**Candida albicans** mutants in the BNI4 gene have reduced cell-wall chitin and alterations in morphogenesis

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The **Candida albicans** BNI4 gene was identified by homology to the Saccharomyces cerevisiae orthologue and encodes a predicted 1655 amino acid protein. In *S. cerevisiae* most cell-wall chitin is associated with primary septum formation and Bni4p is involved in tethering the Chs3p chitin synthase enzyme to the mother-bud neck by forming a bridge between a regulatory protein Chs4p and the septin Cdc10p. CaBni4p shows 20% overall identity to the ScBni4p, with 73% identity over the C-terminal 63 amino acids, which includes a putative protein phosphatase type 1 (PP1) binding domain. Northern blot analysis revealed a transcript of the expected size that was expressed in both yeast and hyphal growth forms. *C. albicans* has more chitin in its cell wall than *S. cerevisiae*, and again most chitin is synthesized by CaChs3p. The function of CaBNI4 was investigated by performing a targeted gene disruption using the ‘Ura-blaster’ method to delete amino acids 1120–1611 that are essential for function. The resulting *Cabni4Δ/Cabni4Δ* null mutants formed lemon-shaped yeast cells and had a 30% reduction in cell-wall chitin, reduced hyphal formation on solid serum-containing medium and increased sensitivity to SDS and increased resistance to Calcofluor White. The *Cabni4Δ/Cabni4Δ* null mutants were unaffected in chitin ring formation, but often exhibited displaced bud sites with more obvious but flattened birth scars. Therefore, unlike in *S. cerevisiae*, the *Cabni4* mutant apparently alters chitin distribution throughout the cell wall and not exclusively at the bud-neck region.

**INTRODUCTION**

Chitin is an essential polysaccharide in the fungal cell wall that is important in determining cell shape, for cytokinesis and as a possible antifungal drug target (Munro & Gow, 2001). In the human fungal pathogen *Candida albicans*, chitin is synthesized by four enzymes encoded by *CaCHS1, CaCHS2, CaCHS3* and *CaCHS8*. CaChs3p is responsible for the synthesis of most chitin in distinct locations of the cell wall including the lateral cell wall, chitin ring and bud scar (Bulawa et al., 1995). In *Saccharomyces cerevisiae*, Bni4p is involved in localizing Chs3p to the bud-neck region where the septum is formed. The mechanism of localization of Chs3p by CaBni4p was the subject of this investigation.

In *C. albicans*, CaChs3p expression is increased in hyphae, which have more chitin than yeast cells (Munro et al., 1998). CaChs1p synthesizes the chitin of the primary septum, is expressed at a low level in both yeast and hyphal cells, and has a potential role in lateral cell-wall stability (Munro et al., 1998, 2001, 2003). CaChs2p is a non-essential enzyme and its expression is increased during the yeast-to-hyphal transition (Gow et al., 1994). CaChs8p also contributes to *in vitro* chitin synthase activity in yeast and hyphal cells and has highest identity to CaChs2p (Munro et al., 2003). Therefore, chitin synthesis is regulated temporally and spatially at the transcriptional and post-translational levels (Roncero, 2002; Munro & Gow, 2001).

The spatial and temporal regulation of Chs3p has been studied in *S. cerevisiae* and involves a number of ancillary proteins including ScChs4p, ScChs5p, ScChs6p and ScChs7p (Trilla et al., 1997, 1999; Santos et al., 1997; Ziman et al., 1998), septins and Bni4p (DeMarini et al., 1997). In both *C. albicans* and *S. cerevisiae*, Chs4p is involved directly or indirectly in the activation of Chs3p (Sudoh et al., 1999; Ono et al., 2000). ScChs5p is required for targeting of ScChs3p to polarized growth sites and for cell fusion during mating (Santos et al., 1997; Santos & Snyder, 2003). ScChs6p is involved in the spatial regulation and recycling of ScChs3p (Ziman et al., 1998), while ScChs7p is required for the export of ScChs3p from the endoplasmic reticulum to the

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**Abbreviations:** PP1, protein phosphatase type 1; TEM, transmission electron microscopy.

The GenBank/EMBL/DDBJ accession number for the sequence reported in this paper is AYS69336.

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plasma membrane (Trilla et al., 1999). ScChs3p is transported through the secretory pathway to the plasma membrane where chitin synthesis takes place, and can also be internalized again via ligand-induced endocytosis (Ziman et al., 1996). ScChs3p can also be mobilized from internal stores in response to cellular stress (Valdivia & Schekman, 2003).

In S. cerevisiae, chitin deposition at the bud site is linked to the septin neck filaments, a family of proteins that have roles in septation and cytokinesis. The septin proteins localize to the incipient bud site and are ordered into higher structures to form a ring of neck filaments. The actin-myosin ring contracts and then the two neck filaments split, resulting in cytokinesis so that the mother and daughter cells each inherit a single septin ring (Longtime et al., 1996; Lippincott et al., 2001; Kinoshita, 2003). In S. cerevisiae there are seven septin genes: CDC3, CDC10, CDC11, CDC12, SHS1/SEP7, SPR3 and SPR28. The latter two genes are expressed only in the sporulation phase. In C. albicans, homologues of all seven septin genes have been recognized. The CaCDC3 and CaCDC10 genes are capable of complementing defects in the respective S. cerevisiae genes and are thus believed to perform similar roles (Di Domenico et al., 1994). Similar to the S. cerevisiae septins, CaCDC3 and CaCDC12 are essential for viability; however, the Cacdc10Δ and Cacdc11Δ mutants were viable but displayed conditional defects in cytokinesis, chitin localization and bud morphology (Warendra & Konopka, 2002). The C. albicans Cdc3p and Cdc11p homologues have been localized during the growth of yeast, pseudohyphae and hyphae (Sudbery, 2001). In true hyphae, an early and transient septin ring is formed that lacks Cdc3p, which does not participate in cytokinesis later in the cell cycle (Sudbery, 2001). Cacdc11A mutants were defective in ability to form hyphae on solid agar (Warendra & Konopka, 2002).

In S. cerevisiae, the septin Cdc10p interacts with Chs4p via Bni4p (bud neck involved). The ScBni4p protein is required for the correct targeting of ScChs3p and its activator ScChs4p to the bud-neck region. Mutants deleted in ScBNI4 had delocalized chitin deposition, with an aberrant cell morphology and enlarged bud necks (DeMarini et al., 1997). Immunolocalization experiments confirmed that ScBni4p was normally localized to the mother-bud-neck region and that localization was dependent upon the presence of septins but not ScChs4p or ScChs3p (DeMarini et al., 1997).

Yeast dihybrid analysis demonstrated that ScBni4p interacts with ScGlc7p (Uetz et al., 2000). ScGlc7p is a protein phosphatase type 1 (PP1) involved in a range of physiological activities including cell polarity, cell-wall integrity and morphology (Andrews & Stark, 2000). ScBni4p is required for the localization of ScGlc7p to the incipient bud neck but not for targeting to the neck at cytokinesis (Kozubowski et al., 2003). Although the precise role for this phosphatase at the bud neck is not known, it could facilitate the association of ScBni4p with the septins. ScBni4p is also believed to be necessary for the targeting of ScCrh2p, a glycosylphosphatidylinositol (GPI)-anchored mannoprotein involved in cell-wall assembly, at cytokinesis (Rodriguez-Pena et al., 2002).

Chitin synthesis in C. albicans is significantly different from that in S. cerevisiae in a number of respects (Munro & Gow, 2001; Munro et al., 2003), and we therefore examined the role of Cabni4p in growth and cellular morphogenesis in C. albicans. Here we describe the isolation and analysis of the C. albicans BNI4 homologue by reverse genetics. Disruption of Cabni4 resulted in cells that had a phenotype that was again different, in some aspects, to that of the bni4 mutation in S. cerevisiae. These were depleted in total chitin and had abnormal cell shape and bud-scar morphology and defects in hypha formation when growing on solid surfaces.

**METHODS**

**Strains, growth conditions.** The C. albicans strains used in this study are listed in Table 1. Strains were grown in YPD [1% (w/v) yeast extract, 2% (w/v) peptone, 2% (w/v) glucose] or SD [0-67% nitrogen source].

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**Table 1. C. albicans strains used in this study**

<table>
<thead>
<tr>
<th>Strain</th>
<th>Relevant genotype</th>
<th>Parent</th>
<th>Reference</th>
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<tbody>
<tr>
<td>CAF2-1</td>
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<td>SC5314</td>
<td>Fonzi &amp; Irwin (1993)</td>
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<td>This work</td>
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<td>CAI-4</td>
<td>This work</td>
</tr>
<tr>
<td>NGY81b</td>
<td>CAI-4 bni4Δ::his-G-URA3-hisG/BNI4</td>
<td>CAI-4</td>
<td>This work</td>
</tr>
<tr>
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<td>CAI-4 bni4Δ::hisG/BNI4</td>
<td>NGY81a</td>
<td>This work</td>
</tr>
<tr>
<td>NGY82b</td>
<td>CAI-4 bni4Δ::hisG/BNI4</td>
<td>NGY81b</td>
<td>This work</td>
</tr>
<tr>
<td>NGY83a</td>
<td>CAI-4 bni4Δ::hisG-URA3-hisG/bni4Δ::hisG</td>
<td>NGY82a</td>
<td>This work</td>
</tr>
<tr>
<td>NGY83b</td>
<td>CAI-4 bni4Δ::hisG-URA3-hisG/bni4Δ::hisG</td>
<td>NGY82b</td>
<td>This work</td>
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<tr>
<td>NGY84a</td>
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<tr>
<td>NGY84b</td>
<td>CAI-4 bni4Δ::hisG/bni4Δ::hisG</td>
<td>NGY83b</td>
<td>This work</td>
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(w/v) yeast nitrogen base, 2% (w/v) glucose] at 30 °C. The hyphal form of C. albicans was grown in 20% (v/v) newborn calf serum or Lee’s minimal medium pH 6.5 (Lee et al., 1975) at 37 °C. Solid media contained 2% (w/v) agar (Oxoid). Ura+ strains were supplemented with 50 μg uridine ml−1. Hyphal colonies were grown on 20% serum agar for 2–5 days at 37 °C.

Media for integrative transformation. Gene knockout was performed using the ‘Ura-blaster’ protocol described by Fonzi & Irwin (1993). Ura+ transformants were streaked on SD plates; single colonies were picked and grown in 5 ml SD medium. Genomic DNA was extracted for Southern analysis and diagnostic PCR. Counterselection of Ura- segregants was done on SD medium containing 1 mg 5-fluoro-orotic acid (5-FOA, Melford) ml−1 and 50 μg uridine ml−1.

Bacterial strains and plasmids. Escherichia coli DH5α and XL1Blue (Stratagene) were used for preparation of plasmid DNA. Plasmids pGEM-T, pBluescript and pBR322 (Promega) were used for cloning gene fragments. For sequencing and disruption cassette construction, the CaBNI4 gene sequence was cloned as two overlapping fragments. Attempts to clone the whole gene were unsuccessful due to frequent recombination events in E. coli.

Plasmids p5921 and pMB7 were used for construction of Ura-blaster cassettes (Fonzi & Irwin, 1993; Gow et al., 1994). A 543 bp fragment from the middle of the coding region of CaBNI4 and a 543 bp fragment covering the 3' coding and non-coding region of CaBNI4 were obtained by PCR using restriction-site-ended primers, to facilitate the disruption of nucleotides 3630–4833 from the 4968 nucleotide ORF. Plasmids p59BN1 and pMBN2 were digested with SacI and HindIII restriction enzymes to release the bni4α/Ura-blaster disruption cassette. The digestion products were extracted with phenol/chloroform, resuspended in TE (10 mM Tris/HCl, 1 mM EDTA, pH 7.5) to a concentration of >100 ng μl−1 in a volume of 20 μl. Transformation used the lithium acetate method (Bulawa et al., 1995; Sanglard et al., 1997). Despite numerous attempts to clone the entire BNI4 gene both in-frame and out-of-frame, the size of this gene and spontaneous recombination events prevented its cloning in E. coli. Hence constituted strains could not be generated as controls for aberrations due to transformation. Therefore, Cabni4Δ/Cabni4Δ mutants were generated from independent lineages of strains and these subjected to parallel phenotypic analysis to ensure that resulting phenotypes were a consequence of gene disruption and not a result of any unforeseen changes induced by the transformation process. This procedure has been adopted in the analysis of other large genes in C. albicans (Cassola et al., 2004; Zaragoza et al., 2000).

Analysis of nucleic acids. C. albicans genomic DNA was extracted using the mechanical lysis method by vortexing in Triton mix [2% (w/v) Triton X-100, 1% (w/v) SDS, 100 mM NaCl, 10 mM Tris/HCl, pH 8.0 and 1 mM EDTA] with glass beads (Sigma, 425–600 μm in diameter) followed by phenol/chloroform extraction. DNA samples were digested with restriction endonucleases, separated on a 0–8–1% (w/v) agarose gel and transferred to nylon membranes. Total RNA was extracted from 50–100 mg (wet wt) yeast and hyphal C. albicans cells using the Qiagen RNeasy mini extraction kit following lysis in a Hybaid Ribolyser. RNA samples were heated at 50 °C for 60 min in 55% DMSO, 1 M Glyoxal, separated on a 1:4% (w/v) non-denaturing agarose gel and again transferred to nylon membranes.

Southern and Northern blots were probed with α-32P-radiolabelled fragments of CaBNI4. DNA sequencing was performed using the dideoxy-termination method (Sanger et al., 1977) and sequences were aligned and analysed using the GCG v.10 software from HGMP (http://www.hgmp.mrc.ac.uk). Northern blots were re-probed with a radiolabelled CaTEF3 fragment as loading controls (Di Domenico et al., 1992). The entire gene was sequenced and submitted to GenBank: accession number AY569336.

Chitin contents. C. albicans cell-wall chitin was determined by the enzymatic method (Bulawa et al., 1986; Mellado et al., 1996; Munro et al., 1998) and acid hydrolysis methods described previously (Kapteyn et al., 1990). Triplicate samples of 50–100 mg (wet wt) yeast cells were used in the enzymatic analysis and 20–30 mg (wet wt) cell-wall material were used for the acid-hydrolysis method.

Morphological observations. Yeast and hyphal cells were fixed in 10% (v/v) neutral buffered formalin (Sigma). Chitin was stained with 50 μg Calcofluor ml−1 (Sigma, fluorescent brightener 28). Transmission electron microscopy (TEM) was performed on exponential-phase yeast cells after fixation with 3% glutaraldehyde (v/v) in 0.1 M sodium phosphate buffer pH 7.4. Secondary fixation was performed in 1% osmium tetroxide in distilled H2O and cells were embedded in TAAB resin. Ultrathin silver or gold defracting sections were stained with uranyl acetate and lead citrate and examined with a Philips 301 transmission electron microscope at an accelerating voltage of 80 kV.

Table 2. Primers used in the construction of Ura-blaster cassettes

<table>
<thead>
<tr>
<th>Name</th>
<th>Sequence</th>
<th>Position and orientation</th>
</tr>
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<tbody>
<tr>
<td>SACIDIS</td>
<td>5′-GAAGAGCTCCACACTGTTAACAATGGG-3′</td>
<td>Nucleotides 3087–3106 of BNI4 ORF →</td>
</tr>
<tr>
<td>BGLIDIS</td>
<td>5′-GAAGAGCTCCACACTGTTAACAATGGG-3′</td>
<td>Nucleotides 3630–3611 of BNI4 ORF ←</td>
</tr>
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<td>SALIDIS</td>
<td>5′-GAAGAGCTCCACACTGTTAACAATGGG-3′</td>
<td>Nucleotides 4833–4852 of BNI4 ORF →</td>
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<td>HINDIDIS</td>
<td>5′-GAAGAGCTCCACACTGTTAACAATGGG-3′</td>
<td>382–500 nucleotides downstream of BNI4 stop codon ←</td>
</tr>
</tbody>
</table>
**RESULTS**

Isolation of the *CaBNI4* gene, expression analysis and search for other BNI4-like homologues

The *CaBNI4* gene was originally identified by homology searches to the Stanford *C. albicans* genome database using *ScBNI4* nucleotide and protein sequences. A contig was identified that contained a 202 bp sequence which showed 73% identity to *ScBNI4* at the amino acid level and 68% identity at the nucleotide level and corresponded to the 3’ region of the gene. The complete ORF for *CaBNI4* of 4968 kb (orf 6.2835 of contig 6.2168) shares 20% overall identity to *ScBNI4*.

![Diagram](https://example.com/diagram.png)

**Fig. 1.** (a) Alignment of the predicted protein sequences of *ScBni4p* and *CaBni4p* based on CLUSTALW analysis at the EBI web site (http://www.ebi.ac.uk). The three regions of homology are outlined, with the corresponding percentage identities. The coiled-coil regions were predicted using the COILSCAN program in GCG version 10 and are shown by the hatched box. The region disrupted in *C. albicans bni4 Δ/bni4 Δ* is shown by the shaded box. (b) Local alignment of *ScBni4p* and *CaBni4p* with the highest identity at the C-terminal region. The grey box shows the conserved PP1 binding domain and the shaded box below the sequence shows the 19 amino acids included in the corresponding region deleted in *Cabni4 Δ/Cabni4 Δ*.
identity to ScBni4p, and alignment of ScBni4p and CaBni4p sequences revealed three main regions of homology, at the N-terminal, mid-protein and C-terminal regions (Fig. 1a). The highest identity is at the C-terminal 63 amino acids; this region also contains the putative Glc7p binding domain, GVRF (Fig. 1b). Attempts to clone full-length CaBNI4 in pBluescript were unsuccessful; therefore, CaBNI4 was cloned as two overlapping fragments of 3.7 kb and 2.7 kb. A 5.5 kb fragment containing the full-length CaBNI4 gene was successfully cloned into the low-copy plasmid pBR322, but this was susceptible to recombination in E. coli. No evidence was found for another BNI4-like sequence in the C. albicans genome database and no homologous sequence was identified by low-stringency Southern hybridization using a probe specific to the 3’ region of the CaBNI4 gene (not shown).

Northern analysis of CaBNI4 revealed a transcript of the expected size in both exponential-phase yeast cells and 4 h after induction of hyphal growth (Fig. 2).

**Disruption of the CaBNI4 gene**

To determine the role of CaBNI4 we disrupted both chromosomal copies of the gene, in parallel lineages of strains generated using the Ura-blaster protocol. Disruption was confirmed by Southern analysis (Fig. 2a) and the absence of transcript in the null mutants was confirmed by Northern analysis (Fig. 2b). Growth rates of the yeast form in YPD and hypha formation in Lee’s medium were the same for CAI-4 and the Cabni4Δ/Cabni4Δ (NGY83a, NGY83b, NGY84a, NGY84b) mutants (not shown). Growth rates were measured in liquid culture in YPD at 30 °C for yeast and germ-tube formation was measured in Lee’s medium at 37 °C for both Ura+ and Ura- strains. No effect was seen on hypha formation in the Ura+ and
Ura<sup>−</sup> *C. albicans* mutants induced in Lee’s medium at pH 6.5 and 37°C. However, the *Cabni4Δ/Cabni4Δ* mutants displayed a reduced ability to form hyphae when grown on solid 20% serum (Fig. 3). In contrast, *Cachs3Δ/Cachs3Δ* mutants were not affected in hypha formation on serum agar (Fig. 3).

**Phenotype of the *bni4* mutant**

The *Cabni4Δ/Cabni4Δ* mutants were screened against SDS (0–0.01–0.05%), Calcofluor White (100–400 μg ml<sup>−1</sup>) (Fig. 4), NaCl (0–2–1 M), and Hygromycin B (100 μg ml<sup>−1</sup>) (not shown) to determine their sensitivity to these plasmolysing or cell-wall-damaging agents. SDS sensitivity was slightly increased for the *Cabni4Δ/Cabni4Δ* mutants compared to the CAF2-1 parent, whilst an increased resistance to Calcofluor White was observed, indicative of a reduction in cell-wall chitin (Fig. 4).

The chitin contents of yeast cells and cell walls of yeast and hyphae were determined using chitinase-digestion and acid-digestion methods (acid-hydrolysis data shown in Fig. 5). In both cases the *Cabni4Δ/Cabni4Δ* mutants contained significantly (*P > 0.01*) less chitin compared to the wild-type strain (Fig. 5). Overall, in *Cabni4Δ/Cabni4Δ* mutant strains, yeast cells had 30% less chitin and hyphal cells 40% less chitin compared to the parental strain.

![Fig. 3. Reduced hypha formation of *Cabni4Δ/Cabni4Δ* mutant (NGY83a) compared to CAF2-1 parent and *Cachs3Δ/Cachs3Δ* mutant on 20% serum agar. Scale bars, 1 mm.](image)

![Fig. 4. Increased sensitivity of *Cabni4Δ/Cabni4Δ* mutant to SDS and increased resistance to Calcofluor White compared to CAF2-1. *C. albicans* strains were grown as a starter culture of yeast cells in YPD overnight. Serial dilutions corresponding to 5 × 10<sup>4</sup>–5 × 10<sup>4</sup> yeast cells were spotted across solid medium containing (a) SDS or (b) Calcofluor White and plates were incubated at 30°C for 2–5 days.](image)
Morphological alterations

The effect of the chitin reduction for the Cabni4Δ/Cabni4Δ null mutants was visualized using Calcofluor White staining (Fig. 6). Mutant hyphal cells stained less brightly with Calcofluor. Only minor differences were noted between the Calcofluor staining of yeast cells in the mutant. A slightly aberrant bud-scar pattern was observed in the Cabni4Δ/Cabni4Δ mutant, in which bud scars appeared to be more randomly positioned over the yeast cell surface. Chitin rings in dividing cells were difficult to detect using Calcofluor White in both wild-type and Cabni4Δ/Cabni4Δ mutants. Yeast cells were more elongated, and ‘lemon-shaped’ cells were frequently observed (Fig. 6k).

Analysis of Cabni4Δ/Cabni4Δ by TEM showed that the primary septum was intact and normal and again suggested there were minor differences in the budding pattern (Fig. 7f) and the formation of lemon-shaped cells (Fig. 7d).

DISCUSSION

We isolated and characterized a C. albicans gene that is the only homologue of the BNI4 of S. cerevisiae in the C. albicans genome sequence. The gene product of ScBni4 has been implicated in the spatial deposition of chitin to the bud-neck region by forming a complex by which Chs3p is linked to the septin bud-neck filaments via Chs4p and Bni4p. Immunolocalization studies confirmed the position of ScBni4p at the bud-neck region (DeMarini et al., 1997). The similarity between ScBni4p and CaBni4p is mostly in the C-terminal region and deletion of 492 amino acids in the C-terminal region caused loss of the BNI4 transcript and influenced subtly the phenotype of both yeast and hyphal cells. In the C. albicans mutants, bud scars and primary septa were formed but only minor changes in the shape and distribution of the bud scars was found.

In S. cerevisiae it has been shown that Bni4p interacts with
Chs4p and the septin Cdc10p whilst Chs4p interacts with Cdc12p (DeMarini et al., 1997). Therefore, if the same is true in C. albicans, then the Chs4p–Cdc12p interaction may be sufficient for targeting of Chs3p to the bud site since the bud neck and primary septum were not markedly affected in the mutant. To date no other ScBNI4 homologue has been identified in the C. albicans genome sequencing project and no homologues were identified here by low-stringency hybridization; therefore, no evidence exists for the formal possibility that function of Bni4p can be achieved by an alternative homologous protein.

Changes in the structural integrity of the Candida cell wall are expressed as changes in the sensitivity of cells to various inhibitors that stress the wall in various ways. Sensitivity to Hygromycin B, SDS, Calcofluor and NaCl have been shown to depend on the permeability, porosity or chitin content of the cell wall, and several glycosylation or chitin synthase mutants have increased sensitivity to these compounds (Timpel et al., 1998, 2000; Warit et al., 2000; Binley et al., 1999; Navarro-Garcia et al., 1995). The Cabni4Δ/Cabni4Δ mutant had decreased sensitivity to Calcofluor White, reflecting the reduced chitin content, and increased sensitivity to SDS that may reflect reduced integrity of the wall.

We have demonstrated a reduction in cell-wall chitin in the Cabni4Δ/Cabni4Δ null mutant, indicating that in C. albicans, Bni4p is involved in targeting of Chs3p to the cell surface. However, disruption of CaBNI4 caused loss of chitin over the whole cell wall as visualized by Calcofluor staining. We propose that CaBni4p may have a global, septin/bud-neck-independent role in the deposition of chitin, by either the targeting or activation of the Chs3p chitin synthase enzyme.

The lemon shape of the bni4Δ/bni4Δ mutants suggests that Chs3p targeting and chitin content are vital for normal yeast morphology. The C. albicans bni4Δ/bni4Δ mutant was also reduced in hyphal formation on 20 % serum agar. Germ-tube formation was, however, normal in both Lee’s

Fig. 7. TEM of parent CAI-4 (a, c, e) Cabni4Δ/Cabni4Δ null mutant (NGY84a) (b, d, f) showing protuberant and flattened bud scars, birth scars and lemon-shaped cells (d). Vacuoles (v) are indicated; bars, 0.5 μm.
Although the phenotype of the synthase enzymes to the surface has yet to be fully explored.

that Bni4p is involved in the targeting of other chitin Chs proteins was identified by dihybrid analysis in (EUROCELL WALL QKL3-2000-01537).

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Sequence data for Candida albicans were obtained from the Stanford DNA Sequencing and Technology Center website at http://www-

REFERENCES


