



# Echinocandin MICs against *Candida* species at hospitals that routinely perform susceptibility testing of bloodstream isolates

GA Eschenauer, MH Nguyen, S Shoham, JA Vazquez, AJ Morris, WA Pasculle, CJ Kubin, KP Klinker, PL Carver, KE Hanson, S Chen, SW Lam, BA Potoski, LG Clarke, RK Shields, CJ Clancy

A collaboration among investigators from nine centers in the United States, Australia and New Zealand



eP232

## Background

- Reference broth microdilution methods of testing *Candida* strains for susceptibility to echinocandins are limited by inter-laboratory variability in caspofungin minimum inhibitory concentrations (MICs)
- Revised Clinical Laboratory Standards Institute (CLSI) breakpoint MICs for echinocandin non-susceptibility may not be valid for commercial assays employed in hospital microbiology laboratories

## Goals

- To report on echinocandin susceptibility testing methods, echinocandin MICs, and susceptibility patterns for *Candida* bloodstream isolates (BSI), as determined by hospital microbiology laboratories that perform routine testing

## Methods

- We performed a retrospective, multicenter study of nine hospitals in the United States, Australia and New Zealand that routinely tested *Candida* for echinocandin susceptibility from 2005-2013
  - University of Pittsburgh, Johns Hopkins, Henry Ford Hospital, New York Presbyterian, University of Florida, University of Utah, Cleveland Clinic, Auckland City Hospital, Westmead Hospital
- C. glabrata* strains with discrepant echinocandin susceptibility profiles (caspofungin-R or I/others-S) were sequenced for *FKS* mutations

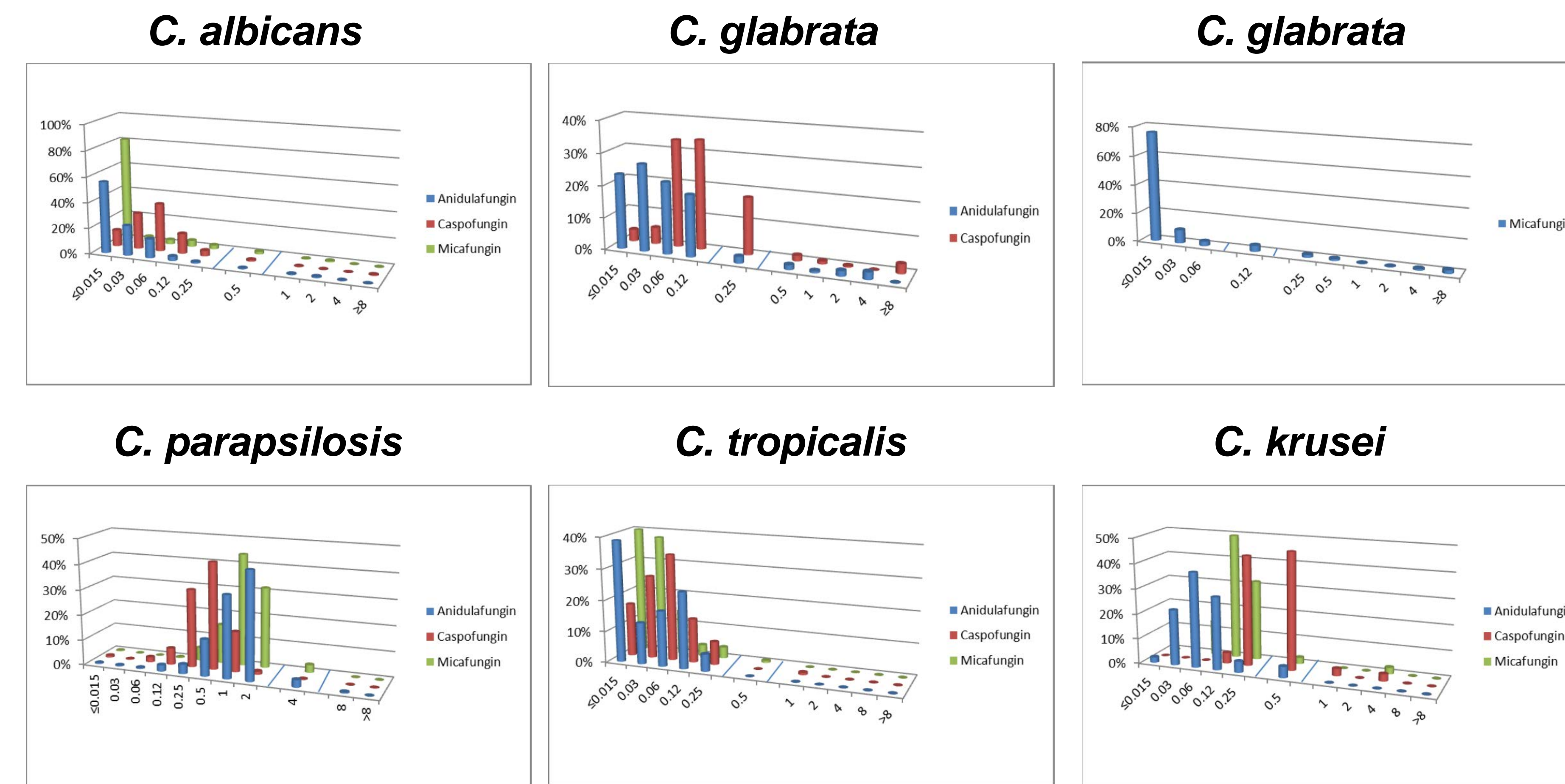
## Results

- We first surveyed 15 large tertiary care hospitals in the U.S., and determined that 53% (8/15) routinely performed echinocandin susceptibility testing of *Candida* BSI
- At the nine centers in this study, 2,897 BSI were tested
  - Anidulafungin (1,467), Caspofungin (2,355), Micafungin (2,004)
  - 8/9 centers used YeastOne; 1/9 used CLSI broth microdilution

Table 1. Echinocandin MICs against *Candida* spp.

Species	Agent	n	MIC						
			≤0.06	0.125	0.25	0.5	1	≥8	
<i>C. albicans</i>	ANF	555	93.7%	3.2%	1.1%	0.5%	0.5%	0.2%	0%
	CSF	906	77.9%	15.6%	4.3%	1.2%	0.3%	0.1%	0.6%
	MCF	704	88.8%	4.8%	3.0%	2.0%	0.4%	0.9%	0.1%
<i>C. glabrata</i>	ANF	480	72.7%	19.2%	2.1%	1.5%	0.6%	1.7%	2.3%
	CSF	754	42.3%	34.0%	17.8%	1.7%	0.9%	0.4%	2.9%
	MCF	634	88.3%	4.3%	2.1%	1.3%	0.3%	1.1%	2.4%
<i>C. parapsilosis</i>	ANF	241	1.2%	2.5%	3.7%	14.5%	32.4%	42.3%	2.9%
	CSF	396	3.0%	6.6%	30.8%	42.2%	15.9%	1.3%	0.3%
	MCF	329	0.3%	0.3%	5.2%	15.5%	44.1%	31.0%	3.0%
<i>C. tropicalis</i>	ANF	90	70.0%	24.4%	5.6%	0.0%	0.0%	0.0%	0.0%
	CSF	135	77.8%	14.1%	7.4%	0.0%	0.7%	0.0%	0.0%
	MCF	140	92.1%	3.6%	3.6%	0.7%	0.0%	0.0%	0.0%
<i>C. krusei</i>	ANF	45	62.2%	28.9%	4.4%	4.4%	0.0%	0.0%	0.0%
	CSF	71	10.9%	4.2%	43.7%	46.5%	2.8%	0.0%	0.0%
	MCF	79	13.9%	49.4%	31.6%	2.5%	0.0%	2.5%	0.0%
<i>C. lusitanae</i>	ANF	31	12.9%	51.6%	22.6%	12.9%	0.0%	0.0%	0.0%
	CSF	44	15.9%	15.9%	34.1%	27.3%	4.5%	0.0%	2.3%
	MCF	44	50.0%	38.6%	2.3%	9.1%	0.0%	0.0%	0.0%
<i>C. dubliniensis</i>	ANF	16	50.0%	37.5%	0.0%	0.0%	0.0%	0.0%	12.5%
	CSF	26	61.5%	30.8%	0.0%	0.0%	0.0%	0.0%	7.7%
	MCF	26	88.5%	3.8%	0.0%	0.0%	0.0%	0.0%	7.7%

Figure 1. Echinocandin MICs against five most common *Candida* spp.

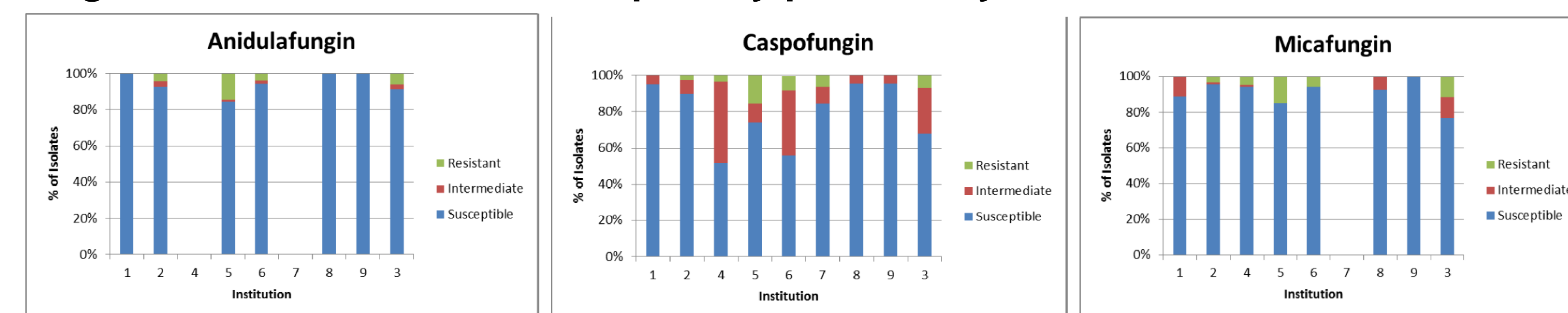


- Modal MICs and susceptibility patterns were essentially unchanged if data were only taken from centers that used YeastOne

Table 2. Echinocandin MIC distribution by center

MIC	Anidulafungin									Caspofungin									Micafungin											
	Center	1	2	4	5	6	7	8	9	3	Center	1	2	4	5	6	7	8	9	3	Center	1	2	4	5	6	7	8	9	3
≤0.008	1	8	0	0	1	NT	6	0	0	0	≤0.015	9	5	3	1	5	0	3	4	85	≤0.008	8	42	73	70	48	NT	23	36	0
0.015	2	44	0	42	17	NT	10	28	150	0.03	56	48	2	41	29	21	19	28	10	0.015	0	40	65	24	9	NT	5	23	106	
0.06	5	22	1	29	29	NT	7	18	18	0.06	75	39	1	34	37	51	18	26	56	0.03	0	1	17	3	3	NT	0	4	1	
0.125	0	13	0	23	12	NT	4	15	15	0.125	32	4	0	20	22	20	9	8	26	0.06	0	0	3	1	1	NT	2	1	16	
0.25	0	0	0	2	1	NT	2	6	2	0.25	10	1	4	2	5	5	0	1	11	0.125	0	1	1	0	1	NT	0	0	35	
0.5	0	0	0	2	1	NT	1	0	2	0.5	1	0	0	6	1	0	0	3	3	0.25	0	0	0	1	0	NT	0	0	20	
1	0	0	0	0	2	NT	0	0	1	1	0	0	0	1	0	0	0	2	2	0.5	0	0	0	0	1	NT	0	0	13	
2	0	0	0	0	0	NT	0	1	2	2	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	NT	0	0	3
≥4	0	0	0	0	0	NT	0	0	1	≥4	0	0	0	1	1	2	0	1	0	≥4	0	0	0	0	0	0	NT	0	0	1

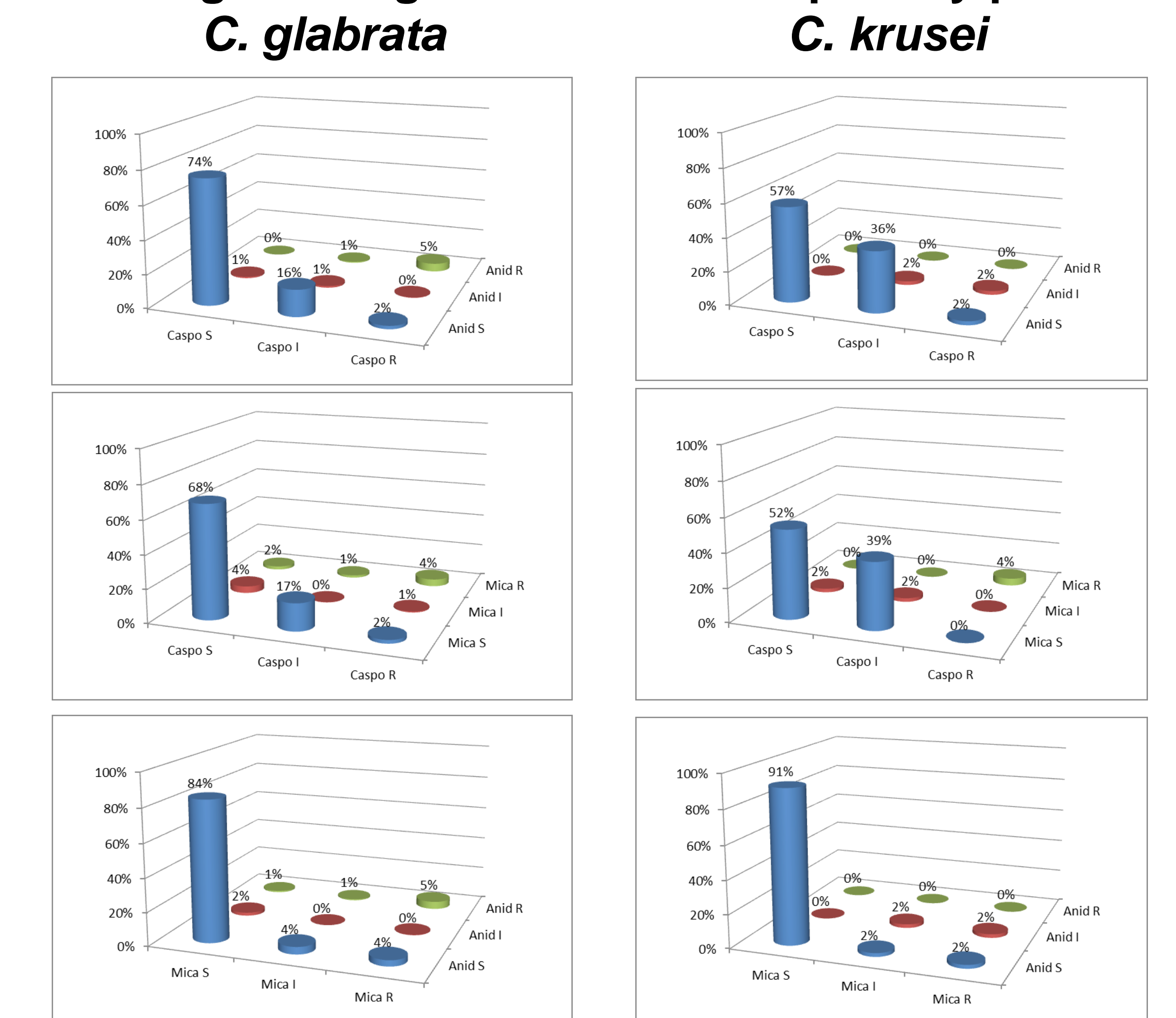
Figure 2. Echinocandin susceptibility patterns by center



- C. glabrata* resistance rates for each agent were comparable across centers
- C. glabrata* intermediate rates varied more for caspofungin (5% to 45%) than anidulafungin (0% to 3.1%) or micafungin (0% to 11.5%)

- Intercenter variability in MICs was lessened if only YeastOne data were considered
  - Modal caspofungin MICs were within 2 dilutions against *C. glabrata* and a single dilution against other spp.
  - Modal anidulafungin and micafungin MICs were within a single dilution against each of the 5 most common *Candida* spp.

Figure 3. Categorical agreement in susceptibility patterns



- Using CLSI breakpoints, 18% and 19% of *C. glabrata* were anidulafungin-susceptible/caspofungin-non-susceptible and micafungin-susceptible/caspofungin-non-susceptible, respectively
- Likewise, 38% and 39% of *C. krusei* were anidulafungin-susceptible/caspofungin-non-susceptible and micafungin-susceptible/caspofungin-non-susceptible, respectively
- Only 6.7% (2/30) of *C. glabrata* strains with discrepant susceptibility patterns (caspofungin-non-susceptible/other agents-susceptible) had *FKS* mutations

## Conclusions

- YeastOne assays employed in hospitals may reduce the inter-laboratory variability in caspofungin MICs against *Candida* spp. that are observed between reference laboratories using CLSI or EUCAST broth microdilution methods
- Echinocandin resistance was most common for *C. glabrata* and *C. krusei*, but rates were stable over the study period
- Hospitals may overstate caspofungin-non-susceptibility rates among *C. glabrata* and *C. krusei* by using CLSI breakpoints to interpret YeastOne MICs
- The classification of *C. glabrata* strains as caspofungin-non-susceptible and anidulafungin/micafungin susceptible is likely a breakpoint artifact, as few strains carry *FKS* mutations.