Deletion of Individual mRNA Capping Genes Is Unexpectedly Not Lethal to *Candida albicans* and Results in Modified mRNA Cap Structures

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Eukaryotic mRNAs are modified at the 5′ end with a cap structure. In fungal cells, the formation of the mRNA cap structure is catalyzed by three enzymes: triphosphatase, guanylyltransferase, and methyltransferase. Fungal capping enzymes have been proposed to be good antifungal targets because they differ significantly from their human counterparts and the genes encoding these enzymes are essential in *Saccharomyces cerevisiae*. In the present study, *Candida albicans* null mutants were constructed for both the mRNA triphosphatase-encoding gene (*CET1*) and the mRNA methyltransferase encoding gene (*CCM1*), proving that these genes are not essential in *C. albicans*. Heterozygous deletions were generated, but no null mutants were isolated for the guanylyltransferase-encoding gene (*CGT1*), indicating that this gene probably is essential in *C. albicans*. Whereas these results indicate that Cet1p and Ccm1p are not ideal molecular targets for development of anticandidal drugs, they do raise questions about the capping of mRNA and translation initiation in this fungus. Southern blot analysis of genomic DNA indicates that there are not redundant genes for *CET1* and *CCM1* and analysis of mRNA cap structures indicate there are not alternative pathways compensating for the function of *CET1* or *CCM1* in the null mutants. Instead, it appears that *C. albicans* can survive with modified mRNA cap structures.

Candida albicans infections are a serious health risk for immunocompromised patients, such as transplant recipients, cancer patients, neonates, human immunodeficiency virus-positive patients, and hospital patients with intravenous tubes or catheters. Few drugs are available for treating disseminated candidiasis, and there is a need for new antifungal compounds to treat these infections (13). There is a common presumption that antifungal agents can be developed from inhibitors of enzymes that catalyze essential functions. Although this presumption has not yet been proven, it has generated interest in the identification of essential genes in *C. albicans*. Enzymes involved in mRNA capping, especially the mRNA triphosphatase, have been proposed as potentially good antifungal targets because they are significantly different from the human enzymes and are reportedly essential for cell growth (32). In all eukaryotes, mRNA cap structures are purported to play critical roles in stability, processing, and nuclear export of mRNA, as well as in translation initiation (45). While cap-independent translation does occur, cap-dependent translation is believed to be the major pathway for translation initiation in eukaryotes (20).

The formation of the 7-methylguanylated mRNA cap (m7GpppN) in eukaryotes occurs in three steps (10). The first step is catalyzed by the mRNA triphosphatase which dephosphorylates the terminal nucleotide (pppN → ppN). In the second step, guanylyltransferase "caps" the diphosphate with guanosine 5′-monophosphate (GMP): ppN + GMP → GpppN. The third step is the transfer of a methyl group to the capped

nucleotide by the methyltransferase (GpppN + *S*-adenosylmethionine → m7GpppN + *S*-adenosylhomocysteine). In mammals, two genes encode the three enzymatic steps of capping, whereas in fungi each of the three capping reactions is catalyzed by a distinct gene product (32). Fungal mRNA 5′-triphosphatase has a completely different structure and catalytic mechanism than the mammalian counterparts (14). The genes encoding mRNA 5′-triphosphatase (*CET1*), guanylyltransferase (*CGT1*), and methyltransferase (*CCM1*) have all been shown to be essential in the model fungal organism, *Saccharomyces cerevisiae* (references 34, 19, and 39, respectively). In a recent publication, Pei et al. (27) concluded the *CET1* gene is essential in *C. albicans* because they were unable to construct a null deletion mutant. However, we show here that both alleles of *CET1* can be deleted in *C. albicans* and the null mutants are viable. We were also able to delete both alleles of *C. albicans CCM1*.

Construction of null mutants in *C. albicans* is complicated because this diploid organism lacks a sexual cycle. Techniques to evaluate gene essentiality by using sequential disruption of both alleles of a target gene in *C. albicans* were introduced by Fonzi and Irwin (9), and more recently the Mitchell laboratory has developed additional methods for generating *C. albicans* null mutants (7, 42, 43). In the two-step transformation method, alleles are knocked out in sequential transformations selecting for homologous recombinations (42). An alternative deletion strategy, the single-transformation method, first selects for transformants that are Arg⁺ due to the insertion of the *ura3Δ3′-ARG4-ura3Δ5′* (UAU1) cassette at the targeted locus (7). Transformants with the desired UAU1 cassette integration are then grown on synthetic complete (SC) medium lacking arginine and uridine to select Arg⁺ Ura⁺ cells. These cells have undergone a mitotic recombination event in which

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TABLE 1. Oligonucleotide sequences

Primer	Sequence (5′ - 3′)[a]
CaCET5′-DR	ctactgcataccataaaccttctgttcatgaacgtcattcaataacgagcatgttgaatgacacGTTTTCCCAGTCACGACGTT
CaCET3′-DR	cttcaattaattcctccaatctaagattatctaccccctttctggattttatcaatagcagcTGAATTGTGAGCGGATA
CaCET1F	catcaagtgggaatgcgaatg
CaCET1R	cttgttcaatctattattgagag
CET1 probe F	ccgtcagattcaactccaac
CET1 probe R	cataacacccgcctccaactc
CET1-restore 5′	*acgcatgtcga*ctttaaactgtatatatttgtagc
CET1-restore 3′	*acgcatgtcgac*gaaagtgggcgcggttc
CaCGT5′-DR	ctatacacttttatgattcaattagaagaaagagaaattcctgtaataccaggtaataaacGTTTTCCCAGTCACGACGTT
CaCGT3′-DR	caatttattcgtcgtcactatcttcataagtggggtatgtcattaagtatttgttgcagtgTGAATTGTGAGCGGATA
CaCGT1F	caaggctagtctttagaaattc
CaCGT1R	ccagaaaccgagaaagaatc
CaCCM5′-DR	ctacaccactagcatgtctaccgattcgtacactccctcacaagagcctggctcaaagcGTTTTCCCAGTCACGACGTT
CaCCM3′-DR	cctataccttctcaaatacaaatcctatgtaaaatgccactgcttccttttcgtcgcctgTGAATTGTGAGCGGATA
CaCCM1F	gagttgaaacatgaatcattag
CaCCM1R	gctacacactacccagacata
CCM1 probe F	gacaggcgaatctgtatttgc
CCM1 probe R	cagcaccgtacttgccatcac
CCM1-restore 5′	*acgcatgtcgac*gaaaagccaatgttatagatg
CCM1-restore 3′	*acgcatgtcgac*acgatgcgtccggcgtagag
ARG4 primer	gaactatctattcgatgatg

[a] Lowercase roman letters indicate nucleotides that provide homology to *C. albicans* genomic DNA. Nucleotides in uppercase indicate the 5′ DR and 3′ DR sequences that anneal to flanking sequence of marker cassettes from the plasmids (42). Lowercase italic nucleotides indicate sequences added for cloning convenience.

one allele of the nonessential gene is replaced with the UAU1 cassette and the other allele of the nonessential gene is replaced with a functional *URA3* gene. In the case of an essential gene, insertional deletion of two alleles of the target gene can only be generated if an allelic duplication occurs such that the strain becomes triploid for the target gene locus. This maintenance of a wild-type allele under the selective pressure for homozygous deletions is strong evidence that a gene is essential.

We initially applied the single transformation method (7) to determine whether *CET1*, *CGT1*, and *CCM1* are essential genes in *C. albicans*. After generating *cet1*-null mutants by this technique, we were also able to generate *cet1*-null mutants by using the two-step transformation knockout strategy (42), confirming that the *C. albicans CET1* gene is nonessential. *C. albicans ccm1*-null mutants were generated by using the two-step transformation method. *CGT1* heterozygous deletions were generated by both techniques, but we were unable to recover any isolates completely lacking a wild-type *CGT1*, indicating that this is probably an essential gene in *C. albicans*.

The viability of *C. albicans cet1*- and *ccm1*-null mutants raises questions about the mechanics and role of cap-dependent translation initiation in this fungal pathogen. There are several possible explanations why *CET1* and *CCM1* are not essential in *C. albicans*, e.g., redundant genes encoding mRNA capping enzymes, alternative mRNA capping pathways, or the possibility that *C. albicans* can survive with modified mRNA cap structures. Our analysis and characterization of mRNA cap structures indicates that the *C. albicans cet1*- and *ccm1*-null mutants do make modified mRNA-cap structures, and these modified mRNA-caps are sufficient for *C. albicans* to effectively translate mRNA and survive.

MATERIALS AND METHODS

Reagents. *Taq* polymerase was purchased from Applied Biosystems (Foster City, Calif.). Restriction endonucleases and deoxynucleotidyl transferase were purchased from Invitrogen (Rockville, Md.). All enzymes were used according to manufacturers' protocols. PCR primers used in the present study were purchased from Sigma-Genosys and are described in Table 1. Plasmids pGEM-URA3, pGEM-HIS1, and pRS-ARG4−Δ*Spe*I (42), as well as the UAU1 cassette-containing plasmid pBME101 (7), were generous gifts from A. P. Mitchell. Synthetic complete (SC) media were made by using dropout base mixes available from Bio 101 (Vista, Calif.) with glucose added to a final concentration of 2%. Southern blot analyses were performed using probes labeled with the DIG High Prime kit and the DIG chemiluminescent detection kit (Roche, Indianapolis, Ind.). Amphotericin B, cycloheximide, hygromycin B, and actinomycin D were purchased from Sigma (St. Louis, Mo.), and blasticidin S was purchased from Calbiochem (Darmstadt, Germany). Tobacco acid pyrophosphatase (TAP) was obtained from Epicentre Technologies (Madison, Wis.). Nuclease P1, NaIO$_4$, and polyethyleneimine-coated thin-layer chromatography (TLC) plates were purchased from VWR (Batavia, Ill.). The capped nucleotide analog standards, m7GpppA, m7GpppG, GpppA, and GpppG, were purchased from New England Biolabs, Inc. (Beverly, Mass.). Nucleotide standards, adenosine 5′-monophosphate (AMP) and GMP, were bought from Sigma. NaB[^{3}H]$_4$ (15 Ci/mmol) was purchased from American Radiolabeled Chemicals, Inc. (St. Louis, Mo.).

Strains and growth conditions. Strains used in the present study are described in Table 2. For transformation, *C. albicans* BWP17 was grown overnight in YEPD (1% yeast extract, 2% Bacto Peptone [Difco], 2% glucose) supplemented with uridine at 80 μg/ml, subcultured 1:100 into 50 ml of the same medium, and grown for two doublings at 30°C. Where indicated, uridine was added to a final concentration of 80 μg/ml, and arginine was added to a final concentration of 50 μg/ml. All transformants were plated onto SC lacking arginine (SC−arginine), SC plus arginine but lacking uridine (SC+arginine−uridine), or SC lacking both arginine and uridine (SC−arginine−uridine) as appropriate for the selectable marker(s) and incubated at 30°C for 2 to 3 days. For the selection of Arg$^+$ Ura$^+$ segregants of *CET1* heterozygotes disrupted with the UAU1 cassette, isolated colonies were grown overnight in YEPD lacking uridine (YEPD−uridine). A total of 1 ml of each culture was washed with sterile water and then resuspended in 1 ml of H$_2$O, and a 100-μl portion of the cells was plated onto SC−arginine−uridine, followed by growth for 2 to 3 days at 30°C. Growth studies were performed in round-bottom 96-well plates with cells inoculated in 200 μl of YEPD+uridine to a final concentration of 2,000 to 3,000 cells/ml, incubated at 30 or 37°C for 60 h. Growth was monitored in a SpectraMax 250 (Molecular Dynamics) at 595 nm, with readings taken every 30 min after shaking for 5 s.

DNA methods. Genomic DNA was prepared from overnight cultures of *C. albicans* grown at 30°C in 5 ml of YEPD by using the glass bead lysis method (3). PCR amplifications of deletion cassettes and analytical PCRs with genomic DNA were carried out as described in Wilson et al. (42). Before transformation of *C.*

TABLE 2. *C. albicans* strains used in this study

Strain	Genotype	Description	Source
BWP17	Δ*ura3*::λ*imm434*/Δ*ura3*::λ*imm434* *his1*::*hisG*/*his1*::*hisG arg4*::*hisG arg4*::*hisG*	Parent strain for deletions, allows selection of three different markers (*URA3, ARG4, HIS1*)	A. P. Mitchell (42)
CQF125	BWP17 Δ*cet1*::*UAU1*/*CET1*	Heterozygote of *CET1* from single transformation method	This study
CQF136	BWP17 Δ*cet1*::*UAU1*/Δ*cet1*::*URA3*	Temperature-sensitive null mutant of *cet1* from single transformation method	This study
CQF160	BWP17 Δ*cet1*::*UAU1*/Δ*cet1*::*URA3*	Null mutant of *cet1* from single transformation method	This study
CQF142	BWP17 Δ*cet1*::*ARG4*/*CET1*	Heterozygote of *CET1* from two-step transformation method	This study
CQF141	BWP17 Δ*cet1*::*UAU1*/Δ*cet1*::*URA3*/*CET1*	Trisomic isolate for *CET1* locus generated from single transformation method	This study
CQF152	BWP17 Δ*cet1*::*ARG4*/Δ*cet1*::*URA3*	Null mutant of *cet1* from two-step transformation method	This study
CQF248	BWP17 Δ*cet1*::*ARG4*/Δ*cet1*::*URA3* *his1*::*hisG*::*CET1*	*CET1* restored to null in *trans* by recombination at *his1*::*hisG* locus	This study
CQF153	BWP17 Δ*cgt1*::*ARG4*/*CGT1*	Heterozygote of *CGT1* from two-step transformation method	This study
CQF170	BWP17 Δ*cgt1*::*ARG4*/Δ*cgt1*::*URA3*/*CGT1*	Trisomic for *CGT1* locus from two-step transformation method	This study
CQF154	BWP17 Δ*ccm1*::*ARG4*/*CCM1*	Heterozygote of *CCM1* from two-step transformation method	This study
CQF171	BWP17 Δ*ccm1*::*ARG4*/Δ*ccm1*::*URA3*	Null mutant of *ccm1* from two-step transformation method	This study
CQF250	BWP17 Δ*cet1*::*ARG4*/Δ*cet1*::*URA3* *his1*::*hisG*::*CET1*	*CCM1* restored to null in *trans* by recombination at *his1*::*hisG* locus	This study

albicans with insertional deletion cassettes, the PCR fragments were blocked with ddATP by using terminal deoxynucleotidyl transferase according to the protocol described by Shah-Mahoney et al. (33). PCR-amplified DNA was purified by using phenol-CHCl₃-isoamyl alcohol (25:24:1), followed by ethanol precipitation before and after the blocking reaction. High-stringency Southern blot analysis (36) was performed on 1 to 3 μg of genomic DNA that was digested with *Bgl*II and separated on 0.8% agarose gels for capillary transfer to membrane (Hybond N; Amersham). Probes were PCR amplified from genomic DNA of *C. albicans* BWP17 with primers *CET1* probe F and *CET1* probe R for the *CET1* probe and *CCM1* probe F and *CCM1* probe R for the *CCM1* probe. Membranes were hybridized with 1 μg of DIG-labeled probe under high-stringency conditions (42°C), followed by stringent wash conditions (two 5-min room temperature washes in 2× SSC [0.15 M NaCl, 10 mM sodium citrate, pH 7] plus 0.1% sodium dodecyl sulfate [SDS], followed by two 20-min washes at 68°C in 0.5× SSC plus 0.1% SDS). Southern blots were developed by using anti-DIG-Fab fragments, which are conjugated to alkaline phosphatase, and CSPD chemiluminescent detection. The anti-DIG was diluted 1:10,000 in blocking buffer and the CSPD was diluted 1:100 in detection buffer as recommended by the supplier.

Genetic manipulations of *C. albicans*. *C. albicans* competent cells were prepared as described by the method of Braun and Johnson (2). *C. albicans* BWP17 and derivatives were transformed with 80 μl of the PCR-amplified disruption cassettes as described previously (42).

In vitro susceptibility tests. MICs were determined by using NCCLS standard protocols for broth microdilution assays with the colorimetric modification (28).

RNA methods. Total RNA was isolated from *C. albicans* cells by hot phenol-chloroform extraction and ethanol precipitation as described by Lin et al. (18). Poly(A) mRNA was enriched from 1 mg of total RNA by using the Qiagen (Valencia, Calif.) RNeasy kit, as per the manufacturer's specification. To label the mRNA, 35 μg of precipitated mRNA was dissolved in 11 μl of 2.5 mM EDTA (pH 7.0), heated to 65°C for 1 min, and placed on ice for 5 min. Then, 5 μl of 8 mM NaIO₄ was added, and the oxidation reaction was allowed to proceed at 4°C in the dark for 90 min. The samples were mixed with 4 μl of 1 M sodium acetate (pH 5.5), and the mRNA was precipitated with ethanol. The mRNA pellets were dissolved in 12 μl of 0.1 M potassium phosphate buffer (pH 6.8). A total of 2 μl of NaB[³H]₄ (15 Ci/mmol; 55 mM in 0.1 M potassium hydroxide) was added to the oxidized RNA, and the reaction was allowed to proceed at room temperature in the dark for 60 min. Next, 75 μl of 0.2 M sodium acetate was added, and the samples were incubated for an additional 15 min. The RNA was ethanol precipitated, dissolved in 100 μl of water, and purified by using the RNeasy kit (Qiagen). The volume of purified radiolabeled mRNA solutions was

adjusted to 50 μl with water, and the samples were split in half for nuclease P1 or TAP digestions. For P1 digestion, 25-μl samples were adjusted to a final concentration of 50 mM ammonium acetate (pH 5.3) and treated with nuclease P1 (100 μg/ml) at 37°C for 18 h. The remaining 25-μl fractions were digested with TAP by adding 2.9 μl of 10× TAP reaction buffer (500 mM sodium acetate [pH 6.0], 1% β-mercaptoethanol, and 0.1% Triton X-100) and 1.1 μl of TAP (10 U) and incubated at 37°C for 4 h.

Cap structure resolution. Next, 20 μl of the RNA samples digested with nuclease P1 or TAP were spotted onto polyethyleneimine-cellulose, along with unlabeled nucleotides, AMP and GMP, and cap standards, m7GpppG, m7GpppA, GpppG, and GpppA. After they dried, the TLC plates were developed in 0.1 M sodium phosphate buffer (pH 6.8)–ammonium sulfate–*n*-propanol (100:60:2 [vol/wt/vol]) at room temperature. Markers were detected under UV light, and the positions of tritiated cap structures were identified by phosphorimaging.

RESULTS

***C. albicans CET1* deletions.** Targeted deletions of the triphosphatase encoding gene, *CET1*, were constructed by using two different methods: the single-step transformation procedure of Enloe et al. (7), and the sequential two-step transformation method (42). In the single-step transformation method, the first allele was deleted by transforming *C. albicans* with a UAU1 PCR cassette-amplified from pBME101 by using primers *CaCET1*5′-DR and *CaCET1*3′-DR. Transformants were selected on SC−arginine. As detected by analytical PCR, three of four Arg⁺ transformants had the UAU1 disruption cassette integrated in the *CET1* genomic locus. These three Δ*cet1*::*UAU1*/*CET1* heterozygotes were streaked out on SC−arginine plates to generate isolated colonies, and 15 isolated colonies from each were grown overnight in YEPD−uridine at 30°C. Overnight cultures were harvested and washed in water and plated on SC−arginine−uridine to select for mitotic recombinants. PCR analysis of genomic DNA
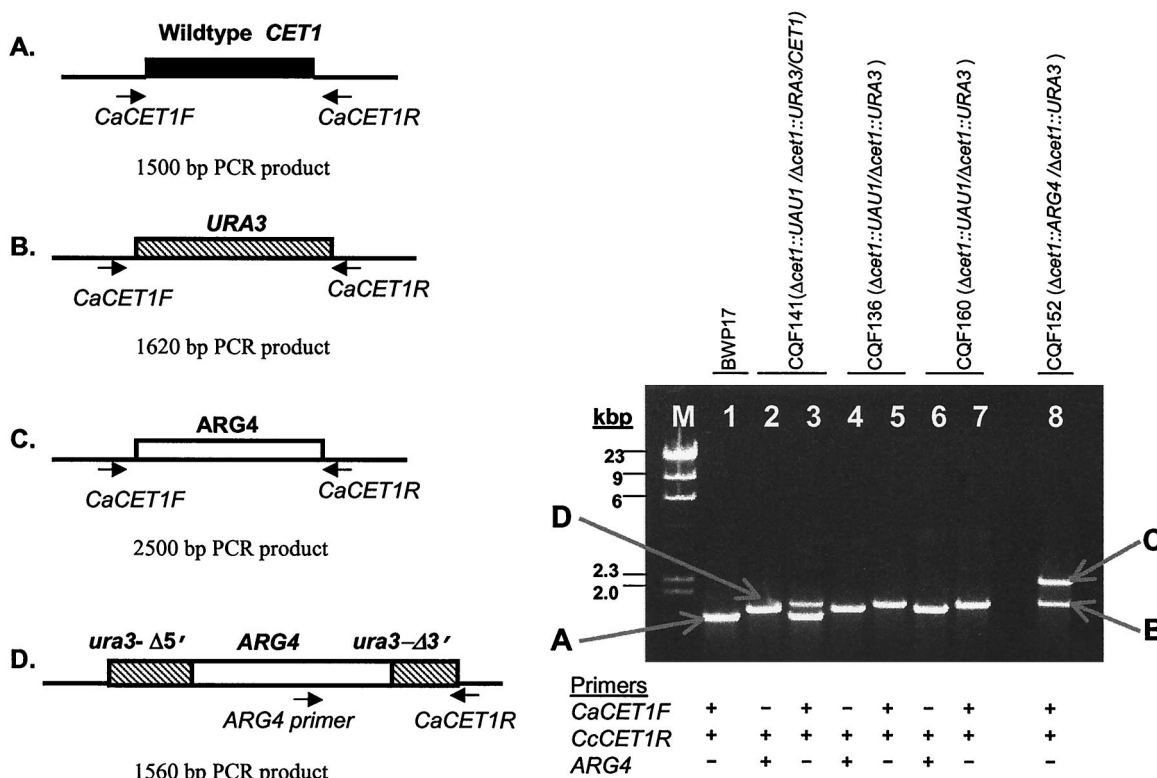
FIG. 1. Analytical PCR of genomic DNA from *C. albicans* BWP17 parent strain and *CET1* deletion strains. (Left panel) Schematic diagrams of wild-type or insertional deletion mutants for *C. albicans* chromosomal DNA at the *CET1* locus with oligonucleotide binding sites and predicted PCR fragments. (Right panel) PCR fragments separated on 1% agarose gel. Lane M, DNA size standards; lane 1, *C. albicans* BWP17 genomic DNA PCR amplified with *CaCET1F* and *CaCET1R* primers; lane 2, *C. albicans* CQF141 genomic DNA PCR amplified with *ARG4* and *CaCET1R* primers; lane 3, *C. albicans* CQF141 genomic DNA PCR amplified with *CaCET1F* and *CaCET1R* primers; lane 4, *C. albicans* CQF136 genomic DNA PCR amplified with *ARG4* and *CaCET1R* primers; lane 5, *C. albicans* CQF136 genomic DNA PCR amplified with *CaCET1F* and *CaCET1R* primers; lane 6, *C. albicans* CQF160 genomic DNA PCR amplified with *ARG4* and *CaCET1R* primers; lane 7, *C. albicans* CQF160 genomic DNA PCR amplified with *CaCET1F* and *CaCET1R* primers; lane 8, *C. albicans* CQF152 genomic DNA genomic DNA PCR amplified with *CaCET1F* and *CaCET1R* primers.

for the 78 Arg$^+$ Ura$^+$ segregants from this selection showed that 12 were null mutants ($\Delta cet1$::*UAU1*/$\Delta cet1$::*URA3*) and 44 were trisomic for the *CET1* locus ($\Delta cet1$::*UAU1*/$\Delta cet1$::*URA3*/*CET1*). The remaining 12 segregants probably had rearrangements or ectopic recombinations that we could not identify.

The two-step transformation method was also used to confirm that *CET1* is not essential in *C. albicans*. Heterozygous *CET1* deletion mutants were identified after selection on SD−arginine after transformation of *C. albicans* BWP17 with a PCR cassette amplified from pRS-ARG4−$\Delta SpeI$ with the primers *CaCET15′-DR* and *CaCET13′-DR*. Two of the nine Arg$^+$ transformants had targeted insertions in one *CET1* allele. One of these heterozygotes ($\Delta cet1$::*ARG4*/*CET1*) was then transformed with a *URA3* marker cassette PCR amplified from pGEM-URA3 with the primers *CaCET5′-DR* and *CaCET3′-DR*. Eight Arg$^+$ Ura$^+$ transformants were screened, and six were null mutants ($\Delta cet1$::*ARG4*/$\Delta cet1$::*URA3*).

Analytical PCR of *CET1* deletion strains are shown on the gel in Fig. 1. The PCR amplifications were designed to detect the four possible chromosomal constructs at this locus (depicted in Fig. 1A to D). PCR amplification of the wild-type *CET1* allele (Fig. 1A) with primers *CaCET1F* and *CaCET1R* should produce a PCR product of 1,500 bp. Using the same primers,

PCR amplification of DNA from isolates with the $\Delta cet1$::*URA3* allele (Fig. 1B), the $\Delta cet1$::*ARG4* allele (Fig. 1C), or the $\Delta cet1$::*UAU1* allele produce larger products (1,620 bp for *URA3*, 2,600 bp for *ARG4*, and 4,000 bp for $\Delta cet1$::*UAU1*). Because the PCR product for the $\Delta cet1$::*UAU1* allele obtained with the flanking primers is so large, amplification of it is not favored when the smaller alleles are present. Therefore, to determine whether this allele is definitively present, we also analyzed genomic DNA of UAU1 transformants by using the *ARG4* primer paired with the *CaCET1R* primer. This primer pair should produce a product of 1,560 bp from the $\Delta cet1$::*UAU1* allele (D). As expected, one PCR product was amplified from *C. albicans* BWP17 genomic DNA with the *CaCET1R* and *CaCET1F* primers (Fig. 1, lane 1), and this band corresponds to the wild-type allele (*CET1*; Fig. 1A). PCR analysis of genomic DNA from isolate CQF141 indicates it is trisomic, with primers *ARG4* and *CaCET1R* producing a band corresponding to the $\Delta cet1$::*UAU1* allele (lane 2) and the *CaCET1R* and *CaCET1F* primers producing two bands corresponding to the wild-type *CET1* allele and the $\Delta cet1$::*URA3* allele (lane 3). The PCR products for isolates CQF136 and CQF160 are the same and indicate that both are *cet1*-null mutants. With primers *ARG4* and *CaCET1R*, both isolates
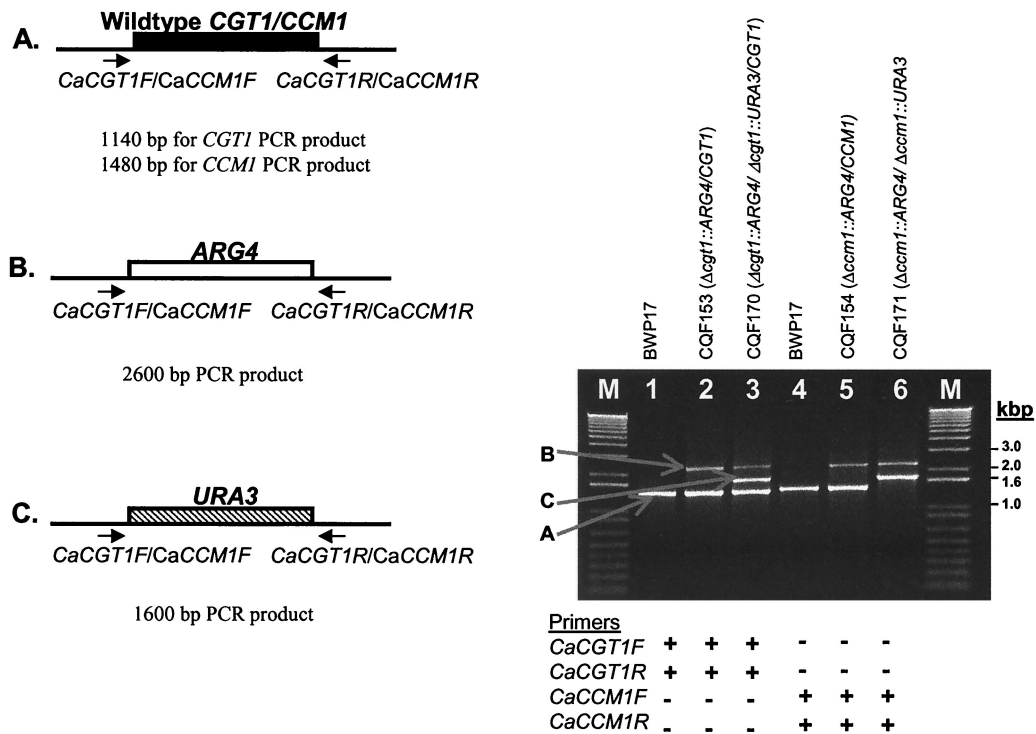
FIG. 2. Analytical PCR of genomic DNA from *C. albicans* BWP17 parent strain and *CGT1* or *CCM1* deletion strains. (Left panel) schematic diagrams of wild-type or insertional deletion mutants for *C. albicans* chromosomal DNA at the *CGT1* and *CCM1* loci with oligonucleotide binding sites. The expected sizes for the PCR products indicated for the genomic structures are as follows: 1,140 bp for wild-type *CGT1* and 1,480 bp for wild-type *CCM1* (A); 2,600 bp for both Δ*cgt1*::*ARG4* and Δ*ccm1*::*ARG4* (B); and 1,600 bp for both Δ*cgt1*::*URA3* and Δ*ccm1*::*URA3* (C). (Right panel) PCR fragments separated on 0.8% agarose gel. Lane M, DNA size standards; lane 1, *C. albicans* BWP17 genomic DNA PCR amplified with *CGT1F* and *CGT1R* primers; lane 2, *C. albicans* CQF153 genomic DNA PCR amplified with *CGT1F* and *CGT1R* primers; lane 3, *C. albicans* CQF170 genomic DNA PCR amplified with *CGT1F* and *CGT1R* primers; lane 4, *C. albicans* BWP17 genomic DNA PCR amplified with *CCM1F* and *CCM1R* primers; lane 5, *C. albicans* CQF154 genomic DNA PCR amplified with *CCM1F* and *CCM1R* primers; lane 6, CQF171 genomic DNA PCR amplified with *CCM1F* and *CCM1R* primers.

yield the band corresponding to the Δ*cet1*::*UAU1* allele (lanes 4 and 6), whereas only the band corresponding to the Δ*cet1*::*URA3* allele is seen with *CaCET1F* and *CaCET1R* primer amplifications (lanes 5 and 7). Isolate CQF152 was generated from the two-step transformation method so only the *CaCET1F* and *CaCET1R* primers were needed for analysis. Lane 8 shows that this isolate has the two deletion alleles (Δ*cet1*::*URA3* and Δ*cet1*::*ARG4*) and no wild-type *CET1* allele.

C. albicans CGT1 and CCM1 deletions. The single transformation method of Enloe et al. (7) was initially applied to deletion analysis of the *CGT1* and *CCM1* genes in *C. albicans*. The marker deletion cassettes were PCR amplified from pBME101 by using primers *CaCGT5'-DR* and *CaCGT3'-DR* or *CaCCM15'* DR and *CaCCM13'-DR*. *C. albicans* BWP17 was transformed with the UAU1 PCR cassettes, and Arg⁺ transformants were selected. DNA isolated from these transformants was screened by analytical PCR to identify isolates with the correct heterozygous deletions. Heterozygous deletions were constructed for both genes. In this gene deletion procedure, the second step requires selection for a mitotic recombination event where the UAU1 cassette recombines into the second allele and the cells become Arg⁺ Ura⁺. We were unable to generate null mutants or even trisomic isolates for either of these two genes by this method.

A second method for generating *C. albicans* gene knockouts was also tested for *CGT1* and *CCM1* (42). *C. albicans* BWP17 was first transformed with *ARG4* cassettes PCR amplified from pRS-ARG4-Δ*Spe*I with primers *CaCGT5'-DR* and *CaCGT3'-DR* or primers *CaCCM5'-DR* and *CaCCM3'-DR*. A heterozygous strain for each of these genes was then transformed with a URA3 marker cassette PCR amplified from pGEM-URA3 with primers *CaCGT5'-DR* and *CaCGT3'-DR* or primers *CaCCM5'-DR* and *CaCCM3'-DR*. Twelve Arg⁺ Ura⁺ transformants were screened for *CCM1* deletions, and two were *ccm1*-null mutants (Δ*ccm1*::*ARG4*/Δ*ccm1*::*URA3*). All 24 of the Arg⁺ Ura⁺ transformants screened for *CGT1* deletions retained a wild-type *CGT1* allele, with 22 isolates being heterozygous (Δ*cgt1*::*ARG4*/*CGT1*) and 2 isolates being trisomic (Δ*cgt1*::*ARG4*/Δ*cgt1*::*URA3*/*CGT1*).

The generation of *ccm1*-null mutants demonstrates that this is not an essential gene in *C. albicans*, but the *CGT1* gene remains an enigma. We did not generate deletion mutants at this locus in multiple attempts by both deletion approaches. However, heterozygous deletion mutants (Δ*cgt1*::*ARG4*/*CGT1*) can be constructed (Fig. 2), indicating that the deletion cassette can integrate into at least one allele at the desired locus. The failure to generate the double deletion could be due to preferential insertion of the deletion cassette at one allelic variant. Yesland and Fonzi (46) have reported that sequence heterology biases insertion to the allele with the best sequence

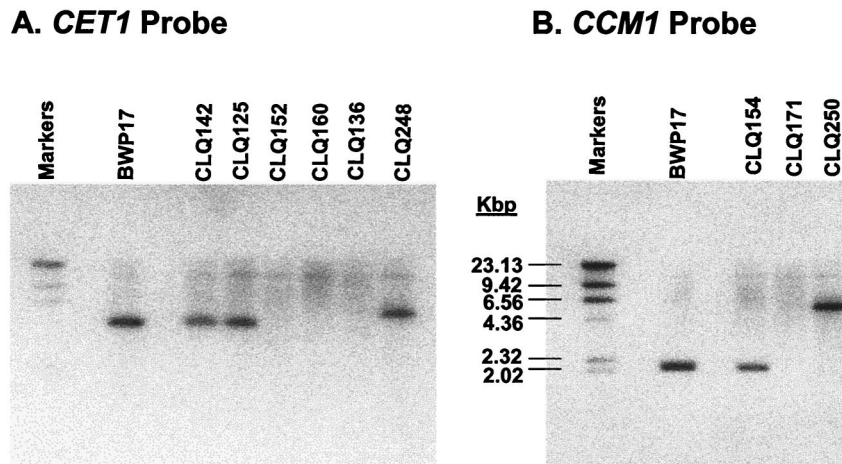## A. *CET1* Probe

B. *CCM1* Probe

FIG. 3. Southern blot analysis of *Bgl*II-digested genomic DNA isolated from *C. albicans*. (A) Probe was *CET1* DNA (covering codons 51 to 479). Sources of genomic DNA: BWP17 (*CET1/CET1*), CQF125 (Δ*cet1*::*UAU1/CET1*), CQF141 (Δ*cet1*::*UAU1*/Δ*cet1*::*URA3/CET1*), CQF136 (Δ*cet1*::*UAU1*/Δ*cet1*::*URA3*), CQF142 (Δ*cet1*::*ARG4/CET1*), CQF152 (Δ*cet1*::*ARG4*/Δ*cet1*:: *URA3*), CQF248 (Δ*cet1*::*ARG4*/Δ*cet1*::*URA3* with *CET1* restored). (B) Probe was *CCM1* DNA (covering codons 18 to 455). Sources of genomic DNA: BWP17 (*CCM1/CCM1*), CQF154 (Δ*ccm1*::*ARG4/CCM1*), CQF171 (Δ*ccm1*::*ARG4*/Δ*ccm1*::*URA3*), CQF250 (Δ*ccm1*::*ARG4*/Δ*ccm1*::*URA3* with *CCM1* restored).

homology with the transforming DNA. However, our sequence analysis of the *C. albicans* BWP17 *CGT1* locus shows that none of the allelic variations in this gene are found in the sequences that would hybridize to the flanking homology provided by the *CaCGT*5′-DR and *CaCGT*3′-DR oligonucleotides in the PCR deletion cassette (data not shown). Therefore, we believe that we are not seeing the allelic bias and that *CGT1* is likely an essential gene in *C. albicans*. Another group has reported failure to generate a *cgt1*-null mutant in *C. albicans* (5), supporting an essential nature for this gene.

Figure 2 shows the PCR analysis for the *CGT1* and *CCM1* deletions. PCR amplification with *CaCGT1F* and *CaCGT1R* results in PCR product sizes of 1,140 bp for the wild-type *CGT1* allele (Fig. 2A), 2,600 bp for the Δ*cgt1*::*ARG4* allele (Fig. 2B), and 1,600 bp for the Δ*cgt1*::*URA3* allele (Fig. 2C). Amplification of genomic DNA with primers *CaCGT1F* and *CaCGT1R* produces a PCR product the size of the expected wild-type *CGT1* allele for *C. albicans* BWP17 (lane 1). Two bands are seen for isolate CQF153 (lane 2), with sizes of the wild-type *CGT1* allele and the size of the Δ*cgt1*::*ARG4* allele, and all three bands (A, B, and C) are seen for isolate CQF170 (lane 3). PCR amplification with *CaCCM1F* and *CaCCM1R* results in PCR product sizes of 1480 for the wild-type *CCM1* allele (A), 2,600 bp for the Δ*ccm1*::*ARG4* allele (B), and 1,600 bp for the Δ*ccm1*::*URA3* allele (C). Amplification of genomic DNA with primers *CaCCM1F* and *CaCCM1R* produces a PCR product the size of the expected wild-type *CCM1* allele for *C. albicans* BWP17 (lane 4), whereas two bands are seen for isolate CQF154 (lane 5) with sizes of the wild-type *CCM1* allele and the size of the Δ*ccm1*::*ARG4* allele. With these primers, both the deleted alleles, Δ*ccm1*::*URA3* and Δ*ccm1*::*ARG4*, are seen for isolate CQF171 (lane 6) but no wild-type *CCM1* allele.

Southern blot analysis. In order to eliminate the formal possibility that *cet1*- and *ccm1*-null mutants survive because a transposed copy of the wild-type *CET1* allele or *CCM1* allele exists in another chromosomal location, *C. albicans* chromo-

somal DNA was analyzed by Southern blot (Fig. 3). Genomic DNA from *C. albicans* BWP17; the *CET1* heterozygotes CQF142 (Δ*cet1*::*ARG4/CET1*) and CQF125 (Δ*cet1*::*UAU1/ CET1*); the *cet1*-null mutants CQF152 (Δ*cet1*::*ARG4*/Δ*cet1*:: *URA3*), CQF160 (Δ*cet1*::*UAU1*/Δ*cet1*::*URA3*), and CQF136 (Δ*cet1*::*UAU1*/Δ*cet1*::*URA3*); the *CCM1* heterozygote CQF154 (Δ*ccm1*::*ARG4/CCM1*); and the *C. albicans ccm1*-null mutant CQF171 (Δ*ccm1*::*ARG4*/Δ*ccm1*::*URA3*) was analyzed by Southern blot (Fig. 3). Genomic DNA was digested with *Bgl*II restriction endonuclease. After gel electrophoresis, the DNA was transferred to a nylon membrane for probing. For *CET1* (Fig. 3A), the DNA probe encompassed codons 51 to 480 of the 520 codon *CaCET1* open reading frame. For *CCM1* (Fig. 3B), the DNA probe encompassed codons 18 to 455 of the 474 codon *CaCCM1* open reading frame. Southern hybridization showed that, as expected, only one DNA band hybridized to the *CET1* probe and one DNA band hybridized to the *CCM1* probe in *C. albicans* BWP17 (Fig. 3). The *CET1* or the *CCM1* band is seen in the heterozygote isolates but not in the *cet1*- or *ccm1*-null mutants. There was no evidence that the wild-type *CET1* or *CCM1* was transposed in the null mutants.

Growth of capping gene deletion mutants. Growth in YEPD at both 30 and 37°C was measured for *C. albicans* BWP17 parent strain; the *CET1*, *CGT1*, and *CCM1* heterozygous deletion mutants and the *cet1*- and *ccm1*-null mutants (Fig. 4). The wild-type parent and the heterozygous strains all had very similar growth curves at both temperatures. The null mutants grew slower at both temperatures, but the difference is more pronounced at 37 than at 30°C. The lag in growth was much longer for the null mutants at 37°C than for the heterozygotes or the parent. One of the null mutants constructed from the one-step transformation method was temperature sensitive, with almost no growth over 96 h at 37°C.

Sensitivity to antifungal compounds. Prompted by a publication describing a *C. albicans* Δ*cgt1/CGT1* heterozygous deletion mutant that is resistant to the protein synthesis inhibitor hygromycin B (5), we decided to test the sensitivity for each of
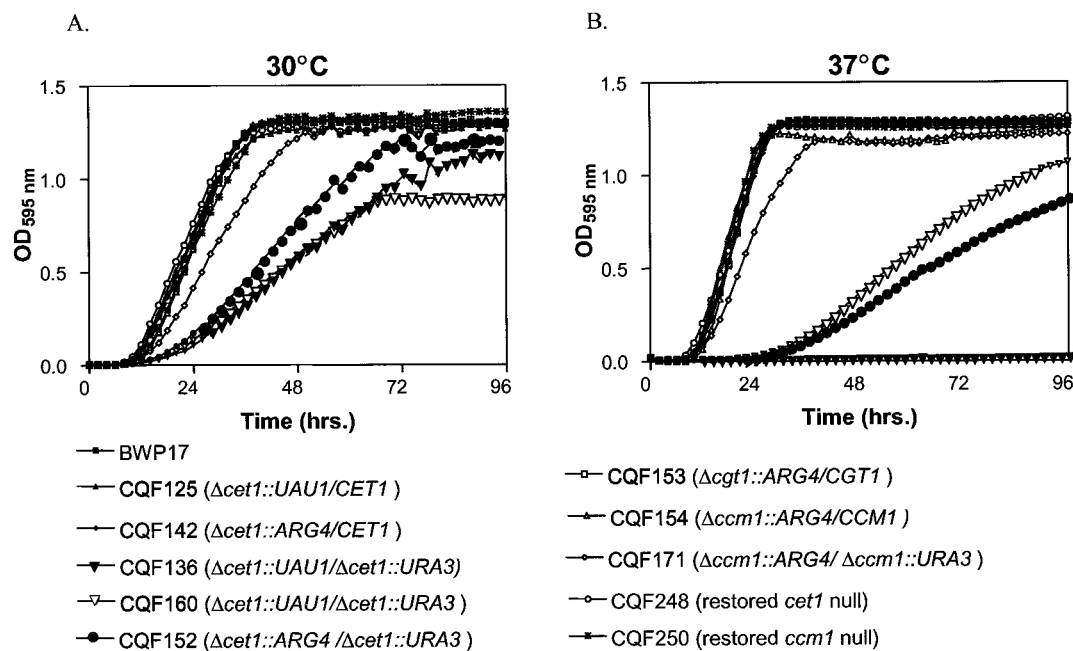
A.

B.

FIG. 4. Growth curves for *C. albicans* parent strain and capping gene deletion mutants at 30 and 37°C. Cultures were grown in 200 μl of YEPD+uridine in 96-well plates with starting inoculum sizes of ca. 2,000 to 3,000 cells/ml. Growth was monitored in a Spectramax plate reader every 30 min after the plates were shaken for 5 s.

our capping gene deletion mutants to antifungal compounds (Table 3). The compounds tested included the following: amphotericin B, a polyene that interacts with ergosterol in the fungal membrane (6); cycloheximide, which inhibits peptide synthesis (24); blasticidin S, an aminohexosyl-cytosine nucleoside that inhibits ribosomal peptidyltransferase (15, 16); hygromycin B, which inhibits peptide chain elongation by disruption of EF-2-dependent translation (8); and actinomycin D, a polypeptide that inhibits DNA-dependent RNA synthesis (1). For standard yeast broth microdilution assays, drug concentrations were tested at twofold dilutions, and MIC endpoints were determined at 48 h; however, the MICs for the *cet1*-null strain (CQF152) were determined at 72 h because no growth was observed in the microtiter plate for this strain even in the no-drug controls at 48 h. MICs that are within two dilutions are not considered significantly different (23). All strains showed very similar sensitivities to amphotericin B and actinomycin D.

The heterozygote deletion mutants for all three genes had similar sensitivities as the BWP17 parent to all drugs tested. Our *C. albicans* Δ*cgt1*/*CGT1* heterozygous deletion mutant was not more resistant to hygromycin B than the parent strain. However, our Δ*cet1*/Δ*cet1* mutant and our Δ*ccm1*/Δ*ccm1* mutants were slightly more sensitive to hygromycin B than the other strains tested. The Δ*cet1*/Δ*cet1* mutant was more sensitive to cycloheximide than any of the other strains.

Characterization of mRNA cap structures. mRNA was purified from *C. albicans* BWP17, CQF152 (*cet1*-null mutant), CQF248 (the *CET1* restored null), CQF171 (*ccm1*-null mutant), and CQF250 (the *CCM1* restored null) by using hot phenol extraction (18). Treatment of mRNA with tritiated sodium borohydride labels the 2′,3′-*cis*-diols on the ribose rings of both mRNA cap structures and the terminal nucleotides at the 3′ end of mRNA (12). In order to separate the cap structures for TLC analysis, the radiolabeled mRNA was

TABLE 3. In vitro susceptibility of *C. albicans* parent strain and capping gene deletion mutants to antifungal compounds

C. albicans strain (relevant phenotype)	MIC (μg/ml)[a]				
	Amphotericin B	Cycloheximide	Blasticidin S	Hygromycin B	Actinomycin D
BWP17 (parent)	0.5	>128	>32	64	128
CQF142 (Δ*cet1*/*CET1*)	0.5	>128	>32	>128	128
CQF152 (Δ*cet1*/Δ*cet1*)	0.5	32	32	8	32
CQF248 (*CET1* restored null)	0.5	>128	>32	>128	128
CQF153 (Δ*cgt1*/*CGT1*)	0.5	>128	>32	>128	128
CQF154 (Δ*ccmI*/*CCM1*)	0.5	>128	>32	>128	128
CQF171 (Δ*ccm1*/Δ*ccmI*)	0.5	>128	>32	32	64
CQF250 (*CCM1* restored null)	0.5	>128	>32	>128	128

[a] All MIC values were determined after 48 h of incubation, except for strain CQF152, where they were determined after 72 h of incubation due to slow growth even in the no-drug controls.
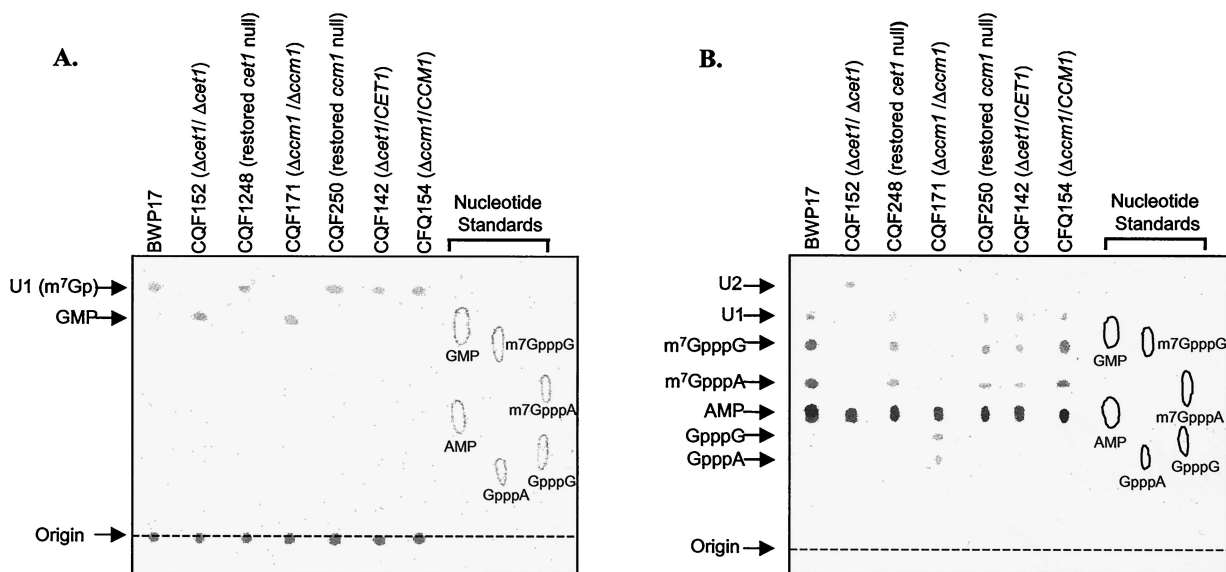
FIG. 5. TLC analysis shows altered mRNA cap structures for *cet1*- and *ccm1*-null mutants. TAP (A)- and P1 (B)-digested mRNA was purified from *C. albicans* BWP17, CQF152 (Δ*cet1*::*ARG4*/Δ*cet1*::*URA*), CQF248 (Δ*cet1*::*ARG4*/Δ*cet1*::*URA3* with *CET1* restored), CQF171 (Δ*ccm1*::*ARG4*/Δ*ccm1*::*URA3*) CQF250 (Δ*ccm1*::*ARG4*/Δ*ccm1*::*URA3* with *CCM1* restored), CQF142 (Δ*cet1*::*ARG4*/*CET1*), and CQF154 (Δ*ccm1*::*ARG4*/*CCM1*), all labeled with NaB[³H]₄. The location of the standards separated on the TLC plate were visualized by UV light and are indicated on the right side of the image.

treated with TAP or P1 nucleases. TAP hydrolyzes a variety of nucleoside-linked pyrophosphate bonds, including those found in cap structures; however, phosphodiester bonds, which link nucleosides downstream of the 5′ terminal cap structure in mRNA, are not cleaved by TAP (35). Hence, TAP digestion of mRNA removes the 5′-terminal guanylate in capped transcripts, leaving the rest of the polynucleotide intact. In contrast, P1 nuclease possesses no pyrophosphatase activity, thus rendering cap structures impervious to its hydrolytic activity. Instead, the enzyme is a phosphodiesterase that cleaves the phosphate bond between nucleosides in mRNA, generating 5′-nucleotide monophosphates, and releasing the unhydrolyzed 5′-terminal cap structures (11, 12). TAP and P1 nuclease digests of the radiolabeled mRNA were separated by TLC and analyzed by phosphorimaging (Fig. 5). Unlabeled standards were also separated on TLC and visualized with UV light to aid in identification of the radiolabeled spots in the samples. For the TAP digestions of all samples (Fig. 5A), there was a radiolabeled spot at the origin of the TLC, corresponding to the 3′-end labeled polynucleotide. In BWP17 the cap structure migration did not correspond to any of the standards (and is identified as U1) but is consistent with a m7Gp that would be released from TAP digestion of mRNA that has the wild-type m7GpppN structure. TAP digestion of labeled mRNA that was isolated from CQF171 (the *ccm1*-null mutant) and CQF152 (the *cet1*-null mutant) did not produce the same unidentified spot as seen in the BWP17 sample (U1); instead, they both had a spot that corresponds to GMP. Nuclease P1 digestion of the samples also produced very different results for parent and null mutants (Fig. 5B). For BWP17, there were spots corresponding to AMP, m7GpppA, and m7GpppG standards, as well as an unidentified spot indicated as U2. As expected, the spot corresponding to AMP and representing the labeled AMP

residue from the 3′ end of the nuclease P1-digested mRNA was seen for both null mutants. Also, as expected, there were no methylated cap structures seen for CQF171 (the *ccm1*-null mutant). Instead, the cap structures corresponded to the GpppG and GpppA standards. Nuclease P1 digestion of mRNA from CQF152 (the *cet1*-null mutant) released a product that migrated much farther than any of the standards or other digestion products (U3). We speculate that this spot also represents a cap structure since mRNA digested with TAP generates a product that migrates with GMP. This finding is consistent with TAP-mediated hydrolysis of cap structures lacking a methyl moiety at the N7 position of the 5′-terminal guanylate. Under the TLC conditions used here, U3 must represent a product with a greater polarity than any of the standards or other products. This could be the result of an extra phosphoryl group on the cap structure and would be consistent with the mutant being unable to catalyze the mRNA triphosphatase reaction.

Restoration of null mutants. As a formal proof that the phenotypes associated with loss of *cet1* and *ccm1* in the null mutants are due to the loss of the respective gene functions rather than disruption of the genetic loci, we inserted wild-type copies of the genes back into the genome at the Δ*his1*::*hisG* locus (42). The wild-type genes and upstream sequence were PCR amplified from *C. albicans* BWP17 genomic DNA with primers for *CET1* (*CET1*-restore 5′ and *CET1*-restore 3′) and primers for *CCM1* (*CCM1*-restore 5′ and *CCM1*-restore 3′). After cloning the PCR fragments into the *Sal*I site of pGEM-HIS (42), the resulting plasmids were linearized with *Nru*I and used to transform the respective null mutants (CQF152 and CQF171). The sequence homology between the genomic *HIS1* flanking sequence and pGEM-HIS1 vector provides a target sequence for recombination and insertion of the genes into the genome. Colonies with *CET1* or *CCM1* insertions were iden-

tified by analytical PCR of Ura$^+$ Arg$^+$ His$^+$ transformants, and the genomic insertions were confirmed by Southern blot analysis (Fig. 3). These strains with CET1 or CCM1 restored in trans in the genome were phenotypically similar to the wild-type BWP17 strain in growth studies (Fig. 4), susceptibilities to antifungal compounds (Table 3), and cap structures (Fig. 5).

DISCUSSION

Two features of fungal mRNA capping enzymes indicate they might be good targets for antifungal drug development. First, mRNA capping enzymes have distinct catalytic mechanisms and gene structures from their functional human counterparts (14, 26). Second, mRNA capping is essential in S. cerevisiae (32) and is widely reported to be critical for efficient translation in all eukaryotes (for reviews, see references 17, 20, and 30). All three genes encoding the enzymes involved in mRNA capping have been shown to be essential in S. cerevisiae (19, 34, 39). Although gene essentiality in S. cerevisiae is often consistent with essentiality for the homologous genes in Candida, there are many notable exceptions. Therefore, we wanted to validate mRNA capping as a good antifungal drug target by determining whether the genes encoding the capping enzymes are essential in C. albicans. The C. albicans mRNA capping enzymes have been characterized and the three genes encoding the mRNA capping enzymes in C. albicans (CET1, CGT1, and CCM1) have been identified (31, 44, 45), but null mutants have previously not been constructed for these genes. We were able to construct null deletion mutants of both CET1 and CCM1 in C. albicans by the methods of Enloe et al. (7) and Wilson et al. (42). This contrasts with a recent report by Pei et al. (26), who were unable to delete both alleles of CET1 in C. albicans by using the UAU1 one-step transformation method (7).

We initially used the one-step transformation method of Enloe et al. (7) and were able to generate null mutants of CET1 in C. albicans. However, the recovery of null mutants was originally very low (1 of 44 initial Arg$^+$ Ura$^+$ segregants), and this one cet1-null mutant isolated by the UAU1 mitotic recombination procedure was temperature sensitive (Fig. 4). These two observations raised the possibility that we might have generated a compensatory mutation during the mitotic recombination allowing us to isolate a null mutant for a gene that really is essential. To test this hypothesis, 16 additional Arg$^+$ Ura$^+$ segregants generated from the other two CET1 heterozygotes with UAU1 targeted insertions were screened. Four of these isolates were cet1-null mutants, and none of these four mutants showed the temperature-sensitive growth phenotype seen with the first cet1-null mutant (Fig. 4). These results suggest that the temperature-sensitive phenotype was not related to the loss of CET1 function but may be due to, for example, duplication of a recessive mutation adjacent to the insertionally deleted CET1 allele when this locus was converted to homozygosity in the mitotic recombination step.

As an additional verification that the CET1 gene is not essential, we were also able to generate cet1-null mutants by a two-step transformation method for disrupting both alleles (42). This method relies on sequential transformation of ARG4 and URA3 markers into the two CET1 alleles and led to the identification of 7 null mutants in the 9 Arg$^+$ Ura$^+$ transformants that were screened.

Null deletion mutants of CCM1, the methyltransferase-encoding gene, were constructed in C. albicans by using the two-step transformation method (Fig. 2). However, we were unable to generate null mutants at this locus by using the single-step transformation method. The high rate of success and relative ease in generating cet1- and ccm1-null mutants with the two-step transformation method versus the one-step transformation method highlights the importance of testing multiple approaches in determining whether genes are essential in C. albicans. The reason for the differences in the two methods remains unexplained, but it could be due to a physical constraint of the DNA at specific loci that inhibits the mitotic recombination event required to select homozygous deletions in the single transformation method.

De Backer et al. (5) showed, with their C. albicans Δcgt1/CGT1 heterozygous mutant, that the mutant was temperature sensitive and resistant to the translational inhibitor hygromycin B. We did not observe temperature sensitivity for our Δcgt1::ARG4/CGT1 heterozygous strain (Fig. 4). The MICs for hygromycin B were similar for this strain and the CGT1/CGT1 parent strain (Table 3). The C. albicans cet1- and ccm1-null mutants are more sensitive to hygromycin B than the heterozygotes and the strains with capping genes added back in trans (MICs = 16 μg/ml versus >128 μg/ml). In addition, the cet1-null mutant is more sensitive to the protein translation inhibitor cycloheximide. Hypersensitivity to a compound that inhibits protein translation would be an expected phenotype for a mutant strain that has altered levels of expression for a component of protein translation. The drug sensitivity data are not conclusive but are consistent with the theory that C. albicans CCM1 and CGT1 deletion mutants may have less-efficient protein translation.

The fact that cet1- and ccm1-null mutants can be generated in C. albicans raises multiple questions about the processing of mRNA and translation in this organism. Possible explanations for why CET1 and CCM1 are not essential in C. albicans include (i) redundant genes encoding the capping functions, (ii) an alternative capping pathway, (iii) the ability to survive with cap-independent translation, or (iv) the ability to effectively translate mRNA with a modified cap. Based on the results we show here, we favor the latter hypothesis.

There are many examples of important enzymes encoded by redundant genes in C. albicans, including genes encoding chitin synthase (21); the GSC1, GSL1, and GSL2 genes involved in β-1,3-glucan synthase (22), and protein mannosyltransferases (38). However, by using sequence analysis and Southern blots we have found no evidence of redundant genes for CET1 or CCM1 in the C. albicans genome. A search of the publicly available C. albicans genomic sequence (assembly 6, Stanford Genome Technology Center, http://www-sequence.stanford.edu/group/candida/index.html) did not identify any other locus encoding an open reading frame with significant amino acid sequence homology to CET1p or CCM1p. The Southern blot analysis showed only one band hybridized to CET1 or CCM1 fragments in the parent strain and this was lost in the cet1- or ccm1-null mutants (Fig. 3). If mRNA triphosphatase or methyltransferase capping activities are essential in C. albicans, there are more likely to be nonhomologous genes encoding the functions or an alternative capping pathway. However, our data indicate that modified guanylated caps are formed in the

null mutants and are sufficient for protein translation in *C. albicans*.

We were unable to delete, under the growth conditions used to select for deletion mutants, both alleles of *CGT1* in *C. albicans*. This suggests that the mRNA-guanylyltransferase modification is essential even if the triphosphatase and methyltransferase activities are not. However, it is possible that the essential nature of *CGT1* is due to an unknown function of this gene.

Analysis of the mRNA cap structure in the *C. albicans cet1*- and *ccm1*-null mutants indicates guanylated cap structures that are distinct from the mRNA cap structure in the wild-type cells (Fig. 5). The mRNA cap structure in the BWP17 cells migrates as expected with the m7GpppN standard. In the *ccm1*-null mutant, it is quite clear that the mRNA cap structures are not methylated (GpppN). Based on the pattern of labeled nucleotides seen in the TLC analyses, our hypothesis is that, in the *cet1*-null mutants, mRNA is guanylated without the third phosphate being removed and that it is not methylated (GppppN). Tetraphosphate linkages have been previously identified in cap structures formed by virus particles lacking RNA triphosphatase activity (4), indicating that viral guanylyltransferase activity is independent of RNA triphosphatase. If the cap structure in the *cet1*-null mutant contains a tetraphosphate linkage, the *C. albicans* guanylyltransferase activity must be independent of RNA triphosphatase. This conclusion is supported by a recent publication from Takagi et al. (37), who cite a fundamental divergence in mRNA capping machinery between *S. cerevisiae* and *C. albicans*. They report that activity of *S. cerevisiae* mRNA guanylyltransferase (CGT1p) depends on interaction with the RNA triphosphatase subunit (CET1p). However, their results showed that *C. albicans* CGT1p does not require interaction with CET1p for guanylyltransferase activity, a conclusion reinforced by our demonstration of guanylated mRNA caps in the *cet1*-null mutant. Further studies will be needed to determine the exact structures of the cap nucleotides in the null mutants, but they are definitely different than the cap structures in the parent strain.

The question remains as to whether any mRNA cap is essential for translation in *C. albicans*. The 5′-cap on mRNA binds the eukaryotic initiation factor eIF4e and is involved in the recruitment of the ribosome to form an initiation complex involving both the 5′-cap and the 3′-polyadenylated tail (41). Whereas most eukaryotic translation is thought to involve mRNA with 5′ caps (29), there are many examples of cap-independent translation in eukaryotes. Viral mRNAs have been reported to have 3′-end sequences that mimic the cap function (41), and cap-independent translation initiation that is facilitated by internal ribosome entry sites has been widely studied (47). Although eIF4e has been reported to be essential in *S. cerevisiae* (40), a recent report clarifies that eIF4e is not essential in starved cells (25). The proposal that mRNA capping is only essential in rapidly growing cells is supported by the growth studies with our *C. albicans* capping gene deletion mutants. Growth defects for the *cet1*- and *ccm1*-null mutants compared to parent strain are much more pronounced at 37°C than at 30°C (Fig. 4). The slower-growth phenotype for the *cet1*- and *ccm1*-null mutants could be due to a variety of reasons but, again, it is a phenotype expected for mutants with alterations in protein translation efficiency. The survival of the *cet1* and *ccm1*-null mutants demonstrates that the complete m7GpppN mRNA cap structure is not absolutely required in *C. albicans* and the mRNA cap probably contributes to efficiency but is not essential.

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