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The *Candida albicans HYR1* Gene, Which Is Activated in Response to Hyphal Development, Belongs to a Gene Family Encoding Yeast Cell Wall Proteins

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A hyphally regulated gene (*HYR1*) from the dimorphic human pathogenic fungus *Candida albicans* was isolated and characterized. Northern (RNA) analyses showed that the *HYR1* mRNA was induced specifically in response to hyphal development when morphogenesis was stimulated by serum addition and temperature elevation, increases in both culture pH and temperature, or *N*-acetylglucosamine addition. The *HYR1* gene sequence revealed a 937-codon open reading frame capable of encoding a protein with an N-terminal signal sequence, a C-terminal glycosylphosphatidylinositol-anchoring domain, 17 potential N glycosylation sites, and a large domain rich in serine and threonine (51% of 230 residues). These features are observed in many yeast cell wall proteins, but no homologs are present in the databases. In addition, Hyr1p contained a second domain rich in glycine, serine, and asparagine (79% of 239 residues). The *HYR1* locus in *C. albicans* CAI4 was disrupted by "Ura-blasting," but the resulting homozygous Δ*hyr1*/Δ*hyr1* null mutant displayed no obvious morphological phenotype. The growth rates for yeast cells and hyphae and the kinetics of germ tube formation in the null mutant were unaffected. Aberrant expression of *HYR1* in yeast cells, when an *ADH1-HYR1* fusion was used, did not stimulate hyphal formation in *C. albicans* or pseudohyphal growth in *Saccharomyces cerevisiae*. *HYR1* appears to encode a nonessential component of the hyphal cell wall.

Candida albicans is a major fungal pathogen in humans (44, 45). Most frequently it causes superficial, irritating infections of the oral and urogenital tracts. However, serious deep-seated or systemic infections can develop, particularly in immunocompromised individuals.

A number of factors are thought to promote the virulence of *C. albicans*. Many of these factors relate to properties of the *C. albicans* cell surface, for example, the ability to adhere to host tissues (7, 8, 27) and the immunomodulatory effects of various cell wall components (40, 72). Another potential virulence factor is the ability to undergo a morphological transition from a budding yeast to a hyphal form, but this has not been established unambiguously (12, 39, 48, 57, 60, 61). Changes in the *C. albicans* cell surface accompany the morphological transition (9, 15, 16, 31, 38, 64), and hence morphogenesis is intimately linked with other virulence factors such as adherence. Processes germane to the regulation of the yeast-to-hypha transition are therefore important in establishing the role of this transition in the pathogenicity of *C. albicans*.

Several factors influenced our experimental approach. First, classical genetic approaches were inappropriate because *C. albicans* is asexual and diploid (55). Second, nonstandard usage of the CTG codon in *C. albicans* (52, 53, 78) precluded the use of standard reporter genes, and until recently (62), no sensitive reporter genes for *C. albicans* were available. Hence, we attempted to identify *C. albicans* genes which are regulated specifically in response to morphogenesis. Using various approaches, we identified numerous genes that are regulated during morphogenesis, including *HSP90*, *TEF3*, *ADH1*, *PYK1*, *RP10*, and *GFA1* (59, 65–67, 69). However, in all cases we showed that these genes were responding to changing growth conditions rather than to morphogenesis. Nevertheless, we did identify a morphogenetically regulated sequence via a serendipitous route. This *C. albicans* cDNA, which was a false positive in an immunological screen for β-subunits of heterotrimeric G proteins (18), was used as a probe in Northern (RNA) analyses of yeast and hyphal RNAs as part of a routine screen for morphogenetically regulated sequences. The corresponding mRNA was not detected in yeast cells but was abundant in hyphae. Hence, the gene was called *HYR1* (for hyphally regulated).

This paper describes the isolation and characterization of the *HYR1* gene. We show that *HYR1* is expressed specifically during hyphal development and that it appears to encode a nonessential component of the hyphal cell wall.

MATERIALS AND METHODS

Strains and culture conditions. The following *C. albicans* (Robin) Berkhout strains were used: ATCC 10261 (58), 3153A (Public Health Laboratory Services Mycology Reference Laboratory, Department of Microbiology, University of Leeds, Leeds, United Kingdom), and CAI4 (Δ*ura3*::*imm434*/Δ*ura3*::*imm434*) and its wild-type parent, SC5314 (21). *Saccharomyces cerevisiae* W303-1B (*MAT*α *ade2 his3 leu2 trp1 ura3*) was used (71). *Escherichia coli* DH5αF′ [K-12 Δ(*lac ZYA-argF*)$_{U169}$ *supE44 thi1 recA1 endA1 hisR17 gyrA relA1* (ϕ80lacZΔM15)F′] was used for the manipulation of cDNA and genomic clones.

The dimorphic transition was induced under three different sets of experimental conditions. (i) *C. albicans* was grown in the yeast form to late exponential growth phase (optical density at 600 nm, about 0.6) in YPD (2% glucose, 2% bacteriological peptone, 1% yeast extract) at 25°C with shaking at 200 rpm. To induce hyphal growth, 10 ml of this culture was used to inoculate 100 ml of YPD containing 10% bovine calf serum at 37°C (approximately 2×10^7 cells per ml). Samples were removed at various times up to 120 min. Control cultures were

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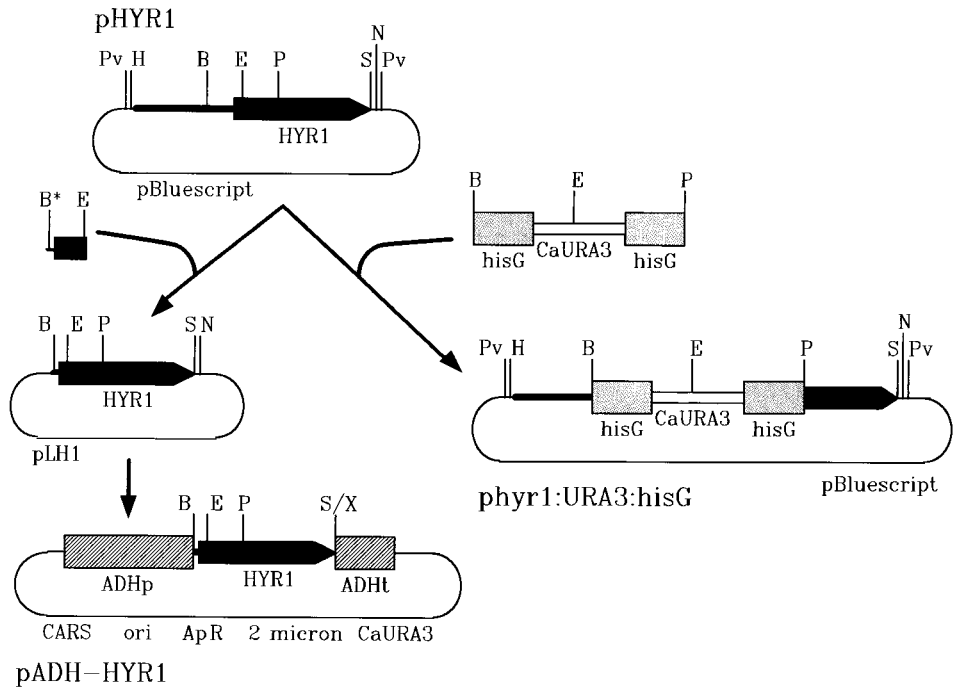

FIG. 1. Construction of *HYR1* plasmids for gene disruption and expression. The plasmid pHYR1 contains the entire *HYR1* coding region and 1.3 kbp of 5′ sequences cloned into pBluescript. The *hisG*::*URA3*::*hisG* cassette from pMB-7 was cloned between the *Bgl*II and *Pst*I sites in pHYR1 to generate phyr1:URA3:hisG, which was used to make a *C. albicans* Δ*hyr1* null mutant (see Materials and Methods). The *ADH1-HYR1* fusion was created essentially in two steps. First, the 2.7-kbp *Eco*RI-*Not*I fragment from pHYR1 (containing most of the *HYR1* coding region), and a 0.1-kbp PCR product with an artificial 5′ *Bgl*II site and a natural 3′ *Eco*RI site (representing the 5′ end of the *HYR1* coding region) were cloned in a three-way ligation into pLH1. Second, the resulting *Bgl*II-*Not*I fragment containing the complete coding region was subcloned into the *C. albicans* expression vector YPB-ADHpt to generate pADH-HYR1. This expression plasmid carries the *HYR1* coding region under the control of the *C. albicans ADH1* promoter and terminator as well as *C. albicans* and *S. cerevisiae* replication origins (CAARS and 2μm) and the *C. albicans URA3* gene. Solid arrow-like boxes, *HYR1*; stippled boxes, *hisG* sequences; white rectangle, *URA3*; hatched boxes, *ADH1* promoter (ADHp) and terminator (ADHt); thin lines, backbone vector sequences. Abbreviations for restriction enzymes: B, *Bgl*II (B*, artificial *Bgl*II site); E, *Eco*RI; H, *Hin*dIII; N, *Not*I; P, *Pst*I; Pv, *Pvu*II; S, *Sal*I; X, *Xho*I. Drawings are not to scale.

grown in fresh YPD at 25°C without serum, 25°C with serum, or 37°C without serum. (ii) *C. albicans* was grown in the yeast form to late exponential growth phase in Soll's medium at 25°C and pH 4.5 with shaking at 200 rpm. Hyphal growth was induced by inoculating 10 ml of this culture into 100 ml of Soll's medium at 37°C and pH 6.5 (approximately 2×10^7 cell per ml) (61), and samples were removed for analysis at various times up to 180 min. Control cultures were grown in Soll's medium at 25°C and pH 4.5, 25°C and pH 6.5, or 37°C and pH 4.5. Soll's medium refers to the defined medium of Lee et al. (34) as modified by Buffo et al. (6). (iii) Hyphal growth was induced with *N*-acetylglucosamine as described previously (41), and samples were removed for RNA analysis at various times thereafter. Cell numbers and morphology were monitored by light microscopy with an improved Neubauer hemocytometer.

Isolating the *HYR1* gene. The genomic library, which was derived from *C. albicans* ATCC 10261, was provided by M. Payton (Glaxo Institute for Molecular Biology, Geneva, Switzerland). The library was constructed by inserting DNA partially digested with *Sau*3A into YCp50 (58). Colony hybridization (49) was performed with the 1.4-kbp *Hin*dIII fragment from the *HYR1* cDNA as a probe following radiolabelling by random priming (17).

DNA sequencing. Dideoxy DNA sequencing (50) was performed with synthetic oligonucleotide primers (Oswel, Southampton, United Kingdom). Double-stranded DNA templates were sequenced with Sequenase (Amersham International, Little Chalfont, United Kingdom) and ^{35}S-dATP according to the manufacturers' instructions. DNA sequences were analyzed with the Genetics Computer Group programs (14) on the SERC computer at the Daresbury Laboratory.

Preparation and analysis of nucleic acids. Genomic DNA (26) and total RNA (5, 36) were prepared from *C. albicans* and *S. cerevisiae* as described previously. Southern blotting (51) and Northern analysis (42) were performed with radiolabelled probes prepared by random priming (17) the purified 1.4-kbp *Hin*dII fragment from the *HYR1* coding region. For Northern blotting, yields of total RNA were measured by spectrophotometry at 260 nm, and approximately equal amounts of RNA were loaded in each lane. Following electrophoresis on formaldehyde-containing gels, the RNA was transferred to nylon membranes by vacuum blotting, and hybridizations were performed under conditions of probe excess (42). To date, there has been no report of a reasonably abundant *C. albicans* mRNA that remains at sufficiently constant levels during the dimorphic transition to use as an internal loading control on Northern blots (3, 11, 59, 65–67, 69). Therefore, mRNA levels were measured relative to those of the rRNAs by loading equal amounts of total RNA in each lane of the Northern gels (3, 11, 59, 65–67, 69).

RNA 5′ mapping. The 5′ end of the *HYR1* mRNA was mapped by primer extension using standard procedures (49). Briefly, 400 ng of oligonucleotide primer (5′-TGAATTCCACCACGGTC-3′; Oswel) was end labelled with [γ-^{32}P]ATP (35). Labelled primer (200 ng) was precipitated with 160 μg of *C. albicans* RNA prepared from hyphal cells. After denaturing and annealing this mixture, primer extension was performed in a total volume of 20 μl with 48 U of avian myeloblastosis virus reverse transcriptase (Boehringer Mannheim UK Ltd., Lewes, East Sussex, United Kingdom). A sequencing reaction was performed with the same primer and electrophoresed alongside the primer extension reaction on a 6% urea–polyacrylamide gel.

Disruption of *HYR1*. The *hisG*::*URA3*::*hisG* "Ura-blaster" cassette from pMB7 (21) was isolated by digestion with *Bgl*II and *Pst*I and used to replace the 1.4-kbp *Bgl*II-*Pst*I fragment in pHYR1 to create phyr1:URA3:hisG (Fig. 1). The 9.6-kb Δ*hyr1*::*hisG*::*URA3*::*hisG* insert was released from pBluescript by digestion with *Pvu*II and used to transform *C. albicans* CAI4 (33). Late logarithmic cells (50 ml) were harvested, spheroplasted with β-glucuronidase (type H2; Sigma, St. Louis, Mo.), and transformed with approximately 5 μg of DNA. Cells were plated onto SD medium [2% glucose, 0.17% yeast nitrogen base without amino acids, 0.5% $(NH_4)_2SO_4$] containing 1 M sorbitol and lacking uridine. Approximately three to four transformants per μg of DNA were visible after incubation at 30°C for 3 days. Primary transformants were replated onto SD medium lacking uridine and then patched onto minimal medium containing uridine (50 μg/ml) and 5′-fluoroorotic acid (FOA) (1 mg/ml). FOA-resistant colonies were used for a second round of transformation with the Δ*hyr1*::*hisG*::*URA3*::*hisG* fragment to disrupt the second *HYR1* allele. Cells were subjected to Southern analysis at each stage of this process.

Overexpression of *HYR1*. The 5′ end of the *HYR1* coding region was PCR amplified with primers designed to introduce a *Bgl*II site at position −13 with respect to the first nucleotide of the coding region. The primer sequences were 5′-CAATTTCAAGATCTATAACAAC*ATG*AAGTGG-3′ (the *Bgl*II site is un-

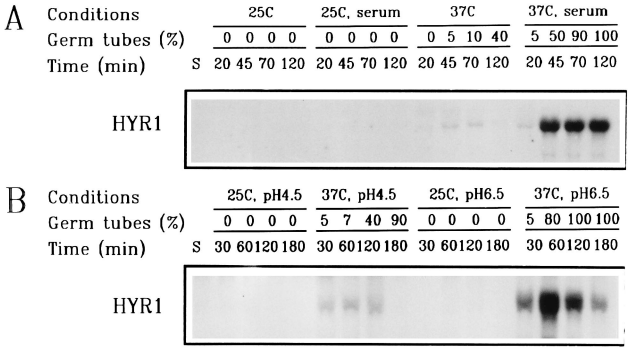

FIG. 2. The *HYR1* mRNA is induced in response to morphogenesis. The yeast-to-hypha transition was induced in *C. albicans* 3153A with different stimuli. Northern analysis of the *HYR1* mRNA was performed at various times thereafter with approximately 20 μg of RNA in each lane, and the proportion of cells forming germ tubes was determined by light microscopy. (A) An overnight starter culture grown in YPD at 25°C (S) was used to inoculate either YPD at 25°C (25C), YPD containing serum at 25°C (25C, serum), YPD at 37°C (37C), or YPD containing serum at 37°C (37C, serum). (B) An overnight starter culture grown in Soll's medium at pH 4.5 and 25°C (S) was used to inoculate fresh Soll's medium either at pH 4.5 and 25°C (25C, pH 4.5), pH 4.5 and 37°C (37C, pH 4.5), pH 6.5 and 25°C (25C, pH 6.5), or pH 6.5 and 37°C (37C, pH 6.5).

derlined and the initiation codon is shown in italics) and 5′-CCTTGATTTGTA GCTGG-3′. The PCR product was digested with *Bgl*II and *Eco*RI to release a 100-bp fragment which was mixed with the 2.7-kbp *Eco*RI-*Not*I fragment from pHYR1 and ligated into the vector pLH1 (Amersham International) (Fig. 1). After being subjected to resequencing to check its integrity, this construct was digested with *Bgl*II and *Sal*I and the 2.8-kbp *HYR1* coding region was cloned between the *Bgl*II and *Xho*I sites in the *C. albicans* expression vector YPB-ADHpt to generate pADH-HYR1 (Fig. 1). YPB-ADHpt carries the *C. albicans ADH1* promoter and terminator regions (3), the *C. albicans URA3* marker, and *C. albicans* (CAARS) and *S. cerevisiae* (2μm) replication origins (2a). pADH-HYR1 was transformed into *C. albicans* CAI4 (33) and *S. cerevisiae* (30).

Nucleotide sequence accession number. The *HYR1* sequence was submitted to the EMBL database and given accession number Z50123.

RESULTS

The *C. albicans HYR1* gene is morphogenetically regulated. In an effort to identify genes that are regulated specifically in response to the yeast-to-hypha transition, we routinely analyzed the expression of newly isolated *C. albicans* clones. As part of this process, we performed Northern analyses of yeast and hyphal RNAs using a cDNA clone isolated as a false positive in an immunological screen for β-subunits of *C. albicans* trimeric G proteins (18). This *C. albicans* cDNA detected an approximately 3-kb-long mRNA which was strongly induced when the yeast-to-hypha transition was induced by a combination of serum addition and temperature elevation (Fig. 2A), by increasing both the pH and temperature of the cultures (Fig. 2B), or by *N*-acetylglucosamine addition (not shown). The presence of this mRNA correlated with the formation of germ tubes rather than the induction conditions themselves. For example, weak induction of *HYR1* correlated with the slow emergence of germ tubes at pH 4.5 and 37°C (Fig. 2B). Therefore, this mRNA was induced specifically in response to hyphal growth, and hence the corresponding locus was named *HYR1* (for hyphally regulated).

Isolation and sequencing of *HYR1*. The *HYR1* cDNA contained only 2.6 kb of the 3-kb mRNA. Hence, the cDNA was used to isolate the gene from a *C. albicans* genomic library. The sequences of the *HYR1* cDNA (derived from a *C. albicans* 3153A library [68]) and gene (derived from a *C. albicans* 10261 library [58]) were identical over their 2.2-kb overlap (Fig. 3). However, the *HYR1* genomic clones were truncated, lacking 400 bp at the 3′ end. Hence, the complete *HYR1* open reading frame was PCR amplified from *C. albicans* ATCC 10261 with primers corresponding to the 5′ and 3′ untranslated regions. The sequence of this PCR product confirmed that the 3′ end of the *HYR1* gene in ATCC 10261 was identical to that in 3153A. The 3′ *Pst*I-*Sal*I fragment from the PCR product was ligated to the 5′ *Hin*dIII-*Pst*I fragment from the genomic clone to reconstruct the full-length *HYR1* gene in plasmid pHYR1 (Fig. 1).

The *HYR1* sequence revealed a 2,810-bp open reading frame capable of encoding a 937-amino-acid protein with a predicted molecular mass of 94.1 kDa (Fig. 3). No homologs were identified in the databases. Computer analyses of the predicted amino acid sequence suggested the existence of an N-terminal signal sequence. Also the presence of a hydrophobic C-terminal tail preceded by consensus cleavage sites was consistent with the attachment of a glycosylphosphotidylinositol (GPI) anchor (19, 73). A large hydrophilic domain (residues 346 to 576) was rich in serine and threonine (51% of the residues). A second domain (residues 577 to 816) was rich in asparagine, serine, and glycine (79% of residues). The protein sequence carried 17 potential N-glycosylation sites, the last of which is unlikely to be used if the protein is GPI anchored (Fig. 3).

Mapping the *HYR1* transcription unit. The transcriptional start sites on the *HYR1* gene were mapped by primer extension (Fig. 4). The major transcriptional start site was at −60 with respect to the predicted translational start codon which represented the 5′-proximal ATG on the *HYR1* mRNA (Fig. 3). A TATA-like sequence (4, 14) existed 27 bp upstream from the major transcriptional start site. Analyses of the cDNA sequence revealed that 3′ polyadenylation occurred between nucleotides 2999 and 3000. It was not clear whether the last A residue was part of the primary transcript or added posttranscriptionally as part of the poly(A) tail (Fig. 3). The length of the transcription unit (2,935 bp) was consistent with the length of the mRNA observed on Northern blots (about 3 kb).

A *C. albicans* Δ*hyr1*/Δ*hyr1* mutant displays no obvious phenotype. A *C. albicans* Δ*hyr1*/Δ*hyr1* mutant was constructed with a view to establishing the function of the *HYR1* gene. We exploited the Ura-blasting procedure (21, 51), which was first developed for sequential gene disruptions in *S. cerevisiae* (1). The plasmid phyr1:URA3:hisG was created essentially by inserting the *hisG*::*URA3*::*hisG* cassette from pMB-7 between the *Bgl*II and *Pst*I sites in the *HYR1* gene (Fig. 1), thereby deleting 290 bp of the 5′ region and 1.1 kbp of the coding region, and leaving about 1 kbp of 5′ sequence and 2 kbp of 3′ sequence flanking the *hisG*::*URA3*::*hisG* cassette for targeted integration into the *HYR1* locus. No upstream open reading frames were affected by this insertion (not shown). The 9.8-kbp *Pvu*II fragment carrying the Δ*hyr1*::*hisG*::*URA3*::*hisG* cassette was transformed into *C. albicans* CAI4, selecting for Ura^+ transformants. Following Southern analysis to confirm the correct disruption of the first *HYR1* allele, spontaneous Ura^- segregants were selected on the basis of their resistance to FOA. Southern analysis confirmed the loss of the *URA3* gene from the Δ*hyr1* allele via intrachromosomal recombination between the tandem *hisG* repeats (Fig. 5). To disrupt the second *HYR1* allele, this *HYR1*/Δ*hyr1*::*hisG* mutant was transformed with the Δ*hyr1*::*hisG*::*URA3*::*hisG* cassette and Ura^+ transformants were selected. FOA-resistant, Ura^- segregants were selected once again, and the construction of a *C. albicans* Δ*hyr1*/Δ*hyr1* mutant was confirmed by Southern analysis (Fig. 5). This also confirmed the existence of a single *HYR1* locus in *C. albicans*.

The phenotype of the *C. albicans* Δ*hyr1*/Δ*hyr1* mutant was compared with that of its isogenic parent, CAI4. The mutant showed normal doubling times in minimal (2.1 h) and rich (1.2 h) media, no change in the kinetics of germ tube formation

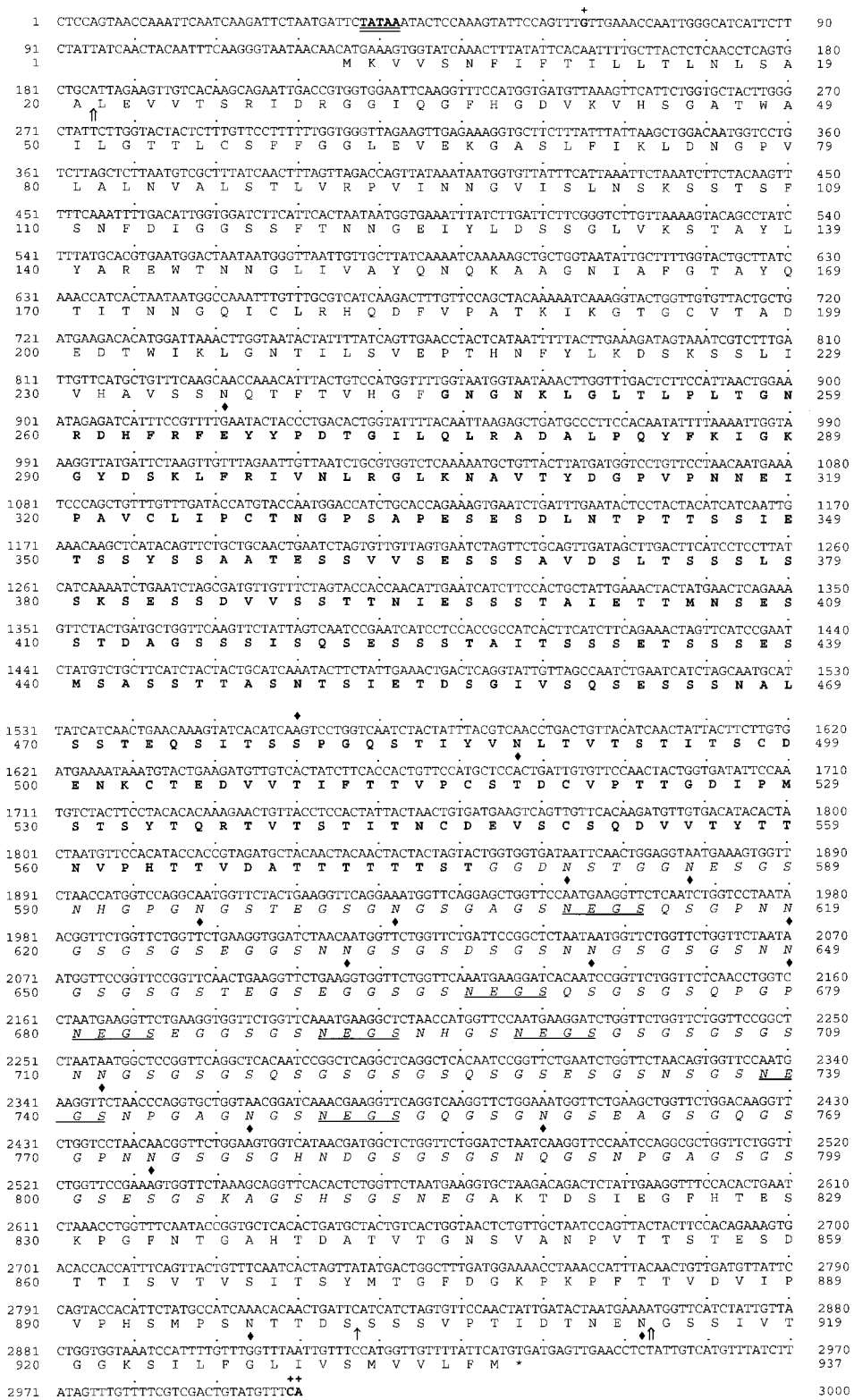

FIG. 3. Nucleotide and predicted amino acid sequences of the *C. albicans HYR1* gene. Regarding the nucleotide sequence, the positions of the major transcriptional start site at nucleotide 65 (see Fig. 4) and the 3′ cleavage and polyadenylation sites at nucleotides 2999 and 3000 are marked with crosses above the sequence. A TATA-like sequence at nucleotides 38 to 42 is indicated by double underlining. The 2.2-kbp cDNA sequence is identical to the 3′ end of the gene sequence. With respect to the predicted amino acid sequence, the serine- and threonine-rich domain is shown in boldface type, whereas the glycine-, serine-, and asparagine-rich domain is shown in italics (see text). The sequence NEGS, which is repeated seven times in the latter domain, is underlined. Potential N glycosylation sites are represented by diamonds below each target asparagine residue. The predicted cleavage site for the N-terminal signal sequence is illustrated with an arrow below the site. The most likely cleavage site for the C-terminal GPI-anchoring domain is shown by the large arrow between residues 913 and 914, and a second possible cleavage site is indicated by the small arrow between residues 902 and 903.

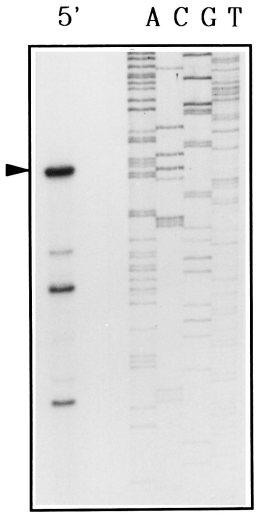

FIG. 4. The *HYR1* transcriptional start site. The transcriptional start site was mapped by primer extension (lane 5′) and electrophoresed alongside an *HYR1* sequencing reaction (lanes A, C, G, and T) performed with the same primer. The position of the major start site on the *HYR1* sequence (Fig. 3) is shown (arrowhead).

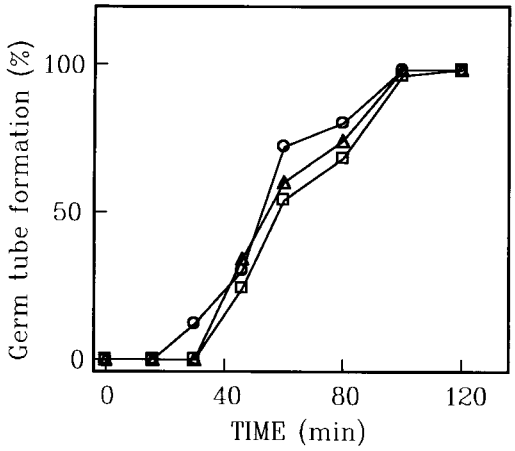

FIG. 6. Kinetics of germ tube formation in *C. albicans HYR1* mutants. The wild-type parental strain (SC5314) (squares), the *hyr1* null mutant (Δ*hyr1*::*hisG*/Δ*hyr1*::*hisG*) (circles), and the pADH-HYR1 transformant (triangles) were grown overnight in YPD at 25°C and then inoculated at the same cell density into YPD at 37°C containing 10% serum. The proportion of cells forming germ tubes was determined by light microscopy at various times thereafter (errors were less than 5%).

(Fig. 6), and no significant difference in its sensitivity to caffeine or calcofluor white. Microscopic analyses revealed no abnormal cell morphologies for this mutant compared with CAI4.

Forced expression of *HYR1* in yeast cells of *C. albicans* and *S. cerevisiae*. Since no obvious phenotype was observed upon disruption of *HYR1*, we tested the effects of expressing this hypha-specific gene in the yeast form of *C. albicans*. To achieve this, the *HYR1* coding region was amplified by PCR, resequenced, and cloned into the *C. albicans* expression vector YPB-ADH1pt to create pADH-HYR1 (Fig. 1). pADH-HYR1 was transformed into *C. albicans* CAI4, and Northern analysis confirmed the aberrant expression of *HYR1* during the growth of the yeast form (Fig. 7). The level of *HYR1* expression in yeast cells transformed with pADH-HYR1 was roughly equivalent to that observed upon induction of hyphal growth in untransformed cells. This did not affect the growth rate of the transformed yeast cells, their sensitivity to caffeine or calcofluor white, or their cell morphology. Germ tube formation in these transformants was not observed under conditions which favored the growth of the yeast form.

The plasmid pADH-HYR1 was also transformed into *S. cerevisiae* W303-1B. Northern analysis revealed high levels of the *ADH1-HYR1* mRNA (Fig. 7), consistent with a high plasmid copy number, generated by the 2 μm sequences in the vector and the efficient expression of the *C. albicans ADH1* gene in *S. cerevisiae* (3). Again, no obvious phenotype in the

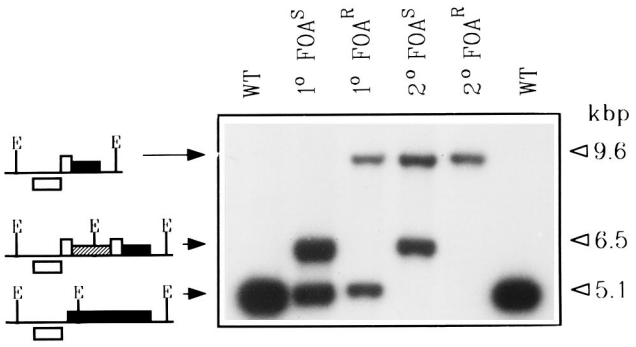

FIG. 5. Disruption of the *C. albicans HYR1* locus. Southern analysis was performed on *Eco*RI digested DNA from the parental strain CAI4 (lanes WT), a first-round Ura3$^+$ transformant (*HYR1*/Δ*hyr1*::*hisG*::*URA3*::*hisG*) (lane 1° FOA^S), a first-round FOA-resistant segregant (*HYR1*/Δ*hyr1*::*hisG*) (lane 1° FOA^R), a second-round Ura3$^+$ transformant (Δ*hyr1*::*hisG*::*URA3*::*hisG*/Δ*hyr1*::*hisG*) (lane 2° FOA^S), and a second-round FOA-resistant segregant (Δ*hyr1*::*hisG*/Δ*hyr1*::*hisG*) (lane 2° FOA^R). The blot was probed with the radiolabelled 5′ *Hin*dIII-*Bgl*II fragment from pHYR1 (Fig. 1). The lengths of the *Eco*RI fragments detected are shown to the right of the gel. Cartoons representing wild-type and disrupted loci are shown opposite the corresponding *Eco*RI fragments, on the left. Black boxes, *HYR1* coding region; horizontal lines, *HYR1* 5′ and 3′ regions; boxes below cartoons, *HYR1* probe; white rectangles, *hisG* sequences; hatched rectangle, *CaURA3* sequence; E, *Eco*RI site.

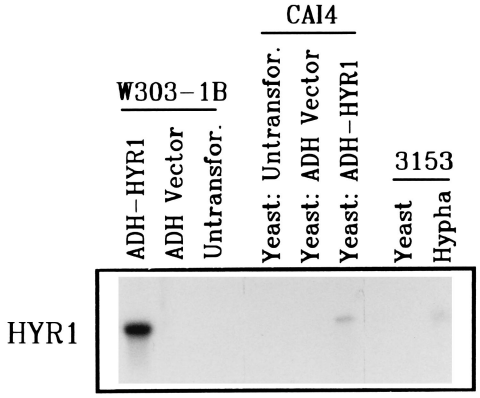

FIG. 7. *HYR1* mRNA levels in *C. albicans* and *S. cerevisiae* transformed with pADH-HYR1. Northern analysis of the *HYR1* mRNA was performed on approximately 5 μg of RNA: *S. cerevisiae* W303-1B transformed with pADH-HYR1 (ADH-HYR1), W303-1B transformed with the empty *ADH1* expression vector (ADH Vector), untransformed W303-1B (Untransfor.), untransformed *C. albicans* CAI4 growing in the yeast form (Yeast: Untransfor.), CAI4 transformed with the empty *ADH1* expression vector and growing in the yeast form (Yeast: ADH Vector), CAI4 transformed with pADH-HYR1 and growing in the yeast form (Yeast: ADH-HYR1), and *C. albicans* 3153A growing in the yeast form (yeast) and the hyphal form (Hypha). All lanes in this composite figure were taken from the same Northern gel; an underexposed autoradiograph was used because of the high *HYR1* mRNA levels in *S. cerevisiae*.

pADH-HYR1 transformants was observed. *HYR1* expression had no significant effect upon their growth rate, did not force the growth of pseudohyphae (11, 23), and did not promote increased self-agglutination of yeast cells.

DISCUSSION

We isolated and characterized the *HYR1* gene because it is one of only three morphogenetically regulated *C. albicans* genes characterized to date. We define these as genes that have been shown to be expressed specifically in response to the yeast-to-hypha transition. *HYR1* fulfils this criterion, the mRNA being detected only in cultures forming germ tubes and expression being independent of the method used to induce hyphal growth (Fig. 2). A recent report describes *HWP1* which encodes a hypha-specific cell surface protein that differs from Hyr1p in several respects (63). For example, Hwp1p contains numerous proline- and glutamate-rich repeats and does not appear to be N glycosylated. The expression of *ECE1*, which encodes a nonessential intracellular protein of unknown function, correlates with the elongation of hyphal cells, irrespective of the induction conditions (4).

Other *C. albicans* genes are induced during hyphal development, but only under certain specific conditions. These include the pH-responsive gene *PHR1* (54), the serum-induced genes *SAP2*, *SAP4*, *SAP5*, and *SAP6*, encoding secretory aspartyl proteinases (29), and the *ALS1* gene, which is induced in the defined medium RPMI (28). The expression of many other *C. albicans* genes fluctuates in response to the inducing conditions during the yeast-to-hypha transition rather than to morphogenesis itself. These genes encode proteins involved in wide-ranging functions such as glycolysis (*ADH1*, *PYK1*, *GPM1*, and *PGK1* [67]), protein synthesis and folding (*TEF3*, *RP10*, and *HSP90* [65, 66, 69]), cell wall biosynthesis (*CHS1*, *CHS2*, *CHS3*, and *GFA1* [10, 24, 59]), and formation of the cytoskeleton (*ACT1* [13, 66]). We know of only one *C. albicans* mRNA (*HST7*) that remains at relatively constant levels during the yeast-to-hypha transition. This low-abundance mRNA encodes a mitogen-activated protein kinase kinase homolog probably involved in intracellular signalling (11). These findings support the conclusion, based on a two-dimensional gel analysis of proteins from the yeast and hyphal cells, that only a small number of *C. albicans* proteins are form specific (20).

The predicted amino acid sequence of Hyr1p has provided some clues about its possible function. Although no homologs exist in the databases, Hyr1p shares several features with known yeast cell wall proteins, namely, a putative N-terminal signal sequence, a putative C-terminal GPI-anchoring domain, and a serine- and threonine-rich domain (Fig. 8). The *S. cerevisiae* proteins Gas1p (43, 74), Flo1p (70), Agα1p (37, 79), Aga1p (47), and Cwp1p, Cwp2p, and Tip1p (77) all contain these features, as does Phr1p from *C. albicans* (54). All of these proteins reside at the cell surface.

Gas1p and Phr1p are structural (43, 74) and functional (75) homologs. *C. albicans* Δ*phr1*/Δ*phr1* mutants display reduced virulence (22) as well as defects in the formation of germ tubes and yeast buds: enlarged, rounded, and multibudded cells are formed at the restrictive pH (54). This conditional phenotype is observed at the alkaline pHs at which *PHR1* is normally expressed. Deletion of *GAS1* yields similar, if unconditional, morphological defects in *S. cerevisiae* (46) which may arise indirectly through the aberrant targeting or processing of other proteins (43). Significantly, *GAS1* has been shown to encode an abundant N-glycosylated and O-glycosylated cell surface protein (76), the function of which is dependent on its C-terminal GPI-anchoring domain (43).

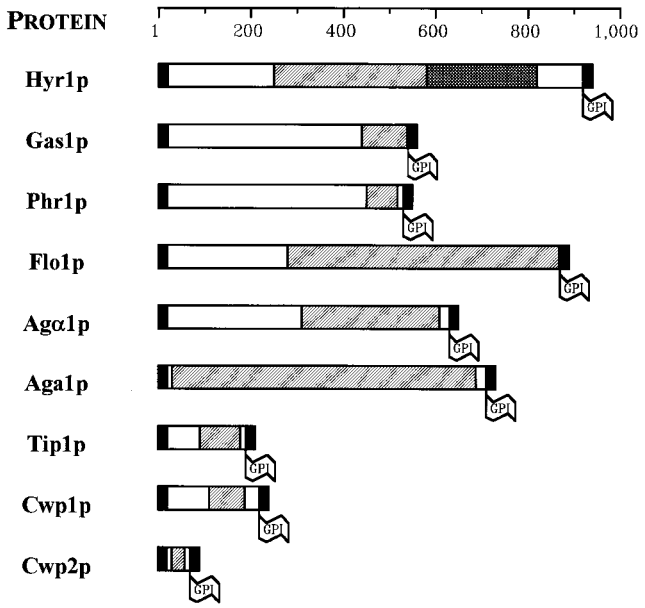

FIG. 8. Hyr1p belongs to a family of yeast cell surface proteins containing N-terminal signal sequences, C-terminal GPI-anchoring domains, and serine- and threonine-rich regions. Each protein sequence is represented diagramatically by a rectangle (approximately to scale [see scale, in amino acid residues, above constructs]; the N terminus is oriented to the left). Signal sequences are represented by the solid boxes at the N termini, and GPI-anchoring domains are illustrated at the C termini as solid boxes with the flag (GPI) below. Serine- and threonine-rich regions are shown as hatched boxes. More than 40% of the residues in these domains are serine or threonine. Hyr1p contains a second region (shaded box) rich in asparagine, serine, and glycine (79% of residues) (Fig. 3). The proteins shown are discussed in references as follows: Hyr1p, this work; Gas1p, Nuoffer et al. (43); Phr1p, Saporito-Irwin et al. (54); Flo1p, Teunissen et al. (70); Agα1p, Lipke et al. (37); Aga1p, Roy et al. (47); and Tip1p, Cwp1p, and Cwp2p, Van Der Vaart et al. (77).

S. cerevisiae Cwp1p, Cwp2p, and Tip1p contain the three main features associated with the family of cell wall proteins shown in Fig. 8, and all three proteins have been shown to correspond to specific glucanase-extractable cell wall proteins (77). Disruption of the *CWP1*, *CWP2*, or *TIP1* gene generates cell wall phenotypes of various intensities, with the *cwp2* mutant showing a significant decrease in the thickness of the electron-dense mannoprotein layer of the yeast cell wall (77).

Flo1p is thought to reside at the *S. cerevisiae* cell surface, stimulating flocculation (or self-aggregation). This protein carries an N-terminal signal sequence and a GPI-anchoring domain and is serine and threonine rich (70). Several repeated motifs appear in the amino acid sequence, one of which might be associated with *FLO1* deletions that affect the ability of host cells to flocculate.

The C-terminal region of *S. cerevisiae* α-agglutinin (encoded by the *AGα1* gene [37]) can direct a heterologous protein to the yeast cell wall (56). Significantly, this C-terminal region is serine and threonine rich and contains a GPI-anchoring domain (37, 79). *S. cerevisiae* Aga1p carries analogous domains (47). This protein appears to be required for the cell surface attachment of **a**-agglutinin since both **a**-agglutinin and the **a**-agglutinin binding subunit are still secreted by *aga1* mutants. Hence, *AGA1* is thought to encode a core subunit of **a**-agglutinin, located at the cell surface (47). A related gene in *C. albicans* has been identified (28). This gene (*ALS1*) appears to encode a secreted, GPI-anchored, serine- and threonine-rich protein which might play a role in the adherence of this asexual yeast to host tissue. However, since no supportive biochemical

or genetic data regarding its cell surface location are available (28), Als1p has not been included in Fig. 8. Nevertheless, it seems likely that Als1p, like Hyr1p, might belong to this family of cell surface glycoproteins.

Hyr1p displays the key features of the protein family shown in Fig. 8, including the serine- and threonine-rich domain which is probably O glycosylated. However, Hyr1p does not show significant sequence similarity to any members of this protein family, and Hyr1p differs from them with respect to the additional asparagine-, glycine-, and serine-rich domain near its C terminus. This domain contains seven copies of the repeated sequence asparagine-glutamate-glycine-serine (NEGS), the significance of which is not known, and it includes numerous potential sites for N glycosylation (Fig. 8). We speculate, therefore, that *HYR1* encodes a hypha-specific cell surface glycoprotein. By analogy with other well-characterized yeast cell wall proteins, Hyr1p might enter the secretory pathway where it might become decorated by N glycosylation and O glycosylation (32) and attached to the membrane via a GPI anchor (19, 73).

The lack of obvious phenotypes for the *HYR1* mutants is not inconsistent with the idea that Hyr1p is a structural component of the hyphal cell wall. The lack of an obvious phenotype for the *C. albicans* Δ*hyr1*/Δ*hyr1* mutant can be explained if Hyr1p provides a nonessential function for the construction of hyphal cell walls, or if, like *CHS2* (25), *HYR1* provides a function overlapping with that of some other cell wall component. Similarly, the aberrant expression of a structural protein (when the *ADH1-HYR1* fusion was used) was unlikely to force hyphal development under conditions which favor the growth of *C. albicans* yeast cells. Finally, the fact that the *ADH1-HYR1* fusion did not affect the self-agglutination of *C. albicans* or *S. cerevisiae* yeast cells suggests that Hyr1p is distinct from a previously isolated *C. albicans* genomic fragment which can promote the self-aggregation of *S. cerevisiae* cells (2).

Whatever the function of *HYR1*, the tight regulation of this gene in response to the yeast-to-hypha transition provides an important handle on morphogenetic regulation in *C. albicans*. Hence, the focus is now on the dissection of the *HYR1* promoter and the identification of the regulatory factors which mediate its transcriptional activation.

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