Eng1 and Exg8 Are the Major β-Glucanases Secreted by the Fungal Pathogen Histoplasma capsulatum

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Fungal cell walls contain β-glucan polysaccharides that stimulate immune responses when recognized by host immune cells. The fungal pathogen Histoplasma capsulatum minimizes detection of β-glucan by host cells through at least two mechanisms: concealment of β-glucans beneath α-glucans and enzymatic removal of any exposed β-glucan polysaccharides by the secreted glucanase Eng1. Histoplasma yeasts also secrete the putative glucanase Exg8, which may serve a similar role as Eng1 in removing exposed β-glucans from the yeast cell surface. Here, we characterize the enzymatic specificity of the Eng1 and Exg8 proteins and show that Exg8 is an endo-β,1,3-glucanase and Eng1 is an endo-β,1,3-glucanase. Together, Eng1 and Exg8 account for nearly all of the total secreted glucanase activity of Histoplasma yeasts. Both Eng1 and Exg8 proteins are secreted through a conventional secretion signal and are modified post-translationally by O-linked glycosylation. Both glucanases have near maximal activity at temperature and pH conditions experienced during infection of host cells, supporting roles in Histoplasma pathogenesis. Exg8 has a higher specific activity than Eng1 for β,1,3-glucans; yet despite this, Exg8 does not reduce detection of yeasts by the host β-glucan receptor Dectin-1. Exg8 is largely dispensable for virulence in vivo, in contrast to Eng1. These results show that Histoplasma yeasts secrete two β,1,3-glucanases and that Eng1 endoglucanase activity is the predominant factor responsible for removal of exposed cell wall β-glucans to minimize host detection of Histoplasma yeasts.

The dimorphic fungal pathogen Histoplasma capsulatum causes respiratory and systemic disease in mammals. Central to the pathobiology of Histoplasma is the ability of pathogenic yeasts to infect and parasitize host phagocytes (1). The cell wall is the first fungal structure encountered by host phagocytes, and thus features of the cell wall contribute to the outcome of the interaction between pathogen and host. Histoplasma’s cell wall-localized Hsp60 protein drives internalization of the yeasts via CD11 family complement receptors (e.g. CR3 (2–4)) while limiting the host response (5–7). Even though this interaction is beneficial to yeasts in facilitating host cell infection, the close association of yeasts with the phagocyte plasma membrane can also activate host receptors that trigger immune responses. Given the polysaccharide nature of the fungal cell wall, many of these pathogen pattern-recognition receptors act as lectins. For example, Dectin-1 is the primary receptor for fungal β-glucans, and Dectin-1 recognition of this polysaccharide stimulates pro-inflammatory responses (8–11) leading to control and elimination of fungal cells. To reduce its detection by Dectin-1, Histoplasma yeasts produce an α-linked glucan polysaccharide that overlays the β-glucans, effectively masking the β-glucan from Dectin-1 (12–14). In addition, Histoplasma yeasts secrete a number of glucanases that can potentially remove exposed immunostimulatory polysaccharides from the yeast cell surface (15, 16).

Two of the glucanases abundantly secreted by Histoplasma are Eng1 and Exg8 (16). Both proteins are highly secreted by yeast cells, but not by avirulent mycelial phase cells, suggesting functional roles in pathogenesis. Histoplasma Eng1 belongs to the glycosyl hydrolase family 81 (GH81), which includes the Eng1 homologs of Candida albicans and Saccharomyces cerevisiae. In C. albicans and S. cerevisiae, Eng1 enzymes participate in cell separation during budding (17, 18). However, in Histoplasma, Eng1 does not contribute to cell separation and instead removes surface-exposed β-glucan molecules to reduce Dectin-1 detection of yeast cells (15). Histoplasma Exg8 is member of the GH55 family. The S. cerevisiae and C. albicans genomes do not contain any genes encoding GH55 proteins, but Aspergillus fumigatus encodes six GH55 proteins (19), including an Exg8 homolog. However, the cellular role for A. fumigatus Exg8 has not been defined. In this study, we provide biochemical characterization of the Histoplasma Exg8 and Eng1 proteins, defining their glucan substrate specificity and their endo- or exo-directed hydrolytic activity, and we investigate the role for Exg8 in Dectin-1 recognition and Histoplasma virulence.

Results

Eng1 and Exg8 Protein Features—Eng1 and Exg8 were identified initially as members of the secreted proteome of Histoplasma yeasts, the genes of which were transcriptionally up-
regulated in pathogenic phase yeasts compared with avirulent mycelia (16). The ENGI gene encodes a GH81 family protein with β-1,3-glucanase activity (supplemental Fig. 1A) (15). The Histoplasma Eng1 protein has high amino acid similarity with other fungal endoglucanases (60% similar to A. fumigatus Eng1), with a series of conserved aspartic acid and glutamic acid residues known to be important for activity (supplemental Fig. 1A) (20). The EXG8 gene encodes a protein that is most similar to the A. fumigatus Exg8 protein (69% amino acid similarity) and is predicted to be in the GH55 family. Similar to other proteins in this family, the Histoplasma Exg8 amino acid sequence contains two pectate lyase domains (supplemental Fig. 1B), as well as a conserved aspartic acid and two conserved glutamic acid residues important for glucanase activity in this family (supplemental Fig. 1B) (21, 22). Both Eng1 and Exg8 have predicted N-terminal secretion signals and N-linked and O-linked mucin-like glycan attachment sites (supplemental Fig. 1, A and B) consistent with extracellular localization.

To determine whether these two proteins are glycosylated, culture filtrates from Histoplasma expressing Eng1-FLAG or Exg8-FLAG-tagged proteins were prepared, and the Eng1 and Exg8 proteins were detected by immunoblotting for the FLAG epitope following electrophoretic separation. To prevent O-linked glycan attachment, fusion proteins were expressed in a mutant lacking O-linked mannosylation (pmt2) instead of wild type (WT). N-Linked glycans were removed by treatment of culture filtrate proteins with PNGaseF. The prevention of O-linked glycan attachment or removal of N-linked glycans are indicated by "−" in contrast to normal presence of the glycans ("+").

The molecular mass (kDa) of protein standards is indicated on the left of the immunoblot.

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Eng1 and Exg8 are β1,3-Glucanases—We previously showed Histoplasma Eng1 can hydrolyze β1,3-glucan (15). To determine the specificity of Eng1 for β1,3-linked glucan and to determine the activity of Exg8, we quantified the hydrolytic activities of Eng1 and Exg8 on polysaccharides with different glycosidic linkages (Fig. 2). The polysaccharides tested include β1,3-glucan (laminarin), β1,6-glucan (pustulan), β1,3,1,6-glucan (scleroglucan), β1,4-glucose (cellulose), α1,4-glucan (amylose), α1,6-glucan (dextran), α1,4,1,6-glucan (pullulan), α1,2-mannose (mannan), and β1,4-N-acetylglucosamine (chitin). Substrates were incubated with purified Histoplasma Eng1 and Exg8 proteins, and the released reducing sugars were measured by reaction with dinitrosalicylic acid (23). Glucanase activity was below the limit of detection after 120 min of incubation for all substrates except laminarin (Fig. 2). Extending the reaction time to 24 h still did not reveal any significant glucanase activity for all substrates except laminarin (data not shown), indicating Eng1 and Exg8 enzymatic activities are specific to β1,3-linked glucans. The specific activity of Exg8 was almost 2-fold higher than Eng1 (Table 1). Exg8 was also more efficient than Eng1, as the $K_{cat}/K_{m}$ for Exg8 was 2.7-fold higher than Eng1, and the $K_{cat}/K_{m}$ was 2.9-fold higher because of the greater substrate affinity of Exg8 for β1,3-glucan.

Of the characterized GH81 family proteins, all are endo-acting glucanases; however, enzymes in the GH55 family can have either endo- or exoglucanase activity (24). To validate Eng1 as an endoglucanase and to determine the action of Histoplasma Exg8, laminarin was digested for 30 min with purified enzymes, and the mono- and oligosaccharide products were analyzed by
mass spectrometry (Fig. 3, A and B). The major products identified were monosaccharides (203 m/z), disaccharides (365 m/z), trisaccharides (527 m/z), tetrasaccharides (689 m/z), and pentasaccharides (851 m/z). Eng1 produced predominantly disaccharides, as well as some tri-, tetra-, and pentasaccharides (Fig. 3A). Very little monosaccharide was produced, consistent with the enzymatic activity acting on internal glycosidic linkages. Extending the digestion time overnight reduced the tetrasaccharide product, leaving predominantly di- and trisaccharides with a very minor amount of mono-, tetra-, and pentasaccharide products (data not shown). This pattern was quite similar to digestion of laminarin with the known endo-glucanase zymolyase (Fig. 3C). Conversely, the predominant product of Exg8 hydrolysis of laminarin was monosaccharides, with minor portions of di- and trisaccharides (Fig. 3B). This pattern is consistent with Exg8 being able to hydrolyze terminal glucose from a glucan chain, indicating exoglucanase activity. Extending digestion of Exg8 overnight results in a similar profile of predominantly monosaccharides with di- and trisaccharides still present, suggesting inefficient hydrolysis of glucose oligomers smaller than 4 units in length (data not shown). To quantify the Eng1 and Exg8 digestion products, the ion intensity of the [M + Na+] ion for each saccharide length was calculated relative to the sum of all [M + Na+] ion intensities (monosaccharide to octosaccharide; Fig. 3D). For Exg8, 49% of the saccharide ions were monosaccharides, compared with only 4% for Eng1 and zymolyase. No quantifiable saccharides longer than 5 units were detected for any enzyme digest after 30 min, expect for zymolyase in which hexasaccharides were calculated at less than 1% of the total saccharide content. These data establish that Eng1 is an endoglucanase and Exg8 is an exoglucanase acting on β1,3-glucan.

Eng1 and Exg8 Are the Major Secreted Histoplasma Glucanases—Examination of the Histoplasma genome identified additional glycosyl hydrolase family proteins in addition to Eng1 and Exg8 (data not shown) raising the possibility of additional secreted glucanases. To determine the relative contribution of Eng1 and Exg8 to the total extracellular glucanase activity of Histoplasma yeasts, we depleted Eng1 and Exg8 activity from Histoplasma yeasts either singly or combined using a gfp sentinel RNAi system (25); Eng1 and/or Exg8 knockdown was monitored by simultaneous knockdown of GFP fluorescence. Transformed yeasts showed at least 85% reduction in GFP fluorescence indicating efficient depletion of the co-targeted ENG1 and/or EXG8 transcripts (data not shown). With depletion lines established, the contribution of each enzyme to the extracellular glucanase activity on β1,3-glucan was determined. Loss of Eng1 function yielded culture filtrates that had 30% less β-glucanase activity compared with wild-type culture filtrates (derived from gfp-RNAi) (Fig. 4A), consistent with previous results (15). Loss of Exg8 function caused a greater reduction in extracellular glucanase activity (66% reduction; Fig. 4A). Simultaneous depletion of both Eng1 and Exg8 depletes 93% of extracellular β-glucanase activity, showing Eng1 and Exg8 constitute the major extracellular β-glucanases. Examination of the β-glucanase activity associated with the surface of Histoplasma yeasts showed slight activity above the limit of detection with wild-type yeasts, and this small amount of activity decreased a statistically significant amount when Exg8 but not Eng1 was depleted from Histoplasma (Fig. 4A). Thus, the major extracellular β-glucanase activity is in the soluble fraction with little associated with the surface of yeast cells. Consistent with this conclusion, abundant Exg8 protein was detected in the culture filtrate; however, only a minute amount of Exg8 protein was in the cell wall fraction (Fig. 4B). Together with the previous demonstration that Eng1 is not associated with the surface of yeast cells (15), these data indicate that Eng1 and Exg8 are responsible for the vast majority of extracellular β-glucanase activity and that this activity is secreted but not associated with the yeast cells themselves.

Despite the reduction in secreted glucanase activity, depletion of Exg8 or depletion of Exg8 and Eng1 together does not increase sensitivity to cell wall-disrupting agents (Table 2); EXG8-RNAi and ENG1:EXG8-RNAi Histoplasma yeasts had no significant change in the 50% inhibitory concentrations (IC50) for cell wall-binding dyes (Congo Red, Uvitex, and Calcofluor White), detergent (SDS), and cell wall glycan-targeting antifungal drugs (Nikkomycin Z and Caspofungin, which impair chitin and β-glucan synthesis, respectively). These results suggest Exg8, like Eng1 (15), is not a glucanase required for major structural modifications or cell intrinsic function of the cell wall.

Eng1 and Exg8 Are Functional in Temperature and pH Conditions of the Phagosome—The pathogenic phase-specific expression of Eng1 and Exg8 suggests these glycans have a function related to pathogenesis. Histoplasma yeasts normally reside within the phagosomal compartment of host macrophages at mammalian temperatures. While in this compartment, the Histoplasma yeast prevents complete acidification and maintains a luminal pH around 5.5 to 6.0 (26–28). To determine whether Eng1 and Exg8 are enzymatically active under conditions that Histoplasma yeasts experience during infection of macrophages, we quantified the hydrolysis of laminarin at various pH and temperatures (Fig. 5, A and B). With respect to pH, Eng1 had maximal activity from pH 5 to pH 8, decreasing only at high alkalinity (pH > 10) and acidity (pH < 3) (Fig. 5A). Exg8 is active from pH 4 to pH 8 with optimal activity at pH 4 to pH 7 (Fig. 5A). Increasing temperature continues to increase activity up to 45 °C for both enzymes (Fig. 5B). At temperatures above 45 °C, Exg8 activity decreases significantly; however, Eng1 activity remains high up to 70 °C. The high glucanase activity at 37 °C and under moderately acidic conditions (pH 5 to 7) indicates Eng1 and Exg8 would be active in the environment within the phagosome.

### Table 1

| Enzyme Kinetics for Histoplasma Eng1 and Exg8 |
|-----------------------------------------------|
| **Vmax** | **Km** | **Kcat** | **Kcat/Km** |
| (units/mg) | (mg/ml) | | (mL/mg) |
| **Eng1** | 17.9 ± 1.1 | 1.62 ± 0.38 | 28.2 ± 1.7 | 71.3 ± 1.4 |
| **Exg8** | 48.1 ± 2.5 | 1.00 ± 0.24 | 75.8 ± 3.9 | 75.8 ± 16.4 |

*Eng1 and Exg8 are the Major Secreted Histoplasma Glucanases.*
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Eng1 is an endoglucanase and Exg8 is an exoglucanase. Hydrolysis products of Eng1 and Exg8 activity on laminarin (β1,3-glucan) are shown. Laminarin was digested for 30 min with 30 ng of purified Eng1 (A), Exg8 (B), or the endo-β-glucanase zymolyase (C), and the products were detected by mass spectrometry. The relative ion intensities for ions between 150 and 1000 m/z are shown with peaks for monosaccharides (mono-, 203 m/z), disaccharides (di-, 365 m/z), trisaccharides (tri-, 527 m/z), tetrasaccharides (tetra-, 689 m/z), and pentasaccharides (penta-, 851 m/z) indicated with arrows. The m/z values for each saccharide peak represent sodiated glucose minus one water per each additional glucose unit.

Exg8 Does Not Reduce Detection of Histoplasma Yeasts—To determine the functional and possible additive roles of Eng1 and Exg1 in virulence, we tested yeasts depleted of Eng1 and/or Exg1 in aspects of Histoplasma pathogenesis. Overall association of yeasts with primary macrophages was unchanged in the absence of either glucanase (Fig. 6A). The response of macrophages to yeasts, as measured by production of the pro-inflammatory cytokines TNFα and IL-6, was unaffected by loss of Exg8; however, loss of Eng1 singly or in combination with Exg8 significantly increased both TNFα and IL-6 (Fig. 7, A and B). This is consistent with Eng1 but not Exg8 affecting recognition of yeasts by signaling receptors but not binding of yeasts to phagocytic receptors on macrophages (i.e. CR3 (2–4)). We previously showed that the Eng1 glucanase activity decreases surface β1,3-glucan exposure on yeasts, thereby enabling yeasts to avoid Dectin-1-dependent recognition by macrophages (15). As both Eng1 and Exg8 are active on β1,3-glucan, we measured the Dectin-1 recognition of yeasts lacking single glucanases or both. To avoid the contribution of other macrophage receptors, yeasts were added to fibroblasts in which only Dectin-1 was expressed. Despite Exg8 having more activity than Eng1, loss of Exg8 had no significant effect on β1,3-glucan recognition, whereas the loss of Eng1 resulted in a nearly 6-fold increase (Fig. 6B). No additional change was seen when both Eng1 and Exg8 were depleted. In the G186A background, in which α-glucan polysaccharides largely mask β-glucans (12, 14), loss of Exg8 similarly had negligible effects on Dectin-1 recognition of yeasts (supplemental Fig. 2). In this same background, depletion of Eng1 results in a 4-fold increase. Again, no additional β1,3-glucans are recognized when both Eng1 and Exg8 are depleted. Pre-incubation of Dectin-1-expressing fibroblasts with laminarin reduced the recognition of yeasts at least 10-fold, confirming the specificity as recognition of yeast β-glucan (Fig. 6B). Together, these data show that Eng1 but not Exg8 reduces β-glucan exposure on yeasts, which minimizes their detection by Dectin-1.

Eng1 Is the Primary Secreted Glucanase That Enhances Histoplasma Pathogenesis—Yeast survival against macrophages in culture was not affected by loss of either glucanase (Fig. 8A). In a murine model of respiratory histoplasmosis, loss of Exg8 function showed only a slight decrease (2-fold) in lung infection (Fig. 8B). Removal of Eng1, however, resulted in an 8-fold reduction compared with wild type (Fig. 8B). Similar to the in vitro effects on Dectin-1 binding, depletion of Exg8 did not further decrease the virulence of yeasts from that caused by single loss of Eng1 function. Thus, the Eng1 endoglucanase functionally contributes more than Exg8 to reducing the β1,3-glucan exposure of yeasts and facilitating infection.

Discussion

The fungal cell wall features centrally in the pathogenesis of H. capsulatum. Unlike many of the opportunistic fungal pathogens, Histoplasma yeast cells have reduced detection of cell wall pathogen-associated molecular patterns (14, 15). Although the
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Eng1 is important for pruning exposed nases (Eng1 and Exg8) important for this latter mechanism. Phagocytes, either through masking or by removal from the cell wall, are essential for fungal viability, consistent with this role, we demonstrate that Eng1 is an endo-acting glucanase specific for 1,3-glucans into monomeric glucose, and removal of β-glucans minimizes immune cell detection of infecting yeasts but preserves invasion mechanisms to bind and enter host macrophages.

In light of the altered Dectin-1 recognition due to Eng1 but not Exg8, and with the demonstrated endo- versus exo-activity of Eng1 and Exg8, respectively, we propose a model in which exposed β-glucans on the Histoplasma cell wall are not simply the exposed ends of glucan chains but instead are polysaccharide “loops” exposed on the surface of the cell wall. In this structure, only an endo-acting glucanase could hydrolyze the β-glucan molecule, whereas an exoglucanase would be ineffective as the exposed β-glucan lacks any terminal ends. Intriguingly, loss of both enzymes is no greater than loss of Eng1 alone with respect to both Dectin-1 recognition and Histoplasma virulence. This indicates hydrolysis of cell wall β-glucans by Eng1 is sufficient to render them undetectable by Dectin-1 without requiring the remaining mono- or disaccharide exposed termini to be hydrolyzed by Exg8. This model fits with the described ligand specificity of Dectin-1 being oligosaccharides of at least seven glucose units (29).

In the environment, secreted glucanases are positioned potentially to hydrolyze polysaccharides of other fungal cell walls, perhaps as a source of glucose that can serve metabolic needs. Although we cannot exclude such a role for Histoplasma Eng1 and/or Exg8, our data indicate that Eng1 and Exg8 have likely evolved to facilitate Histoplasma pathogenesis. First, Eng1 and Exg8 are expressed at high levels by pathogenic yeasts but are only minimally expressed by the environmental mycelia form (16) suggesting Eng1 and Exg8 function specifically in yeast cell biology (i.e. pathogenesis as opposed to the saprobic mycelia). Second, during infection, Histoplasma yeasts are found almost exclusively within the phagosome of host phagocytes in which Histoplasma is the only fungal cell present, making it unlikely that Eng1 and Exg8 act on other fungi. Third, Eng1 and Exg8 have evolved to be compatible with conditions within the host phagosome, whereas glucanase activity is reduced in acidic conditions, common to Histoplasma-containing soils. Finally, Eng1 in particular has been shown to be important for pathogenesis by reducing surface exposure of cell walls, as Histoplasma yeasts effectively minimize cell wall β-glucans that are exposed to host phagocytes, either through masking or by removal from the exposed surface. This study characterizes two secreted glucanases (Eng1 and Exg8) important for this latter mechanism. Eng1 is important for pruning exposed β-glucans (15), and consistent with this role, we demonstrate that Eng1 is an endo-acting glucanase specific for β1,3-glucans (EC 3.2.1.39). Exg8 is an exo-acting glucanase, also specific for β1,3-glucans (EC 3.2.1.58). Together, the action of these enzymes can effectively hydrolyze β1,3-glucans into monomeric glucose, and removal of both enzymes from Histoplasma effectively eliminates extracellular glucanase activity. The enzymes are highly active in conditions that Histoplasma yeasts experience during infection, 37 °C and pH between 5 and 6, which characterizes the lumen of the host cell phagosomes. Thus, Histoplasma Eng1 and Exg8 are factors produced during infection, with the ability to alter the surface of the yeast cell, specifically in reducing immunostimulatory β-glucans of the cell wall.

Although both Eng1 and Exg8 are produced by pathogenic yeasts, Eng1 is the major β-glucanase that removes exposed β-glucans from the yeast cell wall. Functional tests show that loss of Eng1 activity significantly increases Dectin-1 recognition of yeast cell β-glucans, and this translates into reduced virulence in a murine model of respiratory histoplasmosis (15). By comparison, loss of Exg8 activity has only minor effects on Dectin-1 recognition of the yeast cells (Fig. 6B) and minimal impact on Histoplasma virulence (Fig. 8B). Although Eng1 reduces recognition of yeasts by Dectin-1, overall binding of yeasts to macrophages is unaffected by either Eng1 or Exg8. This is not surprising, as association and phagocytosis of Histoplasma yeasts are primarily mediated through binding of yeasts to the complement receptor (2–4). Thus, glucanase removal of β-glucans minimizes immune cell detection of infecting yeasts but preserves invasion mechanisms to bind and enter host macrophages.

FIGURE 4. Eng1 and Exg8 are responsible for the majority of extracellular glucanase activity produced by yeasts. A, extracellular glucanase activity in the soluble fraction or associated with yeast cells. Culture supernatants were separated from yeast cells, and both fractions were tested for hydrolysis of laminarin to determine the activity in culture filtrates (dark bars) or activity associated with the yeast cells (light bars) of wild-type (gfp-RNAi) or glucanase-deficient strains (ENG1-RNAi, EXG8-RNAi, and ENG1/EXG8-RNAi strains). Data represent the glucose equivalents (micromoles) of reducing sugars released after 90 min of incubation with laminarin. Dashed line represents the limit of detection of the assay, and bars represent the mean reducing sugars released ± S.D. among replicate assays (n = 3). B, localization of Exg8 in light bars represents the activity associated with yeast cells (dark bars) or the yeast cells (light bars) of wild-type (gfp-RNAi) or glucanase-deficient strains (ENG1-RNAi, EXG8-RNAi, and ENG1/EXG8-RNAi strains). Data represent the glucose equivalents (micromoles) of reducing sugars released after 90 min of incubation with laminarin. Dashed line represents the limit of detection of the assay, and bars represent the mean reducing sugars released ± S.D. among replicate assays (n = 3). B, localization of Exg8 in cell lysates and cell wall-associated fractions. Soluble and cell-associated fractions were tested for Exg8-FLAG protein by immunoblot of the FLAG epitope. Proteins in the culture filtrate, the soluble yeast cell lysate, and proteins extracted by SDS + DTT or by zymolyase + chitinase digestion of the insoluble cell wall fraction were separated by electrophoresis and probed for the FLAG epitope. Protein samples were derived from equivalent numbers of yeast cells. Numbers represent the molecular mass (kDa) of protein standards. n.s., not significant. *, p < 0.05; ***, p < 0.001.
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**TABLE 2**

Sensitivity of glucanase-deficient *Histoplasma* yeasts to cell wall-destabilizing compounds

| CFV       | CR   | Uvtx | SDS† | Cfl | Flc   | NikZ  |
|-----------|------|------|------|-----|-------|-------|
| gfp-RNAi  | 6.1 ± 2.4 | 1.3 ± 0.1 | 11.0 ± 1.9 | 3.1 ± 1.5 | 10.9 ± 4.2 | 0.68 ± 0.07 | 4.3 ± 1.2 |
| EXG8-RNAi | 5.2 ± 2.0 | 1.1 ± 0.2 | 11.3 ± 0.3 | 4.8 ± 0.2 | 11.4 ± 4.5 | 0.52 ± 0.01 | 5.1 ± 0.4 |
| ENG1/EXG8-RNAi | 5.7 ± 1.8 | 1.1 ± 0.2 | 10.6 ± 1.5 | 4.4 ± 0.6 | 11.7 ± 4.7 | 0.59 ± 0.24 | 4.8 ± 1.6 |

† Concentrations were expressed as milli-percent by volume (m %).

![FIGURE 5. Eng1 and Exg8 are active under phagosome-like conditions.](image)

Glucanase activity is shown for Eng1 (circles) and Exg8 (triangles) at different ranges of pH (A) and temperature (B). Data represent reducing sugar equivalents of glucose released from laminarin after digestion with purified Eng1 or Exg8 for 2 h. Dashed line represents the limit of detection. Data points are the mean amount of reducing sugars released, and error bars represent the standard deviation among replicates (n = 3). Data are representative of two independently purified protein samples of Eng1 and Exg8.

![FIGURE 6. Eng1 and Exg8 do not affect yeast-macrophage association but Eng1 reduces yeast β-glucan recognition.](image)

A, association of yeast with macrophages. Yeasts lacking Exg8 (EXG8-RNAi), Eng1 (ENG1-RNAi), or both Exg8 and Eng1 (ENG1/EXG8-RNAi) were added to peritoneal macrophages (1 mg/ml). Adherent yeasts were quantified by cfu determination. Data represent the mean cell-associated yeast per 2 x 10⁵ macrophages (A) or 2 x 10⁵ Dectin-1-expressing fibroblasts (B) cells with error bars indicating standard deviation among replicate assays (n = 3). Asterisks indicate statistically significant differences in assay results between wild-type (gfp-RNAi) and glucanase-deficient yeasts as determined by Student’s t test (*, p < 0.05; **, p < 0.01; ***. p < 0.001; ns, not significant).

![Yeast-Dectin-1 Binding](image)

B. Relative recognition of glucanase-deficient *Histoplasma* yeasts by Dectin-1. Yeasts were added to Dectin-1-expressing 3T3 fibroblasts in the absence (black bars) or presence (gray bars) of the β-glucan competitor laminarin (1 mg/ml). Yeast-Dectin-1 binding was quantified by cfu determination. Data represent the mean yeast-Dectin-1 binding (CFU/3T3-Dectin-1 Cell) for each treatment with error bars indicating standard deviation among replicate assays (n = 3). Yeast-Dectin-1 binding was increased in the presence of laminarin (gray bars) compared to yeast-Dectin-1 binding in the absence of laminarin (black bars) (***, p < 0.001; ns, not significant).

**Experimental Procedures**

*Histoplasma Strains and Culture—* *H. capsulatum* strains were derived from the wild-type clinical isolates G186A (ATCC 26029) and G217B (ATCC 26032) and are listed in Table 3. *Histoplasma* yeasts were grown in *Histoplasma*-macrophage medium (HMM)⁵ (30) and supplemented with 100 µg/ml uracil when necessary. Hemocytometer counts were used for precise enumeration of yeasts for infection studies.

**β-Glucanase Protein Sequence Analysis—**Fungal homologs of the *Histoplasma* G186A Eng1 and Exg8 protein sequences were identified by BLAST search of *C. albicans*, *S. cerevisiae*, and *Aspergillus* genome databases and the derived protein sequences aligned using ClustalW with the BLOSUM62 matrix.

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⁵ The abbreviations used are: HMM, *Histoplasma*-macrophage medium; GPI, glycosylphosphatidylinositol; m.o.i., multiplicity of infection; nt, nucleotide; PNGaseF, peptide-N-glycosidase F.
Protein features were predicted using SignalP (version 4.0) (31) and the GPI-SOM prediction server (32) for glycosylphosphatidylinositol (GPI) anchor signals. N-Linked glycosylation sites were predicted using the consensus motif (N\(\text{X}(S/T)\)). For prediction of O-linked mucin sites, protein sequences were scanned for regions with at least 40% serine or threonine density within a 40-amino acid window (33).

**Eng1 and Exg8 Localization**—The ENG1 and EXG8 genes were amplified by high fidelity PCR and fused to the FLAG epitope (in plasmid pCR628 (34)) or a hexahistidine tag at the C terminus. Expression plasmids were transformed into *Histoplasma* uracil-auxotroph strains WU15 or WU8 (see Table 3) via *Agrobacterium* tumefaciens-mediated transformation (35). Expression, electrophoretic mobility, and subcellular localization of proteins was monitored by epitope tag immunoblotting (FLAG: M2 clone (Sigma), HIS6: 6G2A9 clone (GenScript)) of culture filtrates following electrophoretic separation of proteins through 10% polyacrylamide with SDS (SDS-PAGE). Potential N- and O-linked glycans were removed by PNGaseF (New England Biolabs) prior to SDS-PAGE.

Potential O-linked mannosylation was tested by expression of proteins in a *Histoplasma* strain that lacks the Pmt2 protein mannosyltransferase, which is required for O-linked glycosylation.5

For subcellular fractionation, 5 \(\times\) 10^8 yeast cells expressing FLAG-tagged Eng1 or Exg8 were separated from culture filtrates by centrifugation and filtration. Cellular lysates were prepared from the yeast by mechanical disruption with 0.5-mm diameter glass beads. The cytosolic fraction was separated from cellular debris by centrifugation (10 min at 14,000 \(\times\) g). Insol-
uble cellular material was treated with 1% SDS and 0.1 m dithi-othreitol (DTT) to extract cell wall-associated proteins or incubated with 3 milliliters/μl zymolyase (GBiosciences) to release glycan-embedded cell wall proteins. Subcellular fractions representing secreted or cellular material from 2 × 10^7 yeasts were probed by immunoblotting.

Eng1 and Exg8 Protein Purification—Histoplasma yeasts expressing Eng1 or Exg8 with the C-terminal hexahistidine tag were grown in liquid HMM, and tagged proteins were purified by affinity chromatography (HisPur Co2).

TABLE 3

| Strain | Genotype* | Other designation |
|--------|-----------|-------------------|
| WU8    | (G186A) ura5-32Δ | WT |
| OSU22  | (G186A) ura5-32Δ zzzpCR482 [hph, gfp] | RNaI sentinel |
| OSU244 | (G186A) ura5-32Δ zzzpCR482 [hph, gfp] zzzpED02 [URA5, gfp-RNAi, EXG8-RNAi] | gfp-RNAi |
| OSU245 | (G186A) ura5-32Δ zzzpCR482 [hph, gfp] zzzpED06 [URA5, gfp-ENG1-RNAi] | ENG1-RNAi |
| OSU205 | (G186A) ura5-32Δ zzzpCR482 [hph, gfp] zzzpAG26 [URA5, gfp-EXG8-RNAi] | EXG8-RNAi |
| OSU214 | (G186A) ura5-32Δ zzzpCR482 [hph, gfp] zzzpAG37 [URA5, gfp-ENG1,EXG8-RNAi] | ENG1,EXG8-RNAi |
| OSU194 | (G217B) ura5-42Δ zzzpAG21 [G418*, gfp] | RNaI sentinel |
| OSU247 | (G217B) ura5-42Δ zzzpAG21 [G418*, gfp] zzzpED02 [URA5, gfp-RNAi, ENG1-RNAi] | gfp-RNAi |
| OSU248 | (G217B) ura5-42Δ zzzpAG21 [G418*, gfp] zzzpED06 [URA5, gfp-ENG1-RNAi] | ENG1-RNAi |
| OSU275 | (G217B) ura5-42Δ zzzpAG21 [G418*, gfp] zzzpAG26 [URA5, gfp-EXG8-RNAi] | ENG1,EXG8-RNAi |
| OSU275 | (G217B) ura5-42Δ zzzpAG21 [G418*, gfp] zzzpAG37 [URA5, gfp-ENG1,EXG8-RNAi] | ENG1,EXG8-RNAi |
| OSU265 | (G217B) ura5-42Δ zzzpQS14 [URA5, PH2B-ENG1-FLAG] | ENG1,FLAG |
| OSU266 | (G217B) ura5-42Δ zzzpAG39 [URA5, PH2B-ENG1-FLAG] | ENG1,EXG8-FLAG |
| OSU313 | (G217B) ura5-42Δ zzzpKD02 [URA5, PH2B-EXG8-FLAG] | EXG8-FLAG |
| OSU314 | (G186A) ura5-32Δ zzzpKD01 [URA5, PH2B,EXG8-FLAG] | EXG8: HIS6 |
| OSU328 | (G217B) ura5-42Δ pmt2::T-DNA [hph] zzzpQS14 [URA5, PH2B-ENG1-FLAG] | pmr2:ENG1,FLAG |
| OSU329 | (G217B) ura5-42Δ pmt2::T-DNA [hph] zzzpKD02 [URA5, PH2B,EXG8-FLAG] | pmr2:EXG8-FLAG |

Strains were constructed in the G186A (ATCC no. 26029) or G217B (ATCC no. 26032) Histoplasma strain backgrounds.

Histoplasma Endo- and Exo-β-glucanases

Determination of Glucanase Activity—Proteins were incubated with polysaccharide substrates in a 30-μl reaction volume (20 μl of substrate and 10 μl of protein solution). Substrates were prepared at 5 mg/ml in PBS, which included laminarin (Sigma), xylan (Inviron), carboxymethylcellulose (Sigma), amylase (Sigma), mannan (Sigma), swollen chitin (Sigma), scleroglukan (Inviron), dextran (Spectrum Chemical), and pullulan (Tokyo Chemical Industry). Polysaccharide hydrolysis was measured by the addition of 3 volumes of dinitrosalicylic acid solution (0.687% w/v) 3,5-dinitrosalicylic acid, 1.28% (v/v) phenol, 19.92% (w/v) potassium/sodium/tartrate, 1.226% (w/v) sodium hydroxide and incubation at 95 °C for 5 min (23, 36). Saccharide-dependent reduction of 3,5-dinitrosalicylic acid to 3-amino-5-nitrosalicylic acid was quantified by absorbance at 540 nm and compared with a standard curve created from glucose or N-acetylglucosamine. Total extracellular and cell-associated glucanase activity was determined using culture filtrate equivalent to media from 2 × 10^7 cells or whole yeasts (2 × 10^7 cells), respectively.

Optimal temperatures for glucanase activities were determined by enzyme reactions carried out between 15 and 90 °C in 5 °C intervals. 30 ng of Eng1 or Exg8 protein was added to 5 mg/ml laminarin for 120 min, and reducing sugars were quantified. Similarly, the pH optimum was carried out in reactions incubated for 120 min at 37 °C using 25 mM buffer to control pH: sodium citrate (pH 3.0–5.0), MES (pH 6.0), HEPES (pH 7.0–9.0), and glycine (pH 10.0–11.0).

Kinetic Analysis of Eng1 and Exg8 Activity—Steady-state kinetic values were estimated using increasing concentrations (0, 0.5, 1, 2.5, 5, 10, 15, and 20 mg/ml) of laminarin. Reactions were carried out in a 30-μl reaction volume in 25 mlll MES buffer, pH 6.0. Reducing sugars were quantified after 0, 1, 2, 5, and 15 min, and the slope of the linear region of the regression curve was calculated for each substrate concentration. Kinetic values were calculated using nonlinear least squares fitting to the expression ν = V_{max} [S]/(K_m + [S]) using Prism 5.03 software (GraphPad).

Mass Spectrometry of Digestion Products—Digests of the laminarin samples were subjected to nano-electrospray mass spectrometry analysis using a Waters Synapt G2 or Synapt G2-S instrument (Waters). 30 ng of protein was incubated with 5 mg/ml laminarin in water for 30 min at 37 °C and then diluted 20-fold with 50:50 water/LC-MS grade acetonitrile (Fisher). Samples were sprayed into the mass spectrometer using a pulled fused silica capillary fitted around a platinum electrode posed at the capillary voltage from the MassLynx 4.1 software (Waters). Acquisitions were from 50 to 5000 m/z.Typical voltages and amplitudes are as follows: capillary, 1.1 kV; source temperature, 30 °C; cone, 20 V; source offset, 5 V; trap collision energy, 4 V; transfer collision energy, 2 V. Ion mobility parameters as follows: helium gas flow, 180 ml/min; ion mobility gas flow, 45 ml/min; wave height, 7 V; wave velocity, 450 m/s.

After collection of the mass spectra, relative quantitation of the [M + Na]+ peaks of glucose oligomers (mono- to octomers) was performed by using ion mobility drift times of the first four isotopic peaks of the ion of interest using the DriftScope 2.0 software (Waters). The ratios of the individual saccharides to the sum intensity of all saccharides (mono- through octosaccharides) were then determined for the specific enzymatic digestions.

Depletion of Glucanase Function(s)—Eng1 and/or Exg8 function was depleted from Histoplasma yeasts by RNA interference (RNAi) (25) using coding regions as follows: ENG1: nucleotides (nts) 445–2091; EXG8: nts 1744–2561; ENG1: EXG8 double knockdown fused ENG1 (nts 445–1521) and
EXG8 (nts 1744–2561). RNAi plasmids were transformed into the RNAi sentinel strains OSU22 and OSU194 using A. tumefaciens-mediated transformation (35, 37), and Ura<sup>+</sup> transformants were selected. GFP fluorescence of individual transformants was quantified using a modified gel documentation system (25) and ImageJ software (version 1.44p).

**Cell Wall Sensitivity Assays**—Yeast cells were grown in 96-well microtiter plates (38) with graded concentrations of antifungal compounds (fluconazole (Glenmark Generics); caspofungin (Merck); and nikkomycin Z (gift from John Galgiani)) and cell wall-stabilizing compounds (Calcofluor White (Sigma); Congo red (MP Biomedicals); SDS; and Uvitex (39)). Growth after 4 days was measured by optical density at 595 nm and compared with the turbidity of wells lacking inhibitors. 50% inhibitory concentration (IC<sub>50</sub>) values were computed by nonlinear regression of the dose-response data.

**Yeast-Macrophage Interaction Assays**—Peritoneal macrophages were harvested from C57BL/6 mice (Charles River) by peritoneal lavage and infected with yeast at 0.5:1 m.o.i. (yeast/macrophage). For association, nonadherent yeast were removed after 2 h. Yeasts were quantified by lysis of mammalian cells in water and plating of the lysate on solid HMM for colony-forming units (cfu). Yeast cells were determined after 8 h.

**Cytokine Analysis**—Peritoneal macrophages were infected at 0.5:1 m.o.i. with yeast, and supernatant was collected after 8 h. Cytokines (TNFα and IL-6) were quantified by ELISA (R&D Systems) and compared with standard curves.

**Murine Model of Respiratory and Disseminated Histoplasmosis**—C57BL/6 mice (Charles River) were infected with *Histoplasma* yeast by intranasal delivery of ~1 × 10<sup>4</sup> yeast cells (15). At 8 days post-infection, lungs and spleens were collected and homogenized. Serial dilutions of the homogenates were plated on solid HMM to determine the fungal burden (cfu) in each organ.

**Dectin-1 Binding Assay**—Dectin-1-expressing 3T3 fibroblasts (3T3-D1) (8, 12) were cultured in Dulbecco’s modified Eagle’s medium (DMEM) supplemented with 10% fetal bovine serum (FBS) at 37 °C in 5% CO<sub>2</sub>, 95% air. 3T3-D1 cells were adhered to wells of a 24-well plate (3 × 10<sup>4</sup> cells/well). Yeast cells were added to the 3T3-D1 cells for 2 h at 37 °C at an m.o.i. of 50:1 (yeast/3T3 cells) in the absence or presence of 1 mg/ml laminarin. Unbound yeasts were removed by washing with PBS. Fibroblast-associated yeasts were released by lysing the 3T3-D1 cells with water and the yeasts quantified by plating of the lysate to enumerate cfu.

**Statistical Analyses**—All assays were performed with independent biological replicates (n = 3 unless otherwise noted) and statistically significant differences from wild type or other parental backgrounds (p < 0.05) as determined by one-tailed Student’s t test.

**Ethics Statement**—All animal experiments were performed in compliance with the National Research Council’s Guide for the Care and Use of Laboratory Animals and were approved by the Institutional Animal Care and Use Committee at Ohio State University (protocol 2007A0241). Animal infections were performed under anesthesia, and all efforts were made to minimize suffering.

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