

Stepwise Development of a Homozygous S80P Substitution in Fks1p, Conferring Echinocandin Resistance in *Candida tropicalis*

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Three *Candida tropicalis* isolates were obtained from a patient with acute lymphoblastic leukemia. The first isolate was susceptible to all drug classes, while isolates 2 and 3, obtained after 8 and 8.5 weeks of caspofungin treatment, respectively, were resistant to the three echinocandins. Multilocus sequence genotyping suggested a clonal relation among all isolates. *FKS1* sequencing revealed a stepwise development of a heterozygous and finally a homozygous mutation, leading to S80S/P and S80P amino acid substitutions.

It is well recognized that long-term antifungal treatment entails a risk for *in vivo* selection of resistant fungi. Accordingly, an increasing number of reports demonstrate acquired echinocandin and azole resistance associated with both hetero- and homozygous mutations in the *FKS* and *ERG11* genes, which encode antifungal target proteins in *Candida* (1–6). This is of clinical importance, as resistant *Candida* isolates are associated with breakthrough candidiasis, treatment failures, and increased mortality (7). *Candida tropicalis* is identified as one of the five most common pathogenic *Candida* species, with a geographically determined proportion ranging from 3 to 66% of candidemia cases (8–10). Unfortunately, acquired fluconazole resistance is increasing, with ranges from approximately 7% in Denmark (9) to 9% in a global study (11) and 40% in Japan (12). Based on such findings, echinocandins are increasingly being utilized in the management of candidiasis caused by *C. tropicalis* (10, 13–15).

In this study, we analyzed three sequential *C. tropicalis* isolates (isolates 1, 2, and 3) obtained over a 4-month period from a patient with acute lymphoblastic leukemia who had been referred for allogeneic bone marrow transplantation. The patient was initially blood culture positive on 19 December 2010 for *C. tropicalis* (isolate 1) while receiving voriconazole prophylaxis. Caspofungin treatment was initiated (70/50 mg/day [70 mg on day 1 as a loading dose, followed by 50 mg daily thereafter]) (Fig. 1) and contin-

ued for a total of 8.5 weeks, interrupted by a 3-week fluconazole step-down treatment (Fig. 1). During the initial caspofungin treatment, nine serum samples tested positive for *Candida* mannan antigen, peaking at 479 pg/ml but stabilizing around 250 pg/ml on 20 January 2011 (Fig. 1). *C. tropicalis* was again detected in the blood on 5 March 2011 (isolate 2, after approximately 8 weeks of caspofungin treatment), and treatment was switched to amphotericin B (3 mg/kg/day) on 9 March. The patient was blood culture negative from 16 March, but the final *C. tropicalis* isolate (isolate 3, after approximately 8.5 weeks of caspofungin treatment) was obtained on 18 March from an oral swab, and treatment was changed to posaconazole (800 mg/day) on 31 March 2011. A Hickman catheter was kept in place, but sterilization was attempted with acid and fluconazole lock. Susceptibility testing was done according to EUCAST EDef 7.2 (azoles, anidulafungin, and micafungin) (16) and by Etest (amphotericin B and caspofun-

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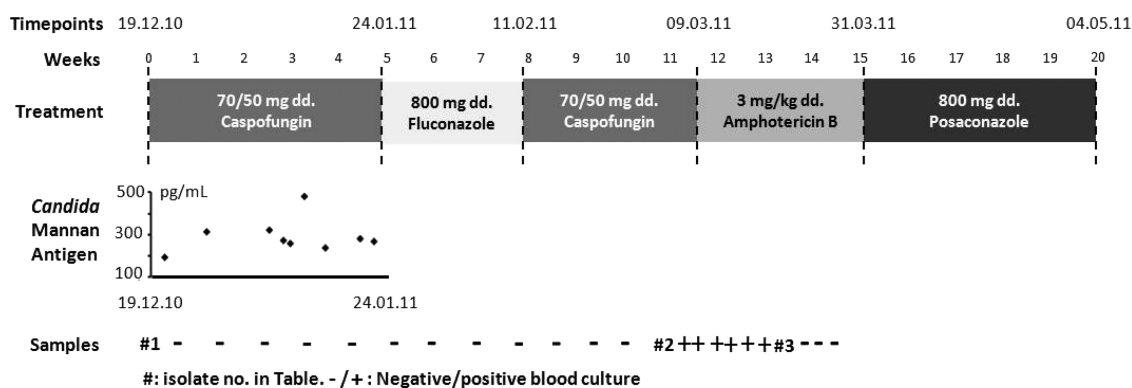


FIG 1 Systemic antifungal treatment of the leukemic patient illustrated in boxes with drugs administered as daily doses (dd.). Nine serum samples were positive for *Candida* mannan antigen during the first caspofungin treatment period, and subsequently, several positive blood cultures were obtained. Three isolates (isolates 1, 2, and 3) were chosen and sequenced for resistance mechanisms and genotyping.

TABLE 1 Origins, resistance mechanisms, genotypes, and susceptibility data for the three study and two control *C. tropicalis* isolates

Isolate	Specimen origin	Collection date (day.mo.yr)	<i>FKS1</i> resistance mechanism	Allelic profile according to PubMLST (<i>ICL1-MDR1-SAPT2-SAPT4-XYR-ZWF</i>)	MIC ($\mu\text{g/ml}$) ^a							
					EUCAST (EDef 7.1)						Etest	
					ANI	MICA	POS	VOR	ITR	FLU	AMB	CAS
1	BC ^b	19.12.10	Wild type	16-20-4-10-25-5	≤ 0.03	≤ 0.008	≤ 0.03	≤ 0.03	≤ 0.03	1	0.5	0.25
2	BC-CVC ^c	05.03.11	S80S/P	16-20-4-10-25-5	0.25	1	≤ 0.03	≤ 0.03	≤ 0.03	0.5	0.5	>32
3	Cavum oris	18.03.11	S80P	16-20-4-10-25-5	0.5	>1	≤ 0.03	0.06	≤ 0.03	2	1	>32
REF-1 ^d	BC ^b	08.07.10	Wild type	1-7-4-6-2-4	≤ 0.03	≤ 0.008	≤ 0.03	≤ 0.03	0.03	≤ 0.125	1	0.25
REF-2 ^d	BC ^b	23.01.11	Wild type	1-3-1-7-2 (99.7%) ⁻¹	≤ 0.03	≤ 0.008	≤ 0.03	≤ 0.03	0.125	0.5	0.5	0.125

^a ANI, anidulafungin; MICA, micafungin; POS, posaconazole; VOR, voriconazole; ITR, itraconazole; FLU, fluconazole; AMB, amphotericin B; CAS, caspofungin.

^b Unspecified blood culture.

^c Blood culture obtained via the intravenous Hickman catheter.

^d Susceptible reference isolate from unrelated patients, used for comparison.

gin). Etest was chosen for caspofungin susceptibility testing, as the biological potency of pure substance has been associated with an unacceptable lot-to-lot variation, with the most recently obtained powder giving rise to elevated MICs (17–19). Echinocandin susceptibility was evaluated using the EUCAST breakpoint for anidulafungin EUCAST MICs (susceptibility [S] ≤ 0.06 mg/liter) but adopting the revised CLSI breakpoint for interpretation of caspofungin Etest results (S ≤ 0.25 mg/liter) (20, 21). CLSI breakpoints were adopted for interpretation of the caspofungin Etest MICs as recommended by the manufacturer, as this has been found to be appropriate for *Candida albicans* and *C. tropicalis* (22). EUCAST breakpoints for micafungin have not yet been established, but 185 of 186 wild-type *C. tropicalis* isolates tested in our laboratory had a EUCAST MIC of ≤ 0.03 mg/liter, which was used to define susceptibility. Two unrelated isolates of *C. tropicalis* (REF-1 and REF-2) were included as wild-type *FKS1* reference isolates. The *FKS1* gene was amplified and sequenced using primers targeting hot spot 1 (FKS1-F, TCATTGCTGTGGCCACTTTAG; FKS1-R, TAGAATGAACGACCAATGGAGA) and hot spot 2 (FKS8-F, CTCTGCGTTGATTGGATTA; FKS8-R, ACCACCAACGGTCA AATCAG) and compared to the *C. tropicalis FKS1* reference sequence (GenBank accession no. EU676168). Genetic relatedness was analyzed by multilocus sequence typing (MLST) based on polymorphisms in 6 sequenced housekeeping genes (*ICL1*, *MDR1*, *SAPT2*, *SAPT4*, *XYR1*, and *ZWF1a*) as described previously (23) by applying the PubMLST database, covering 205 diploid sequence types (<http://pubmlst.org/ctropicalis>).

Isolate 1 and the two reference isolates were susceptible to all tested antifungals, whereas isolates 2 and 3 were categorized as echinocandin resistant (Table 1). Isolate 1, REF-1, and REF-2 were wild type in both hot spot 1 and 2 in the *FKS1* sequence, while isolate 2 harbored a heterozygous T238C mutation and isolate 3 a homozygous T238C mutation in hot spot 1 of *FKS1*, leading to S80S/P and S80P amino acid substitutions, respectively. The MLST data suggested that isolates 1, 2, and 3 were clonally related, since the diploid sequences in the 6 housekeeping genes were 100% identical (Table 1).

In vivo selection for echinocandin resistance has been demonstrated for several *Candida* species, including *C. albicans* (1, 24–27), *C. glabrata* (24, 28–31), *C. krusei* (5, 24, 32), and *C. parapsilosis* (33). However, to our knowledge, this is the first study to demonstrate the stepwise *in vivo* progression of a wild-type *C. tropicalis* strain to a homozygous *fkS1* mutant exhibiting echinocandin resistance. Even the heterozygous mutant isolate was classified as echinocandin resistant, with a significant ≥ 3 to 7 two-fold-dilution step increase in echinocandin MICs, illustrating the

significance of the S80 codon in *FKS1* in *C. tropicalis*. Nevertheless, the MICs indicated that the homozygous mutant (isolate 3) may be slightly more resistant to echinocandins (at least 1 dilution step, as suggested by the increase in anidulafungin and micafungin MICs). Other homozygous mutations in *C. tropicalis fks1* have been associated with elevated echinocandin MICs and amino acid substitutions, including L79W (4), F76S (6), and F76L (34). Moreover, heterozygous S80S/P mutants that display echinocandin resistance have been found (34, 35), but interestingly, the homozygous S80P mutation has not been described previously. This is in contrast to the findings for *C. albicans*, where a homozygous alteration at the corresponding codon (S645) has been detected in several resistant isolates (17, 36–38). Several factors may contribute to this difference. First, fitness cost when the second allele is mutated may vary, as supported by previous observations associating homozygous *fkS1* mutations in *C. albicans* with both fitness and virulence costs (39). Second, the resistance conferred by the heterozygous mutation may be sufficient to allow escape in S80S/P *C. tropicalis* during caspofungin treatment, whereas the homozygous variant may be required for high-level echinocandin resistance in *C. albicans* (37, 40).

Our and related studies contribute to the overall understanding of resistance development *in vivo* as a consequence of antifungal treatment, including understanding the duration of treatment and which compounds allow selection of resistant mutants. Finally, this study may assist in determining treatment guidelines for the management of *C. tropicalis* infections, as the development of echinocandin resistance should be acknowledged as a rising concern in the treatment of patients with long-term echinocandin exposure.

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H.K.J. has nothing to declare.

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