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Antifungal susceptibility testing results of New Zealand yeast isolates, 2001–2015: Impact of recent CLSI breakpoints and epidemiological cut-off values for *Candida* and other yeast species

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ABSTRACT

Objectives: We reviewed the antifungal susceptibility testing results of local yeast isolates (2001–2015) to record the impact of recently updated interpretive criteria and epidemiological cut-off values (ECVs) for yeast species.
Methods: Susceptibility testing was performed using Sensititre® YeastOne®. The results were interpreted following CLSI criteria or YeastOne-derived ECVs.
Results: A total of 2345 isolates were tested; 62.0% were from sterile body sites or tissue. Application of new CLSI interpretative criteria for fluconazole increased the proportion of non-susceptible isolates of *Candida parapsilosis*, *Candida tropicalis* and *Candida glabrata* ($P \leq 0.03$ for all species). For voriconazole, the greatest increase was for *C. tropicalis* ($P < 0.0001$). Application of new CLSI interpretive criteria for caspofungin increased the proportion of non-susceptible isolates for *C. glabrata* and *Pichia kudriavzevii* ($P < 0.0001$ for both). The new amphotericin ECV ($\leq$2 mg/L) did not reveal any non-wild-type (non-WT) isolates in the five species covered. YeastOne itraconazole ECVs detected 2%, 5% and 6% non-WT isolates for *P. kudriavzevii*, *C. tropicalis* and *C. glabrata*, respectively. No itraconazole non-WT isolates of *Clavispora lusitaniae* were detected.
Conclusions: Whilst most results are similar to other large surveys of fungal susceptibility, the new CLSI interpretive criteria significantly altered the proportion of non-susceptible isolates to fluconazole, voriconazole and caspofungin for several *Candida* spp. Application of CLSI and YeastOne-derived ECVs revealed the presence of a low proportion of non-WT isolates for many species. The results serve as a baseline to monitor the susceptibility of *Candida* and other yeast species in New Zealand over time.
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1. Introduction

Fungi cause serious infections, especially in immunocompromised patients, and *Candida* spp. also cause troublesome mucocutaneous infections [1,2]. The incidence of non-*albicans* *Candida* spp. has been increasing and several of these species have reduced susceptibility to azole antifungal agents [1,3,4].

Significant work has been undertaken to improve antifungal susceptibility testing both for yeast and moulds [4–8]. There is also good evidence that antifungal susceptibility testing results help predict those yeast isolates more likely to respond, or more importantly unlikely to respond, to antifungal therapy [4,6,9,10]. Current interpretive criteria take into account pharmacological data, wild-type minimum inhibitory concentration (MIC) distributions, epidemiological cut-off values (ECVs), as well as molecular and clinical data [7–13]. In addition, there are encouraging moves to align Clinical and Laboratory Standards Institute (CLSI) and European Committee on Antimicrobial Susceptibility Testing (EUCAST) interpretive criteria [9,11].

ECVs are useful in distinguishing between wild-type (WT) isolates, without mutational or acquired resistance mechanisms, and non-WT isolates, which are more likely to harbour mutational or acquired resistance mechanisms [9,10,14–16].

Whilst there are limited data on the susceptibility of *Candida* spp. in New Zealand, they are several years old or are limited to nail isolates of non-*albicans* *Candida* spp. [17–19]. Likewise, there are limited Australian data [20,21]. The aims of this study were to analyse the antifungal susceptibility testing results of yeast isolates

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tested at the New Zealand Mycology Reference Laboratory at Auckland City Hospital (Auckland, New Zealand) for the period 2001–2015 in order to determine the impact of recent CLSI interpretive criteria and to record the local prevalence of non-WT strains using the new CLSI and other recent ECVs for yeast species [14–16,22,23].

2. Methods

All isolates from Auckland City Hospital, or those referred from other New Zealand hospitals, for the 15-year period 2001–2015 were included in this study. Antifungal susceptibility testing was performed in the National Mycology Reference Laboratory. Antifungal susceptibility results are entered into the laboratory information system, which was searched for all entries for the 15-year period. Extracted data were analysed using Microsoft Excel (Microsoft Corp., Redmond, WA).

2.1. Isolates

Only the first isolate of any species was included for each patient. If there were multiple isolates of the same species recovered from a patient at the same time, the more resistant isolate was included for analysis. If susceptibility results were the same, the most invasive isolate was included. In the early years, identification methods were carbohydrate fermentation or assimilation (bioMérieux ID32C; bioMérieux, Marcy-l'Étoile, France) and morphology; from 2004, CHROMagar™ *Candida* (Fort Richards Laboratory, Auckland, New Zealand) was used to identify *Candida albicans*; and from 2012, matrix-assisted laser desorption/ionisation time-of-flight (MALDI-TOF) (VITEK® MS; bioMérieux) replaced carbohydrate utilisation tests and morphology for non-*albicans Candida* spp. Only rare isolates were identified by molecular methods.

2.2. Antifungal susceptibility testing

All isolates were tested by the broth colorimetric microdilution method Sensititre® YeastOne® (TREK Diagnostic Systems, East Grinstead, UK). Procedures followed manufacturer and CLSI methods [12–14,24,25]. The YO-3 panel was used until July 2005, the YO-5 panel until May 2006 and the YO-6 until February 2007, when the YO-8 was introduced. In March 2012, YO-10 was used for systemic isolates. Microtitre broths were read manually by recording the lowest antifungal concentration showing inhibition of growth as indicated by the colour change in the colorimetric growth indicator broth as specified by the manufacturer. All cryptococci were read at 72 h and other species were read at 24 h. Rare isolates were read at 48 h if required for the growth control to become positive.

Amphotericin B (AmB), 5-fluorocytosine (5FC), ketoconazole, fluconazole (FLU) and itraconazole (ITR) were tested throughout the 15-year period. Voriconazole (VRC), caspofungin (CAS) and posaconazole (POS) testing was introduced in late 2002, mid-2005 and mid-2006, respectively. For *Clavispora lusitaniae* (formerly *Candida lusitaniae*) isolates, the AmB broth MIC was checked by performing AmB disk susceptibility testing [23]. As no discrepancies in interpretation were observed, the broth AmB MICs were used in the data analysis. FLU was tested using a 0.12–256 mg/L dilution series, 5FC using 0.03–64 mg/L and the other six agents were tested using 0.008–16 mg/L. The control organisms *Candida krusei* ATCC® 6258 and *Candida parapsilosis* ATCC® 22019 were used for quality control of each delivery of Sensititre® YeastOne® plates, which was ca. every 2 months. An isolate's results were only recorded and reported when the MICs for the control organisms were within the acceptable range. CLSI interpretive criteria were used [12,13]. ECV evaluation followed a cascade approach: first, with YeastOne-derived ECVs for azoles [22] and CAS [23], then using CLSI ECVs [14] and then CLSI method-derived ECVs [15,16]. Where the CLSI-derived ECVs differed between these references, the later 2014 ECVs were used [16].

In recent years, two other New Zealand laboratories also perform antifungal susceptibility testing on yeasts. These were contacted and asked how many tests they would perform in a year.

Differences in non-susceptible rates between the previous and revised breakpoints were assessed for significance by Fisher's exact test. A P-value of ≤ 0.05 was considered statistically significant.

3. Results

3.1. Isolates

Over the 15-year period (2001–2015), 2345 initial isolates from 2167 patients were tested. Most isolates (1649/2345; 70.3%) were from Auckland patients, including 1289 (55.0%) from Auckland City Hospital itself, whereas 505 (21.5%) were from other North Island laboratories and 191 (8.1%) were from South Island laboratories.

Candida spp. predominated (2188/2345; 93.3%), followed by *Cryptococcus* spp. (88/2345; 3.8%) and other yeast species (69/2345; 2.9%). Cryptococci included *Cryptococcus neoformans* ($n = 85$), *Cryptococcus gattii* ($n = 1$) and *Cryptococcus laurentii* ($n = 2$). Other yeasts included *Saccharomyces* spp. ($n = 28$), *Rhodotorula* spp. ($n = 18$), *Pichia* spp. other than *Pichia kudriavzevii* (formerly *Candida krusei*) ($n = 6$), *Trichosporon* spp. ($n = 7$), *Magnusiomyces capitatus* ($n = 3$), *Malassezia pachydermatis* ($n = 2$), *Kodamaea ohmeri* ($n = 1$), *Lodderomyces elongisporus* ($n = 1$), *Pseudozyma* sp. ($n = 1$) and non-speciated ($n = 2$) .The most common *Candida* and other species were *C. albicans* ($n = 1036$; 47.3% of *Candida* spp. and 44.2% of all isolates), *Candida glabrata* complex ($n = 448$; 20.5% and 19.1%, respectively), *C. parapsilosis* complex ($n = 422$; 19.3% and 18.0%, respectively), *Candida tropicalis* ($n = 89$; 4.1% and 3.8%, respectively), *Meyerozyma guilliermondii* (formerly *Candida guilliermondii*) ($n = 49$; 2.2% and 2.1%, respectively), *P. kudriavzevii* ($n = 51$; 2.3% and 2.2%, respectively), *C. lusitaniae* ($n = 44$; 2.0% and 1.9%, respectively) and *Candida dubliniensis* ($n = 16$; both 0.7%). Other species were *Candida haemulonii* ($n = 7$ isolates), *Kluyveromyces marxianus* ($n = 7$), *Pichia norvegensis* ($n = 5$), *Wickerhamomyces anomalus* ($n = 2$), *Candida variabilis* ($n = 2$), *Candida utilis* ($n = 2$), *Candida rugosa* ($n = 2$), *Candida inconspicua* ($n = 1$), *Yarrowia lipolytica* ($n = 1$) and non-speciated *Candida* ($n = 4$).

More than one-third of the isolates (811; 34.6%) were from blood cultures, followed by the genital tract (541; 23.1%), abdomen (199; 8.5%), continuous ambulatory peritoneal dialysate fluid (174; 7.4%), urine (152; 6.5%), respiratory tract (139; 5.9%), musculoskeletal (79; 3.4%), wound (56; 2.4%), central nervous system (43; 1.8%) and other sites (151; 6.4%). Overall, 62.0% of isolates were from sterile body sites or tissue, including bronchial wash or bronchoalveolar lavage specimens.

3.2. Antifungal susceptibility testing results

Full yeast antifungal susceptibility testing results for all agents, as well as breakpoint and ECV MICs used for each main species/complex, are available in the Supplementary tables. Summary categorical results for the three antifungal agents with CLSI interpretive criteria [13] for species with ≥ 20 isolates are shown in Table 1. Azole results showed activity for most agents, apart from the expected reduced activity against *P. kudriavzevii* (Supplementary Table S1) and *C. glabrata*. The 2012 CLSI interpretive criteria for FLU significantly changed the proportion of susceptible dose-dependent (SDD) and resistant isolates for all four species with updated criteria ($P \leq 0.03$ for all species; data not shown). For

Table 1
Susceptibility of New Zealand yeast species/complexes to antifungal agents with Clinical and Laboratory Standards Institute (CLSI) clinical breakpoints.

Species	Descriptor	FLU	VRC	CAS
Candida albicans	*N*	1035	878	654
	MIC range (mg/L)	≤0.125 to >64	≤0.016 to >16	0.16–0.5
	MIC_{90} (mg/L)	1	0.03	0.125
	S (%)	94.9	96.5	98.9
	SDD or I (%)	1.7	1.8	1.1
	R (%)	3.4	1.7	0
Candida glabrata complex	*N*	448		342
	MIC range (mg/L)	0.5 to ≥64		0.16–2
	MIC_{90} (mg/L)	≥64		0.125
	S (%)	NA		92.7
	SDD or I (%)	88.6		6.4
	R (%)	11.4		0.9
Meyerozyma guilliermondii	*N*			30
	MIC range (mg/L)			0.16 to ≥16
	MIC_{90} (mg/L)			1.0
	S (%)			96.6
	R (%)			3.4
Pichia kudriavzevii	*N*		48	45
	MIC range (mg/L)		0.06–4	0.125–1
	MIC_{90} (mg/L)		0.5	0.5
	S (%)		91.7	66.7
	SDD or I (%)		6.3	31.1
	R (%)		2.1	2.2
Candida parapsilosis complex	*N*	421	366	276
	MIC range (mg/L)	≤0.125 to ≥64	≤0.016–0.5	0.03 to ≥16
	MIC_{90} (mg/L)	4	0.06	1.0
	S (%)	85.3	98.4	99.3
	SDD or I (%)	10.7	1.6	0
	R (%)	4	0	0.7
Candida tropicalis	*N*	88	74	51
	MIC range (mg/L)	0.5 to ≥64	≤0.016–8	0.016–1
	MIC_{90} (mg/L)	8	0.5	0.125
	S (%)	79.5	66.3	96.1
	SDD or I (%)	9.1	29.7	0
	R (%)	11.4	4	3.9

FLU, fluconazole; VRC, voriconazole; CAS, caspofungin; MIC, minimum inhibitory concentration; MIC_{90}, MIC for 90% of the isolates; S, susceptible; SDD, susceptible dose-dependent; I, intermediate; R, resistant; NA, not applicable.

VRC, the proportion of non-susceptible strains significantly increased for *C. albicans*, *C. parapsilosis* and *C. tropicalis* when the 2012 CLSI criteria were applied ($P \leq 0.03$ for all species; data not shown). There is no VRC CLSI breakpoint for *C. glabrata* complex but the suggested resistance breakpoint of ≥1 mg/L [26] indicated 13.3% resistant (Supplementary Table S2). The YeastOne-derived ECV (≤2 mg/L) for VRC against *C. glabrata* [22] put the non-WT proportion at only 2.7% (Table 2). Other than for *P. kudriavzevii*, the CAS MICs for most local yeast isolates were susceptible by CLSI breakpoints [13]. The new CLSI interpretive criteria for CAS significantly impacted the classification of *C. glabrata* and *P. kudriavzevii*, where the proportion of non-susceptible isolates rose from 0% to 7% and 33% respectively ($P < 0.0001$ for both species). The latter was due to the new breakpoint bisecting the MIC distribution (Supplementary Table S8).

The proportion of WT isolates for species/complexes without CLSI breakpoint criteria is shown in Table 2. For AmB, MICs for most isolates (98%) fell within the narrow range of 0.25–1.0 mg/L, and MICs were rarely >1 mg/L. The AmB MICs for *C. lusitaniae* were all ≤1.0 mg/L, and disk testing confirmed the YeastOne® MIC results. All isolates from all five species covered by the new CLSI AmB ECVs were WT strains (i.e. MICs ≤ 2 mg/L) or for *C. lusitaniae* published ECV also ≤2 mg/L [15] (Table 2). YeastOne ITR ECVs [22], which match the new CLSI ECVs [14], detected 2%, 5% and 6% non-WT isolates for *P. kudriavzevii*, *C. tropicalis* and *C. glabrata*, respectively (Table 2). No ITR non-WT isolates of *C. lusitaniae* were detected. Overall, AmB and CAS had the greatest proportion of isolates classified as being susceptible/WT (Tables 1 and 2).

In the earlier years of the study period almost all susceptibility testing in New Zealand was performed by the New Zealand Mycology Reference Laboratory. From information provided, New Zealand Mycology Reference Laboratory now performs ca. 75% of yeast susceptibility testing in New Zealand [personal communication, Dr A. Werno (Christchurch Hospital, Christchurch, New Zealand) and Dr C. Mansell (Waikato Hospital, Hamilton, New Zealand)].

4. Discussion

This study significantly updates antifungal susceptibility data for New Zealand. Direct comparisons with previous data are difficult because of either the testing method used (i.e. Etest [17]), lack of MIC data [18] or limited to non-*albicans Candida* spp. causing onychomycosis [19]. As far as comparisons can be made, it would appear that there has not been a shift in the susceptibility of *Candida* spp. in the past 15–20 years. A recent candidaemia report from Australia reported the Sensititre® YeastOne® susceptibility profiles of 494 isolates [20], and most of the MIC_{90} values in the current study were within a dilution of that report for the main species/complexes. Whilst we observed a small, but consistent,

Table 2
Proportion of wild-type New Zealand yeast species/complexes for those with epidemiological cut-off value (ECV) criteria only.

Species	Descriptor	FLU	VRC	POS	ITR	AmB	CAS
Candida albicans	*N*			559	1018	1034	
	MIC range (mg/L)			≤0.008 to >8	≤0.08 to >8	0.016–1	
	MIC_{90} (mg/L)			0.06	0.125	1	
	ECV			≤0.25[a]	≤0.5[a]	≤2[b]	
	WT (%)			96.4	98.3	100	
Candida glabrata complex	*N*		414	317	439	448	
	MIC range (mg/L)		≤0.016 to >16	0.016 to >8	0.03 to >8	0.125–2	
	MIC_{90} (mg/L)		1	2	2	1	
	ECV		≤2[a]	≤4[a]	≤4[a]	≤2[b]	
	WT (%)		97.3	90.5	94.1	100	
Meyerozyma guilliermondii	*N*	49	41	28	47	49	
	MIC range (mg/L)	0.5–32	≤0.016–0.5	0.016–0.5	0.03–1	0.125–1	
	MIC_{90} (mg/L)	16	0.25	0.5	1	0.5	
	ECV	≤8[c]	≤0.12[c]	≤0.5[c]	≤1[d]	≤2[d]	
	WT (%)	87.8	85.4	100	100	100	
Pichia kudriavzevii	*N*	51		44	51	51	
	MIC range (mg/L)	32 to ≥256		0.06–1	0.03–8	0.25–2	
	MIC_{90} (mg/L)	128		0.5	0.5	1	
	ECV	≤256[a]		≤1[a]	≤1[a]	≤2[b]	
	WT (%)	100		100	98	100	
Clavispora lusitaniae	*N*	44	42	33	44	44	37
	MIC range (mg/L)	≤0.125 to ≥64	≤0.016–0.5	≤0.008–0.25	≤0.008–0.5	≤0.016–1	≤0.008–0.5
	MIC_{90} (mg/L)	8	0.125	0.125	0.5	0.5	0.5
	ECV	≤1[c]	≤0.06[c]	≤0.06[c]	≤1[b]	≤2[d]	≤1[e]
	WT (%)	56.8	88.1	84.5	100	100	100
Candida parapsilosis complex	*N*			247	418	422	
	MIC range (mg/L)			≤0.008–0.5	≤0.008–0.5	0.06–2	
	MIC_{90} (mg/L)			0.125	0.25	1.0	
	ECV			≤0.12[a]	≤0.5[a]	≤2[b]	
	WT (%)			98.8	100	100	
Candida tropicalis	*N*			48	88	89	
	MIC range (mg/L)			0.016 to >8	0.03–8	0.25–1	
	MIC_{90} (mg/L)			1	0.5	1	
	ECV			≤2[a]	≤0.5[a]	≤2[b]	
	WT (%)			97.9	95.5	100	

FLU, fluconazole; VRC, voriconazole; POS, posaconazole; ITR, itraconazole; AmB, amphotericin B; CAS, caspofungin; MIC, minimum inhibitory concentration; MIC_{90}, MIC for 90% of the isolates; WT, wild-type.
[a] Reference [22].
[b] Reference [14].
[c] Reference [16].
[d] Reference [15].
[e] Reference [23].

higher proportion of resistant or non-WT isolates for most species/antifungal agent pairs, there were a few where we appeared to have more non-WT isolates: in the *C. glabrata* complex for VRC and POS (35% vs. 9.8% and 19% vs. 3%, respectively); for *P. kudriavzevii* and FLU (49% vs. 23.1%); and the proportion of non-susceptible isolates in the *C. parapsilosis* complex for fluconazole (14.7% vs. 1.2%). A recent review summarised the susceptibility of *Candida* spp. causing invasive disease in the Asia-Pacific region [27]. The AmB results in the current study matched regional MICs and all were WT isolates. The current results for FLU, VRC, POS, ITR and 5FC (Supplementary Table S7) were mostly the same or within the range of susceptibilities reported in countries in this region, with exceptions where we observed a higher proportion of resistant or non-WT isolates including: *C. albicans* for FLU (3.4% vs. <1% regionally); and *C. glabrata* complex for VRC and POS (35.3% vs. ≤17.8% and 19.2% vs. ≤10%, respectively). Overall, however, the current susceptibility results are very similar to Australian and regional blood culture isolates of *Candida* spp. [20,27].

In this report, interpretive CLSI breakpoints were used to categorise isolates by MICs generated with the Sensititre® YeastOne® method. CLSI and CLSI method-derived ECVs were also used where no Sensititre® YeastOne® ECVs existed. This was done for a number of reasons. First, the two methods generate similar MICs for many species/antifungal combinations [28–31]. In comparisons between Sensititre® YeastOne® and CLSI-generated ECVs for nine antifungals and six species, the median YeastOne ECVs were within one dilution of CLSI method ECVs for 37 (73%) of the 51 species/antifungal pairings and within two dilutions for 48 (94%) comparisons [22,32]. The third is simply pragmatic. The Sensititre® YeastOne® method is the most common yeast susceptibility testing method used in clinical laboratories. Without method-specific criteria, laboratories adopt CLSI criteria to report their results. Finally, our results will be comparable with those generated by many laboratories globally.

Others have either reported on the impact of the recent CLSI interpretive criteria [26] or have MIC data that allow the change to be calculated [9,33]. Fothergill et al. reviewed their CLSI method-derived results and observed a significant increase in the proportion classified as resistant for VRC in *C. glabrata* complex and for FLU in *C. albicans* [26]. We observed for FLU and *C. parapsilosis* complex an increase in non-susceptible isolates from 1.5% to 14.7% (Supplementary Table S1); the corresponding

changes reported by Pfaller et al. [9] and Schmalreck et al. [33] were from 2.6% to 6.8% and from 4.7% to 70%, respectively.

The proportion of *P. kudriavzevii* isolates for which the CAS MIC is above the CLSI criterion for susceptibility (i.e. 0.25 mg/L) has varied in recent studies. In their collection of global invasive isolates of *P. kudriavzevii*, Pfaller et al. observed that whilst overall 3.7% of isolates were non-susceptible, the proportion varied between 0% to 18.5% (median 5.1%) over the period 2001–2009 [34,35]. Among 16 isolates of *P. kudriavzevii* in the 2009 SENTRY study, the CAS MIC_{50} and MIC_{90} values were 0.5 mg/L and 1.0 mg/L, respectively, and the CAS MIC for 12.5% of the isolates was >0.5 mg/L [36]. In Europe, for 46 German and Austrian *P. kudriavzevii* isolates the CAS MIC range was 0.06–2.0 mg/L and the MIC_{50} and MIC_{90} values were 0.25 mg/L and 1.0 mg/L, respectively, and for 12.5% of isolates the MIC was >0.25 mg/L [37]. Whilst all 13 recently reported Australian blood isolates of *P. kudriavzevii* were susceptible to CAS [20], the proportions of non-susceptible isolates in recently published MIC distributions were 3.7% and 15.2% [10,33]. Our proportion of non-susceptible isolates (33%) appears high compared with other reports. Whilst this may partly reflect the Sensititre® YeastOne® method used, it was not due to the generation of a wide range of MICs as reported with CLSI and EUCAST methods for CAS [38], as 43 (96%) of the 45 MICs were either 0.25 mg/L or 0.5 mg/L. This is in keeping with the low modal MIC variability of Sensititre® YeastOne®-derived CAS MICs reported by Eschenauer et al. [39]. Nevertheless, it would be useful to have information relating CAS MICs derived by the Sensititre® YeastOne® method to clinical outcome or *fks1/fks2* mutation testing in order to allow a better understanding of the application of the CLSI breakpoint criteria to this species/antifungal/test method combination. In the meantime, we agree with the suggestion that either anidulafungin or micafungin can provide the desired susceptibility result for this antifungal class [38].

This study has strengths and weaknesses. Most isolates came from Auckland, a city with the country's largest population and concentration of tertiary/quaternary clinical services. More than 60% of isolates were from sterile body sites and represent the majority of deep-seated infections, and antifungal susceptibility testing was performed in one laboratory, by the same method, by a small number of staff (mainly KR and WPMK). However, there are limitations to the study. The data are not a fully representative of testing in New Zealand as other laboratories perform yeast susceptibility testing. That said, this report covers >75% of tests performed during the 15-year study period. The referred isolates, particularly genital isolates, may have been more likely to have been sent because of clinical relapse/failure following antifungal therapy. This may have increased the number of isolates exposed to antifungal agents and therefore more likely to be non-WT. Lastly, no molecular testing was performed for acquired azole or echinocandin resistance mechanisms. This would be informative given the association between non-WT MICs and the presence of resistance mechanisms [9,10,15,16].

5. Conclusions

These results show that the updated CLSI interpretive criteria have increased the reporting of non-susceptible isolates locally. Application of Sensititre® YeastOne®- and CLSI-generated ECVs show the presence of non-WT isolates for several *Candida* spp. Reporting these isolates with the comment that the MIC is above the WT MIC and that this could indicate the presence of a mutational or acquired mechanism of resistance will enable more informative results to clinicians [40]. We have now instituted this approach where no CLSI interpretative criteria exist for a given yeast/antifungal combination. Finally, the results add to the global literature and will enable the monitoring of local yeast susceptibility over time.

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None.

Competing interests

None declared.

Ethical approval

Not required.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at https://doi.org/10.1016/j.jgar.2018.02.014.

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