Antifungal Chemical Compounds Identified Using a C. elegans Pathogenicity Assay

The Harvard community has made this article openly available. Please share how this access benefits you. Your story matters

| Citation         | Breger, Julia, Beth Burgwyn Fuchs, George Aperis, Terence I. Moy, Frederick M. Ausubel, Eleftherios Mylonakis, and Brendan P. Cormack. 2007. Antifungal Chemical Compounds Identified Using a Pathogenicity Assay. PLoS Pathogens 3:e18. |
|------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Published Version| doi:10.1371/journal.ppat.0030018                                                                                                                                                                                                                           |
| Citable link     | http://nrs.harvard.edu/urn-3:HUL.InstRepos:4513032                                                                                                                                                                                                                      |
| Terms of Use     | This article was downloaded from Harvard University’s DASH repository, and is made available under the terms and conditions applicable to Other Posted Material, as set forth at http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA                                                                 |
Antifungal Chemical Compounds Identified Using a C. elegans Pathogenicity Assay

Julia Breger1, Beth Burgwyn Fuchs1, George Aperis1, Terence I. Moy2, Frederick M. Ausubel2-3, Eleftherios Mylonakis1*

1 Division of Infectious Diseases, Massachusetts General Hospital, Boston, Massachusetts, United States of America, 2 Department of Molecular Biology, Massachusetts General Hospital, Harvard Medical School, Boston, Massachusetts, United States of America, 3 Department of Genetics, Harvard Medical School, Boston, Massachusetts, United States of America

There is an urgent need for the development of new antifungal agents. A facile in vivo model that evaluates libraries of chemical compounds could solve some of the main obstacles in current antifungal discovery. We show that Candida albicans, as well as other Candida species, are ingested by Caenorhabditis elegans and establish a persistent lethal infection in the C. elegans intestinal track. Importantly, key components of Candida pathogenesis in mammals, such as filament formation, are also involved in nematode killing. We devised a Candida-mediated C. elegans assay that allows high-throughput in vivo screening of chemical libraries for antifungal activities, while synchronously screening against toxic compounds. The assay is performed in liquid media using standard 96-well plate technology and allows the study of C. albicans in non-planktonic form. A screen of 1,266 compounds with known pharmaceutical activities identified 15 (~1.2%) that prolonged survival of C. albicans-infected nematodes and inhibited in vivo filamentation of C. albicans. Two compounds identified in the screen, caffeic acid phenethyl ester, a major active component of honeybee propolis, and the fluoroquinolone agent enoxacin exhibited antifungal activity in a murine model of candidiasis. The whole-animal C. elegans assay may help to study the molecular basis of C. albicans pathogenesis and identify antifungal compounds that most likely would not be identified by in vitro screens that target fungal growth. Compounds identified in the screen that affect the virulence of Candida in vivo can potentially be used as “probe compounds” and may have antifungal activity against other fungi.

Introduction

The discovery of substantial commonality between microbial pathogenesis in mammals and nonvertebrate model hosts, such as the nematode Caenorhabditis elegans, has provided the foundation for the development of high-throughput genetic analysis of microbial virulence factors in live animal models (reviewed in [1,2]). We sought to extend the use of the C. elegans infection models to identify chemical compounds with antifungal activity against Candida species, the most common human pathogenic fungus.

Candida spp. are the fourth most common cause of nosocomial blood-stream infections, and disseminated candidiasis continues to have an attributable mortality rate of over 25% [3]. The mortality rate for device-associated Candida infection can be even higher [4]. In the United States, the overall excess cost attributable to candidemia is estimated at $1 billion per year and the average cost of candidemia for a single episode is about $40,000 (1997 United States dollar) [5,6]. However, efforts to identify new antifungal compounds have been hindered by the fact that most compounds that have antifungal activity in vitro are also toxic to mammalian cells. A facile bioassay compatible with high-throughput screening technologies, which simultaneously evaluated libraries of chemical compounds for antifungal activity and host toxicity in the context of a whole-animal Candida infection model, could solve some of the main obstacles in current antifungal discovery.

Here, we show that Candida albicans, as well as other Candida strains, can kill C. elegans. We used these findings to develop a C. elegans-based infection model that is performed in standard 96-well plates in liquid media, thereby enabling automated addition of compounds. An important feature of the assay is that the first assay endpoint is nematode survival, which automatically eliminates highly toxic compounds that affect nematode viability. Moreover, important components of Candida pathogenesis in mammals are involved in nematode killing, and filamentation becomes apparent as the nematode dies, providing a second clinically relevant endpoint. We demonstrate how this model enables the screening of a chemical library for compounds that prolong nematode survival or inhibit Candida filamentation. Importantly, the screen identifies compounds that prolong survival in a hematogenous murine model of candidiasis.

Results

Killing of C. elegans by Candida Species

C. elegans nematodes eat microorganisms, but they die when fed a variety of human bacterial and fungal pathogens [1,2]. In

Copyright: © 2007 Breger et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Abbreviations: ATCC, American Type Culture Collection; BHI, brain-heart infusion; CAPE, caffeic acid phenethyl ester; CFU, colony-forming unit; GFP, green fluorescent protein; MIC, minimum inhibitory concentration; PBS, phosphate-buffered saline,YPD, yeast-peptone dextrose

* To whom correspondence should be addressed. E-mail: emylonakis@partners.org
Author Summary

_Candida_ spp. are among the most significant causes of nosocomial infections, and disseminated candidiasis continues to have an attributable mortality rate of over 25%. For this reason, we have developed a liquid media assay using the model nematode _Caenorhabditis elegans_ as a model organism for _Candida_ infection. The worms are infected on solid media lawns and then moved to pathogen-free liquid media. Unless antifungal compounds are added to the wells, the majority of worms die within 3–4 d. This model is similar to the infection process in humans, in that _Candida_ cells are able to produce filaments, which are essential for the infection process in humans. We used this pathogen model to create a semi-automated, high-throughput screen using _C. elegans_ to evaluate the antifungal effectiveness of many types of chemical compounds. Through this process, we have identified three compounds that we show have varying degrees of antifungal activity in _C. elegans_, in vitro, and in mice.

the laboratory, _C. elegans_–killing assays are typically carried out by transferring nematodes from lawns of _Escherichia coli_ strain OP50 (their normal laboratory food) to lawns of pathogenic bacteria or yeast grown on solid agar media. However, screening chemical libraries using an agar-based _C. elegans_–killing assay is not readily compatible with the use of robots for filling assay plates and pin transfer of compounds, homogeneous distribution of chemicals in the medium, or the use of automated plate readers or automated screening microscopes to monitor nematode survival. We therefore sought to develop a _C. elegans_–_Candida_ spp.–killing assay that could be performed in liquid media. We found that when wild-type L4 stage N2 nematodes were fed _Candida_ spp. on solid brain–heart infusion (BHI) medium for 2 h and then transferred to a liquid medium consisting of 20% BHI and 80% M9 minimal medium, the longevity of the worms was significantly reduced compared to worms not infected with _Candida_ (Figure 1A). We tested different times of exposure to _Candida_ spp. on solid BHI medium (from 5 min to 24 h) and in all cases the longevity of the worms was significantly reduced compared to uninfected worms (unpublished data).

Although _Candida_ spp. killed wild-type _C. elegans_ in liquid medium, the killing did not occur rapidly enough to prevent the production of progeny produced by 3- and 4-d-old hermaphroditic nematodes. The presence of a brood in the assay mix made it difficult to score the viability of the infected parents. Indeed, in the assay described above and shown in Figure 1A, it was necessary to painstakingly remove progeny nematodes that survived beyond the L1 or early L2 developmental stage. Production of progeny during the assay had another undesirable consequence in the scoring of the assay; namely, _Candida_–infected wild-type nematodes exhibited significant matricidal death (over 30%) involving the premature hatching of eggs in the _C. elegans_ uterus (which is not necessarily directly associated with an infectious-like process) around day 3 of the experiment. To avoid these problems associated with progeny production, we substituted _C. elegans_ glp-4 mutants for wild-type in the _Candida_ spp. killing assay. _C. elegans_ glp-4 mutant animals have normal morphology and brood sizes at 15 °C, but do not make gonads and are unable to produce eggs at 25 °C [7–10]. As shown in Figure 1A, _Candida_ spp. also killed _glp-4_ nematodes, but the rate of killing was significantly slower than for wild-type worms (Figure 1A), similar to results reported previously for the killing of glp-4 and other sterile mutants by bacterial pathogens.

Although glp-4 mutant worms could have potentially been used in an antifungal screening assay, we sought to increase the rate of killing of the glp-4 mutant by utilizing _glp-4;sek-1_ double mutant worms. _sek-1_ encodes a mitogen-activated protein kinase kinase that functions directly upstream of the _C. elegans_ homolog of the mammalian p38 mitogen-activated protein kinase that was shown previously to be an important component of the _C. elegans_ defense response to pathogens [7,11]. As shown in Figure 1A, the _C. elegans_ _glp-4;sek-1_ double mutant was significantly more susceptible to _Candida_ than the _glp-4_ mutant (p < 0.001), suggesting that the _C. elegans_ homolog of the mammalian p38 mitogen-activated protein kinase (which is involved in mammalian response to candidiasis [12]) plays a significant role in the _C. elegans_ response to _Candida_. This finding is consistent with the observation that _sek-1_ mutants are more susceptible to a variety of pathogens [7,11]. When _glp-4_ and _glp-4;sek-1_ mutants were moved from OP50 plates to pathogen-free liquid media, their survival was not significantly different from N2 worms in the presence of _E. coli_ in liquid media (unpublished data). Notably, when we exposed _glp-4;sek-1_ worms to DAY185 for 2 h and then moved them to lawns of an _E. coli_ OP50 strain that expresses green fluorescent protein (GFP), over 70% of the worms had no GFP-expressing bacteria in their intestine, suggesting that the grinder is still operational, at least in the majority of the nematodes. Because the _glp-4;sek-1_ mutant was similarly susceptible to a variety of _C. albicans_ strains as well as to the non- _C. albicans_ strains _Candida krusei_ and _Candida parapsilosis_ (Figure 1B), because it did not produce progeny, and because we found it compelling to study _Candida_ pathogenesis in immunocompromised nematodes (in some ways analogous to candidiasis in immunocompromised humans), we utilized the _glp-4;sek-1_ strain in all of the further studies described below.

**Progression of _Candida_ Filamentation within _C. elegans_**

_Candida_ yeast cells have the ability to develop filaments that are usually differentiated to hyphae (long continuous germ tubes separated by true septin rings) or pseudohyphae (chains of distinct cells that fail to separate). Development of human candidiasis involves adhesion to the substratum (which allows the yeast to colonize surfaces, such as the gastrointestinal tract and intravascular catheters), development of biofilm, and formation of hyphae and pseudohyphae [13–15]. Filamentation is instrumental in _Candida_ virulence in mammals; nonfilamentous mutants of _C. albicans_ are highly attenuated [16]. _Candida_ hyphae invade host tissues and exert mechanical force through cells and tissues, enabling escape of _C. albicans_ from the host bloodstream [17,18]. Notably, there is significant coregulation between adherence, biofilm, and filament pathways [15,19,20]. For example, genes involved in biofilm formation are required for hyphal development, while filaments are a prominent feature of _C. albicans_ biofilms that support biofilm integrity [4,21–23].

Persistence in the intestine appears to be a critical first step during _Candida_ infection in _C. elegans_. Indeed, nematodes exposed to _Candida_ lawns are unable to clear the _Candida_ infection when they are transferred to _Candida_-free liquid
Candida is important for filamentation, as it is not observed during Notably, it appears that the interface between solid and liquid alleles by homologous recombination (unpublished data).

suv3 and in killing between the wild-type and strains in which the wild-type strain DAY185). There was no significant difference 0.0001, respectively for the two mutants, compared to the of the yeast strains compared to control nematodes that were exposed to E. coli OP50 (∼65 nematodes/group).

doi:10.1371/journal.ppat.0030018.g001

(A) N2, glp-4, or glp-4;sek-1 L4 nematodes feeding on E. coli OP50 were transferred to C. albicans strain DAY185 for 2 h and then transferred to pathogen-free liquid media. Dead nematodes were counted and removed daily. N2 worms transferred from E. coli OP50 directly to liquid media were used as control. Survival of glp-4;sek-1 is significantly shorter compared to the strain glp-4 (p < 0.001).

(B) Survival of C. elegans glp-4;sek-1 feeding on lawns of C. albicans ATCC#90028, C. parapsilosis ATCC#20019, or C. krusei ATCC#6258, p < 0.001 for each of the yeast strains compared to control nematodes that were exposed to E. coli OP50 (∼65 nematodes/group).

doi:10.1371/journal.ppat.0030018.g002

media (Figures 2 and S1). Even when nematodes were exposed to Candida lawns for as little as 5 min and then transferred to pathogen-free liquid media or lawns of E. coli OP50, 100% of the nematodes remain colonized (unpublished data). As a result, Candida cells fill the nematode pharynx and intestine (Figure S1B and unpublished data). Also, we placed the worms on lawns of C. albicans strain MLR62, a strain that constitutively expresses GFP, and then we moved them onto the non-GFP parent strain DAY185. Over a 24-h period, the GFP-expressing Candida cells were displaced by non-GFP-expressing cells, suggesting that Candida cells are not too big to be defecated.

To evaluate the hypothesis that biofilm formation and filamentation are involved in C. elegans killing, we infected C. elegans with C. albicans kem1 and suv3 mutants that are defective in hyphal production [24]. As shown in Figure 3, C. elegans killing by kem1 (strain MLR74) and suv3 (strain GKO443) mutants was significantly attenuated compared to the isogenic parental strain DAY185 (p = 0.0008 and p < 0.0001, respectively for the two mutants, compared to the wild-type strain DAY185). There was no significant difference in killing between the wild-type and strains in which the kem1 and suv3 mutations had been reconstituted with wild-type alleles by homologous recombination (unpublished data). Notably, it appears that the interface between solid and liquid is important for filamentation, as it is not observed during Candida–C. elegans interaction on solid media (unpublished data and [25]). Because the C. albicans biofilm defective mutants that were used in our studies were also defective in filamentation, the study of the role of Candida biofilm in C. elegans pathogenesis requires further experimentation.

Interestingly, in the absence of C. elegans, none of the Candida species tested in the liquid assay formed filaments. Nevertheless, after nematodes died, extensive filamentation was observed in the colonized worms with numerous filaments exiting through the nematode cuticle (Figure 4A and 4B). Moreover, after the integrity of the cuticle was breached, the yeast cells did not dissipate within the liquid medium, but rather remained connected, resulting in C. elegans “ghosts” in which the transition from mostly yeast-like Candida cells to the filaments outlined where the cuticles used to be (Figure 4C–4F).

We used a C. albicans reporter strain that expresses yeast-enhanced GFP (yEGFP3) from the promoter for the gene Hyphal Wall Protein 1 (HWP1) to evaluate whether true hyphae are formed during the infectious process in C. elegans. This strain confers developmental expression of yEGFP3 in germ tubes and hyphae, but not in yeasts or pseudohyphae [18,26,27]. As shown in Figure 5, yEGFP3 expression was observed in filaments as they penetrated the nematode cuticle, confirming that C. albicans forms hyphae in the course of C. elegans infection. No yEGFP3 expression was detected prior to filamentation.

Figure 2. Intact C. albicans Cells Persist within the C. elegans Intestine

C. elegans strain glp-4;sek-1 L4 worms were transferred from OP50 to C. albicans for 30 min and then moved to Candida-free liquid media for 6 d when the worms were photographed. Intact yeast cells are seen within the (A) proximal and (B) distal intestine. White arrows in (A) point to the pharyngeal grinder organ. Black arrows point to the intestinal lumen. Scale bars are 31.58 μm.

doi:10.1371/journal.ppat.0030018.g002
Antifungals Prolong Nematode Survival

To develop a system that allows high-throughput screening for antifungal compounds, we first evaluated whether established antifungals prolong the survival of nematodes infected with *Candida* spp. For this, we used different *C. albicans* isolates as well as non-*C. albicans* strains, including those used as reference strains by clinical microbiology laboratories [28]. Notably, all strains tested were susceptible to amphotericin B and caspofungin, but had different susceptibilities to fluconazole [24,26,29,30] (Table 1). We found that antifungals that are active against a particular *Candida* strain resulted in prolongation of *C. elegans* survival when the nematodes were infected with the relevant *Candida* strain (Figure 6A–6D).

Caspofungin, a fungicidal agent that is active against *Candida* biofilm [31,32], and also the fungicidal agent amphotericin B, were the most active agents tested in prolonging nematode survival to *C. albicans* strain MLR62 (Figure 6A), *C. krusei* American Type Culture Collection (ATCC) #6258 (Figure 6B), *C. parapsilosis* ATCC#20019 (Figure 6C and 6D), and *C. albicans* ATCC#90028 (unpublished data). In the case of *C. krusei* ATCC#6258, the most resistant to fluconazole among the strains we tested, caspofungin and amphotericin B were more effective than fluconazole (in both cases *p* < 0.0001; Figure 6B). Antifungal agents were also effective at lower concentrations; for example, caspofungin was effective at concentrations as low as 1 µg/ml in the case of *C. albicans* strain MLR62 (*p* < 0.0001). Since filament formation was only seen after the *Candida* cells overwhelmed and killed the nematode, there were significantly fewer nematodes with filaments in the wells that contained antifungal compounds (unpublished data).

Interestingly, at high concentrations, the beneficial effect of fluconazole was lost and the nematodes died faster than untreated infected worms. Fluconazole up to 32 µg/ml was effective in prolonging survival of nematodes exposed to the fluconazole-susceptible strain *C. parapsilosis* ATCC#20019, but at higher concentrations (100 µg/ml) nematode survival was diminished, even compared to the nematodes in the untreated control group (*p* = 0.01; Figure 6D). Probably this toxicity is present at even lower concentrations, but the beneficial effect from the antifungal activity outweighs the toxic effect. For example, when nematodes were exposed to the fluconazole-resistant strain *C. krusei* ATCC#6258, fluconazole at 32 µg/ml not only had no effect on nematode survival, but killing in the fluconazole group was significantly faster than untreated worms (*p* = 0.02; Figure 6B). Taken together, these observations suggest that the *C. elegans–Candida* model can be used for the concurrent screen for antifungal activity and host toxicity.

We also evaluated the effect of antifungal agents in reducing fungal burden in the nematode intestine. For example, in a representative experiment, after 48 h, untreated *C. elegans* infected with *C. albicans* MLR62 had an average of 170.8 ± 63.5 colony-forming units (cfu) per worm, whereas caspofungin-treated animals (at 8 µg/ml) had almost cleared the infection with an average of 0.3 ± 0.2 cfu per worm (*p* < 0.001). Fluconazole and amphotericin B also significantly decreased the concentration of *Candida* cfu in the nematodes, and...
microscopic examination of the worms confirmed that treatment with antifungals was effective in clearing the worm intestine of visible Candida cells (unpublished data).

Antifungal Compounds Identified Using the C. elegans–Candida-Killing Assay

To facilitate adaptation of the C. elegans–Candida-killing assay to screening chemical libraries for antifungal compounds, we used C. albicans strain MLR62 that expresses GFP (linked to the constitutively active TEF1 promoter) and that exhibits similar killing kinetics to the parent strain DAY185 in the C. elegans assay. Using this strain, nematodes exposed to compounds that have significant antifungal efficacy exhibited sinusoidal movement and no green fluorescence in the intestine at the endpoint of the assay (Figure 7A), whereas nematodes exposed to compounds without antifungal efficacy did not move, were rod-shaped, exhibited high levels of intestinal fluorescence (Figure 7B), and developed filaments (Figure 7C).

As an initial test of the C. elegans–Candida compound screening assay, we utilized libraries of compounds made available through the Institute of Chemistry and Cell Biology (ICCB) at Harvard Medical School that include known compounds that affect diverse cellular pathways as well as the United States Food and Drug Administration approved drugs that are known to be safe and bioactive in humans.

Table 1. C. albicans Strains Used in This Study

| Candida Strain | Description | Relevant Characteristics or Phenotype | Reference |
|----------------|-------------|--------------------------------------|-----------|
| DAY185         | Arg⁺ Ura⁺ His⁺ reference strain | Forms meshwork comprised almost exclusively of long hyphae MIC: 0.5 μg/ml for amphotericin B, 2 μg/ml for fluconazole and caspofungin | [24] |
| MLR28          | KEM1 reconstituted strain | Restored the ability to form normal hyphae | [24] |
| GKO443         | suv3 | Biofilm-defective mutant that is defective in hypha production | [24] |
| MLR3           | SUV3 reconstituted strain | Produced thick biofilms containing hyphae and excluded calcofluor from the basal cell layers | [24] |
| MLR74          | kem1 deletion mutant | Biofilm-defective mutant that is defective in hypha production | [24] |
| MLR62          | GFP-expressing WT | GFP gene linked to the constitutively active TEF1 promoter | [29] |
| C. albicans ATCC#90028 WT | Isolated from blood, Iowa MIC: 2 μg/ml for amphotericin B and 1 μg/ml for caspofungin | [28] |
| C. krusei ATCC6258 WT | Isolated from sputum of patient with bronchomycosis, Sri Lanka MIC: 2 μg/ml for amphotericin B, 32 μg/ml for fluconazole, and 0.5–2 μg/ml caspofungin | [28] |
| C. parapsilosis ATCC22019 WT | Isolated from case of sprue, Puerto Rico MIC: 2 μg/ml for amphotericin B, 2 μg/ml for fluconazole, and 0.5–2 μg/ml caspofungin | [28] |
| C. albicans HGFP3 | Transformed with pHWP1GFP3 | Expresses GFP in a hyphae-specific manner | [26] |

WT, wild-type.

doi:10.1371/journal.ppat.0030018.t001
We screened a total of 1,266 compounds and identified 15 (~1.2%) that prolonged nematode survival and completely or almost completely inhibited filamentation (Table S1). An additional 57 (~4.5%) compounds prolonged nematode survival but had no or minimal effect on filamentation (Table S1). To the best of our knowledge, the C. elegans screen identified all of the compounds among the 1,266 tested with established, clinically documented antifungal activity against Candida (Table S1).

Among the known antifungals, ketoconazole and butoconazole were among the most effective compounds identified (Table S1). We selected three compounds identified in the screen, which are not established antifungals, for further analysis. By design, we selected compounds that have a positive safety profile in mammals and exhibit variable efficacy in the C. elegans assay, including compounds that both affected or did not affect filamentation. The three compounds selected for further evaluation were caffeic acid phenethyl ester (CAPE), enoxacin, and lapachol (Figure 8 and Table S1).

CAPE is a major active component of propolis, a natural antimicrobial resinous product derived from plants, which is collected and used by honeybees to seal cracks or large potentially infectious objects (such as carcasses) that honeybees cannot remove from their hives ([33,34] and Table S1).

Enoxacin, a fluoroquinolone antibiotic, was shown previously to marginally enhance the in vitro antifungal activity of amphotericin B and mepartricin [35]. Lapachol is a naphthoquinone found in the seeds and heartwood of tropical plants that exhibits anti-leishmanicidal activity [36–38]. Enoxacin did not inhibit C. albicans filament formation in the C. elegans-killing assay.

To determine whether CAPE, enoxacin, and lapachol play a role in mammalian virulence, we evaluated their efficacy in
an established murine model of systemic *Candida* infection. After tail vein injection of $1 \times 10^6$ blastospores, both CAPE and enoxacin prolonged the survival of mice inoculated with *C. albicans* strain DAY185 (Figure 9). Among these three compounds, CAPE, which was the most effective agent in the *C. elegans* screen, was also the most effective agent in the murine assays ($p = 0.008$, compared to the control of mice that received placebo). Notably, intravenous enoxacin was effective in once-a-day dosing of 25 mg/kg ($p = 0.03$; 12 mice per group), whereas CAPE was not statistically effective in once-a-day dosing (unpublished data). Lapachol (150 mg/kg) was not active in the mouse model (unpublished data), consistent with previous work that suggested that lapachol may be transformed into inactive metabolite(s) or neutralized in mammals [36–38].

All three compounds were also evaluated in vitro for their activity in *Candida* biofilm formation. CAPE strongly inhibited both filamentation and biofilm formation (Figures 10 and S2 and Text S1). Interestingly, lapachol also exhibited a modest effect on biofilm formation, suggesting that metabolites of lapachol that are not transformed into inactive metabolite(s) or neutralized in mammals [36–38] may be useful antifungal agents. Of note is that the antifungal activity of the three compounds tested is most likely not due to their ability to inhibit the growth of yeast. Among the three compounds, only CAPE inhibited growth of *C. albicans* in vitro, and that was at a minimum inhibitory concentration (MIC) of 64 gg/ml, which was higher than the concentration (33 gg/ml) used in the *C. elegans* screen. Moreover, CAPE was effective in the *C. elegans–Candida* assay to a concentration as low as 4 gg/ml (unpublished data). Enoxacin and lapachol did not inhibit the growth of *C. albicans* strain DAY185 at the highest concentration tested (256 gg/ml).

To evaluate for toxicity, CAPE, enoxacin, and lapachol were evaluated in vitro using sheep erythrocytes [7] and in vivo using *glp-4;sek-1* worms in liquid media with *E. coli* OP50. Neither CAPE nor lapachol hemolyzed the red blood cells, as compared to DMSO and Triton X-100 controls, though enoxacin exhibited a marginal amount of hemolysis; however, none of the three compounds had any acute toxicity to uninfected *C. elegans glp-4;sek-1* worms (unpublished data).

**Discussion**

The objective of the studies detailed in this paper was to develop a semi-automated, high-throughput, whole-animal *C. elegans* assay that can be used to identify chemical compounds with antifungal activity. Key features of the *C. elegans* assay are that it allows concurrent evaluation of toxicity and antifungal activity and that it identifies compounds that target important pathways associated with human *Candida* infection, including filament formation. Moreover, the assay allows the study of *Candida* cells that are in non-planktonic form and identification of antifungal compounds in a system where both the pathogen and the host can be genetically manipulated.

The *C. elegans* whole-animal screen has several advantages compared to in vitro screens that use planktonic cells. Some virulence traits are induced only in the host, and therefore...
the identification of compounds that are effective against these virulence traits may require detection in vivo. Also, the whole-animal approach provides two relatively unambiguous assay endpoints in the survival/death of the worms and filamentation, and allows the use of liquid-handling robots for filling assay plates and for pin transfer of compounds from library stock plates to assay plates. The current rate-limiting step in the assay is the manual scoring of worm viability and filament formation. Thus far, scoring of live/dead and filamented/nonfilamented worms has been done by direct human observation of movement and morphology of the nematodes on a microscope or by reviewing microscopic images. A quantifiable automated scoring assay that is compatible with the use of high-throughput automated screening microscopes is currently under development and would greatly increase the throughput of the assay. This is possible using a commercially available worm-dispensing robot. Moreover, in the future, we believe that it will be possible to robotically dispense both Candida and C. elegans to the wells, thereby eliminating the labor-intensive infection and wash steps.

The C. elegans assay has many advantages compared to screens using mammalian models. The study of pathogenesis in mammals is complicated by difficulty of handling, long reproductive cycles, small brood sizes, complexity of mammalian hosts, high cost, and ethical considerations. In vivo models for Candida biofilm are particularly cumbersome and expensive, as they usually entail the placement of vascular catheters in rabbits [39] or rats [40,41]. Overall, the whole-animal C. elegans screen can help identify compounds that most likely would not be identified by in vitro screens or would be too costly and inefficient using an in vivo mammal approach. In addition to the Candida assay, members of our group have screened libraries of chemical compounds to identify those that have antimicrobial activity against C. elegans [7]. However, it should be noted that the use of C. elegans for the identification of antimicrobial agents also has obvious limitations. First, it is unlikely that the use of C. elegans (or other invertebrate model hosts) will completely eliminate toxic compounds, even though there is a reasonable correlation between the toxicities of a variety of compounds in mammals and C. elegans [7,42–44]. In addition, the small size that makes C. elegans less expensive and amenable to high-throughput screens makes it very difficult to use this model to study pharmacokinetic variables such as impact of protein binding, absorption, and distribution that are automatically assayed in other, larger animal models.

In addition to providing a facile system for screening chemical libraries for antifungal compounds, the experiments detailed above support the hypothesis that natural
selection in nonmammalian hosts may have aided the evolution and maintenance of virulence-related genes in pathogenic human fungi [8,45]. In previous work from our laboratories, we showed that Cryptococcus neoformans, another important human opportunistic fungal pathogen, is also a potent C. elegans pathogen, supporting previous conclusions that the pathogenic potential of C. neoformans may have evolved as a by-product of avoiding predation by soil organisms, including nematodes and amoebae that feed on yeasts [46]. Thus, even though C. albicans is not necessarily found in the same environment as C. elegans, other fungal pathogens are found in the soil, and the interactions between C. elegans and fungi in general can be seen as a representation of the evolutionary arms race between fungi and soil-borne predators such as C. elegans [47]. Interestingly, however, C. neoformans and Candida use different approaches to kill C. elegans. Cryptococcal cells, which are larger than Candida cells, do not persist in the nematode intestine, and nematodes exposed to cryptococcal lawns are able to deface the cryptococcal cells upon transfer to liquid media and thus can clear the cryptococcal infection ([8] and unpublished data). In contrast, Candida, a common colonizer of the intestinal track of humans, establishes a persistent infection in the C. elegans intestine, forms biofilm, dissolves nematode tissues, and breaks through the nematode cuticle by forming an impressive network of filaments (Figures 2, 4, and 5).

It is expected that the C. elegans--Candida-killing assay will not only identify compounds that affect the growth of the pathogen in vitro, but also compounds that affect the virulence of the pathogen in vivo, or, even immuno-modulate the host. For example, CAPE is known to inhibit NfκB [48] in mammals, and murine mouse studies suggest that it has immunomodulatory effects in vivo [49,50]. Since C. elegans appears not to have an NF-kB-like protein, if CAPE also affects C. elegans immunity, the mechanism presumably does not involve NF-kB inhibition. Since the compounds identified through this screen have no obvious similarities with current classes of antifungals and thus may have a different mechanism of action, combination of these compounds with established antifungal agents could have additive or synergistic action that should be studied further.

Materials and Methods

Strains and media. The Candida strains used in these experiments are summarized in Table 1 or described in the text. Yeast cultures were maintained on yeast peptone dextrose (YPD) (Difco, http://www.difco.com), agar, or as frozen stocks. The C. elegans strains were propagated on E. coli strain OP50 or E. coli strain HB101 using established procedures (detailed below and in [7,51]).

C. elegans liquid medium killing assays. Candida strains were inoculated into 2 ml of YPD and grown at 30 °C for 24 h. Lawns were prepared by spreading 30 μl of each culture on 35-mm tissue culture plates (BD Falcon, http://www.bdbiosciences.com) containing solid BHI media (Difco) with kanamycin (45 μg/ml), ampicillin (100 μg/ml), and streptomycin (100 μg/ml). The plates were incubated at 30 °C for 24 h followed by 25 °C for 24 h, glp-4(sek-1) and glp-4 worms were grown at 15 °C until they reached the L2 stage, and then they were transferred to 25 °C for 24 h. N2 wild-type worms were grown at 15 °C for 72 h, until they reached the L4 stage. Approximately 100 worms were picked onto each lawn and allowed to feed for 30 min to 2 h. The worms were washed off the plates with M9 buffer and allowed to crawl on unseeded BHI plates to remove yeast cells from their cuticles. Roughly 70–80 worms were then picked to wells in a six-well microtiter dish that contained 1.5 ml liquid medium of 70% M9 buffer, 20% BHI, 10 μg/ml cholesterol in ethanol, and 90 μg/ml kanamycin. The plates were incubated at 25 °C overnight and then examined at 24-h intervals for survival. Worms were considered dead and removed when they did not respond to being touched by a platinum wire pick.

C. elegans filamentation staining. C. albicans strains DAY185 and HGFP3 lawns were prepared, and C. albicans glp-4(sek-1) worms exposed to C. albicans as described above for the killing assays. The worms were then transferred to the appropriate media described above with the presence and absence of 32 μg/ml fluorescein. At 24, 48, 144, and 192 h, 20–40 worms exposed to DAY185 were stained in 200 μl of 10 μM FUN-1 (Invitrogen, http://www.invitrogen.com) and 25 μg/ml Concanavalin A-Alexafluor 488 (Invitrogen, http://www.leva-microsystems.com). Pictures were taken with a confocal laser microscope (TCS NT, Leica Microsystems, http://www.leica-microsystems.com). FUN-1 is a fluorescent yellow dye that is absorbed by metabolically active fungal cells and fluoresces red when illuminated with 488 nm (fluorescence emission). Concanavalin A-Alexafluor (fluorescence emission at 519 nm) is a fluorescent green dye that binds to polysaccharides and stains spores and spore stains for 72 h, until they reached the L4 stage. Approximately 100 worms were picked onto each lawn and allowed to feed for 30 min to 2 h. The worms were then moved to pathogen-free liquid media and incubated at 25 °C for 72 h. Lawns were then photographed on days 0 and 1 with the confocal laser microscope described above. For the second experiment, sek-1 glp-4 worms were placed on DAY185 for 2 h, thoroughly washed, and then pipetted onto OP50-GFP NGM plates. Worms were thoroughly washed and then photographed with a confocal laser microscope at 24, 48, and 48 h. Additionally, living and dead worms on day 1 were moved to pathogen-free liquid media in the presence of kanamycin (90 μg/ml) and incubated for 24 h.

Evaluation of fungal burden within C. elegans. The number of C. albicans cfu in C. elegans was quantified based on the protocol detailed in [45,53] with a few modifications. C. albicans strain MLR62 lawns were prepared on BHI as described above. C. albicans glp-4(sek-1) worms were exposed to the lawns for 30 min and then transferred to liquid media and incubated at 25 °C in the presence or absence of antifungal agents. At appropriate time points, three groups of ten worms each were washed twice in 8-μl drops of M9 medium on BHI agar plates, in order to remove surface Candida. Each group of ten worms was then disrupted using a Pellet Pestle Motor (Kontes, http://www.kimble-kontes.com) and plated on YPD agar containing kanamycin (45 μg/ml), ampicillin (100 μg/ml), and streptomycin (100 μg/ml). The plates were incubated for 48 h at 30 °C and colonies were counted. Statistical significance was determined by the Mann-Whitney test using STATA6 statistical software (Stata, http://www.stata.com). A P-value of less than 0.05 was considered to be significant.

Screen of compound library in C. elegans. For testing the efficacy of chemical compounds, C. albicans strain MLR62 was inoculated into 2 ml of YPD and grown at 30 °C for 24 h. 10 μl of the culture was spread onto tissue culture plates (BDFalcon) containing 79% M9 buffer, 20% BHI agar (BD Falcon), and streptomycin (15 μg/ml). The plates were incubated at 30 °C for 24 h. C. elegans animals at the L4 developmental stage (grown as detailed above under C. elegans liquid medium killing assays) were transferred from a lawn of E. coli HB101 onto C. albicans lawns on BHI medium, incubated at 25 °C for 30 min, and then pipetted in 50 μl into 96-well plate wells that contained 100 μl liquid medium (79% M9 buffer, 20% BHI media, 10 μg/ml cholesterol in ethanol, and 90 μg/ml kanamycin). C. elegans glp-4(sek-1) nematodes were pipetted into 96-well plates that contained 1 ml of YPD and grown at 25 °C for 24 h. Approximately 100 wells were picked onto each lawn and allowed to feed for 30 min to 2 h. The worms were washed off the plates with M9 buffer and allowed to crawl on unseeded BHI plates to remove yeast cells from their cuticles. Roughly 70–80 worms were then picked to wells in a six-well microtiter dish that contained 1.5 ml liquid medium of 70% M9 buffer, 20% BHI, 10 μg/ml cholesterol in ethanol, and 90 μg/ml kanamycin. The plates were incubated at 25 °C overnight and then examined at 24-h intervals for survival. Worms were considered dead and removed when they did not respond to being touched by a platinum wire pick.
developed filamentation, were rod-shaped, or did not respond to the well being tapped. Each compound was also scored by the number of dead worms in the well that developed hyphae (Table S1). Compounds were considered to have completely or almost completely inhibited filament formation if fewer than 25% of the dead worms in the well developed hyphae. Compounds were categorized as having a minimal effect on filament formation if 25%–75% of the dead worms developed hyphae. The compounds that had no effect on filament formation allowed over 75% of the dead worms to form hyphae.

Approximately 25 nematodes were used to analyze each chemical compound tested. Two controls were used in all plates. The positive control was the antifungal caspofungin (which allows >75% survival at day 6). Phosphate-buffered saline (PBS) was the negative control (<25% of nematodes in PBS are alive at day 6). In this pilot screen, we considered a result as a “hit” when survival in the compound well was 50% and above of the median survival of the control wells.

Evaluation of MIC. Cells were maintained in YPD (1% yeast extract, 2% peptone, and 2% dextrose) at ~80 °C until used. The MIC was evaluated for each of the above compounds according to the Clinical and Laboratory Standards Institute (formerly the National Committee for Clinical Laboratory Standards, NCCLS) microdilution protocol (M27-A) [28].

Hemolysis assay. CAPE, exonoin, and lapachol were evaluated for hemolysis of sheep erythrocytes as described by Moy et al. [7, DMSO and Triton X-100 were used as controls.

Compound toxicity in uninfected gfp-fsek-1 worms. To test whether CAPE, exonoin, and lapachol were toxic to the worms at the concentration used in the hemolysis assay, gfp-fsek-1 L4s were prepared as described above. The nematodes were moved from E. coli OP50 to pathogen-free liquid media containing 2% DMSO or 2% Triton X-100 or 100 mg/ml CAPE, exonoin, or lapachol. The worms were incubated for 4 h at 25 °C; at hourly intervals dead worms were counted and removed.

Murine models of virulence. BALB/c mice (22–24 g, female, Charles River Laboratories) were used in all studies. In brief, C. albicans strain DAY185 was grown at 30 °C with shaking overnight in YPD to late-log phase. The yeast cells were centrifuged, washed in PBS, and re-suspended to a concentration of 5 × 10⁶ blastospores/ml (measured with a hemocytometer). 200 μl of this suspension were inoculated into the lateral tail vein (1 × 10⁶ blastospores). In all mammalian experiments, the concentration of yeast cells in the inoculum was confirmed by plating serial dilutions and enumerating cfus 24–48 h later. The murine protocols were approved by the Massachusetts General Hospital Committee on Research, Subcommittee on Research Animal Care and special attention was given to minimizing the suffering of the mice.

In vitro biofilm growth on silicone pads. The effect of CAPE, lapachol, and exonoin on biofilm growth on silicone pads was evaluated as described by Richard et al. [24] and Nobile et al. [41]. The C. albicans strain DAY185 was inoculated in 2 ml of YPD and grown at 30 °C for 24 h. The DAY185 culture was diluted into SD media plus 50 mM glucose to an OD560 of 1.0. After the 90-min incubation and PBS wash, caspofungin (positive control), CAPE, exonoin, or lapachol were added for 4 h at 25 °C; at hourly intervals dead worms were counted and removed.

Microscopic visualization of silicone pads. The silicone pads were visualized as reported in [24,29]. DAY185 cells were incubated at 37 °C for 60 h on silicone squares in SD media with 50 mM glucose. Biofilms were stained with 25 μg/ml Concanaval A-Alexafluor 488 (Invitrogen) for 1 h in the dark. Pictures were taken with a confocal laser microscope (TCS NT, Leica Microsystems).

Biofilm dry mass measurements. The biofilm dry mass was evaluated as described by Nobile et al. [29]. Statistical significance was determined by the Mann-Whitney test using STATA 6. A p-value of less than 0.05 was considered to be significant.

Statistical analysis. Murine and C. elegans-killing curves were plotted, and estimation of differences (log-rank and Wilcoxon tests) in survival analyzed with the Kaplan-Meier method performed using STATA 6. A p-value of less than 0.05 was considered to be significant.

Supporting Information

Figure S1. Candida species accumulate in the C. elegans intestine (A) C. elegans nematode strain gfp-fsek-1 exposed to C. parapsilosis strain ATCC™ 29219 for 2 h and then moved to microbe-free liquid media. 1 d later, there were a significant number of yeast cells within the nematode resulting in distention of the nematode intestine. The round structure (white arrows) is the pharyngeal grinder organ, which functions to disrupt ingested organisms. Black arrows with borders point to the intestinal lumen. (B) As the infection within the nematode progresses, the nematode cells are essentially replaced by yeast cells, and staining of nematodes with FUN-1 shows yeast cells to be metabolically active (C. elegans gfp-fsek-1 nematode 4 d after infection with C. parapsilosis strain ATCC™ 29219).

Found at doi:10.1371/journal.ppat.0030018.sg001 (1.6 MB TIF).

Figure S2. In vitro efficacy of CAPE, Exonoin, and Lapachol Biofilm on the Surfaces of Wells of Microtiter Plates

When evaluated using the XTT reduction assay, CAPE and lapachol inhibited the formation of biofilm (A), while all three compounds had an effect in pre-formed biofilm (B). Found at doi:10.1371/journal.ppat.0030018.sg002 (58 KB TIF).

Table S1. Compounds identified through a pilot screen in C. elegans Found at doi:10.1371/journal.ppat.0030018.s001 (349 KB DOC).

Acknowledgments

We appreciate the support of the New England Regional Center of Excellence for Biodefense Emerging Infectious Diseases Research funded by National Institutes of Health grant AI057159. We thank Su Chiu, Dave Fletcher, and Brian Kraybill at the Institute of Chemistry and Cell Biology (ICCB) at Harvard Medical School for providing expertise during the screening of the compound libraries and Drs. A. P. Mitchell and P. Sundstrom for providing the C. albicans HGP33 strain.

Author contributions. BBF and GA contributed equally to this work.

Funding. Support was provided by the National Institutes of Health K08 award AI63084 to EM, a New Scholar Award in Global Infectious Diseases from the Ellison Medical Foundation to EM, and NIH grant R21 AI059483 to FA.

Competing interests. The authors have declared that no competing interests exist.

References

1. Mylonakis E, Aballay A (2005) Worms and flies as genetically tractable animal models to study host-pathogen interactions. Infect Immun 73: 3834–3841.

2. Exwark J (2002) Tackling both sides of the host-pathogen equation with Caenorhabditis elegans. Microbes Infect 4: 247–256.

3. Slavin M, Fastenau J, Sukarom I, Mavros P, Crowley S, et al. (2004) Burden of hospitalization of patients with Candida and Aspergillus infections in Australia. Int J Infect Dis 8: 111–129.

4. Kojic EM, Darouiche RO (2004) Candida infections of medical devices. Clin Microbiol Rev 17: 255–267.

5. Rentz AM, Halpert MT, Bowden R (1998) The impact of candidemia on length of hospital stay, outcome, and overall cost of illness. Clin Infect Dis 27: 781–788.

6. Miller LG, Hajjeh RA, Edwards JE Jr (2001) Estimating the cost of nosocomial candidemia in the United States. Clin Infect Dis 32: 1110.

7. Moy TI, Ball AR, Anklesaria Z, Casadei G, Lewis K, et al. (2006) Nosocomial candidemia in the United States. Clin Infect Dis 32: 1110.

8. Mylonakis E, Sussel BM, Perfect JR, Heitman J, Calderwood SB (2002) Killing of C. albicans elegans by Cryptococcus neoformans as a model of yeast pathogenesis. Proc Natl Acad Sci U S A 99: 15675–15680.

9. Beanan MJ, Strome S (1992) Characterization of a germ-line proliferation suppression gene in C. elegans. Genes Dev 6: 2342–2359.

10. Mylonakis E, Ausubel FM, Perfect JR, Heitman J, Calderwood SB (2002) Nosocomial candidemia in the United States. Clin Infect Dis 32: 1110.

11. Moy TI, Ball AR, Anklesaria Z, Casadei G, Lewis K, et al. (2006) Nosocomial candidemia in the United States. Clin Infect Dis 32: 1110.

12. Mylonakis E, Sussel BM, Perfect JR, Heitman J, Calderwood SB (2002) Killing of C. albicans elegans by Cryptococcus neoformans as a model of yeast pathogenesis. Proc Natl Acad Sci U S A 99: 15675–15680.
10. Roussel DL, Bennett KL (1993) gh-1, a germ-line putative RNA helicase from <i>Candida albicans</i>, has four zinc fingers. Proc Natl Acad Sci U S A 90: 9300–9304.

11. Kim DH, Feinbaum R, Alloing G, Emerson FE, Garsin DA, et al. (2002) A conserved p38 MAP kinase pathway in <i>Candida albicans</i> elegans innate immunity. Science 297: 623–626.

12. Deva R, Shankaranarayanan P, Ciccoli R, Nigam S (2003) <i>Candida albicans</i> induces selectively transcriptional activation of cylooxygenase-2 in HeLa cells: Pivotal roles of Toll-like receptors, p38 mitogen-activated protein kinase, and NF-kappa B. J Immunol 171: 3047–3053.

13. Odds EC (1997) Switch of phenotype as an escape mechanism of the intruder. Mycoses 40 (Suppl 2): 9–12.

14. Berman J, Sudbery PE (2002) <i>Candida albicans</i>: A molecular revolution built on lessons from budding yeast. Nat Rev Genet 3: 918–930.

15. Kobayashi SD, Cutler JE (1998) <i>Candida albicans</i> hyphal formation and virulence: Is there a clearly defined role? Trends Microbiol 6: 92–94.

16. Lo HJ, Kohler JR, DiDomenico B, Loebenberg D, Cacciapuoti A, et al. (1997) Nonfilamentous <i>C. albicans</i> mutants are avirulent. Cell 90: 939–949.

17. Kumamoto CA, Vinces MD (2005) Contributions of hyphae- and hypha-coregulated genes to <i>Candida albicans</i> virulence. Cell Microbiol 7: 1546–1554.

18. Staab JF, Bradway SD, Fidel PL, Sundstrom P (1999) Adhesive and mammalian transglutaminase substrate properties of <i>Candida albicans</i> Hwp1. Science 283: 1553–1558.

19. Kumamoto CA (2002) <i>Candida</i> biofilms. Curr Opin Microbiol 5: 608–611.

20. Gow NA (2002) <i>Candida albicans</i> switches mates. Mol Cell 10: 217–218.

21. Verstrepen KJ, Reynolds TB, Fink GR (2004) Origins of variation in the fungal cell surface. Nat Rev Microbiol 2: 533–540.

22. Douglas LJ (2003) <i>Candida</i> biofilms and their role in infection. Trends Microbiol 11: 30–36.

23. Ramage G, VandeWalle K, Lopez-Ribot JL, Wickes BL (2002) The <i>Candida albicans</i> Hwp1. Science 283: 1535–1538.

24. Richard ML, Nobile CJ, Bruno VM, Mitchell AP (2005) <i>Candida albicans</i> biofilm-defective mutants. Eukaryot Cell 4: 1493–1502.

25. Sifri CD, Enloe B, Mylonakis E, Qin X, Singh KV, et al. (2001) A simple method for generating <i>Candida albicans</i> transposon mutants. Antimicrob Agents Chemother 46: 3591–3596.

26. Staab JF, Bahn YS, Sundstrom P (2003) Integrative, multi-functional plasmids for hypha-specific or constitutive expression of green fluorescent protein in <i>Candida albicans</i>. Microbiology 149: 2977–2986.

27. Sundstrom P (2002) Adhesion in <i>Candida</i> albicans: Pivotal roles of Toll-like receptors, p38 mitogen-activated protein kinase, and NF-kappa B. J Immunol 171: 3047–3055.

28. Sifri CD, Enloe B, Mylonakis E, Qin X, Singh KV, et al. (2004) Rabbit model of <i>Candida albicans</i> biofilm infection: Liposomal amphotericin B antifungal lock therapy. Antimicrob Agents Chemother 48: 1727–1732.

29. Andes D, Nett J, Oschel P, Albrecht R, Marchillo K, et al. (2004) Development and characterization of an in vivo central venous catheter <i>Candida albicans</i> biofilm model. Infect Immun 72: 6023–6031.

30. Nobile CJ, Andes DR, Nett JE, Smith EJ, Yue F, et al. (2006) Critical role of Bcr1-dependent adhesins in <i>C. albicans</i> biofilm formation in vitro and in vivo. PLoS Pathog 2: e63. doi:10.1371/journal.ppat.0020063.

31. Sochova I, Hofman J, Holoubek I (2006) Using nematodes in soil ecotoxicology. Environ Int 32: 374–383.

32. Williams PL, Dusenbery DB (1988) Using the nematode <i>Caenorhabditis elegans</i> to predict mammalian acute lethality to metallic salts. Toxicol Ind Health 4: 469–478.

33. Cole RD, Anderson GL, Williams P (2004) The nematode <i>Caenorhabditis elegans</i> as a model of organophosphate-induced mammalian neurotoxicity. Toxicol Appl Pharmacol 194: 248–256.

34. Tang RJ, Breger J, Idrumm A, Gerik KJ, Lodge J, et al. (2005) <i>Cryptococcus neoformans</i> gene involved in mammalian pathogenesis identified by a <i>C. elegans</i> progeny-based approach. Infect Immun 73: 8219–8225.

35. Steenbergen NJ, Shuman HA, Casadevall A (2001) <i>Cryptococcus neoformans</i> interactions with amoebae suggest an explanation for its virulence and intracellular pathogenic strategy in macrophages. Proc Natl Acad Sci U S A 102: 17542–17550.

36. Kumamoto CA, Vinces MD (2005) Alternative <i>Candida albicans</i> lifestyles: Growth on surfaces. Annu Rev Microbiol 59: 113–133.

37. Watabe M, Hishikawa K, Takayangi A, Shimizu N, Nakaki T (2004) Caffeic acid phenethyl ester induces apoptosis by inhibition of NFkappaB and activation of Fas in human breast cancer MCF-7 cells. J Biol Chem 279: 6017–6026.

38. Park JH, Lee JK, Kim HS, Chung ST, Eom JH, et al. (2004) Immunomodulatory effect of caffeic acid phenethyl ester in BabL/c mice. Int Immunopharmacol 4: 429–436.

39. Ho CC, Lim SS, Chou MY, Chen FL, Hu CC, et al. (2005) Effects of caffeic acid phenethyl ester on HIV replication in vitro and modulation of cytokines in vivo. J Amicrib Chemother 56: 372–379.

40. Brenner S (1974) The genetics of <i>Candida albicans</i> species. Genetics 77: 71–94.

41. Li X, Yan Z, Xu J (2003) Quantitative variation of biologms among strains in natural populations of <i>Candida albicans</i>. Microbiology 149: 353–362.

42. Garsin DA, Sifri CD, Mylonakis E, Qin X, Singh KV, et al. (2001) A simple model host for identifying gram-positive virulence factors. Proc Natl Acad Sci U S A 98: 10892–10897.