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Differential Virulence of *Candida glabrata* Glycosylation Mutants


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Differential Virulence of *Candida glabrata* Glycosylation Mutants*

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**Background:** *Candida glabrata* virulence is poorly understood at the molecular level.

**Results:** Inactivation of components of the *C. glabrata* glycosylation machinery results in changes in fungal mannan structure and altered virulence.

**Conclusion:** Changes in *C. glabrata* cell wall architecture impact the host-pathogen interactions.

**Significance:** Greater understanding of *C. glabrata* virulence will provide insights that can be adopted for development of novel diagnostic and therapeutic interventions.

The fungus *Candida glabrata* is an important and increasingly common pathogen of humans, particularly in immunocompromised hosts. Despite this, little is known about the attributes that allow this organism to cause disease or its interaction with the host immune system. However, in common with other fungi, the cell wall of *C. glabrata* is the initial point of contact between the host and pathogen, and as such, it is likely to play an important role in mediating interactions and hence virulence. Here, we show both through genetic complementation and polysaccharide structural analyses that *C. glabrata* *ANP1*, *MNN2*, and *MNN11* encode functional orthologues of the respective *Saccharomyces cerevisiae* mannosyltransferases. Furthermore, we show that deletion of the *C. glabrata* *ANP1*, *MNN2*, and *MNN11* mannosyltransferases directly affects the structure of the fungal N-linked mannan, in line with their predicted functions, and this has implications for cell wall integrity and consequently virulence. *C. glabrata* *ANP1* and *MNN2* mutants showed increased virulence, compared with wild-type (and *mnn11*) cells. This is in contrast to *Candida albicans* where inactivation of genes involved in mannan biosynthesis has usually been linked to an attenuation of virulence. In the long term, a better understanding of the attributes that allow *C. glabrata* to cause disease will provide insights that can be adopted for the development of novel therapeutic and diagnostic approaches.

The fungal pathogen *Candida glabrata* is a major cause of life-threatening disease in the immunocompromised patient population, causing up to 30% of all candidemias and having a higher attributable mortality than *Candida albicans* (1, 2). As with other pathogenic *Candida* species, the cell wall of *C. glabrata* is the point of contact between host and fungus. In addition, it performs many other functions, protecting the fungal cell from hostile environments, enabling adherence to host surfaces, and maintaining cell shape. The cell walls of *Saccharomyces cerevisiae* and *C. albicans* have both been investigated in detail and extensively reviewed in the literature (3–5). Common to many other fungi, the central core of their cell walls is a branched β-(1,3)-, β-(1,6)-glucan linked to chitin via a β-(1,4)-glucan linkage. This core structure is generally found close to the cell membrane, with chitin innermost, and the β-(1,6)-glucan structure/linkages displayed outwards acting as a linker to the outer cell wall mannanproteins. Some of the chitin and glucan chains extend throughout the entire depth of the cell wall structure (6, 7). The outer glycoprotein layer of the fungal cell wall plays a major role in host recognition (8–15).

These glycoproteins are decorated with both *N*- and *O*-linked sugars, principally mannans, the precise nature of which varies among species but can result in addition of up to 200 mannose units (16). Structural studies indicate that *C. glabrata* mannan is more closely related to that of *S. cerevisiae* than *C. albicans* (17–19), and it shows some inter-strain variation (20). Despite this variation in mannan structure, the core biosynthetic machinery appears to be relatively well conserved, a fact that facilitates the analysis of *C. glabrata* glycosylation. *N*-Linked protein glycosylation occurs in two stages. First, assembly of the core oligosaccharide structure takes place at the membrane of the endoplasmic reticulum (21). The completed core structure is a branched oligosaccharide of residues Glc3Man9GlcNAc2, which is transferred en bloc from its lipid
TABLE 1

Fungal strains used in this study

<table>
<thead>
<tr>
<th>Species</th>
<th>Strain</th>
<th>Genotype or description</th>
<th>Source</th>
</tr>
</thead>
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<tr>
<td>C. glabrata</td>
<td>ATCC 2001</td>
<td>Wild type</td>
<td>ATCC</td>
</tr>
<tr>
<td>C. glabrata</td>
<td>ΔH76</td>
<td>Δhis3::ScURA3 Δtrp1</td>
<td>This study</td>
</tr>
<tr>
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<td>Δhis3::ScURA3 Δtrp1 Δanp1::HIS3</td>
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<tr>
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<td>XFS-1P</td>
<td>Δhis3::ScURA3 Δtrp1 Δanp1::HIS3 pGACT14 (TRP1)</td>
<td>This study</td>
</tr>
<tr>
<td>C. glabrata</td>
<td>LJW-5RLP</td>
<td>Δhis3::IRA3 Δtrp1Δanp1::ANP1 pGACT14 (TRP1) pGACH3 (HIS3)</td>
<td>This study</td>
</tr>
<tr>
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<td>This study</td>
</tr>
<tr>
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<td>LJW-2P</td>
<td>Δhis3::IRA3 Δtrp1Δanp1::HIS3 pGACT14 (TRP1)</td>
<td>This study</td>
</tr>
<tr>
<td>C. glabrata</td>
<td>LJW-2RLP</td>
<td>Δhis3::IRA3 Δtrp1Δanp1::MNN2 pGACT14 (TRP1) pGACH3 (HIS3)</td>
<td>This study</td>
</tr>
<tr>
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<td>Δhis3::IRA3 Δtrp1Δanp1::HIS3 mnn1::HIS3</td>
<td>This study</td>
</tr>
<tr>
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<td>This study</td>
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<tr>
<td>C. glabrata</td>
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<td>BY4741</td>
<td>MATa Δhis3 Δleu2 Δmet15 Δura3</td>
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<tr>
<td>S. cerevisiae</td>
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<td>Δhis3::IRA3 Δtrp1 Δanp1::HIS3 plJW5 (TRP1 ScANP1)</td>
<td>This study</td>
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<tr>
<td>S. cerevisiae</td>
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<td>This study</td>
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</table>

anchor to the target asparagine residues on a nascent peptide (22). Once attached, the oligosaccharide is trimmed to leave Man₃GlcNAc₂ (23). The second part of the N-linked glycosylation process occurs in the Golgi complex, where a single α-(1,6)-linked mannose is added to Man₃GlcNAc₂ core by Och1 (24). Proteins either then receive a core-type structure by the addition of two further mannoses or a much more highly decorated α-(1,6)-linked backbone structure, branched by α-(1,2)- and α-(1,3)-mannoses (25, 26). In S. cerevisiae this process requires both the MNN and KTR/KRE/MNT families of mannosyltransferases, including Anp1, Mnn2, and Mnn11 (27–35). It is this final stage in processing that accounts for the huge diversity of glycans decorating fungal glycoproteins. Interestingly, many of these fungal mannosyltransferases are absent from human cells, and hence their analysis has potential with respect to the development of novel antifungal and immunotherapy.

With this in mind, the enzymes involved in both the processing of N- and O-linked mannans in C. albicans have been analyzed and shown to be required for the virulence of this organism, including those specifically involved in both N-glycosylation (36) and O-glycosylation (37, 38). In addition glycosylation appears to be important in mediating virulence in Cryptococcus neoformans (39, 40). Indeed, in C. neoformans the polysaccharide capsule that includes mannose-based components is essential for the virulence of this fungus (41). Furthermore, a heterogeneous group of mannoproteins are critical antigens in stimulating T cell responses (42). This importance in virulence may be due in part to differential host recognition. N- and O-linked mannans are major pathogen-associated molecular patterns and, along with β-glucans, play important roles in triggering host innate immunity. Recent findings in C. albicans have highlighted how a coordinated immune response, with stimulus from both N- and O-linked glycans of the mannoproteins, and also the β-glucan triggers the immune cascade (6). This underlines the fact that multiple components of the cell wall are involved in fungal recognition. Some of the proteins that manufacture these specific epitopes are also required for virulence of C. albicans (36, 43, 44).

These studies have resulted in an understanding of how glycosylation of C. albicans proteins influences fungal host-pathogen interaction and virulence. However, little is known regarding the role of glycosylation in the pathogenesis of C. glabrata. Simultaneous deletion of the BMT2–6 genes encoding five β-mannosyltransferases yielded a strain that was unable to induce weight loss or chronic inflammation in a murine colitis model (45). Furthermore, nothing is known regarding the conservation of the glycosylation machinery in this species. We therefore sought to determine the effect of inactivation of three putative components of the C. glabrata N-linked glycosylation machinery (Anp1, Mnn2, and Mnn11) on cell wall, specifically mannan structure and virulence. We show that there is functional conservation of these enzymes between C. glabrata and S. cerevisiae. ANP1 and MNN11 encode α-(1–6)-mannosyltransferases, and MNN2 encodes an α-(1–2)-mannosyltransferase. Inactivation of each gene results in altered N-linked mannan structure consistent with these functions. Furthermore, deletion of the genes differentially affects virulence, and this variability may be partially explained by resultant changes in cellular adhesion.

EXPERIMENTAL PROCEDURES

Strains, Media, and Culture Conditions—All strains used and constructed in this study are listed in Table 1. Fungal cells were routinely cultured in yeast extract peptone dextrose (YPD) (2% (w/v) peptone, 2% (w/v) glucose, 1% (w/v) yeast extract), yeast extract peptone maltose (YPM) (2% (w/v) peptone, 2% (w/v) maltose, 1% (w/v) yeast extract), or synthetic dropout medium (SD) (0.68% (w/v) yeast nitrogen base without amino acids (Difco), 2% (w/v) glucose, and appropriate dropout mix (Clontech) at 30 °C (S. cerevisiae) or 37 °C (C. glabrata) at 180 rpm. For culture on solid media 2% (w/v) agar was added prior to autoclaving. For phenotypic assays, selective media were made as described by Hampsey (46). Strains were stored at room temperature for up to 4 weeks on solid agar plates or for long term storage in 50% (v/v) glycerol at −80 °C.

Construction of C. glabrata Mutants—To disrupt C. glabrata genes, a one-step PCR-based approach was adopted (47). DNA fragments were amplified using primer pairs such that the PCR product would contain 60 bp of homology to the gene of interest at both the 5′ and 3′ ends and 20-bp tails homologous to the C. glabrata HIS3 gene, which was amplified from pTW25 (48). Primer sequences are available upon request. The disruption cassette was transformed into C. glabrata ΔHT6, and histidine prototrophs were selected on appropriate dropout media. To reconstitute C. glabrata genes of interest, the SAT1 flipper method was used (49). Southern analysis was used to confirm gene disruption at the correct locus and single integration.
The C. glabrata anp1 null mutant was constructed by removing 1344 bp of the C. glabrata ANP1 gene (CAGL0I01331g, +1 to +1344 with respect to the start codon, and the stop codon is at +1342) via homologous recombination. Four independent transformants were selected. These strains were all screened in a full phenotypic assay (data not shown), and one mutant was selected for further study, C. glabrata XFS-1 (anp1). This was made prototrophic by transformation with pCgACT14 (50) to give C. glabrata XFS-1P.

To reconstitute ANP1 in C. glabrata XFS-1 plasmids, plJW6 and plJW7 were constructed as follows. A NotI-SacII downstream fragment of the C. glabrata ANP1 gene (positions +1322 to +1772) was amplified from C. glabrata 2001 genomic DNA. The resulting 459-bp downstream fragment was digested with NotI and SacII and cloned into NotI-SacII-digested pSFS2 (49) to generate plasmid plJW6. A KpnI-Xhol fragment containing the complete open reading frame as well as 0.44 kb of upstream and 0.30 kb of downstream flanking sequences of the ANP1 gene was amplified from C. glabrata 2001 genomic DNA. The resulting 2164-bp fragment was digested with KpnI and Xhol and cloned into KpnI-Xhol digested plJW6 to generate plJW7. The insert from plasmid plJW7 was excised as a KpnI-SacII fragment for transformation into C. glabrata LJW-2 (anp1) via homologous recombination. Four independent transformants were selected. These strains were all screened in a full phenotypic assay (data not shown), and one mutant, C. glabrata LJW-2 (anp1), was selected for further study.

The C. glabrata mnn2 null mutant was constructed by removing 1839 bp of the C. glabrata MNN2 gene (CAGL0I014532g, +1 to +1839 with respect to the start codon; the stop codon is at +1837) via homologous recombination. Four independent transformants were selected. These strains were all screened in a full phenotypic assay (data not shown), and one mutant, C. glabrata LJW-2 (mnn2), was selected for further study. This was made prototrophic by transformation with pCgACT14 to give C. glabrata LJW-2P.

To reconstitute MNN2 in C. glabrata, LJW-2 plasmids plJW8 and plJW9 were constructed as follows. A NotI-SacII downstream fragment of the C. glabrata MNN2 gene (positions +1820 to +2250) was amplified from C. glabrata 2001 genomic DNA. The resulting 331-bp downstream fragment was digested with NotI and SacII and cloned into NotI-SacII digested pSFS2 to generate plasmid plJW8. An ApaI-Xhol fragment containing the complete open reading frame as well as 0.44 kb of upstream and 0.30 kb of downstream flanking sequences of the MNN2 gene were amplified from C. glabrata 2001 genomic DNA. The resulting 2583-bp fragment was digested with ApaI and Xhol and cloned into ApaI-Xhol-digested plJW8 to generate plJW9. The insert from plasmid plJW9 was excised as an ApaI-SacII fragment for transformation into C. glabrata LJW-2 by electroporation, and re-integrants were selected, made prototrophic, and confirmed as above to yield C. glabrata LJW-2RLP (mnn2::CgMNN2).

The C. glabrata mnn11 null mutant was constructed by removing 1326 bp of the C. glabrata MNN11 gene (CAGL0G07491g, +1 to +1326 with respect to the start codon, the stop codon is at +1324) via homologous recombination. Four independent transformants were selected. These strains were all screened in a full phenotypic assay (data not shown), and one mutant, C. glabrata LJW-3 (mnn11), was selected for further study. This was made prototrophic by transformation with pCgACT14 to give C. glabrata LJW-3P. MNN11 was not reconstituted.

Cross-species Complementation—To determine whether the functions encoded by the C. glabrata and S. cerevisiae ANP1, MNN2, and MNN11 orthologues have been conserved, we performed a series of cross-species complementation experiments. First, we sought to determine whether S. cerevisiae ANP1 could complement phenotypes of the C. glabrata anp1 mutant. To achieve this, the entire S. cerevisiae ANP1 open reading frame (−760 to +2480, the stop codon is at +1501) was amplified from S. cerevisiae BY4741 genomic DNA. The resulting 3287-bp product was cloned directly into pGEM-T Easy (Promega), excised with BamHI, and cloned into BamHI-digested pCgACT14 to give plasmid plJW1. plJW1 was transformed into C. glabrata XFS-1 (anp1), and tryptophan prototrophs were selected. A representative strain was selected and designated C. glabrata LJW-6 (anp1::ScANP1).

Next, we sought to determine whether C. glabrata MNN2 and MNN11 could complement the phenotypes of the S. cerevisiae mnn2 and mnn11 mutants, respectively. To achieve this, the entire C. glabrata MNN2 (−1265 to +2376, the stop codon is at +1837) and MNN11 (−1916 to +1911, the stop codon is at +1324) open reading frames plus flanking regions were amplified from C. glabrata 2001 genomic DNA. The resulting 3661- and 3779-bp products were cloned directly into pGEM-T Easy, excised with BamHI, and cloned into BamHI-digested pCgACT14 to give plasmids plJW3 and plJW4, respectively. plJW3 was transformed into S. cerevisiae mnn2, and leucine prototrophs were selected. A representative strain was selected and termed S. cerevisiae LJW-8 (mnn2::CgMNN2). plJW4 was transformed into S. cerevisiae mnn11, and leucine prototrophs were selected. A representative strain was selected and termed S. cerevisiae LJW-9 (mnn11::CgMNN11).

Virulence Analysis—We then sought to determine how inactivation of ANP1, MNN2, and MNN11 impacted the ability of C. glabrata to cause disease in a well established murine model of systemic candidosis. To achieve this virulence, analysis was performed essentially as described previously (53–55). Briefly, groups of 10–22 out-bred male CD1 mice were immunosuppressed with 200 mg of cyclophosphamide/kg of body weight on day −3 and every 4th day thereafter. Animals were infected with $7 \times 10^7$ C. glabrata yeast cells in 200 μl of saline via tail vein injection. Following infection, mice were weighed and observed daily and sacrificed at predetermined end points, e.g. 20% weight loss.
Candida glabrata Glicosylation Mutants

Ethics Statement—All animal work was performed under the auspices of the “Animals (Scientific Procedures) Act 1986” at Imperial College London, United Kingdom. All protocols were approved by the Home Office under project license PPL 70/6487.

Alcian blue Binding Assay—Alcian blue binding assays were performed essentially as described previously to determine the extent of mannan phosphorylation (58). Briefly, a suspension of \( 1 \times 10^7 \) washed exponential phase cells was suspended in 1 ml of 30 \( \mu \)g/ml Alcian blue in 0.02 M HCl (pH 3), incubated at room temperature for 10 min, and pelleted by centrifugation. Then \( A_{600} \) values of 100 \( \mu \)l of supernatant samples were determined in a spectrophotometer. Alcian blue concentration was determined by reference to a standard curve (microgram of Alcian blue bound per \( A_{600} \) unit of cell suspension).

Mannan Isolation—To analyze the consequences of gene deletion on mannan structure, mannan was isolated using a modified method first described by Kocourek and Ballou (59). Briefly, 1 liter of saturated culture was collected by centrifugation, and the cells were washed in double distilled water. Washed cells were resuspended in an excess of acetic acid; the cells were collected by centrifugation, and the supernatant was removed. The cells were dried over Drierite® and under vacuum. The cells were rehydrated in 200 ml of double distilled water and subjected to autoclaving for 3 h, and after cooling the solid extract was collected by centrifugation and the remaining supernatant subjected to Fehling precipitation. An equal volume of Fehling’s solution (50:50 Fehling’s Solution No. 1 and No. 2) was added to the extracted mannan mixture with stirring, and a precipitate of copper-mannan was then formed and allowed to settle. The remaining supernatant was removed, and the copper complex was dissolved in 6 ml of 3 M HCl. The resulting solution was poured slowly, with stirring, into a 100-ml (8:1) mixture of methanol/acetic acid, and the resulting precipitate was allowed to settle overnight. The supernatant was decanted, and the precipitate was stirred with a fresh methanol/acetic acid mixture to remove the copper complex. This was repeated until the solution appeared colorless. The precipitate was collected and washed several times with methanol and allowed to dry under vacuum.

Proton and Carbon-13 NMR—Structural analysis of the mannan extracts was performed using one- and two-dimensional proton (60) and carbon-13 NMR (61). NMR spectra were collected on a JEOL Eclipse + 600 NMR spectrometer operating at 80 ± 1 °C in 5-mm NMR tubes. Mannan was dissolved in D$_2$O at 80 ± 1 °C. Proton chemical shifts were referenced to sodium 3-trimethylsilylpropionate-2,2,3,3-d$_4$. C-13 chemical shifts were referenced to external acetone. Proton one-dimensional NMR spectral collection and processing parameters were as follows: 25 ppm spectral width centered at 7.5 ppm, 32,768 data points, 1024 scans, 15 s relaxation delay, 2.18 s acquisition time, and exponential apodization. C-13 one-dimensional NMR spectral collection and processing parameters were as follows: 250 ppm spectral width centered at 110 ppm, 65,536 data points, 3161 scans, 5 s relaxation delay, 1.74 s acquisition time, and exponential apodization. Homonuclear gradient COSY two-dimensional NMR spectra were collected and processed as follows: 512 × 128 point matrix was zero-filled to 512 × 1024 points, 256 scans per row with 4 dummy scans, 3 ppm sweep width centered at 4.5 ppm, sinebell apodization in both dimensions, and 1 s relaxation delay. NMR spectra were processed using JEOL DELTA software running on the Eclipse+ 600 NMR and on a Macintosh MacBook Pro.

Flow Adhesion Assay of C. glabrata Mutants—To determine whether gene deletion affected cellular adherence, we used a well established endothelial flow assay performed essentially as described previously (64). Briefly, C. glabrata was cultured overnight in liquid YPD at 37 °C. 180 rpm, washed three times with sterile Hanks’ buffered salt solution (Invitrogen), counted, and resuspended at 1.0 × 10^6 yeast/ml in Hanks’ buffered salt solution. Glass slides coated with confluent HMEC-1 endothelial cell monolayers were mounted in a parallel plate flow chamber (GlycoTech, Rockville, MD), and C. glabrata cells were perfused through the flow chamber and over the endothelial cell monolayer, using an automated syringe pump at 0.25 dynes/cm^2 (Harvard Apparatus, Natick, MA). All experiments were performed on a 37 °C stage, in an environmental microscope chamber also maintained at 37 °C. Adhesion events were visualized using a Zeiss Axiovert 200 M inverted fluorescence microscope. An integrated high resolution AxiosCam digital camera (Nikon) with Axiosvision 4.6 software (Imaging Associates Ltd., Bicester, UK) was used to record the flow experiments. C. glabrata suspensions were allowed to perfuse the flow chamber for 2 min before commencing recording. Results consisted of 15-min recordings of a random field of view (0.15 mm^2) using a ×20 objective. Each experiment was repeated with three separate confluent endothelial cell slides on at least two occasions. Cell motion analysis was performed using time-lapse software. Images were then acquired over 15 min into a video file at 2 frames/min, and the total number of adherent cells/mm^2 was recorded.

3 The abbreviations used are: GPC/MALLS, gel permeation chromatography-multilangle laser light scattering; r.m.s., root mean square.
RESULTS

ANP1, MNN2, and MNN11 Gene Functions Are Conserved between C. glabrata and S. cerevisiae—To determine whether C. glabrata ANP1, MNN2, and MNN11 encode functional homologues of the S. cerevisiae α-(1–6)-mannosyltransferases (Anp1 and Mnn11) and α-(1–2)-mannosyltransferase (Mnn2), we conducted a series of cross-complementation experiments. S. cerevisiae ANP1 was able to successfully rescue the caffeine, SDS, Calcofluor White, hygromycin B, and NaCl sensitivities of the C. glabrata anp1 null mutant (Fig. 1, A–C, and data not shown). Similarly C. glabrata MNN2 and MNN11 were able to rescue phenotypes associated with S. cerevisiae mnn2 and mnn11 null mutants, respectively (Fig. 1, D–I, and data not shown). This demonstrates that the genes in the two species encode at least partial functional homologues.

In addition to these complementation studies, we determined the consequences of the individual C. glabrata gene deletions to various perturbations. As anticipated, all three mutants had phenotypes consistent with a weakened cell wall. The C. glabrata anp1 null mutant was hypersensitive to the cell wall perturbing agents Calcofluor White and SDS and the stress-inducing agent NaCl. Furthermore, analogous to glycosylation-defective strains in S. cerevisiae, the C. glabrata anp1 null mutant was hypersensitive to hygromycin B (Fig. 2, A–C, data not shown). Comparatively, C. glabrata mnn2 was unaffected for growth on hygromycin B, NaCl, and SDS but harbored a cell wall defect of sorts as the null mutant was hypersensitive to Calcofluor White and sodium orthovanadate (Fig. 2, D–F, data not shown). C. glabrata mnn11 was hypersensitive to Calcofluor White, NaCl, hygromycin B, sodium orthovanadate, and to growth at 42 °C (Fig. 2, G–I). In liquid culture, all three null mutants exhibited slight growth defects with doubling times of 54 min (mnn11), 60 min (mnn2), and 70 min (anp1) in YPD at 37 °C compared with 45 min for C. glabrata 2001. In addition, C. glabrata mnn2 and mnn11 tended to form small cellular aggregates that could be largely dispersed by vigorous vortexing. These data strongly support the hypothesis that C. glabrata Anp1, Mnn2, and Mnn11, as expected for mannosyltransferases, play roles, as do their counterparts in S. cerevisiae, in maintaining cell wall integrity.

Structure of C. glabrata Mannan—Our cross-complementation experiments strongly suggest that C. glabrata ANP1, MNN2, and MNN11 encode functional homologues of the respective S. cerevisiae mannosyltransferases. Hence, we would anticipate that their inactivation should result in changes to mannan structure, specifically that the anp1 and mnn11 mutants would have shorter α-(1–6)-polymannosyl backbones, as they would have reduced α-(1–6)-mannosyltransferase activity, and the mnn2 null would lack α(1–2) mannose side chains, due to loss of α(1–2)-mannosyltransferase. To verify this, we carried out a series of physicochemical and structural analyses.

Initially, GPC/MALLS was used to compare the molecular weight and r.m.s. radii of mannans from C. glabrata 2001, anp1, mnn2, and mnn11 strains. Pullulan was used as a control. The mannans from all three mutants showed polymer distributions that were different from C. glabrata 2001. Specifically, mannans from the mutants were characterized by a larger quantity of lower molecular weight polymers (Fig. 3A and Table 2). For example, the polymer distribution of C. glabrata mnn2 mannan is clearly shifted downfield in the GPC/MALLS chromatogram (Fig. 3B) which is indicative of a lower molecular weight mannan compared with the wild-type C. glabrata 2001 strain. This was also the case for mannans from anp1 and mnn11 cells, as would be expected if the mannan polymers had a lower degree of polymerization as a result of a shorter α-(1–6) backbone or missing α-(1–2) side chains. The r.m.s. radius provides an indication of the volume that the molecules occupy in three-dimensional space. C. glabrata mnn2 mannan has a 47.4% reduction in r.m.s. radius compared with C. glabrata 2001, suggesting that it contains the fewest mannose monosaccharides of all strains tested. Reductions of 29.2 and 29.9% were observed in the anp1 and mnn11 mannans (Table 2).
To further characterize these differences we performed \(^1\)H NMR studies. Chemical shift assignments for the anemic proton, H1, and H2 of the mannosyl repeat units in the backbone and side chain structural fragments were obtained from COSY spectra (data not shown). These studies show (Table 3) that \(C.\ glabrata\) 2001, \(anp1\), and \(mnn11\) mannans (Fig. 4, A–C, respectively) are distinctly different from the mannan isolated from \(C.\ glabrata\) mnn2 (Fig. 4D). Specifically, the \(C.\ glabrata\) 2001, \(anp1\), and \(mnn11\) mannans exhibit resonances that are assigned to structural fragments in \(\alpha\)-(1,2)-linked (60) and possibly \(\alpha\)-(1,3)-linked (65) mannosyl repeat units in side chains attached to the \(\alpha\)-(1,6)-linked backbone chain with all backbone repeat units containing side chains (Table 3). Also, the presence of mannosyl repeat units associated with the phosphodiester linkage between acidic and acidic labile portions of the mannan structure is evident for 2001, \(anp1\), and \(mnn11\). In addition, the proton NMR spectrum of \(mnn11\) mannan (Fig. 4C) indicates a reduced level of \(\beta\)1–2\(\alpha\)1, side chains compared with 2001 and \(anp1\) mannans based on the reduced intensity of the resonances near 4.78 and 5.18 ppm (Fig. 4C, indicated by vertical arrows). These resonances are assigned to the anemonic protons of the \(\beta\)1- and -2\(\alpha\)1 structural fragments, respectively, of the \(\beta\)1–2\(\alpha\)1 side chain structural fragment. The predominant resonances for \(C.\ glabrata\) mnn2 mannan support the presence of backbone mannosyl repeat units without attached side chains based upon the major anemonic proton resonance at 4.91 ppm. This singlet resonance at 4.91 ppm is assigned to an anemonic proton of the \(\alpha\)-(1,6)-linked backbone mannose repeat unit (-\(\alpha\)1–6\(\alpha\)1–6\(\alpha\)1-\(\alpha\)1-) containing no side chains (66, 67). Also, significant side chain structural fragments containing \(\alpha\)-(1,2)-linked and possibly \(\alpha\)-(1,3)-linked mannosyl repeat units (60, 65) are not indicated based upon the reduced level of these resonances in the 5.0–5.3 ppm spectral region. The side chains in the mnn2 mannan are considerably shorter than in 2001, \(anp1\), and \(mnn11\) mannans.
**TABLE 3**

Significant mannosyl structural fragments present in the mannans purified from *C. glabrata* 2001, *anp1*, *mnn2*, and *mnn11*

<table>
<thead>
<tr>
<th>Structural fragments</th>
<th>2001</th>
<th><em>anp1</em></th>
<th><em>mnn11</em></th>
<th><em>mnn2</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>α-1–2 Mα1→PO₄</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>α-1–2 Mα1→2</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Mβ1→2 Mα1→(2(3))</td>
<td>Yes</td>
<td>Yes</td>
<td>Minor</td>
<td>No</td>
</tr>
<tr>
<td>α1→2 Mα1→2</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Mα1→α-1–2 Mα1α1→6 Mα1→(2(3))</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>α1→6 Mα1→2</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>α1→6 Mα1→6</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Mβ1→2 Mβ1→2 Mα1→(2(3))</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
</tbody>
</table>

* Structural fragment identifications are based upon analysis of COSY two-dimensional NMR spectra observed for each isolate. In each fragment, “M” refers to the mannosyl repeat unit. The number represents the point of attachment within the specified mannosyl repeat unit. Proton numbering is indicated in the monomer structure shown in Fig. 4. α and β indicate the conformation at the anomeric carbon.

* 2(3)” indicates that the point of attachment to the neighboring mannosyl repeat unit could be either at the 2- or 3-position.

The mannan from *C. glabrata mnn2* is distinct from other mannans because it lacks resonances in the 5.0–5.3 ppm spectral region for anomeric protons associated with acid-labile mannosyl repeat units in side chains attached to a phosphodiester linkage are not evident (Table 3). 13C NMR (Fig. 5) with six resonances whose chemical shifts compare favorably with an α-(1,6)-mannan dimer model compound (61) confirms this structural assignment. Proton and 13C NMR chemical shift assignments along with structural fragment and dimer chemical shifts for *C. glabrata mnn2* mannan are summarized in Table 4. Therefore, *C. glabrata mnn2* expresses nearly pure α-(1,6)-mannan with fewer or shorter side chains, whereas *C. glabrata 2001*, *anp1*, and *mnn11* express mannan containing side chains (Table 3).

The Alcian blue assay showed that inactivation of *MNN2* resulted in a 75% reduction in mannosyl phosphorylation compared with wild-type cells, whereas the relative reduction was only 50% when *ANP1* or *MNN11* was deleted (Fig. 6). Furthermore, the *C. glabrata 2001* 1H NMR spectrum shows a doublet resonance at 5.57 ppm from phosphorylation of the mannan (Fig. 4B), which the *C. glabrata mnn2* spectrum lacks (Fig. 4D). This supports the data from the Alcian blue experiments of decreased mannosyl phosphorylation in the *mnn2* null mutant.
and it suggests that the α-(1,2)-mannose side branches are important sites for mannosyl phosphate linkage.

Taken together, these data strongly support the view that Anp1, Mnn2, and Mnn11 function as mannosyltransferases in C. glabrata, and both S. cerevisiae and C. glabrata mannans are structurally similar but distinct from C. albicans mannan (65).

Role of C. glabrata Anp1, Mnn2, and Mnn11 in Virulence—Having determined that C. glabrata ANP1, MNN2, and MNN11 encode functional homologues of the orthologous S. cerevisiae proteins, we sought to investigate their role in virulence. To achieve this, we used an established murine model of Candida albicans hypervirulence with 100% mortality by day 4, compared with 20% survival over 14 days for the wild-type control (Fig. 7B, p < 0.0001). Reconstitution of MNN2 restored virulence to wild-type levels with 20% survival over 14 days (p > 0.05). Therefore, inactivation of C. glabrata anp1 results in a hypervirulent phenotype in our mouse model. Similarly, the C. glabrata mnn2 null was significantly increased in virulence with 100% mortality by day 4, compared with 20% survival over 14 days for the wild-type control (Fig. 7B, p < 0.0001). Reconstitution of MNN2 restored virulence to wild-type levels with 20% survival over 14 days (p > 0.05). Therefore, inactivation of C. glabrata mnn2 results in a hypervirulent phenotype in our mouse model.

In contrast, the C. glabrata mnn11 null was unaffected in virulence with 40% survival by day 14, compared with 20% survival over 14 days for the wild-type control (Fig. 7C, p > 0.5). No MNN11 reconstitution experiments were performed as virulence was wild type in the mnn11 null. Hence, deletion of MNN11 has no effect on virulence in our mouse model.

C. glabrata mnn2 Cells Are Hyperadherent to Endothelial Cells—To determine whether the structural differences in the cell wall were able to affect the adherence capacity of the strains, and hence at least partially explain the differences in virulence observed, we employed a flow adhesion assay. C. glabrata cells were perfused through a flow chamber over a confluent layer of HMEC-1 endothelial cells for 15 min. Adhered cells were scored at 0, 5, 10, and 15 min for each strain, and the results from a representative experiment (three technical replicates) are shown in Fig. 8. C. glabrata adhesion to the endothelial cells was extremely rapid with adhesion noted for C. glabrata mnn2 strain, and both α-(1,6)-mannan dimer (61). The 13C NMR spectrum of α-(1,6)-mannan extracted from C. glabrata mnn2 cells is shown. Resonance chemical shifts are assigned to specific carbons in Table 4. Resonances are labeled and assigned based on the α-(1,6)-linked mannan dimer shown (61).

TABLE 4
C. glabrata mnn2 mannann1H and 13C NMR chemical shifts

<table>
<thead>
<tr>
<th>Nucleus</th>
<th>1H NMR</th>
<th>13C NMR</th>
</tr>
</thead>
<tbody>
<tr>
<td>This work</td>
<td>Reference</td>
<td>This work</td>
</tr>
<tr>
<td>1</td>
<td>4.911</td>
<td>4.920 (66)</td>
</tr>
<tr>
<td>2</td>
<td>4.002</td>
<td>4.009 (66)</td>
</tr>
<tr>
<td>3</td>
<td>3.854</td>
<td>3.856 (60)</td>
</tr>
<tr>
<td>4</td>
<td>3.736</td>
<td>66.64</td>
</tr>
<tr>
<td>5</td>
<td>3.854</td>
<td>70.86</td>
</tr>
<tr>
<td>6</td>
<td>3.943</td>
<td>65.56</td>
</tr>
<tr>
<td>6′</td>
<td>3.812</td>
<td></td>
</tr>
</tbody>
</table>

4. C-13 chemical shifts were referenced to external acetone.

C. glabrata and C. albicans mannans are moderate with the reference assignments for protons, and an α-(1,6)-mannan dimer (61) for C. glabrata and C. albicans mannans are moderate with the reference assignments for protons, and an α-(1,6)-mannan dimer (61) for 13C. Proton labels are shown in the mannose monomer structure in Fig. 4. The structure of the dimer with carbon labels is shown in Fig. 5. Proton and 13C NMR spectra were collected on a JEOL Eclipse 600 NMR spectrometer operating at 1 °C. Proton chemical shifts were referenced to sodium 3-trimethylsilylpropionate-2,2,3,3-d4 at UNIV OF EXETER on September 1, 2014http://www.jbc.org/ Downloaded from
**Candida glabrata Glycosylation Mutants**

FIGURE 7. *C. glabrata anp1 and mnn2 are hypervirulent*. A, survival curves for mice infected with *C. glabrata* 2001 (open squares), anp1 (closed diamond), and anp1:ANP1 (closed triangles). Intravenous infection with the *C. glabrata* anp1 null mutant at $7 \times 10^7$ cells/mouse resulted in a hypervirulent phenotype with 100% mortality within 5 days, compared with the wild-type strain at the same dose resulting in 20% survival over 14 days. This result is significant ($p < 0.01$, Kaplan-Meier log rank analysis). The reintegrant control restored virulence to wild-type levels with 20% survival over 14 days ($p > 0.05$, Kaplan-Meier log rank analysis). B, survival curves for mice infected with *C. glabrata* 2001 (open squares), mnn2 (closed diamond), and mnn2::MNN2 (closed triangles). Intravenous infection with the *C. glabrata* mnn2 null mutant at $7 \times 10^7$ cells/mouse resulted in a hypervirulent phenotype with 100% mortality within 4 days, compared with the wild-type strain at the same dose resulting in 20% survival over 14 days. This result is significant ($p < 0.0001$, Kaplan-Meier log rank analysis). The reintegrant control restored virulence to wild-type levels with 20% survival over 14 days ($p > 0.05$, Kaplan-Meier log rank analysis). C, survival curves for mice infected with *C. glabrata* 2001 (open squares) and mnn11 (closed diamond). Intravenous infection with the *C. glabrata* mnn11 null mutant at $7 \times 10^7$ cells/mouse resulted in a wild-type phenotype with 40% survival over 14 days, compared with the wild-type strain at the same dose with 20% survival over 14 days. This result is not significant ($p > 0.5$, Kaplan-Meier log rank analysis). Groups ($n = 22$ wild-type cells; $n = 10$ for all mutants) of outbred CD1 mice were immunosuppressed with cyclophosphamide and infected with $7 \times 10^7$ *C. glabrata* yeast cells via tail vein injection. Following infection, mice were weighed and observed daily and sacrificed at predetermined end points, e.g. 20% weight loss.

adherence compared with *C. glabrata* 2001 for all measured time points. Hence, both the *C. glabrata* mnn2 and anp1 endothelial cell interactions were altered as characterized by a hyperadherent phenotype in vitro, albeit modest in the case of *C. glabrata* anp1 cells.

**DISCUSSION**

Complementation analyses showed that the *C. glabrata* ANP1, MNN2, and MNN11 encode functional homologues of the respective *S. cerevisiae* proteins. Therefore, we predict that both *C. glabrata* Anp1 and Mnn11 are $\alpha$-(1,6)-mannosyltransferases, whereas Mnn2 functions as an $\alpha$-(1,2)-mannosyltransferase (26). As anticipated, inactivation of each gene resulted in phenotypic consequences suggestive of changes in cell wall structure and integrity.

To investigate the structural basis for these phenotypic changes, we compared the mannans in each mutant to wild-type *C. glabrata*. All three mutants had mannans that exhibited lower molecular weight than mannan isolated from wild-type cells. The 48% reduction in molecular weight of *C. glabrata* mnn2 demonstrates that this mannan contains the fewest mannosyl repeat units of all strains tested, which we suggest is due to an inability of the mutant to catalyze the addition of $\alpha$-(1–2)-mannose residues to the $\alpha$-(1–6)-linked mannosyl backbone resulting in long unbranched mannans. This is in agreement with a lack of $\alpha$-(1–2)-mannose residues seen in an *S. cerevisiae* mnn2 strain (68). In contrast, the *C. glabrata* anp1 and mnn11 strains display a less dramatic decrease in their molecular weight (degree of polymerization). Although their mannan backbone chains are shorter, $\alpha$-(1–2)-mannose residues can still attach. Thus, the overall molecular weight of the anp1 and mnn11 mannan polymers is higher than that observed for *C. glabrata* mnn2 mannan.

The Alcian blue assay showed that inactivation of MNN2 resulted in a 75% reduction in mannosyl phosphorylation compared with wild-type cells, whereas the relative reduction was only 50% when ANP1 or MNN11 was deleted. The mannosyl phosphorylation that was observed is likely due to attachment of phosphomannan to either the N-linked core structure or O-mannan. However, the lower level of mannosyl phosphorylation in *C. glabrata* mnn2 cells indicates that the $\alpha$-(1,2)-mannose side chains harbor mannosyl phosphorylation linkage points, as seen in *S. cerevisiae* N-glycans (69) and similar to what has been reported in *C. glabrata* N-glycan structural studies (17, 18). The $^1$H NMR spectrum of mannan extracted from...
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FIGURE 8. C. glabrata anp1 and mnn2 are hyperadherent to HEMC-1 endothelial cells. Adhesion of C. glabrata 2001, anp1, mnn2, and mnn11 to HEMC-1 endothelial monolayers under conditions of shear flow. C. glabrata 2001, anp1, mnn2, and mnn11 cells were perfused through a flow chamber over an HMEC-1 monolayer, and adhered cells were counted at 0-, 5-, 10-, and 15-min time points. C. glabrata cells were suspended at 1.0 x 10⁶ yeast/ml in Hanks’ buffered salt solution and perfused over glass slides coated with confluent HMEC-1 monolayers, mounted in a parallel plate flow chamber. Adhesion events were visualized from a random field of view (0.15 mm²) using a Zeiss Axiovert 200 M inverted fluorescence microscope. Images were then acquired over 15 min into a video file at 2 frames/min, and the total number of adherent cells/mm² was recorded. All experiments were performed in a controlled environment chamber at 37 °C, and each experiment was repeated with three separate confluent endothelial cell slides on at least two occasions. The results shown are the pooled triplicate data from a representative experiment, and the standard deviation indicated. *, p < 0.05; **, p < 0.001; t test.

FIGURE 9. Predicted mannan structures of C. glabrata anp1, mnn2, and mnn11. A, predicted structure of the C. glabrata mnn2 mannan as essentially a linear α-(1,6)-mannotan with minimal α-(1,2)-linked side chain branching, and lacking the majority of mannosyl phosphorylation. B, predicted structure of C. glabrata anp1 and mnn11 mannans. These contain a shorter α-(1,6)-mannotan backbone; however, they retain secondary and tertiary side chain branching and some mannosyl phosphorylation. The precise structure of the secondary and tertiary branches is not known and is predicted from the mannann structural work described herein.

C. glabrata mnn2 confirmed the lower level of mannosyl phosphorylation in this strain.

Our results indicate that C. glabrata 2001 has a mannan structure composed of α-(1,6)-linked mannosyl backbone that has α-(1,2)-linked mannosyl side chains that are the principal site of mannosyl phosphorylation and that some of these side chains terminate in α-(1,3)-mannose residues. In mnn2 cells, this is replaced by a structure that lacks α-(1–2)-linked mannosyl side chains and exhibits severely depleted levels of phosphomannan (Fig. 9A). Whereas anp1 and mnn11 cells retain α-(1–2)-linked mannosyl side chains and a greater degree of phosphorymnannan, they have shorter α-(1–6)-linked mannosyl backbones (Fig. 9B). These structures are in broad agreement with the structures recently described in three different C. glabrata strains (20). Additionally, these overall changes in mannan structure very likely reflect differential glycosylation of individual proteins, many of which would have phenotypic implications. Functional analysis of these changes could be extremely revealing.

Changes in C. albicans mannan structure dramatically impact upon cell wall integrity, virulence, and activation of innate immunity (12, 36). Here, we have shown that deletion of C. glabrata mannosyltransferases again impacts cell wall integrity. We have previously shown that inactivation of C. glabrata ACE2, although not directly involved in modulating mannan structure, had a profound impact on the cell wall and secretome that results in massive overstimulation of host innate immunity and increases virulence almost 200-fold (48, 70, 71). We therefore sought to determine the impact of Anp1, Mnn2, and Mnn11 on virulence. In a mouse model of systemic candidosis, both the C. glabrata anp1 and mnn2 mutants were hypervirulent compared with wild-type C. glabrata 2001, whereas C. glabrata mnn11 exhibits wild-type like virulence. C. glabrata ace2 cells form large clumps, and hence it is possible that death is attributable to obstruction of the vasculature. However, in the experiments described here, mice were infected with single cells (C. glabrata anp1) or very small cellular aggregates (C. glabrata mnn2 and mnn11, n < 5) clearly demonstrating that increased virulence can occur in the absence of vascular occlusion. We predict that a septic shock-like response occurs in the C. glabrata anp1- and mnn2-infected mice, as has been observed in mice infected with other hypervirulent C. glabrata mutant strains (48, 72). Certainly, the balance between pro- and anti-inflammatory responses is important in many fungal infections (73). Potent activation of pattern recognition receptors can lead to septicemia and rising levels of pro-inflammatory cytokines such as TNF-α and IL-6, which can reflect the balance between inflammatory responses (74, 75). Cytokine analysis of the serum 24 h post-infection (four mice per group) was conducted to investigate this; however, the variation in absolute cytokine levels between mice was too high to allow comparison within such a small cohort. Hence, we have been unable to confirm or refute this prediction.

Another issue with respect to the virulence characteristics of anp1 and mnn11 strains needs to be addressed. In S. cerevisiae, Anp1 and Mnn11 are both members of the mannosyl polymerase II complex and either contribute to or exhibit α-(1,6)-mannosyltransferase activity (76, 77). Our data strongly suggest that this function is conserved in C. glabrata. So the question arises, why do strains that lack components of the same enzyme complex exhibit different virulence levels? Especially as we have shown that the outer chain mannan structure is similar in C. glabrata anp1 and mnn11 strains (Fig. 9). To address this, we sought to determine whether variations in the ability to elicit
immune activation *in vitro* or adherence to endothelial cells, both important mediators of the host-fungal interaction, could explain this variation. *mnn2*, *mnn11*, and *anp1* cells were hyper-elicitors of TNF-α production from RAW264.7 cells compared with *C. glabrata* 2001 (supplemental Fig. 1), suggesting that they are all capable of overactivation of innate immunity, at least *in vitro*, and hence this cannot explain the virulence difference.

The ability to adhere to cells is a prerequisite for tissue penetration, invasion, and disease progression, and many of the proteins that mediate this interaction are, or are likely to be, glycosylated (78–81). The crucial role of adhesion in *C. glabrata* pathogenesis has been demonstrated by the observation that the glycosylphosphatidylinositol-linked aspartyl proteases encoded by YPS1-11 are essential for virulence (78–81). We therefore sought to determine whether the differences in virulence could be explained by differences in adhesion. Most reported studies of *Candida* adhesion employ static assays where the fungal cells remain in prolonged contact with cultured monolayers (82–84). Flow assays more closely mimic the passing and brief interactions that *Candida* cells have with endothelial cells, under conditions of shear stress and flow that occur in blood vessels (64, 85). In this study we compared the adhesion capacity of *C. glabrata* 2001, *anp1*, *mnn2*, and *mnn11* strains to endothelial cells under conditions of shear flow. In this flow adhesion assay, only *C. glabrata mnn2* cells were convincingly hyper-adherent to endothelial cells, compared with the parent *C. glabrata* 2001 strain, although *anp1* cells were also statistically increased in their ability to adhere to HMEC-1 cells. Hence, there is no distinct difference in this crucial aspect of the host-pathogen interaction that can explain the difference in virulence seen between *anp1*, *mnn2*, and *mnn11* cells. It remains to be elucidated what, if any, other structural differences there are between *anp1/mnn2* and *mnn11* cells and how this subsequently affects the interaction with the host. However, it is possible to speculate that the glycossylation of specific adhesins may influence these interactions significantly (78–81).

Finally, we have shown that inactivation of *C. glabrata ANP1* and MNN2 results in an increased ability to cause disease, whereas loss of MNN11 has no impact on virulence. This is in contrast to *C. albicans*, and other fungi, where changes in the external glycan structure often result in attenuation. Hence, it is not prudent to draw predictions of what we may expect to observe in *C. glabrata* based upon studies in *C. albicans*. *C. glabrata* and *C. albicans* are not particularly closely related phylogenetically (57), and it is not surprising that they have different virulence traits. It is vitally important, with the growing incidence of this pathogen and its innate resistance to many currently available antifungal drugs, that we dissect virulence attributes directly in *C. glabrata*.

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