The Ess1 prolyl isomerase is dispensable for growth but required for virulence in Cryptococcus neoformans

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Cryptococcus neoformans is an important human fungal pathogen that also serves as a model for studies of fungal pathogenesis. C. neoformans contains several genes encoding peptidyl-prolyl cis/trans isomerases (PPIases), enzymes that catalyse changes in the folding and conformation of target proteins. Three distinct classes of PPIases have been identified: cyclophilins, FK506-binding proteins (FKBPs) and parvulins. This paper reports the cloning and characterization of ESS1, which is believed to be the first (and probably only) parvulin-class PPIase in C. neoformans. It is shown that ESS1 from C. neoformans is structurally and functionally homologous to ESS1 from Saccharomyces cerevisiae, which encodes an essential PPIase that interacts with RNA polymerase II and plays a role in transcription. In C. neoformans, ESS1 was found to be dispensable for growth, haploid fruiting and capsule formation. However, ESS1 was required for virulence in a murine model of cryptococcosis. Loss of virulence might have been due to the defects in melanin and urease production observed in ess1 mutants, or to defects in transcription of as-yet-unidentified virulence genes. The fact that Ess1 is not essential in C. neoformans suggests that, in this organism, some of its functions might be subsumed by other prolyl isomerases, in particular, cyclophilins Cpa1 or Cpa2. This is supported by the finding that ess1 mutants were hypersensitive to cyclosporin A. C. neoformans might therefore be a useful organism in which to investigate crosstalk among different families of prolyl isomerases.

INTRODUCTION

Cryptococcus neoformans is an opportunistic fungal pathogen that occurs worldwide and causes fatal nervous system infections, predominantly in immunocompromised individuals (Mitchell & Perfect, 1995). It is a basidiomycete; sexual reproduction involves the formation of a specialized structure (basidium) in which nuclear fusion, meiosis and spore formation occur to generate infectious basidiospores. The diploid phase is transient and the cells grow vegetatively as haploids. C. neoformans also differentiates to produce several enzymes and structures that are crucial for virulence in animal models of cryptococcal meningitis. For example, production of the pigment melanin is important for virulence and is thought to protect the organism from toxic oxygen radicals produced by host phagocytes (Kozel, 1995), while production of the metalloenzyme urease, which catalyses the hydrolysis of urea to ammonia and carbamate, may function by altering host immune function (Cox et al., 2000). A prominent structure associated with virulence is the polysaccharide capsule, which inhibits phagocytosis by host monocytes or macrophages (Fromtling et al., 1982; Kozel & Casin, 1971; Chang & Kwon-Chung, 1994).

Peptidyl-prolyl cis/trans isomerases (PPIases) catalyse the interconversion between cis and trans forms of the peptide bond preceding proline residues in proteins (Fischer, 1994; Fischer et al., 1998; Schiene & Fischer, 2000). Conformational isomerization by PPIases is thought to control the activity of target proteins and their ability to interact with other proteins to form complexes (Schmid et al., 1993; Hunter, 1998). Three families of PPIases that differ in structure and substrate specificity are known: the cyclophilins, the FK506-binding proteins (FKBPs) and the parvulins (Dolinski & Heitman, 1997; Arévalo-Rodríguez et al., 2004). The PPIase activity of cyclophilin A is potently inhibited by the immunosuppressive drug cyclosporin A (CsA).
(Handschumacher et al., 1984; Takahashi et al., 1989). In C. neoformans, there are two cyclophilin A homologues, encoded by linked genes, CPA1 and CPA2 (Wang et al., 2001). Mutations in CPA1 and CPA2 confer a spectrum of cell growth, mating and virulence phenotypes that indicate the homologues have distinct but overlapping roles in C. neoformans (Wang et al., 2001). The second class of PPlases, the FKBP5s, are inhibited by the immunosuppressants FK506 and rapamycin, drugs which also show antifungal activity. In C. neoformans, disruption of the FKBPI2 gene confers rapamycin and FK506 resistance but has no effect on growth, differentiation or virulence of C. neoformans (Cruz et al., 1999, 2001). Prior to this report, no parvulin-class PPlases had to our knowledge been identified in C. neoformans.

Parvulin-class PPlases are named after an Escherichia coli protein called parvulin (Rahfeld et al., 1994). The first eukaryotic parvulin to be discovered was the Ess1 protein from Saccharomyces cerevisiae (Hanes et al., 1989; Hani et al., 1995). Ess1 is the only PPlase that is essential for growth in S. cerevisiae (Hanes et al., 1989; Dolinski et al., 1997). Cells depleted of Ess1 arrest in mitosis and undergo nuclear fragmentation (Lu et al., 1996; Wu et al., 2000). Some evidence suggests that Ess1 and its homologue in humans, Pin1, interact with cell cycle proteins to control mitotic progression (Crenshaw et al., 1998; Shen et al., 1998; Stukenberg & Kirschner, 2001), while other evidence shows that Ess1 binds to the carboxy-terminal domain (CTD) of the large subunit of RNA polymerase II and is important for mRNA transcription (Morris et al., 1999; Wu et al., 2000, 2001). It is thought that Ess1-mediated isomerization of the CTD controls multiple steps in transcription, including initiation and elongation, and pre-mRNA processing (Shaw, 2002; Wu et al., 2003; Xu et al., 2003; Wilcox et al., 2004).

Ess1 homologues have been studied in metazoa such as Drosophila melanogaster (Maleszka et al., 1996; Hsu et al., 2001), Xenopus (Winkler et al., 2000), mice and humans (Fujimori et al., 1999; Lu et al., 1996). In most of these organisms, Ess1/Pin1 is not essential for growth. However, in two other fungi, Candida albicans and Aspergillus nidulans, Ess1 was shown to be essential (Devasahayam et al., 2002; Joseph et al., 2004). In C. albicans, mutants with a reduced gene dosage showed defects in filamentation (Devasahayam et al., 2002) and reduced virulence in a mouse model of candidiasis (Li et al., 2005). Here, we sought to identify an Ess1/Pin1 homologue in C. neoformans, a distantly related human fungal pathogen, and to characterize its requirement for growth, differentiation and virulence. Unlike the case for S. cerevisiae and C. albicans, disruption of ESS1 in C. neoformans was not lethal. No defects were observed in growth rate, capsule formation, response to mating pheromones, or haploid fruiting. However, ess1Δ mutants were avirulent when tested in a murine model of cryptococcosis, and showed reduced levels of melanin production and urease activity, factors known to be important for virulence (Salas et al., 1996; Cox et al., 2000). These results, together with studies in C. albicans, suggest that the Ess1 PPlase might be a useful target for the development of broad-spectrum antifungal drugs.

**METHODS**

**Strains, media and transformations.** Strains used in this paper are listed in Table 1. Standard yeast media, i.e. YPD (yeast extract peptone glucose [dextrose]), and CSM (complete synthetic medium) with relevant amino-acid dropouts were made as described by Guthrie & Fink (1991). Niger seed agar (Alspaugh et al., 1997; Salkin, 1979), urea agar (McGinnis, 1980), and limited-iron medium with EDTA and bathophenanthroline disulfonic acid (Pierini & Doering, 2001) were used for detecting melanin production, urease activity, and capsule formation, respectively. S. cerevisiae transformations were done using the standard lithium acetate procedure (Ito et al., 1983) and C. neoformans transformations were done using biolistic DNA delivery as described by Toffaletti et al. (1993) and Davidson et al. (2000). For biolistic transformation, approximately 5 µg linear DNA was used and transformants were selected on CSM lacking uracil. Cyclosporin A solution (Novartis) was a gift of Dr David Porter (University of Pennsylvania Medical Center, Philadelphia, PA, USA). FK520 was purchased from Calbiochem and dissolved in DMSO.

**Identification, cloning and sequence analysis of the C. neoformans ESS1 gene.** The C. neoformans ESS1 gene was identified using BLAST on the genome sequence at the Stanford Genome Technology Center Genome Project (http://www-sequence.stanford.edu/group/C.neoformans). Oligonucleotides with the sequences 5′-GGAAATTCATATGTCATACAACGGTTGGAGATTC-3′ and 5′-TCATATCCGACCACTTGTGATTTCCATAGCCGTTC-3′ were synthesized and used to amplify the ESS1 gene by PCR from C. neoformans B-3501 genomic DNA. Standard reaction conditions were used (94°C 1 min, 59°C 45 s, 72°C 1 min) and a fragment of approximately 0.7 kb was amplified, cloned and sequenced. Two introns in the ESS1 gene were identified by alignment of the predicted Ess1 protein with other members of Ess1 family of parvulin-class prolyl-isomerases: S. cerevisiae Ess1, C. albicans Ess1, A. nidulans PinA, Drosophila melanogaster Dodo and Homo sapiens Pin1. The introns were deleted using the ‘gene splicing by overlap extension’ method (Horton et al., 1990) and the uninterrupted ORF cloned into the yeast expression vector pJG4-1 (Horton et al., 1990) and the uninterrupted ORF cloned into the yeast expression vector pJG4-1 (Horton et al., 1990). For biolistic transformation, approximately 5 µg linear DNA was used and transformants were selected on CSM lacking uracil. Cyclosporin A solution (Novartis) was a gift of Dr David Porter (University of Pennsylvania Medical Center, Philadelphia, PA, USA). FK520 was purchased from Calbiochem and dissolved in DMSO.

**S. cerevisiae strain construction.** To construct haploid strain YPR-57 (ess1Δ::His3 pGAD-CaESS1), a high-copy plasmid carrying C. albicans Ess1, pgd-CaESS1 (URA3) (Devasahayam et al., 2002), was transformed into the heterozygous Ess1/ess1Δ::His3 (YSH55) strain. Cells were induced to sporulate, tetrads dissected, and His+ Ura+ segregants were selected. To generate YPR-34 (ess1Δ::Ura3/ ESS1), a PCR product of the URA3 gene flanked by 46 nucleotides of homology to 5′ and 3′ ESS1 flanking sequences was transformed into diploid S. cerevisiae strain W303-1A × B and uracil prototrophs were selected. The ess1Δ::Ura3 disruption was confirmed by PCR.

**Complementation experiments.** The temperature-sensitive S. cerevisiae strain ess1H114aK (YGD-ts22W; Wu et al., 2000) was transformed with the plasmid pCnESS1-Δ, a positive-control vector (pRS424-Ess1, which contains a BantH–Xhol fragment of S. cerevisiae Ess1 from plasmid pRS413-Ess1), or vector alone (pG4-1ΔE),
Table 1. Strains used in this study

<table>
<thead>
<tr>
<th>Strain</th>
<th>Parent</th>
<th>Genotype</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. cerevisiae</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>W303-1A × B</td>
<td>MATa/MATα ura3-1/ura3-1 leu2-3,112/leu2-3,112 trp1-1/trp1-1 can1-100/can1-100 ade2-1/ade2-1 his3-11/his3-11 [phi+]</td>
<td>R. Rothstein*</td>
<td></td>
</tr>
<tr>
<td>YSH-55</td>
<td>W303-1AxB</td>
<td>MATa/MATα ade2-1/ade2-1 can1-100/can1-100 his3-11,15/his3-11,15 leu2-3,112/LEU2 ura3-1/ura3-1 ESSI/ESSIΔ:: HIS3</td>
<td>Wu et al. (2000)</td>
</tr>
<tr>
<td>YGD-ts22W</td>
<td>W303-1A</td>
<td>MATa ura3-1/ura3-1 trp1-1/trp1-1 can1-100/can1-100 ade2-1/ade2-1 his3-11,15 [phi+] ess1-H164R</td>
<td>Wu et al. (2000)</td>
</tr>
<tr>
<td>YPR-57</td>
<td>YSH-55</td>
<td>MATa ade2-1 can1-100 his3-11,15 leu2-3,112/LEU2 ura3-1 ess1Δ:: HIS3 + pCaESS1</td>
<td>This study</td>
</tr>
<tr>
<td>YPR-34</td>
<td>W303-1A × B</td>
<td>MATa/MATα ura3-1/ura3-1 leu2-3,112/leu2-3,112 trp1-1/trp1-1 can1-100/can1-100 ade2-1/ade2-1 his3-11/his3-11 ESSI/ESSIΔ:: URA3</td>
<td>This study</td>
</tr>
<tr>
<td>C. neoformans var. neoformans (serotype D)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>B-3501</td>
<td>Wild-type MATα</td>
<td></td>
<td>Kwon-Chung (1978)</td>
</tr>
<tr>
<td>JEC21</td>
<td>Wild-type MATα</td>
<td></td>
<td>Kwon-Chung et al. (1992a)</td>
</tr>
<tr>
<td>JEC20</td>
<td>Wild-type MATα</td>
<td></td>
<td>Kwon-Chung et al. (1992a)</td>
</tr>
<tr>
<td>JEC43</td>
<td>JEC21</td>
<td>MATα ura5</td>
<td>Moore &amp; Edman (1993)</td>
</tr>
<tr>
<td>CnPR68</td>
<td>JEC43</td>
<td>MATα ura5 ess1:: URA5</td>
<td>This study</td>
</tr>
<tr>
<td>CnPR37</td>
<td>CnPR68</td>
<td>MATα ura5 ess1:: ura5</td>
<td>This study</td>
</tr>
<tr>
<td>CnPR170</td>
<td>CnPR37</td>
<td>MATα ura5 ess1:: ura5 ESSI:: URA5</td>
<td>This study</td>
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</tbody>
</table>

*Columbia University, New York, USA.

and the ability of cells to grow at the restrictive temperature (37°C) was tested by streaking on appropriate solid media. For plasmid curing experiments, a haploid S. cerevisiae ess1 deletion strain, YPR-57, carrying a plasmid-borne copy of ESSI was transformed with pCnESS1-ΔI. Transforms were serially passaged in liquid CSM lacking tryptophan for 3 days, i.e. selecting for the pCnESS1-ΔI (TRP1) but not for the pGD-CaESS1 (URA3) plasmid. Cells were plated and the phenotypes of individual colonies were scored by replica-plating to appropriate selective media. For segregation analysis, the heterozygous disruption strain YPR-34 (ess1Δ:: URA3/ESSI) was transformed with pCnESS1-ΔI. Cells were induced to undergo sporulation on 1% potassium acetate plates, tetrads were dissected and haploid segregants were grown on rich medium. Growth was scored after 3 days, and segregation of the Ura⁺ and Trp⁺ phenotypes monitored by replica-plating to detect presence of the ess1:: URA3 disruption and the pCnESS1-ΔI plasmid (TRP1) respectively.

**Disruption of ESSI in C. neoformans and reconstitution of mutant strains.** The ESSI gene was disrupted by homologous recombination using an ess1:: URA3 disruption allele. To generate the disruption allele the following strategy was used. A 2-0 kb fragment containing the C. neoformans URA5 gene was PCR amplified from C. neoformans B-3501 genomic DNA. The primers used incorporated SpeI and MfeI sites at the 5' and 3' ends of URA5, respectively. The fragment was digested with these enzymes and cloned into the same sites of plasmid pUC-CnESS1-Spel. pUC-CnESS1-Spel contains a modified version of ESSI in which the initiator codon was destroyed and replaced with stop codons in all three frames and included a SpeI cloning site (P. Ren & S. D. Hanes, unpublished). The final disruption construct, pUC-CnESS1-URA5, replaces the first 124 nucleotides of the ESSI ORF with the URA5 gene. To use this disruption construct, a 4-1 kb fragment was released by EcoRI and XhoI digestion and used for biolistic transformation of JEC43.

Uracil-protoprototrophic transforms were selected and colony purified. Approximately 60 transforms per µg DNA were obtained. As determined by PCR and Southern analysis, about 1% of the transforms carried homologous gene replacements at the ESSI locus, resulting in strain CnPR68.

A CnPR68 ura5 prototrophic revertant, CnPR37, was obtained by counterselection using 5-fluoroorotic acid (5-FOA) medium (Kwon-Chung et al., 1992b). Strain CnPR37 was used to generate a reconstituted strain by biolistic transformation with plasmid pCn-tel-CnESS1 that was linearized with NotI. pCn-tel-CnESS1 was constructed by insertion of a 2-kb EcoRI–BamHI fragment (consisting of 1-4 kb of upstream untranslated region plus 0-7 kb of the C. neoformans ESSI gene) into plasmid pCn-tel1. pCn-tel1 contains a URA5 selection marker and was kindly supplied by Ping Wang and Joseph Heitman (Duke University, Durham, NC, USA; Davidson et al., 2000; Edman & Kwon-Chung, 1990). The 2-1 kb fragment had been obtained by PCR from C. neoformans B-3501 genomic DNA. The DNA sequence of the C. neoformans ESSI gene in this construct was confirmed by sequence analysis. In the reconstituted strain, CnPR170, the NotI-linearized pCn-tel-CnESS1 was integrated at random into the genome (i.e. not at the ess1:: ura5 locus). The integrated copy of ESSI contained its own promotor region so that it could be expressed normally. The presence of intact ESSI in the reconstituted strain was confirmed using four PCR reactions with different sets of primers.

**Cell morphology, capsule formation, melanin production and urease biosynthesis assays.** To observe the cell morphology, cells were incubated in YPD broth at 25°C to mid-exponential phase and photographed at ×400 magnification using a compound microscope equipped with a digital camera. For capsule formation, the wild-type, ess1 mutant and ess1 + ESSI reconstituted strains were
inoculated into 10 ml limited-iron medium with 100 μM EDTA and 100 μM bathophenanthroline disulphonic acid, and incubated at 30°C for 5 to 7 days with agitation. Cells from these cultures were mixed with a standard India ink preparation and photographed (×400 magnification). To detect melanin or urease production, wild-type, ess1 mutant and ess1+ESS1 reconstituted strains were freshly cultured to mid-exponential phase in YPD broth, and 5 μl of each culture was spotted onto Niger seed agar medium and incubated for 4 days at 30°C, or onto urea agar medium for 2 days at 30°C, respectively.

Virulence in a mouse model of cryptococcal meningitis. Cells of wild-type strain (JEC21), the ess1 mutant strain (CnPR68) and the reconstituted strain (CnPR170) were grown to mid-exponential phase in liquid YPD medium and washed and resuspended in 15 mM PBS. BALB/c male mice (Jackson Laboratory, Bar Harbour, ME, USA, six in a group for each strain) weighing 20–25 g (about 6–8 weeks old) obtained from the Griffin Laboratory (Wadsworth Center) were infected by lateral tail vein injection using 100 μl C. neoformans at 10⁷ cells ml⁻¹. The cell concentrations were determined using a haemocytometer before injection and confirmed by

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**Fig. 1.** (a) Alignment of C. neoformans Ess1 (AF533511) with selected members of the Ess1 family of parvulin-class prolyl isomerases. Dashes indicate gaps. Shaded areas indicate regions of identity with the C. neoformans protein or identity among others. The signature tryptophans of the WW domain (Trp6 and Trp29), and conserved residues Tyr18 and Pro32, are indicated by dots. (b) Phylogenetic relationship among Ess1/Pin1 sequences. The phylogenetic tree is derived using a bootstrap method with neighbour-joining. The numbers are the bootstrap values given as a percentage of 1000 replications (1000 trials). Organism sources and NCBI database accession numbers for the sequences are: C. neoformans Ess1 (AF533511), S. cerevisiae Ess1 (S52764), Ca. albicans Ess1 (AAK00626), A. nidulans PINA (AAC49984), Sch. pombe Pin1 (NP_587913), D. melanogaster Dodo (P54353), M. musculus Pin1 (BAB22743) and H. sapiens Pin1 (NP_006212). The asterisk (*) indicates organisms in which Ess1 has been shown to be essential for cell growth and viability.
plating 100 μl of 10⁻⁴ dilutions of cell suspensions onto YPD plates. Mice were monitored once daily and those that were moribund or in apparent discomfort were sacrificed by CO₂ inhalation. Survival was analysed using the Kaplan–Meier method with SAS software, version 6.12 (SAS Institute, Cary, NC, USA). Brain tissue pieces dissected from the dead mice were spread on Niger seed agar medium and incubated at 30 °C for 5 to 7 days to detect the presence of C. neoformans by microscopic examination after staining with India ink. To confirm the presence of the ess1::URA5 disruption allele in strains from infected brains, colony isolates were subjected to diagnostic PCR.

RESULTS

Isolation of the C. neoformans homologue of ESS1

C. neoformans genomic DNA sequences were searched using BLAST for ORFs with similarity to S. cerevisiae Ess1 protein. A unique ORF was identified, and PCR primers were designed and used to amplify the corresponding DNA sequences (see Methods). No other ESS1-related sequences were identified. After conceptual removal of two small introns, of 50 bp and 64 bp, this region encoded a predicted protein of 178 aa with 39 % identity to S. cerevisiae Ess1, 38 % identity to Ca. albicans Ess1, 39 % to A. nidulans Pin1, 40 % to Drosophila Dodo and 42 % to human Pin1 (Fig. 1a). The overall structure of the encoded protein is conserved with that of all known Ess1/Pin1 homologues; it has an N-terminal WW domain, a short linker region (19 amino acids) and a C-terminal PPIase domain.

WW domains are proline-binding modules found in a variety of signalling proteins and are characterized by two precisely spaced tryptophan residues (Sudol, 1996). The predicted C. neoformans Ess1 protein contains these signature tryptophan residues, properly spaced (by 23 residues), along with other highly conserved residues (e.g. Tyr18 and Pro32 in C. neoformans Ess1). In the PPIase domain, the four putative active-site residues (His157, Cys113, His59 and Ser154 in Pin1) that are predicted on the basis of the crystal structure of human Pin1 (Ranganathan et al., 1997) are conserved (Fig. 1a; underlined residues). These features indicate that the C. neoformans ESS1 encodes a structural homologue of Ess1/Pin1.

To examine the evolutionary relatedness of the predicted C. neoformans Ess1 protein to Ess1/Pin1 homologues in other organisms, the protein sequences were analysed using the neighbour-joining method. We chose seven other fungal species and metazoan species for which at least some functional data on Ess1/Pin1 exist. In the resulting phylogenetic tree (Fig. 1b), the Ess1/Pin1 sequences clearly show the fungal clades to be distinct from those of the fly and mammals. Within the four ascomycetes species, S. cerevisiae and Ca. albicans were grouped in one clade and Schizosaccharomyces pombe and A. nidulans were grouped in another clade. That C. neoformans (a basidiomycete) appeared as a monophyletic group, a sister to the other four fungal species, was as expected. These results support the idea that C. neoformans Ess1 is homologous to Ess1/Pin1 proteins from other organisms.

C. neoformans ESS1 is the functional homologue of S. cerevisiae ESS1

Although the primary sequence features suggest that C. neoformans ESS1 encodes a homologue of Ess1/Pin1, it was necessary to demonstrate a conserved function. To do this, we tested whether C. neoformans ESS1 would functionally complement S. cerevisiae ess1 mutants. This was done using several different methods. After the two introns were deleted from the original isolate of the C. neoformans ESS1 gene (see Methods), the intron-less version, carried on an episomal plasmid (pCnESS1-ΔI), was introduced into a conditional-lethal strain of S. cerevisiae (ess1H164R; Wu et al., 2000). This strain cannot grow at the restrictive temperature of 37 °C due to a mutation in ESS1 (ess1H164R) that renders it temperature-sensitive. The non-growth phenotype of the S. cerevisiae temperature-sensitive strain was fully complemented at the restrictive temperature (37 °C) by the C. neoformans ESS1 gene (data not shown).

While these results are highly suggestive of functional homology, it could be argued that the C. neoformans ESS1-encoded protein (Ess1) was simply stabilizing or restoring the activity of the mutant ess1H164R protein. To rule out this possibility, we tested whether C. neoformans ESS1 could complement S. cerevisiae strains bearing a complete deletion of the ESS1 gene. Since ESS1 is essential in S. cerevisiae, certain manipulations were necessary to create the appropriate genetic background. First, the pCnESS1-ΔI plasmid was introduced into a heterozygous ess1 mutant strain of S. cerevisiae (ess1Δ::URA3/ESS1). The diploid cells were induced to undergo sporulation and the resulting tetrads were dissected. As expected, cells transformed with the vector alone showed a 2:2 segregation for viable: inviable spores (Table 2). In contrast, about half of the tetrads derived from diploids transformed with the pCnESS1-ΔI plasmid yielded a 4:0 segregation of viable: inviable spores.

Table 2. C. neoformans ESS1 complements an S. cerevisiae ess1Δ mutation during spore germination and outgrowth

<table>
<thead>
<tr>
<th>Plasmid</th>
<th>Tetrads dissected</th>
<th>Viable spores per tetrad</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Viable</td>
<td>1</td>
</tr>
<tr>
<td>Vector</td>
<td>40</td>
<td>2</td>
</tr>
<tr>
<td>pCnESS1-ΔI-1</td>
<td>60</td>
<td>1</td>
</tr>
<tr>
<td>pCnESS1-ΔI-2</td>
<td>60</td>
<td>0</td>
</tr>
</tbody>
</table>

Tetrad analysis of a heterozygous ESS1/ess1Δ::URA3 S. cerevisiae strain transformed with two isolates of plasmid pCnESS1-ΔI (TRP1) and induced to undergo sporulation. All viable spores that were Ura⁺ (i.e. ess1Δ) were also Trp⁺, indicating that they contained the complementing plasmid (data not shown).
Percentage loss of the pCaESS1 plasmid (URA3) in a haploid disruption strain (ess1Δ::HIS3) harbouring the indicated plasmid constructs (TRP1). Cells were grown in the absence of selection for the pCaESS1 plasmid for 2 days at 30°C and plated on medium containing 5-FOA.

### Table 3. C. neoformans ESS1 complements an S. cerevisiae ess1 Δ mutation in vegetatively growing cells

<table>
<thead>
<tr>
<th>Plasmid</th>
<th>His⁺</th>
<th>Trp⁺</th>
<th>Ura⁺</th>
<th>5-FOA⁻</th>
<th>Percentage loss of pCaESS1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vector</td>
<td>200</td>
<td>200</td>
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<tr>
<td>pCnESS1-ΔI-1</td>
<td>200</td>
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<tr>
<td>pCnESS1-ΔI-2</td>
<td>200</td>
<td>79</td>
<td>121</td>
<td>60.5</td>
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</table>

indicating that the C. neoformans ESS1 gene complements ess1Δ haploid cells to allow spore outgrowth and cell viability. Note that not all of these tetrads showed 4:0 segregation for viability. This was presumably due to failure of the plasmid to be uniformly maintained during sporeulation, a commonly observed phenomenon. As expected, all of the cells that carried the ess1::URA3 disruption (i.e. were Ura⁺) also carried the pCnESS1-ΔI plasmid (i.e. were Trp⁺; data not shown).

To test whether C. neoformans ESS1 complemented an S. cerevisiae deletion mutation (ess1Δ::HIS3) in vegetatively growing cells, we used plasmid shuffling (Table 3). Here, the pCnESS1-ΔI plasmid was introduced into ess1 deletion cells that carried a plasmid expressing Ca. albicans ESS1. Cells were then grown in the absence of selection for the Ca. albicans ESS1 plasmid, which carried a URA3 marker, and plated onto medium containing 5-FOA. If the C. neoformans ESS1 complements the ess1 deletion, then cells would lose the Ca. albicans ESS1 plasmid (URA3) and grow on 5-FOA medium (which selects against Ura⁺ cells). Indeed, this is what we observed. About 60% of cells showed growth on 5-FOA medium, indicating complementation by C. neoformans ESS1. Thus, the results of all three complementation tests indicate that C. neoformans ESS1 encodes a bona fide (functional) homologue of Ess1/Pin1.

**Fig. 2.** Isolation of ess1 mutant strains of C. neoformans.

(a) Schematic illustration of the ESS1 gene-specific disruption. The ess1::URA5 allele fragment was transformed into the ura5 strain JEC43. Also indicated are approximate positions of diagnostic PCR primers used in (b). (b, left panel) Verification of ess1 gene disruption mutant and reconstituted strains by PCR with ESS1 gene-specific primers. A band of 517 bp indicates an intact ESS1 gene. The large PCR product (~2.5 kb) predicted for the disruption strain is not made under these conditions. (b, right panel) Northern analysis showing the absence of ESS1 RNA in two ess1 mutant strain isolates. Twenty-five micrograms of total RNA was loaded per lane, and the same filter was probed sequentially with the indicated 32P-labelled probes. Film exposure was about five times longer and the specific activity was seven times higher for the ESS1 probe (~600 bp) vs the actin probe (~1400 bp). (c) Southern blot analysis of genomic DNA prepared from isogenic C. neoformans strains containing wild-type or mutant allele of ESS1. Genomic DNA was cleaved with EcoRI or PstI and electrophoresed in a 0.8% agarose gel. The same blot was probed sequentially with ESS1 and UR55 probes. Lanes 1 to 3 contain 1–2 μg EcoRI-digested genomic DNA and lanes 4 to 6 contain 1–2 μg PstI-digested genomic DNA from the following strains: (1, 4) wild-type C. neoformans JEC43; (2, 5 and 3, 6) two Ura5⁻ isolates of JEC43 generated by biolistic transformation with ess1::URA5 allele fragment. Using an ESS1 probe (left panel), the wild-type ESS1 gene yields a 4.4-kb EcoRI fragment and a 3.2-kb PstI fragment, and the ess1::URA5 disruption allele yields a 6.4-kb EcoRI fragment and 3.2-kb PstI fragment. Using a UR55 probe (right panel), the ess1::URA5 disruption allele yields a 6.4-kb EcoRI fragment and a 9.4-kb PstI fragment. The banding pattern using each of the two probes is as predicted by the restriction map based on genomic DNA sequence, thus confirming the expected genotypes.
The ESS1 gene is not essential in C. neoformans

To determine whether ESS1 is essential in C. neoformans, we disrupted it by homologous recombination (Fig. 2a). An ess1::URA5 disruption allele was transformed into a ura5 strain of C. neoformans (JEC43) by biolistic transformation. From a total of about 170 Ura+ transfectants, two isolates were identified that appeared to have undergone homologous recombination to generate ess1 mutations. The structure of the ESS1 genomic locus disrupted in these mutants was verified by PCR (Fig. 2b, left panel) and Southern analysis (Fig. 2c). In contrast to wild-type cells, neither of the mutants expressed ESS1 mRNA as indicated by Northern analysis (Fig. 2b, right panel). Since C. neoformans grows vegetatively as a haploid, our ability to recover mutants in which ESS1 is disrupted (and partially deleted, see Methods) indicates that the gene is not essential for growth of this organism under standard laboratory conditions.

We next generated reconstituted strains in which a wild-type copy of ESS1 with its own promoter region was integrated at random in the genome. Such strains served as important controls for characterizing ess1 mutant phenotypes and for in vivo virulence studies. To make reconstituted strains, the Ura+ phenotype was reverted by plating the ess1::URA5 mutants (two mutant isolates) onto 5-FOA-containing medium and selecting for Ura− cells. This procedure generates ura5 cells that can be reused for transformation with URA5-containing constructs. In our case, the revertants were used as recipients for transformation with a complementing linear DNA fragment containing ESS1 and a URA5 selectable marker. The presence of an intact copy of ESS1 was verified by PCR (Fig. 2b). Several reconstituted strains (ess1::ura5+ESS1) were generated, and the one that we used for most subsequent experiments is called CnPR170 (Table 1).

The reconstituted strain CnPR170 expressed ESS1 mRNA, but at a much lower level than that of wild-type cells (Fig. 2b, right panel). Other reconstituted strain isolates did not show detectable ESS1 mRNA (data not shown). The reason for the low expression is not known, but might be due to missing 5′ or 3′ regulatory sequences (or introns) in the construct we used, or to local repressive effects at the site(s) of insertion. The finding that even low levels of ESS1 expression in CnPR170 can rescue certain in vitro and in vivo phenotypes (see below) may not be surprising given results in S. cerevisiae, which show that Ess1 protein is present in vast excess over the levels required for its essential function (Gemmill et al., 2005).

ess1 mutants show normal growth, morphology and capsule formation

We next compared the C. neoformans mutants lacking a functional ESS1 gene with control strains (wild-type and the reconstituted strain) for general growth properties and the ability to express a standard set of virulence-associated traits. First, we examined the growth rate since slow-growing cells might not be expected to retain virulence in a host organism. The growth rate of ess1 mutants at three different temperatures appeared to be the same compared to the wild-type and the reconstituted strains (Fig. 3a). This can best be seen by comparing the slopes over the 3–4 log units that represent the linear portion of the growth curves. However, at higher temperatures (30 °C and 37 °C) the ess1 mutant cells appeared to reach saturation at slightly lower concentrations than did the wild-type or reconstituted strains. Second, cells were examined microscopically for morphological and capsule formation.
possible defects in overall morphology. No obvious defects could be discerned; cells still appeared normal in size and shape (Fig. 3b, upper panels). Third, we assayed the ability of ess1 mutants to undergo capsule formation, a key differentiation step required for virulence in vivo. Cells were induced to form capsules by growth on standard inducing medium and then stained with India ink. No defects in capsule formation were observed; the size of the capsules appeared to be the same between mutant and control strains (Fig. 3b, lower panels). Finally, we tested for the ability of ess1 mutants to undergo mating and haploid fruiting, and to generate pheromone-induced conjugation tubes. No changes compared to control strains were observed (data not shown). Thus, ess1 mutant cells behaved normally for several basic properties of growth and differentiation.

**ess1 mutants show defects in melanin production and urease activity**

In contrast to the results described above, disruption of ESS1 results in obvious defects in two important virulence-associated factors. As shown in Fig. 4(a) (upper panel), production of the pigment melanin is greatly reduced (or delayed) in the ess1 mutant as compared to the wild-type. That the defect is due to loss of ESS1 function is demonstrated by the fact that melanin production is at least partially restored in the reconstituted strain (CnPR170). Since melanin production is important for virulence, probably due to its role in helping cells resist oxygen-radical-induced killing by host macrophages (Liu et al., 1999), these results were the first hint that ess1 mutants might have a reduced virulence in vivo.

Melanin production depends on the metalloenzyme laccase, which is encoded by the gene LAC1. We therefore examined LAC1 expression in ess1 mutant cells. Surprisingly we found that LAC1 RNA levels appear to go up about threefold (relative to actin) in ess1 mutants vs wild-type cells. (Fig. 4c, upper panel). This result suggests that the defect in melanin production is due either to post-transcriptional defects in laccase activity (see below), or to defects in transcription of other genes (e.g. LAC2) also involved in melanin production (Pukkila-Worley et al., 2005).

Production of the enzyme urease, which is known to be required for virulence in animal models (Cox et al., 2000), was also reduced in ess1 mutant cells. A spot-test assay for urease activity showed that the ess1 mutant strains produce a much smaller zone of substrate utilization than do the wild-type or the reconstituted strain (Fig. 4b). Consistent with this decrease in activity, expression of the URE1 gene, which encodes urease, is reduced slightly (about twofold) in ess1 mutants vs wild-type cells (Fig. 4c, lower panel). As expected, URE1 levels were partially restored in the reconstituted strain.

In addition to direct transcriptional effects on LAC1 and URE1 genes, mutation of ESS1 might affect laccase and urease enzyme activity indirectly, for example, by affecting expression or function of genes such as VPH1, which encodes an intracellular vesicular proton pump. Both

![Fig. 4. C. neoformans Ess1 protein is required for melanin and urease biosynthesis. (a, b) The wild-type (JEC21), ess1 mutant (CnPR68) and ess1::ura5+ESS1 reconstituted (CnPR170) strains were grown as indicated. (a) For 4 days at 30 °C on Niger seed medium to assay melanin production (upper panel) or 5 days at 30 °C on Niger seed medium with 100 μM copper sulphate (lower panel). (b) For 2 days at 30 °C on urea agar to assay urease production. (c) Northern analysis of LAC1 and URE1 expression in wild-type, ess1 mutant and reconstituted strains. Cells were grown in asparagine (LAC1) or YPD (URE1) liquid medium at 30 °C to mid-exponential phase (Ikeda & Jacobson, 1992). The amount of total RNA used per lane was 21 μg (LAC1) or 25 μg (URE1). Probes used are indicated. The numbers indicate the fold change of LAC1 or URE3 vs wild-type, using an actin probe as a control. Values were based on mean density of signal determined using NIH IMAGE software.](image-url)
laccase and urease are metalloenzymes whose activities are greatly reduced in \textit{vph1} mutants (Erickson et al., 2001). The \textit{vph1} defect can be overcome by the addition of excess copper, which, for example, restores laccase activity allowing melanin production (Zhu et al., 2003). Addition of copper sulphate did not seem to restore melanin production to \textit{ess1} mutants (Fig. 4a, lower panel), indicating that the defect is not due to post-transcriptional defects in laccase metallation. The results suggest that \textit{VPH1} may not be affected in \textit{ess1} mutants, consistent with our finding that \textit{ess1} mutants generate normal-looking capsules, whereas no capsules are formed in \textit{vph1} mutants. Thus, some other defect(s) must occur in the pathway leading to melanin production.

These results and those shown in Fig. 3 show that some, but not all, of the standard virulence factors in \textit{C. neoformans} are affected by disruption of the \textit{ESS1} gene. Note that the levels of melanin and urease production are not completely restored in the reconstituted strain. This was not surprising given that the \textit{ESS1} mRNA levels in the reconstituted strain were much lower than in the wild-type (Fig. 2b).

**ESS1 is required for virulence**

We tested if \textit{ESS1} is required for virulence of \textit{C. neoformans} in a murine model of cryptococcosis. Each BALB/c animal was infected by lateral tail vein injection with $10^6$ \textit{C. neoformans} cells. The mean survival of these mice with the wild-type serotype D strain JEC21 was 56 days and all injected mice were moribund or dead after 72 days. In contrast, all mice injected with the \textit{ess1} mutant strain were still viable with no signs of sickness even after 100 days, at which time the experiment was ended. These results indicate that the virulence of the \textit{ess1} mutant strain is severely attenuated compared with the wild-type (Kaplan–Meier analysis log-rank, \(P<0.001\)). Consistent with the idea that the loss of virulence is due to the loss of \textit{ESS1} function, virulence was largely restored in the reconstituted strain (\textit{ess1::ura5+ESS1}) compared with the mutant (\(P<0.001\)).

Results showed that the mean survival of infection of the mice injected with the reconstituted strain was 74 days, and that all mice were moribund or dead after 80 days (Fig. 5). In summary, the results indicate that the \textit{C. neoformans} \textit{ESS1} gene is required for virulence in a murine model for cryptococcosis.

As expected, \textit{C. neoformans} cells were detected in brain tissue obtained post-mortem from mice infected with the wild-type or reconstituted strain. Surprisingly, brain tissue from mice infected with the \textit{ess1} mutant strain still contained \textit{C. neoformans} cells, although qualitatively they appeared to be in lower concentrations compared to brain tissue from mice infected with the wild-type or reconstituted strains (data not shown). These cells were white (no melanin production) and carried the mutant \textit{ess1::URA5} allele as detected by PCR, confirming that the cells were genetically similar to the injected cells. Thus, although some \textit{ess1} mutant cells persist in brain, they do not seem to cause overt disease.

**Ess1 and cyclophilins may have some overlapping functions**

Previous work in \textit{S. cerevisiae} had shown that overexpression of cyclophilin A suppresses \textit{ess1} mutations, and that under some conditions \textit{ess1} mutants are hypersensitive to the effects of the CsA, an inhibitor of cyclophilin A (Arevalo-Rodriguez et al., 2000; Wu et al., 2000). \textit{C. neoformans} is known to have two cyclophilin A homologues (Wang et al., 2001). We therefore tested whether CsA affected the growth of \textit{C. neoformans} \textit{ess1} mutant cells. As shown in Fig. 6(a), CsA strongly inhibited the growth of \textit{ess1} mutant cells as compared to wild-type control cells. At least some of the inhibitory effects of CsA were reversed by adding back a wild-type copy of the \textit{ESS1} gene, as in the reconstituted strain. We obtained similar results at 28°C (data not shown). In this plate assay, \textit{ess1} mutant cells grew slightly slower than the wild-type or the reconstituted strain, even without the addition of drug. However, the magnitude of this difference does not fully account for the CsA inhibitory effect. Note that this experiment was conducted at 25°C because calcineurin (a target of cyclophilins) becomes essential at 30–37°C, and therefore CsA inhibits cell growth even in wild-type cells at elevated temperature (Odom et al., 1997).

In control experiments, no such growth inhibitory effects were observed using the FK506 analogue (FK520), indicating that the effect was specific for cyclophilins.
DISCUSSION

In this study, we isolated and characterized the *C. neoformans* *ESS1* gene. This is believed to be the first study in which a parvulin-class PPIase has been described in this organism. Cyclophilin- and FKBP-class PPIases have been previously described (Cruz et al., 1999, 2001; Wang et al., 2001). We showed that *ESS1* is expressed in vegetatively growing cells but is not required for growth. Instead it appears to be required for differentiated functions and for virulence in *vivo*. Together with these previous reports, our results indicate that PPIases play a crucial role in specialized functions of *C. neoformans* and that at least two of the many PPIases identified by the sequencing of the *C. neoformans* genome are required for virulence of this organism (Cpa1 and Ess1).

The mechanism by which the Ess1 protein contributes to virulence in *C. neoformans* is not yet known. Our findings showed that mice infected with the *ess1* mutant continued to carry at least some viable *C. neoformans* cells, despite having no clinical signs of illness. These results are intriguing and indicate that *ess1* mutant cells can still colonize the brain, at least to some degree, but are unable to cause disease over the time-frame of our experiments (100 days). Thus, we suggest that *ess1* mutant cells have defects in differentiated functions related to disease progression, but this idea will require further investigation to confirm.

The exact function of *C. neoformans* Ess1 is not known. However, studies in the model organism *S. cerevisiae* would suggest that the molecular nature of the *ess1* defect is likely to involve gene-specific changes in transcription regulation. In *S. cerevisiae*, Ess1 binds to and regulates the function of RNA polymerase II (reviewed by Shaw, 2002; Arevalo-Rodriguez et al., 2004). It seems plausible, therefore, that expression of certain virulence-associated genes in *C. neoformans* might be affected by disruption of *ESS1*. Indeed, expression of *URE1*, which encodes an enzyme required for synthesis of urease, was reduced (albeit only twofold) in *ess1* mutant cells (Fig. 4c). In contrast, expression of *LAC1*, which is required for melanin production, showed an unexpected increase in *ess1* mutants. We note that it is possible that expression of the actin gene, which was used as a control, might also vary in *ess1* mutants. A more complete study of gene expression of virulence factors affected by *ess1* deletion could be accomplished by microarray analysis using the *C. neoformans* strains generated in this study.

*ESS1* was first identified as a gene essential for growth in *S. cerevisiae* (Hanes et al., 1989). However, in addition to its non-essentiality in *C. neoformans*, *ESS1* homologues are not essential in several other organisms (reviewed by Arevalo-Rodriguez et al., 2004), including fungi such as *Sch. pombe* (Huang et al., 2001). While functional studies of *ESS1/PIN1* have been undertaken only in a limited number of organisms, phylogenetic analysis using this small dataset (Fig. 1b) reveals that within the ascomycetes group, fungi are divided into two subgroups, one in which Ess1 is essential and one in which it is not essential. Since *C. neoformans* is a basidiomycete and is outside this group, perhaps it should not have been surprising that *ESS1* is not essential in this organism.
One explanation for the fact that ESS1 is essential in some organisms but not others is that under some circumstances, cyclophilin A can substitute for Ess1 (Areávalo-Rodríguez et al., 2000; Wu et al., 2000). These and other studies indicate that Ess1 and cyclophilin A exhibit crosstalk, i.e. that they possess partially overlapping functions (Fujimori et al., 2001). C. neoformans is very unusual in that it has two distinct cyclophilin A homologues, Cpa1 and Cpa2 (Wang et al., 2001). It is possible, therefore, that in ess1 mutant strains, the two cyclophilin A homologues might compensate for many, although not all, of the functions of Ess1 lost by gene disruption. Such an overlap in function might explain why ESS1 is not essential for growth in C. neoformans, despite playing an important role in virulence. Consistent with this idea, ess1 mutant cells were more sensitive than wild-type cells to the cyclophilin inhibitor CsA.

Interestingly, both ess1 and cpa1 cpa2 double mutants are defective in melanin synthesis, and in virulence in a mouse model (this study; Wang et al., 2001). These similarities, and the fact that both Ess1 and cyclophilin A homologues have been implicated in transcription (Areávalo-Rodríguez et al., 2000, 2004; Wu et al., 2000), support the idea of functional overlap. However, there are important differences. For example, unlike ess1 mutants, cpa1 cpa2 double mutants are also defective in capsule formation and mating, and are resistant to the effects of CsA (Wang et al., 2001). Thus, while some pathway overlap probably occurs, Ess1 and cyclophilins clearly have distinct functions in vivo. Further genetic analysis would be useful to investigate these differences.

Based on studies using another human fungal pathogen, Candida albicans, we proposed that parvulin-class PPIases such as Ess1 might be valuable targets for antifungal drug development (Devasahayam et al., 2002). Indeed, ESS1 appears to be important for virulence of Ca. albicans (G. Devasahayam, V. Chaturvedi & S. D. Hanes, unpublished). The present study demonstrates that ESS1 is also required for virulence of C. neoformans in at least one animal model system. It seems reasonable to predict that inhibitors of ESS1 might attenuate the virulence of C. neoformans in humans. Since Pin1, the vertebrate Ess1 homologue, does not appear to be essential in mammals (Fujimori et al., 1999), targeting this family of PPIases might be feasible for human therapeutic applications.

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