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Adaptations of the Secretome of *Candida albicans* in Response to Host-Related Environmental Conditions

Frans M. Klis, Stanley Brul

Department of Molecular Biology and Microbial Food Safety, Swammerdam Institute for Life Sciences, University of Amsterdam, Amsterdam, The Netherlands

The wall proteome and the secretome of the fungal pathogen *Candida albicans* help it to thrive in multiple niches of the human body. Mass spectrometry has allowed researchers to study the dynamics of both subproteomes. Here, we discuss some major responses of the secretome to host-related environmental conditions. Three β-1,3-glucan-modifying enzymes, Mp65, Sun41, and Tos1, are consistently found in large amounts in culture supernatants, suggesting that they are needed for construction and expansion of the cell wall β-1,3-glucan layer and thus correlate with growth and might serve as diagnostic biomarkers. The genes **ENG1**, **CHT3**, and **SCW11**, which encode an endoglucanase, the major chitinase, and a β-1,3-glucan-modifying enzyme, respectively, are periodically expressed and peak in M/G₁. The corresponding protein abundances in the medium correlate with the degree of cell separation during single-yeast-cell, pseudohyphal, and hyphal growth. We also discuss the observation that cells treated with fluconazole, or other agents causing cell surface stress, form pseudohyphal aggregates. Fluconazole-treated cells secrete abundant amounts of the transglucosylase Phr1, which is involved in the accumulation of β-1,3-glucan in biofilms, raising the question whether this is a general response to cell surface stress. Other abundant secretome proteins also contribute to biofilm formation, emphasizing the important role of secretome proteins in this mode of growth. Finally, we discuss the relevance of these observations to therapeutic intervention. Together, these data illustrate that *C. albicans* actively adapts its secretome to environmental conditions, thus promoting its survival in widely divergent niches of the human body.

The fungal pathogen *Candida albicans* is a highly specialized inhabitant of warm-blooded animals (mammals and birds). It preferentially colonizes mucosal surfaces and the skin but can also invade deeper-lying tissues and cause systemic infections that are difficult to treat and frequently lethal (1). To survive under the challenging and divergent conditions associated with the various mucosal surfaces in the human body, *C. albicans* disposes of a wide arsenal of virulence traits that help it to cope with antimicrobial peptides, the complement system, engulfment by macrophages, antibodies, hypoxic conditions, iron restriction, etc. A fascinating trait is its ability to switch reversibly between various growth forms, including among others the single-cell yeast form, which is especially suitable for dispersion of the fungus; the hyphal form, which facilitates adhesion to host tissues and promotes invasive growth and escape from engulfment by immune cells; and an intermediate, pseudohyphal growth form. *C. albicans* also forms biofilms (surface-associated microbial communities), which clinically speaking represent a highly relevant mode of growth and in which yeast, pseudohyphal, and hyphal cells cooccur and become encapsulated by substantial amounts of extracellular, macromolecular material. Biofilm formation on abiotic surfaces of medical devices and prostheses and on teeth has therefore been extensively studied (2, 3). The first contacts between *C. albicans* and host cells occur predominantly at the cell surface, and this presumably explains why the external protein coat of *C. albicans* cell walls consists of a wide variety of glycoproteins with specialized functions, many of which are under tight control, thus promoting survival under diverse stress conditions (4, 5). Equally important, *C. albicans* secretes a variety of glycoproteins that help to forage for nutrients by degrading host proteins, lipids, and glycogen, while others acquire iron and zinc ions and provide protection against antimicrobial peptides. Other glycoproteins help to form and strengthen biofilms and to accumulate extracellular matrix material. Together, we designate these secreted proteins as the secretome *sensu stricto* (see below). The introduction of mass spectrometry in protein research has made it possible to study the protein assortment of entire cells or tissues and also well-defined subsets of proteins (subproteomes such as the cell wall proteome and the secretome), not only qualitatively but also quantitatively. This review discusses recent mass spectrometric explorations of the dynamics of the secretome of *C. albicans* depending, for example, on growth form and pH or in response to cell surface stress. For complementary reviews, the reader is referred to reference 4, which includes an extensive section about secretome proteins, and to a more recent review (6). In addition, the *Candida albicans* PeptideAtlas and the Candida Genome Database are recommended for detailed information about mass spectrometrically identified peptides (7, 8).

**CLASSIFICATION OF MAJOR SECRETOME PROTEINS (SENSU STRICTO) OF C. ALBICANS**

In this review, we will restrict ourselves to the secretome in the narrow sense of the word (secretome *sensu stricto*), that is, we will discuss only those proteins that possess an N-terminal signal peptide for entering the classical secretory pathway and lack internal transmembrane sequences. The major advantages of analyzing...
this protein category separately are that it is physiologically well defined, is limited in size, and is not affected by accidentally released proteins. This facilitates statistical analysis of the data (9), simplifies discussion of the results, and leads to physiologically relevant conclusions and testable hypotheses. For more information about the secretome in the wide sense of the word (secretome sensu stricto), which includes a number of known cytosolic proteins, we refer to references 6 and 10.

The experimentally identified secretome proteins (secretome sensu stricto) (currently, about 70 [9–15]) can be classified into two major groups: nonglycosylphosphatidylinositol (non-GPI) proteins, which lack a C-terminal signal sequence for the addition of a GPI anchor in the endoplasmic reticulum, and GPI proteins (Fig. 1). To avoid an excessively long list, this review focuses on the more abundant secretome proteins that are observed under more than one growth condition and/or have a known or predicted function.

**NON-GPI PROTEINS**

**Modification of cell wall polysaccharides.** Eleven enzymes (distributed over six families of glycosylhydrolases [GHs]) are involved in glucan chain elongation and branching in glucan degradation (for example, during cell separation and emergence of a new bud or hyphal branch). Throughout this paper, we will follow the GH family classification according to the CAZy (for carbohydrate-active enzymes) database (16).

(i) **β-1,3-Glucan-modifying enzymes.** β-1,3-Glucan-modifying enzymes include Xog1 (GH5); Tos1 (GH16); Bgl2, Mp65, and Scw11 (GH17); Eng1 (GH81); Sim1 and Sun41 (GH132); and Dag7 (Barwin-like endoglucanase domain, PF03330) and GH (unspecified) (8).

(ii) **Chitin-degrading enzymes.** Chitin-degrading enzymes include Chl1 and Chl3 (GH18); they carry out degradation of the primary septum between mother and daughter cells, thus initiating cell separation. Note that the GH18 family member Chl2 is a GPI protein.

Three of the 11 corresponding genes (CHT3, which encodes the major chitinase; ENGL, which encodes an endo-β-1,3-glucanase; and SCW11, which encodes a β-1,3-glucan-modifying enzyme) are periodic genes with maximal expression in the M/G1 period of the cell cycle and are target genes of the transcription factor Ace2 (17–20), consistent with a role in cell separation. Agar-grown colonies, mucosal biofilms, and biofilms formed on abiotic surfaces produce abundant amounts of extracellular matrix material (3, 21–23). The transglucosylase Bgl2 and the exoglucanase Xog1 (together with the GPI-modified, putative β-1,3-glucan-elongating enzyme Phr1) seem to be directly involved in formation and modification of extracellular matrix material in biofilms (24).

**Nutrient acquisition.** (i) **Glucoamylases.** Glucoamylases include Gca1 and Gca2 (GH31); the predicted substrates are glycogen and starch (4, 16, 25, 26). Interestingly, maltose, which is a degradation product of both polysaccharides, is a carbon source known to promote hyphal growth (27). It has been suggested previously that Gca1 and Gca2 are directly involved in promoting matrix production in biofilms by enzymatic release of soluble β-1,3-glucan fragments from insoluble β-1,3-glucan chains (28). However, Gca1 and Gca2 possess the hallmarks of an α-glucosidase/glucoamylase, cleaving α-1,4-glucosidic linkages (8), and hence, it seems unlikely that they might cleave β-1,3-glucosidic linkages, which have a spatial structure highly different from that of α-1,4-glucosidic linkages.

(ii) **N-Acetylmuramidase.** HEX1 is a glucose-repressed gene (29). Hex1 (GH20) is found in the periplasm and in the culture supernatant (29). It is possibly involved in the release of GlcNAc residues from host tissues for use as a carbon or nitrogen source (29). Note that GlcNAc also acts as a signaling molecule and induces and maintains hyphal growth in glucose-repressed cells (30–33).

(iii) **Lipid degradation by Lips and Plbs.** Lipids are degraded by lipases (Lips) including Lip1 to Lip6 and Lip8 to Lip10 and by phospholipases (Plbs) including Plb1 and Plb2, reviewed in references 4 and 34.

(iv) **Protein degradation by aspartyl proteases.** Protein degradation by aspartyl proteases includes, for example, degradation of mucins and host immune proteins (4, 34–37), by aspartyl proteases such as Sap1 to Sap8. Note that Sap9 and Sap10 are cell surface-associated GPI proteins (38).

(v) **Metal ion acquisition.** Metal ion acquisition includes acquisition of zinc by Pra1 (39) and, probably, acquisition of heme (iron) by Csa2 (6, 12, 40, 41). Intriguingly, Pra1 is also involved in immune evasion (42, 43).

**Pry family.** The Pry family (11) consists of five members: Pry1, Rbe1, Rbt4, and two uncharacterized open reading frames (ORFs) (19.6200 and 19.2336). Rbe1 and Rbt4 have been often identified in culture supernatants (10–14). Interestingly, whereas Rbe1 is much more abundant in yeast culture supernatants, Rbt4 is much more abundant in hyphal culture supernatants (11–13) (see also Table 2). The virulence of an ∆rbe1 ∆rbt4 double deletion strain in the mouse model for systemic infection is strongly diminished (11), but the precise function of the Pry family proteins is still unknown.

**Coil.** Coil is a small protein of 191 amino acids that is relatively abundant and is consistently found in the medium under all conditions.
growth conditions tested (10–14). Homologous proteins are found in only a limited number of Candida spp.—Candida dubliniensis, Candida orthopsilosis, Candida parapsilosis, and Candida tropicalis—and in Lodderomyces elongisporus (8). Its function is unknown.

Signaling protein Msb2. The signaling protein Msb2 is located in the plasma membrane and involved in signaling through activation of the Cek1 mitogen-activated protein (MAP) kinase (44). Although Msb2 has an internal transmembrane sequence, it is included in this classification and in the secretome sensu stricto, because it has a large extracellular, highly O-glycosylated domain that is shed into the medium and consistently identified in culture supernatants (10–14, 45). Interestingly, it also serves as a broad-range protectant against antimicrobial peptides (45, 46).

**GPI PROTEINS**

GPI proteins are targeted to the plasma membrane or become covalently linked to the β-glucan layer of the cell wall through their GPI anchor or are found at both locations. However, most GPI proteins are also identified in culture supernatants (10–14). There are several (possible) explanations for their presence.

**Target proteins of Sap9 and Sap10.** Some wall-bound GPI proteins are released by the surface-bound aspartyl proteases Sap9 and Sap10, such as Cht2 (47). Other candidates for active and controlled release, such as the adhesion protein Als3 and the transglucosylase Phr1, will be discussed below.

**GPI proteins from the neck region.** In single-cell yeast cultures, wall-bound GPI proteins are released from the neck region during cell separation. The wall between mother cell and growing bud is continuous, and complete cell separation therefore requires not only degradation of the primary septum by chitinase activity but also degradation of the lateral wall in the neck region.

**Accidental release.** Especially in shaken cultures, wall-bound GPI proteins might be released during emergence of a new bud or hyphal branch, which requires localized cell wall softening, or during periods of isotropic growth, which requires insertion of new cell wall polysaccharides and wall proteins into the existing wall.

Wall protein precursors may be washed out into the medium before they become covalently linked to the glucan-chitin network, especially in shaken cultures.

**DYNAMICS OF THE SECRETOME OF C. ALBICANS**

In this section, the term “apparent abundance” is introduced. It is defined as the number of spectral counts per protein divided by the total number of spectral counts of all secretome proteins (sensu stricto) and expressed as a percentage (48). This is a semi-quantitative measure that allows comparison of the individual contributions of the secretome proteins and, importantly, allows estimating and comparing the fold changes of individual secretome proteins upon changes in environmental conditions, including conditions that induce growth as single yeast, pseudohyphal, or hyphal cells. We prefer the use of apparent abundances to that of normalized spectral abundance factors (NSAFs [9, 10, 49]). In the latter approach, the number of spectral counts per protein is normalized for protein length, which for nonglycosylated proteins results in more accurate estimates of protein abundance. However, secretome proteins sensu stricto frequently contain long, heavily O-glycosylated sequences, which rarely result in detectable tryptic peptides and thus lead to serious underestimations of protein abundances (for example, about 10-fold in the case of Msb2 [7, 8]) and decreased accuracy. A rough estimate of the number of secretome proteins per cell present in yeast culture supernatants, based on the data in references 12 and 50 and assuming an average protein mass of 40 kDa, is about 4 × 10^3 to 5 × 10^5.

**Three prominent secretome proteins.** The three β-glucan-modifying enzymes Mp65 (GH17), Sun41 (GH132), and Tos1 (GH16) belong to the most prominent (detectable) secretome proteins, both in single-cell yeast culture supernatants and hyphal culture supernatants and during pseudohyphal-like growth induced by fluconazole (Table 1). Similar values for their apparent abundances have been obtained under diverse growth conditions (6, 9, 10, 12–14). Conceivably, they are involved in various ways in the construction and remodeling of the β-1,3-glucan layer in the cell wall during growth (8, 16, 51–55). Their combined apparent abundance accounts for one-fourth to one-third of all secretome proteins. Consistent with this, the gene sequences of Mp65, Sun41, and Tos1 have a relatively high codon bias index (MP65, 0.71; SUN41, 0.64; TOS1, 0.59 [8]), suggesting that these genes are strongly expressed. Surprisingly, although Mp65 lacks a C-terminal GPI anchor to connect it covalently to the β-glucan network, it is usually also found in (hot-SDS-extracted) cell walls (10, 13, 14, 30, 37, 40). Scw11 and Sim1 belong to the same families as Mp65 and Sun41, respectively, and both show high apparent abundances in single-cell yeast cultures (Tables 2 to 4). However, in hyphal cultures and to a lesser extent also in pseudohyphal-growth cultures, their apparent abundances are considerably lower, suggesting that Scw11 and Sim1 might play a direct role in cell separation.

**Yeast state-enriched secretome proteins: yeast versus hyphal cultures.** In single-cell yeast cultures, the daughter cells become separated from the mother cell, a process that requires chitinase activity to degrade the primary septum formed during cytokinesis and β-1,3-endoglucanase activity to degrade the β-1,3-glucan layer in the lateral wall of the neck region. Conceivably, also transglucosylase activity is needed for repair activity. This results in much higher apparent abundances of the cell separation enzymes Cht3 and Eng1 and the potential repair enzyme Scw11 in the culture solution of unicellular budding yeast than in hyphal cells (Table 2). Although the apparent abundances of Bgl2, Cht1, Dag1, Rbe1, Sim1, and Xog1 in the culture solution of hyphal cultures are also strongly reduced, the corresponding genes do not seem to be periodically expressed (8, 17).

**Hyphal state-enriched secretome proteins: hyphal versus yeast cultures.** Many host-related chemical and physical conditions, such as a neutral pH, a temperature of 37°C, low oxygen levels and high CO₂ concentrations, the presence of GlcNAc (de-

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**TABLE 1 Three prominent secretome (sensu stricto) proteins of C. albicans grown under various conditions**

<table>
<thead>
<tr>
<th>Protein</th>
<th>Yeast abundance (%)</th>
<th>Hyphal abundance (%)</th>
<th>FCZ abundance</th>
</tr>
</thead>
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<tr>
<td>Mp65</td>
<td>12.4</td>
<td>14.3</td>
<td>8.5</td>
</tr>
<tr>
<td>Sun41</td>
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<td>7.4</td>
</tr>
<tr>
<td>Tos1</td>
<td>9.9</td>
<td>12.4</td>
<td>8.7</td>
</tr>
</tbody>
</table>

*Based on data from references 12 to 14. Yeast cultures were grown at 30°C and pH 7.4; hyphal cultures were grown at 37°C and pH 7.4. FCZ, fluconazole-treated cells grown at 37°C and pH 7.4. They form pseudohyphal aggregates (14).
initiate and sustain hyphal growth (31, 32, 59). GlcNAc is, for the human body, a GlcNAc and also GlcNAc derivatives strongly glucose-derepressing conditions, which occur in many niches in connective tissues (60) and is a known inducer of hyphal growth (31, 32, 59). An additional advantage of using GlcNAc to induce hyphal growth is that it, in contrast to bovine serum, allows (mass spectrometric) analysis of the hyphal secretome (12). GlcNAc-induced hyphal cultures contain four additional proteins in the culture medium that become about as equally prominent as Mp65, Rbt4, and Tos1 (Tables 1 and 2), namely, the aspartyl proteases Sap4 and Sap6; the Pry family protein Rbt4, whose function is unknown; and the GPI-modified adhesion protein Als3 (Tables 1 and 2). This is consistent with the strongly increased expression of the corresponding genes in GlcNAc-induced hyphal cultures (31; see also reference 61) for serum-induced hyphal cultures.

### Yeast to Hyphal Change

<table>
<thead>
<tr>
<th>Yeast to hyphal change</th>
<th>Apparent abundance (%)</th>
<th>Yeast</th>
<th>Hyphal</th>
<th>Fold change</th>
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<tbody>
<tr>
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<td>1.9</td>
<td>4.5</td>
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</tr>
<tr>
<td>Scw11†</td>
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<td>1.9</td>
<td>4.5</td>
<td></td>
</tr>
<tr>
<td>Xogl</td>
<td>8.4</td>
<td>1.2</td>
<td>7.1</td>
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</tr>
<tr>
<td>Sim1</td>
<td>7.8</td>
<td>2.6</td>
<td>3.0</td>
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</tr>
<tr>
<td>Eng1†</td>
<td>7.3</td>
<td>ND</td>
<td>&gt;28</td>
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</tr>
<tr>
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<tr>
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<tr>
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### Fold change

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<th>Yeast</th>
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<th>Fold change</th>
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<table>
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<tr>
<th>Hyphal to yeast change</th>
<th>Apparent abundance (%)</th>
<th>Yeast</th>
<th>Hyphal</th>
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<td>&gt;42</td>
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**Major changes in apparent abundance in the secretome of fluconazole-treated cells.** Pseudohyphal (or pseudohypha-like) growth can be induced in various ways, for example, by treating single-cell yeast cultures with sublethal concentrations of the antifungal compound fluconazole (14). Fluconazole blocks an Erg11-mediated demethylation step of the planar ring structure during ergosterol synthesis, and this results in the formation of structurally suboptimal sterols and increased fluidity of the plasma membrane (66). The cells respond by suppression of cell separation and by increased phosphorylation of the MAP kinase Mkc1 (14), which mediates the cell wall integrity pathway. Pseudohypha-like cell aggregates are formed, which separate into single cells when treated with exogenous chitinase (14). These effects are not specific for fluconazole but also occur when the cells are treated with the detergent SDS, grown at the harmful temperature of 42°C, or treated with the cell wall construction-perturbing compound calcifluor white or Congo red (14, 51) (Fig. 2). This suggests that many forms of plasma membrane stress or cell wall stress, together here referred to as cell surface stress, will cause pseudohypha-like growth and constitutively activate the cell wall integrity pathway. Indeed, cell separation suppression is a common phenotype among all genetic mutants that have to cope with a weakened cell wall resulting from defective N- or O-glycosyla-

### Table 2 Yeast state- and hyphal state-enriched secretome proteins

<table>
<thead>
<tr>
<th>Change and protein</th>
<th>Yeast</th>
<th>Hyphal</th>
<th>Fold change</th>
</tr>
</thead>
<tbody>
<tr>
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<tr>
<td>D ag7</td>
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</table>

### Table 3 Main features of the secretomes of fluconazole-supplemented cultures

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<th>Apparent abundance (%)</th>
<th>Yeast</th>
<th>Hyphal</th>
<th>Fold change</th>
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</table>

### Table 4 Main features of secretomes of low-pH-grown cultures

<table>
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<th>Change and protein</th>
<th>Apparent abundance (%)</th>
<th>Yeast</th>
<th>Hyphal</th>
<th>Fold change</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chlt3†</td>
<td>8.0</td>
<td>3.2</td>
<td>2.5</td>
<td></td>
</tr>
<tr>
<td>Bgl2</td>
<td>7.4</td>
<td>2.8</td>
<td>2.6</td>
<td></td>
</tr>
<tr>
<td>Phb4.3†</td>
<td>6.0</td>
<td>ND</td>
<td>&gt;32</td>
<td></td>
</tr>
<tr>
<td>Pir1</td>
<td>3.6</td>
<td>1.1</td>
<td>3.2</td>
<td></td>
</tr>
</tbody>
</table>

**Table 2.** Yeast state- and hyphal state-enriched secretome proteins

**Table 3.** Main features of the secretomes of fluconazole-supplemented cultures

**Table 4.** Main features of secretomes of low-pH-grown cultures
tion of secretory glycoproteins (67–70) or lack proteins involved in cell wall formation, such as Bgl2 (71); Ecm33, which is a GPI protein required for cell wall integrity (72); the secretome enzyme Sun41 (51, 52); and the GPI-modified and cell surface-located aspartyl proteases Sap9 and Sap10 (38), as well as Pir1, a putative cross-linker of β-1,3-glucan chains (73), and this list could be easily extended. Interestingly, CHT3 transcription is markedly downregulated in micafungin-treated cells (74), suggesting that this inhibitor of β-1,3-glucan synthesis might also induce cell separation suppression. Similar observations have been described by O’Meara and coworkers, who treated wild-type cultures with serum in combination with various antifungal drugs at sublethal concentrations and found that under these conditions hyphal growth was suppressed and, instead, pseudohyphal cell clusters were formed (see Fig. 2c in reference 75). A relevant implication of these observations is that “cell separation suppression” as a phenotype does not necessarily prove that the mutated gene is directly involved in cell separation.

Consistent with the partial suppression of cell separation in fluconazole-treated cells, resulting in pseudohypha-like growth, the major chitinase Cht3 (GH18), the endo-β-1,3-glucanase Eng1 (GH81), and the β-1,3-glucan-modifying enzyme Scw11 are all decreased in the supernatants of fluconazole-treated cultures, although less so than in hyphal cultures (Tables 2 and 3). Other chitin- and β-1,3-glucan-modifying enzymes, namely, Cht1 (GH18) and Sim1 (GH132), are also decreased in fluconazole-treated and hyphal cells. How exactly suppression of cell separation is regulated in response to cell surface stress is currently unknown. As CHT3, ENG1, and SCW11 are known target genes of the transcription factor Ace2 (18–20), a regulator of cell separation that controls the expression of M/G1-specific genes, it seems likely that fluconazole treatment and many other forms of cell surface stress lead to suppression of Ace2 activity in cell separation. Possibly, cell separation is suppressed through phosphorylation of the transcription factor Efg1, which in turn represses Ace2 target genes and promotes pseudohypha-like growth (76).

Another striking observation is the high apparent abundance of the GPI protein Phr1 in the medium of fluconazole-treated cells, whereas it is not detectable in the medium of single-cell yeast cultures and hyphal cultures. This observation is consistent with the finding that the antifungal compounds ketoconazole and caspofungin stimulate the expression of PHR1 (77). Phr1 (GH72) is a pH-responsive transglucosylase and probably involved in expansion of the β-1,3-glucan layer (78, 79). It also plays an important role in the accumulation of β-1,3-glucan in the extracellular matrix of biofilms, possibly by extending the β-1,3-glucan chains there and thus increasing the cohesiveness of the biofilm (24). This raises the interesting question of whether biofilm-associated Phr1 in fluconazole-treated cells might contribute to protection against fluconazole. It is currently unknown how Phr1 is released from the cell surface. However, Phr1 contains two consecutive lysine residues (K145 and K152), suggesting that it might be a substrate of Sap9/10 (47).

Finally, the culture medium of fluconazole-treated yeast cultures contains several low-abundance secretory proteins that do not necessarily prove that this secretome response is specific for fluconazole-treated cells, because, as we have seen above, many other conditions lead to cell surface stress, and this might be in itself enough to trigger the release of members of this subset of proteins.

**Secretome proteins increased at low pH**. Acidic conditions are found on the skin (80); in the vagina, due to formation of lactic acid by vaginal epithelial cells and by lactobacilli (81); and in dental plaque, where they are caused by the formation of lactic acid by *Streptococcus mutans* (82). Two GPI-modified wall proteins (Plb4.5 and Utr2) and the β-1,3-glucan-linked wall protein Pir1 become much more abundant in the culture medium upon lowering the environmental pH, either because at acidic pH their incorporation into the cell wall becomes less efficient or because they are actively released from the wall (Table 4). The apparent abundance of the non-GPI, β-1,3-glucan-modifying protein Bgl2 (GH17) also shows a considerable increase. As this protein contributes to β-1,3-glucan accumulation in biofilms (24), this might mean that at acidic pHs biofilms produce more extracellular matrix.

**Lactate-induced secretome proteins**. Although at many infections sites glucose levels are low and, consequently, *C. albicans* cells are in a glucose-derepressed state, depending instead on alternative carbon sources for growth, glucose-grown cells are often used for research. The results obtained in this way can therefore not always be directly extrapolated to glucose-derepressed cells (83). For example, the levels of three secretome proteins, glucoamy-lase(s) Gca1/2 (GH31), the aspartyl protease Sap7, and the exo-β-1,3-glucanase Xog1 (GH15), strongly increase when lactate, a nonfermentable carbon source and a much poorer carbon source than glucose, is used to support growth (9, 84). On the other end of the spectrum, there are also a number of secretome proteins whose apparent abundances strongly decrease in lactate-grown cultures (9). The induction of hyphal growth by GlnNac as discussed above is already blocked at a glucose concentration of 20 mM (33), and this represents another striking example of the importance of selecting the appropriate carbon source and/or glucose concentration in *Candida* research.

**CONCLUDING REMARKS**

Similarly to the wall proteome, the secretome of *C. albicans* operates at the fungus-host interface, and pronounced changes in abundance of individual proteins occur in distinct host niches. For example, the switch from single-cell yeast growth to hyphal growth results in the abundant secretion of the aspartyl proteases Sap4 and Sap6, which significantly contribute to virulence (85). As expected, the pH of the host niche also strongly affects the composition of the secretome. The ability to form biofilms, in which
yeast, pseudoohyophal, and hyphal cells are found, with the concur-
rent accumulation of extracellular matrix material and the often
strongly lowered susceptibility to antifungal agents, is another im-
portant virulence trait. Several secretome proteins, such as Als3,
Bgl2, Mp65, Pfr1, Xog1, and Sun41, are believed to be involved in
biofilm formation (8). In view of their high apparent abundances
under widely diverging growth conditions, the secretome proteins
Mp65, Sun41, and Tso1 seem attractive candidates for diagnostic
purposes. In addition, as Candida infections are usually associated
with invasive, hyphal growth, and as Als3, Rbt4, Sap4, and Sap6
become abundant in the supernatants of hyphal cultures, these
proteins also are potential diagnostic candidates. Two secretome
proteins, Als3 (actually, a recombinant protein that covers the
N-terminal immunoglobulin-like domain of Als3) and Sap2, are
currently being actively pursued for vaccine development (86–
88). Als3 is an abundant, multifunctional GPI-modified cell wall
protein (86, 89, 90) and as such is a highly attractive vaccine can-
didate. The finding that Als3 also becomes an abundant secretome
protein in hyphal cultures (12) with a proposed role in biofilm
formation further increases its attractiveness. It has been argued
that a multivalent vaccine might be more effective to combat the
various types of Candida infections (91). Conceivably, a recombi-
nant protein consisting of two or three of the most immunogenic
epitopes from various cell wall proteins (92) and from secretome
proteins such as the aspartyl proteases Sap4 and Sap6 (12, 85); the
three secretome proteins involved in the formation of biofilm ma-
trix beta-glucan (Bgl2, Pfr1, and Xog1) (24); Sun41 and Sim1, which
form a two-member family and are synthetically lethal (52); and
the Pry proteins Rbe1 and Rbt4 (11), each separated from the
other by a nonimmunogenic linker sequence, might be an option.
Similar approaches might be considered for other pathogenic
fungi. Finally, many regulatory pathways have been shown to be
involved in controlling the abundance of individual secretome
proteins, but more-systematic studies of how the secretome as a
whole is regulated are still scarce.

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REFERENCES
cally important Candida species, p 1–25. In Calderone RA, Clancy CJ
(ed), Candida and candidiasis, 2nd ed. ASM Press, Washington, DC.
heterogeneous, drug-tolerant environment. Curr Opin Microbiol 16:
ed. ASM Press, Washington, DC.
2012. The carbohydrate-active enzymes database (CAZy) in 2013. Nu-
10.1091/mcb.E09-03-0210.
factor Ace2 regulates metabolism and is required for filamentation in
EC.00155-06.
2004. The Candida albicans CaAce2 gene affects morphogenesis, ad-
j.1365-2958.2004.04185.x.
9. Esteban PF, Rios I, García R, Dueñas E, Pla J, Sánchez M, de Aldana CR,
Del Rey F. 2005. Characterization of the CαtENG1 gene encoding an endo-1,3-beta-glucanase involved in cell separation in Candida al-
0066-2.
Candida albicans biofilms form on the vaginal mucosa. Microbiology
13. Taff HT, Nett JE, Zarnowski R, Ross KM, Sanchez H, Cain MT,
pathway for matrix glucan delivery: implications for drug resistance. PLoS
Pathog 8:e1002848. http://dx.doi.org/10.1371/journal.ppat.1002848.
1999. Identification and cloning of GCA1, a gene that encodes a cell sur-
dx.doi.org/10.1080/026928300999.00244.x.
15. Dennerstein GJ, Ellis DH. 2001. Oestrogen, glycogen and vaginal candi-
16. Shepherd MG, Sullivan PA. 1976. The production and growth charac-
teristics of yeast and mycelial forms of Candida albicans in continuous
get proteins necessary for both cellular processes and host-pathogen response to ambient pH. Microbiology


