1,3}; ¹Pharmacy Practice and Translational Research, University of Houston College of Pharmacy, Houston, Texas, ²Department of Infectious Diseases, Infection Control, and Employee Health, The University of Texas MD Anderson Cancer Center, Houston, Texas, ³CHI St. Luke's Health - Baylor St. Luke's Medical Center, Houston, Texas

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Background. Activation of the cell wall integrity pathway and enhanced cell wall chitin synthesis are compensatory mechanisms associated with the incomplete killing of *Candida glabrata* by echinocandins. Echinocandin-induced morphologic changes in *C. glabrata* have also been described, yet their correlation with cell wall composition and macrophage responses to echinocandin treated *C. glabrata* are not well characterized. Elucidating these relationships is needed to understand how *C. glabrata* is capable of resisting both echinocandin killing and host immune responses.

Methods. Three echinocandin-susceptible bloodstream isolates of *C. glabrata* were grown in liquid RPMI with or without inhibitory concentrations of micafungin (MFG; 0.004 µg/mL) or caspofungin (CAS; 0.008 µg/mL). Cells were stained with fluorescent markers specific for cell wall chitin, mannan, and viability, then imaged utilizing high-content single-cell techniques. Phenotypic characteristics of *C. glabrata* cells that survive echinocandin exposure were determined by comparing the morphology and abundance cell wall components among the viable and nonviable cell sub-populations. To identify cellular characteristics of the nonphage phagocytosis, CAS or MFG treated cells were co-incubated RAW 264.7 macrophage and imaged as above. Phenotypic characteristics of the nonphagocytized yeast cells before and after co-incubation with macrophage was compared.

Results. Compared with untreated controls, growth in MFG and CAS significantly increased the proportion of cells with multiple-buds (50% ± 10% and 40% ± 18% vs. 12% ± 6%; P < 0.001) and induced cellular enlargement (biovolume; 35 ± 9 µm³ and 80 ± 58 µm³ vs. 26 ± 5 µm³; P < 0.001). Cell enlargement, reduced cell wall mannan, and increased chitin were highly correlated with survival to MFG and CAS exposure (P < 0.001). Comparison of the drug-exposed yeast cell population before and after co-incubation with macrophage found an increased proportion of viable cells and cells with a large diameter ($\geq 7 \mu$ M) remained un-phagocytized, indicating strong phagocytic cytic preference for small, nonviable yeast cells.

Conclusion. C. glabrata cells that survive echinocandins have distinct cell wall changes and are large in size. These cells tend to evade phagocytosis by macrophages, suggesting a potential mechanism by which C. glabrata may persist despite echinocandin treatment.

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382. Virulence in *Candida glabrata* Is Not Attenuated by FKS Mutations but Associated With the Frequency of Cells With Distinct Morphology

Chenlin Hu, PhD¹; Gary Fong, PharmD² and Nicholas D. Beyda, PharmD, BCPS^{1,2}; ¹Pharmacy Practice and Translational Research, University of Houston College of Pharmacy, Houston, Texas, ²CHI St. Luke's Health – Baylor St. Luke's Medical Center, Houston, Texas

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Background. Echinocandins are the first-line treatment for *C*. glabrata; however, echinocandin resistance is increasingly reported. Acquired *FKS*-mediated echinocandin resistance has been associated with the upregulation of chitin synthesis and attenuated fitness and virulence in *C. albicans*; however, conflicting data are reported in *C. glabrata*. Here, the influence of FKS mutations on fitness, virulence, morphology, and cell wall chitin was assessed among clinical strains of *C. glabrata*.

Methods. Three sets of isogenic paired strains consisting of an index-WT and persistent-*FKS* mutant (S663P), two un-paired *FKS* mutant strains (S663F and S629P), and a WT reference strain (CBS138) were included. Growth kinetics were measured over 24 hours in 96-well microplate containing liquid RPMI. After overnight growth in RPMI and staining with a chitin-specific fluorescent marker, morphology, and chitin were assessed at the single-cell level utilizing high-content imaging technique. Virulence was evaluated in *Galleria mellonella* larvae by injecting 10⁷ cells/larvae. Mortality was assessed daily for 5 days.

Results. Significant differences in growth kinetics, frequency of morphologic phenotypes within the cell populations (nonbudding, single-bud, multiple-buds), and

virulence were observed between strains obtained from different patients (P < 0.05 for each). However, no difference was observed between paired index-WT and persistent-*FKS* S663P mutants. Compared with index-WT and the CBS138 reference strain *FKS* mutant isolates (S663P, S629P, and S663F) had significantly elevated cell wall chitin content (P < 0.05). Neither chitin content, the presence of an *FKS* mutation, nor *in vitro* growth characteristics were found to be associated with virulence. Virulence was strongly correlated with the frequency of multi-bud cells within the population however, with 5-day post-injection survival rates of 4% vs. 28% for high-frequency (>12% multi-bud cells) and low-frequency strains, respectively (P < 0.001).

Conclusion. Acquired FKS-mediated echinocandin resistance induced significant alterations in cell wall chitin content but was not observed to attenuate fitness or virulence. Virulence was highly associated with the frequency of cells with distinct morphology.

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383. An Increased Rate of *Candida parapsilosis* Infective Endocarditis Is Associated With Injection Drug Use

J. Alexander Viehman, MD¹; Cornelius J. Clancy, MD²; Guojun Liu, BS¹; Shaoji Cheng, MD, PhD¹; Louise-Marie Oleksiuk, PharmD³; Ryan K. Shields, PharmD¹ and Minh-Hong Nguyen, MD¹; ¹Infectious Disease, University of Pittsburgh, Pittsburgh, Pennsylvania, ²Infectious Disease, University of Pittsburgh and VA Pittsburgh, Pittsburgh, Pennsylvania, ³Pharmacy and Therapeutics, UPMC Presbyterian Shadyside, Pittsburgh, Pennsylvania

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Background. Candida parapsilosis fungemia typically occurs in patients with intravascular catheters or prosthetic devices. In 2017, we noted an increase in *C. parapsilosis* infective endocarditis (IE).

Methods. We retrospectively reviewed *C. parapsilosis* fungemia and IE from January 2015 to February 2018. Species were identified using MALDI-TOF, and confirmed by ITS sequencing.

Results. Between 2010 and 2017, there was no increase in cases of C. parapsilosis fungemia (mean: 13/year), but there was a significant increase in C. parapsilosis IE (P = 0.048) (Figure 1). From January 2015 to February 2018, 22% (12/54) of C. parapsilosis fungemia was complicated by IE. Demographics of C. parapsilosis fungemia included: community-acquired infection (87%), presence of vascular catheters (80%), opiate noninjection drug use (non-IDU, 44%), IDU (20%), and presence of cardiac devices (18%). Ninety-one percent (49/54) of C. parapsilosis fungemia was caused by C. parapsilosis sensu strictu (Cpss); C. orthopsilosis and C. metapsilosis accounted for 4% (2/54) each (1 isolate could not be subtyped). Cpss, C. orthopsilosis, and C. metapsilosis accounted for 83% (10/12), 8% (1/12), and 8% (1/12) of IE, respectively. Ninety-two% (11/12) of C. parapsilosis IE was left-sided, and 33% (4/12) involved multiple valves. Risk factors for *C*, *parapsilosis* IE were past or active IDU (P < 0.001), community-ac-quired fungemia (P = 0.02), prosthetic heart valve (P = 0.01) or implanted cardiac device (P = 0.03). Receipt of an antibiotic within 30 days was a risk for C. parapsilosis fungemia without IE ($\hat{P} = 0.001$). Median age for IE vs. fungemia was 38 vs. 57 years (P = 0.09). By multivariate logistic regression, IDU (P < 0.0001), prosthetic valve (P = 0.09). 0.006) or implanted cardiac device (P = 0.04) were independent risks for C. parapsilosis IE. 70% (7/10), 20% (2/10), and 10% (1/10) of patients with IDU and C. parapsilosis IE primarily used heroin, buprenorphine/naltrexone, and cocaine, respectively. 50% (6/12) of patients with C. parapsilosis IE underwent surgery; most common initial AF regimens were caspofungin and amphotericin B. Nonsurgical patients were suppressed with long-term azole; one relapsed requiring surgery. Thirty-day and in-hospital mortality for patients with fungemia vs. IE were 32% vs. 17% and 26% vs. 17%, respectively.

Conclusion. C. parapsilosis IE has emerged at our center. Unique aspects of C. parapsilosis pathogenesis that may account for emergence are a propensity to colonize skin, adhere to prosthetic material and form biofilm. C. parapsilosis IE may be an under-appreciated consequence of IDU and opioid abuse.



Figure 1. Cases of C. parapsilosis infective endocarditis

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384. Findings From a *Candida auris* Admission Screening Pilot in New York State Elizabeth M. Dufort, MD¹; Richard Erazo, BS²; Monica Quinn, RN, MS³; Sudha Chaturvedi, PhD⁴; Snigdha Vallabhaneni, MD, MPH⁵; Valerie B. Haley, PhD⁶; Emily Lutterloh, MD, MPH⁶; Jiankun Kuang, MS⁷; Carolyn Stover, BA⁸; Coralie Bucher, MPH⁸; Robert McDonald, MD, MPH¹; Eleanor H. Adams, MD, MPH² and Debra S. Blog, MD, MPH¹; ¹Division of Epidemiology, New York State Department of Health, Albany, New York, ²Healthcare Epidemiology and Infection Control, New York State Department of Health, New Rochelle, New York, ³Health Care Epidemiology and Infection Control, New York State Department of Health, Albany, New York, ⁴Wadsworth Center, New York State Department of Health, Albany, New York, ⁵Mycotic Diseases Branch, Centers for Disease Control and Prevention, Atlanta, Georgia, ⁶Bureau of Health, Albany, New York State Department of Health, Albany, New York, ⁷New York State Department of Health, Albany, New York, ⁶University at Albany School of Public Health, State University of New York, Albany, New York

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Background. Candida auris is an emerging multidrug-resistant yeast which can spread within healthcare facilities and is associated with significant morbidity. Over 160 clinical cases have been reported in NYS. This pilot aims to assess the feasibility of *C. auris* admission screening and to better understand its role in controlling spread of *C. auris* in an area where it has emerged.

Methods. One hospital and two nursing homes (NHs) with known prior cases participated (one NH and hospital are closely associated and are reported together). Patients were screened on admission to any of three hospital intensive care units (medical, cardiac, pulmonary) or to a ventilator unit in the NHs from November 2017 to April 2018. Screening consisted of bilateral nares and axilla/groin swabs sent to the NYS Department of Health Wadsworth Center (WC) for a WC-developed *C. auris* real-time polymerase chain reaction (rt-PCR) test. Specimens with detection of *C. auris* on rt-PCR underwent fungal culture. Facilities were alerted of positive results and infection control precautions were promptly initiated.

Results. To date, 575 patients (1,371 samples) were screened. Of patients not previously known to be colonized, 39 had *C. auris* detected on rt-PCR; 34 confirmed by *C. auris* culture at either site and one culture pending. Of these, 30 (88%) were detected and confirmed from the axilla/groin specimen (Figure 1). Mean age was 76 years and 59% were females. Patients had significant healthcare facility exposure (Figure 2). Eleven (32%) were from NH-A and 23 (68%) from the hospital/NH-B combined. Rates of positivity were 16.2% (11/68) for NH-A and 4.6% (23/498) for the hospital/NH-B.

Conclusion. C. auris rt-PCR is a useful tool within an admission screening program; however, more accessible and affordable rapid laboratory diagnostics are urgently needed. The axilla/groin site detected the majority of colonized individuals. Admission screening was feasible and increased facility knowledge of colonization status, which led to earlier implementation of infection control precautions potentially limiting spread. However, further study is needed to assess transmission dynamics and potential impact of admission screening on control of C. auris within an outbreak or endemic setting.

Figure 1.

Candida auris Positive by Specimen Site (rt-PCR Positive Confirmed by Culture) From an Admission Screening Pilot



Figure 2.

Prior Residence and Healthcare Facility Type at Admission Screen Positive for Candida auris (N=33)





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385. The Value Added From *Candida auris* Point Prevalence and Environmental Studies in New York State

Eleanor H. Adams, MD, MPH1; Monica Quinn, RN, MS, CIC2; Belinda Ostrowsky, MD, MPH³; Karen Southwick, MD⁴; Jane Greenko, RN, MPH, CIC⁵ Rafael Fernandez, MPH⁶; Rutvik Patel, MSW¹; Ronald Jean Denis, BS¹; Richard Erazo, BS¹; Sudha Chaturvedi, PhD⁷; Lynn Leach, MS⁷; Yan Chun Zhu, MS⁷; Valerie B. Haley, PhD²; Sharon Tsay, MD⁸; Snigdha Vallabhaneni, MD, MPH⁹; Emily C. Lutterloh, MD, MPH²; Debra S. Blog, MD, MPH¹⁰ and Elizabeth M. Dufort, MD¹⁰; ¹Healthcare Epidemiology and Infection Control, New York State Department of Health, New Rochelle, New York, ²Bureau of Healthcare-Associated Infections, New York State Department of Health, Albany, New York, ³Dhqp, Centers for Disease Control and Prevention, New York, New York, ⁴New York State Department of Health, Albany, New York, ⁵Healthcare Epidemiology and Infection Control, New York State Department of Health, Central Islip, New York, 6Healthcare Epidemiology and Infection Control, New York State Department of Health, New York, New York Wadsworth Center, New York State Department of Health, Albany, New York, ⁸Epidemic Intelligence Service, Centers for Disease Control and Prevention, Atlanta, Georgia, ⁹Mycotic Diseases Branch, Centers for Disease Control and Prevention, Atlanta, Georgia, ¹⁰Division of Epidemiology, New York State Department of Health, Albany, New York

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Background. As of March 25 2018, 151 clinical cases of *C. auris* were diagnosed in NYS. We conducted point prevalence surveys (PPS) and environmental surveys (ES) to detect surveillance cases and assess the burden of environmental contamination in NYS healthcare facilities from September 12, 2016.

Methods. A PPS was defined as culturing ≥ 2 individuals at a healthcare facility that diagnosed, cared for, or was near a facility with a *C. auris* case. ES involved environmental swabbing in facilities where cases resided or were admitted. Cultures and polymerase chain reaction (PCR) were performed at the NYS Wadsworth Center.

Results. As of March 25, 2018, 81 PPS or ES had been conducted at 55 facilities. From these PPS, a total of 144 (6.1%) individuals were positive for *C. auris* by culture; 125 were PCR positive. The rates of culture positive *C. auris* identified patients varied by facility type: hospitals (38/767, 5.0%), long-term care facilities (LTCF) (88/1,404, 6.3%), long-term acute care (1/35, 2.9%), and co-located hospital and LTCF (17/138, 12.3%). The majority of the LTCF *C. auris* culture-positive cases (80/82) were identified patients ware nearly 10 times as high as other LTCF [86/1,121 (7.7%) vs. 2/284 (0.7%)]. ES identified 86 (3.0%) samples positive by culture and 257 (8.9%) by PCR. Thirty-seven (67%) of the 55 facilities had at least one positive environmental sample by PCR or culture; many of these positive samples were from surfaces or equipment deemed to be "clean." Over 1,900 person-hours were needed to conduct onsite PPS and ES that collected >4,200 human and >2,800 environmental samples and identified opportunities for improving basic infection prevention and environmental cleaning. Ten facilities, including the co-located hospital and LTCF, had multiple positive PPS or ES.

Conclusion. PPS conducted over 17 months detected many colonized individuals and *C. auris* in facility environments, likely indicating a silent reservoir for this organism beyond clinical cases, especially in LTCFs. Serial PPS and ES can help improve *C. auris* detection and inform subsequent infection prevention and control interventions. However, these efforts are resource intensive and can divert resources from other activities.

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