# Comparison of Pathogenesis and Host Immune Responses to Candida glabrata and Candida albicans in Systemically Infected Immunocompetent Mice

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Cytokine-mediated host defense against Candida glabrata infection was compared to that against C. albicans, using immunocompetent murine models of systemic candidiasis. The pathogenesis of infection was evaluated morphologically and by culture of target organs, while the kinetics of induction of cytokine mRNAs and corresponding proteins were determined in kidneys by real-time reverse transcription-PCR and cytokinespecific murine enzyme-linked immunosorbent assays, respectively. Systemic infection with C. glabrata resulted in a chronic, nonfatal infection with recovery of organisms from kidneys, while intravenous inoculation with C. albicans resulted in rapid mortality with logarithmic growth of organisms in kidneys and recovery of C. albicans from the spleen, liver, and lungs. Survival of C. glabrata-infected mice was associated with rapid induction of mRNAs and corresponding immunoreactive proteins for the proinflammatory cytokines tumor necrosis factor alpha (TNF- $\alpha$ ), interleukin-12 (IL-12), and gamma interferon (IFN- $\gamma$ ) and the lack of induction of protein for the anti-inflammatory cytokine IL-10. In contrast, mortality in C. albicans-infected mice was associated with induction of mRNA and corresponding protein for IL-10 but delayed (i.e., TNF-α) or absent (i.e., IL-12 and IFN- $\gamma$ ) induction of immunoreactive proinflammatory cytokines. Mice were subsequently treated with cytokine-specific neutralizing monoclonal antibodies (MAbs) to TNF-α, IL-12, or IFN-γ, and the effect on growth of C. glabrata in kidneys was assessed. Neutralization of endogenous TNF- $\alpha$  resulted in a significant increase in C. glabrata organisms compared to similarly infected mice administered an isotype-matched control MAb, while neutralization of endogenous IL-12 or IFN- $\gamma$  had no significant effect on C. glabrata replication. These results demonstrate that in response to intravenous inoculation of C. glabrata, immunocompetent mice develop chronic nonfatal renal infections which are associated with rapid induction of the proinflammatory cytokines TNF- $\alpha$ , IL-12, and IFN- $\gamma$ . Furthermore, TNF- $\alpha$  plays a key role in host defense against systemic candidiasis caused by either C. glabrata or C. albicans, as the absence of endogenous TNF- $\alpha$  activity was associated with enhanced tissue burden in both infection models.

*Candida glabrata*, a monomorphic haploid yeast, has historically been considered a nonpathogenic saprophyte of normal flora of healthy individuals (22, 27, 77). However, due to the widespread use of immunosuppressive agents and/or broad-spectrum antimycotic therapy, the frequency of mucosal and systemic *C. glabrata* infections has increased significantly, making it the second or third most common cause of candidiasis after *C. albicans* (22, 24, 35, 36, 52, 72, 73, 84). Infections caused by *C. glabrata* are particularly difficult to treat, as resistance to azole antifungal agents including fluconazole is common (22, 31, 36, 69, 79, 82, 83). Consequently, *C. glabrata* infections often result in high morbidity and mortality in immunocompromised hospitalized patients (22).

Despite increasing clinical significance, there are few reports regarding host response to *C. glabrata* infections (22). Previous studies have demonstrated that innate immunity, mediated by granulocytes (polymorphonuclear leukocytes) and monocytes/ macrophages, is crucial to containment and resolution of systemic candidiasis caused by other *Candida* species, including *C. albicans* (5, 13, 18, 55, 66). Phagocytic cells kill *C. albicans* 

yeast, hyphae, and pseudohyphae, using both oxidative and nonoxidative mechanisms (20, 28, 41, 81). Previous in vitro and in vivo studies have demonstrated that polymorphonuclear leukocytes and/or macrophage antifungal activities are modulated by cytokines (1, 61, 62). Specifically, stimulation of phagocytic cells in vitro with proinflammatory cytokines including gamma interferon (IFN- $\gamma$ ) and/or tumor necrosis factor alpha (TNF- $\alpha$ ) enhanced anti-*C*. *albicans* activity, while anti-inflammatory cytokines including interleukin-10 (IL-10) and IL-4 had the opposite effect (6, 15-17, 47, 48, 57-59, 85, 86). Likewise, murine resistance to systemic C. albicans infections was associated with induction of TNF- $\alpha$ , IL-12, and IFN- $\gamma$ , while susceptibility to infection was associated with induction of IL-4 and IL-10 (38, 61, 65, 76). Furthermore, mice depleted of endogenous IL-10 (by administration of cytokine-specific neutralizing monoclonal antibody [MAb], receptor antagonists, or IL-10 knockout mice), developed protective immune responses to systemic C. albicans infection, while inhibition of endogenous TNF- $\alpha$ , IL-12, or IFN- $\gamma$  had the opposite effect (9, 12, 38, 40, 46, 53, 63, 64, 67, 78, 80).

To gain insight into cytokine-mediated host defense against systemic *C. glabrata* infection, immunocompetent Crl:CF-1 mice were inoculated intravenously (i.v.) with either *C. glabrata* or *C. albicans*. The pathogenesis of infection was evaluated morphologically and by culture of target organs, while the

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kinetics of induction of cytokine mRNAs and corresponding proteins for TNF- $\alpha$ , IL-12, IFN- $\gamma$ , and IL-10 were determined in tissues by real-time reverse transcription-PCR (RT-PCR) and cytokine-specific murine enzyme-linked immunosorbent assays (ELISAs), respectively. Subsequently, the biological relevance of induced proinflammatory cytokine activity in host resistance to systemic *C. glabata* infection was assessed using cytokine-specific neutralizing MAbs.

#### MATERIALS AND METHODS

**Mice.** Male specific-pathogen-free outbred immunocompetent CrI:CF-1 mice (11 to 13 g; Charles River) were used for all experiments. Animals were housed in microisolator cages and were cared for in accordance with standard guidelines. All in vivo experiments were approved by the institutional Animal Care and Use Committee.

**Fungal inoculum and animal inoculation.** Clinical isolates of *C. glabrata* and *C. albicans* were grown on Sabouraud's dextrose agar (SDA) (7, 14). For preparation of the inocula, *C. glabrata* and *C. albicans* were quantified from SDA plates that had been incubated for 48 h at  $35^{\circ}$ C and resuspended in phosphatebuffered saline at the desired concentration. Crl:CF-1 mice were inoculated i.v. with *C. glabrata* or with *C. albicans* ( $10^{4}$  to  $10^{8}$  CFU/mouse) via the lateral tail vein.

Quantification of *Candida* sp. in infected tissue homogenates. At 0, 1, 2, 3, 7, 10, 14, and 21 days postinfection (p.i.), mice were euthanized, and target organs (brain, heart, lung, liver, spleen, and kidney) were excised and homogenized in 10 ml of sterile phosphate-buffered saline. Tissue homogenates from individual mice were serially diluted on SDA plates and incubated for 48 h at  $35^{\circ}$ C prior to quantifying *C. glabrata* or *C. albicans*. Results are expressed as CFU log<sub>10</sub> per organ.

**Pathology.** The inflammatory response in target organs of *C. glabrata-* and *C. albicans-*infected mice was assessed by light microscopy. Mice were inoculated i.v. with *C. glabrata* ( $10^8$  CFU/mouse) or with *C. albicans* ( $5 \times 10^6$  CFU/mouse). At 0, 4, 24, 48, 72, 168, 240, 336, and/or 504 h p.i., groups of three surviving mice were euthanized, and tissues were excised and fixed in 10% buffered formalin. Fixed tissues were sectioned, embedded in paraffin, and stained with hematoxylin-cosin and Gomori's silver stain.

Quantitation of cytokine transcripts by real-time RT-PCR. Real-time RT-PCR assays were performed to specifically quantify murine TNF-α, IL-12, IL-10, and IFN-y transcripts. Briefly, kidneys were excised from C. glabrata- and C. albicans-infected mice at specific times p.i. and flash-frozen in liquid nitrogen. Total RNA was extracted using TriReagent (Molecular Research Center, Cincinnati, Ohio) according to the manufacturer's directions and stored at -80°C in nuclease-free water containing 0.1 mM EDTA. Isolated RNA (5 µg) was incubated with 10 U of DNase I (Boehringer Mannheim) in the presence of RNasin (Promega) for 30 min at 37°C. Samples were heat inactivated at 70°C for 10 min, chilled, and reverse transcribed with Superscript II reverse transcriptase (Gibco/ BRL) with 1 µg each of random hexamers and oligo(dT) 12-18. PCR primers were obtained from Perkin-Elmer as predeveloped assay reagents (TNF-a, IL-12 p35, IL-12 p40, IL-10, and IFN-y). Samples were then subjected to 40 cycles of amplification at 95°C for 15 s followed by 60°C for 1 min using an ABI Geneamp 7700 sequence detection system as specified by the manufacturer (Perkin-Elmer). PCR amplification of the housekeeping ubiquitin gene was performed for each sample to control for sample loading and allow normalization between samples as instructed by the manufacturer (Perkin-Elmer). Water controls were included to ensure specificity. Each data point was examined for integrity by analysis of the amplification plot. The ubiquitin-normalized data were expressed as fold induction of gene expression in infected mice compared to that in uninfected mice.

Immunoreactive cytokine analysis of tissue homogenate supernatants. Kidney supernatants were procured from uninfected and infected mice by filtering tissue homogenates (prepared as described above) through a 0.22- $\mu$ m-pore-size filter (Gelman Sciences, Ann Arbor, Mich.). Protein levels of TNF- $\alpha$ , IL-12, IL-10, and IFN- $\gamma$  were subsequently measured using commercially available cytokine-specific murine ELISA kits (Quantikine mouse TNF- $\alpha$ , mouse IL-12 p70, mouse IFN- $\gamma$ , and mouse IL-10; R&D systems, Minneapolis, Minn.) according to the manufacturer's directions.

**Interventional studies.** Endogenous TNF- $\alpha$ , IL-12, and IFN- $\gamma$  activities were blocked by administration of cytokine-specific neutralizing MAbs directed toward TNF- $\alpha$  (30, 32), IL-12 (51), and IFN- $\gamma$  (10). Each neutralizing antibody was given intraperitoneally at a dose of 1 mg of antibody/mouse 24 h prior to systemic

 TABLE 1. Assessment of virulence of C. glabrata and C. albicans in systemically infected Crl:CF-1 mice<sup>a</sup>

Dose (organisms/mouse)	Organism	No. of survivors	% Survival
10 <sup>8</sup>	C. glabrata C. albicans	5 0	100 0
$5 \times 10^7$	C. glabrata C. albicans	5 0	$\begin{array}{c} 100 \\ 0 \end{array}$
$10^{7}$	C. glabrata C. albicans	5 0	$\begin{array}{c} 100 \\ 0 \end{array}$
$5  imes 10^{6}$	C. glabrata C. albicans	5 0	$\begin{array}{c} 100 \\ 0 \end{array}$
$10^{6}$	C. glabrata C. albicans	5 2	$\begin{array}{c} 100 \\ 40 \end{array}$
$5 \times 10^5$	C. glabrata C. albicans	5 5	$\begin{array}{c} 100 \\ 100 \end{array}$
$10^{5}$	C. glabrata C. albicans	5 5	$\begin{array}{c} 100 \\ 100 \end{array}$
$5  imes 10^4$	C. glabrata C. albicans	5 5	$\begin{array}{c} 100 \\ 100 \end{array}$
$10^{4}$	C. glabrata C. albicans	5 5	100 100

<sup>*a*</sup> CrI:CF-1 mice were inoculated i.v. with the indicated doses of *C. glabrata* or *C. albicans* as described in Materials and Methods. Mice were observed once daily for 7 days for clinical signs of illness or mortality. Results are representative of five mice per inoculum.

infection with *C. glabrata*. Similarly infected mice administered an isotypematched immunoglobulin G2a (IgG2a) served as controls.

**Statistical analysis.** The average cytokine mRNA expression for all time points p.i. was compared against that of the initial time point. Analysis of variance was performed to model *dCt* against time, using the following equation:  $dCt_T = dCt_0 - \log_2(\text{fold expression})$ , where *T* is time. The *P* values were computed using a Dunnett adjustment for multiple comparisons.

The average immunoreactive cytokine protein was measured for all time points p.i. and compared to that of the initial time point. Due to the clearly nonnormal nature of the data, a permutation test was performed to make these comparisons.

All *P* values were compared to a significance level of  $\alpha = 0.05$ . Results are presented as mean  $\pm$  standard error of the mean (SEM).

## RESULTS

Comparison of virulence of *C. glabrata* and *C. albicans* in immunocompetent Crl:CF-1 mice. Initial experiments were conducted to compare the pathogenesis of *C. glabrata* and *C. albicans* systemic infection in immunocompetent Crl:CF-1 mice. Mice were inoculated with *C. glabrata* or with *C. albicans* (10<sup>4</sup> to 10<sup>8</sup> organisms in 100  $\mu$ l of saline i.v. via the lateral tail vein) and observed once daily for 7 days for morbidity and mortality. As shown in Table 1, all mice inoculated with *C. glabrata* ( $\leq 10^8$  organisms/mouse) survived and appeared clinically normal. In contrast, systemic infection with *C. albicans* ( $\geq 5 \times 10^6$  organisms/mouse) resulted in 100% mortality within 4 days p.i., which was associated with clinical signs of disease including weight loss, lethargy, and a ruffled appearance. In all subsequent experiments, mice were inoculated



FIG. 1. Growth of *C. glabrata* and *C. albicans* in tissues of immunocompetent CrI:CF-1 mice. Mice were inoculated i.v. with *C. glabrata* (10<sup>8</sup> organisms/mouse) or with *C. albicans* (5 × 10<sup>6</sup> organisms/mouse). At specific time points p.i., mice were euthanized, and net growth of *C. glabrata* and *C. albicans* was quantified in kidneys, hearts, lungs, brains, spleens, livers, and lungs by culture of tissue homogenates. Results represent the mean  $\pm$  SEM of CFU (log<sub>10</sub>)/tissue of three mice per time point.

systemically with either *C. glabrata* (10<sup>8</sup> organisms/mouse) or *C. albicans* ( $5 \times 10^6$  organisms/mouse).

Pathogenesis of systemic *C. glabrata* and *C. albicans* infection in immunocompetent CrI:CF-1 mice. The tissue distribution of *C. glabrata* and *C. albicans* in systemically infected CrI:CF-1 mice was subsequently determined by culturing brains, hearts, lungs, livers, kidneys, and spleens. As shown in Fig. 1a, *C. glabrata* was recovered from all organs within 1 day p.i., and there was no significant net growth of the yeast in any organ over the 21-day duration of infection. However, while the number of *C. glabrata* organisms in the hearts, brains, spleens, livers, and lungs of infected mice declined over the duration of infection ( $<10^3 C. glabrata$  organisms/organ at 21 days p.i.),  $\geq 10^5$  organisms were consistently recovered from kidneys of infected mice for 21 days p.i.

As shown in Fig. 1b, *C. albicans* was also recovered from all organs within 1 day p.i. However, while the number of *C.* 

*albicans* organisms in the heart and liver declined rapidly with time ( $\leq 10^3$  organisms at 3 days p.i.), there was no significant change in the fungal load in the brains, spleens, or lungs of infected mice over the duration of infection ( $10^4$  to  $10^5$  organisms/tissue at 3 days p.i.). Furthermore, the number of *C. albicans* organisms in kidneys of infected mice increased by nearly 2 logs within 3 days p.i. Taken together, these results demonstrate systemic infection with a relatively large inoculum ( $10^8$  CFU/mouse) of *C. glabrata* resulted in a chronic nonfatal infection with persistent recovery of the yeast from the kidneys, while systemic *C. albicans* infection, induced by 100-fold fewer organisms, was rapidly fatal (100% mortality within 4 days p.i.) and was associated with logarithmic growth of the organism in the kidneys and persistent recovery from the brain, spleen, and lungs.

**Pathology.** Gross lesions were not apparent in organs from Crl:CF-1 mice inoculated with *C. glabrata*. In contrast, within 72 h p.i., kidneys from mice infected with *C. albicans* appeared tan and mottled in color with an irregular surface.

Histopathological lesions in *C. glabrata*-infected mice were most prominent in kidneys. Within 4 h p.i., organisms were apparent in the glomerular tuft and within macrophages attached to the renal vascular endothelium (Fig. 2A). The presence of organisms at 4 h p.i. was associated with minimal inflammation. By 48 to 72 h p.i. there were perivascular and periglomerular foci of mixed mononuclear cell infiltrates scattered primarily throughout the renal cortex. These foci infrequently contained organisms (Fig. 2B). The renal mononuclear cell infiltrate persisted until 10 days p.i.; however, organisms were not observed after 7 days p.i. Organisms were also infrequently demonstrated in arterioles and capillaries of the brains, spleens, hearts, and livers of infected mice at 24 to 72 h p.i. These foci were associated with minimal mononuclear cell inflammatory infiltrates which resolved within 10 days p.i.

In sharp contrast, histopathological lesions in mice systemically infected with *C. albicans* were extensive, with multiple foci of hyphal invasion in kidneys, hearts, brains, and spleens of infected mice. Foci were largest and most numerous in kidneys, with a cortical perivascular or periglomerular distribution, and were associated with minimal to severe mononuclear cell inflammatory infiltrates within 24 h p.i. (Fig. 2C). Multiple foci of perivascular oriented hyphae and polymorphonuclear inflammatory cell infiltrates were also apparent in hearts of infected mice within 24 h p.i. (Fig. 2D). These lesions were associated with foci of minimal mononuclear cell inflammatory infiltrates and cardiac myodegeneration and/or necrosis within 72 h p.i. Hyphae were also visible in brains (Fig. 2E) and spleens (Fig. 2F) of infected mice within 48 h p.i. and were associated with mild inflammatory cell infiltrates.

Temporal induction of cytokine mRNA in kidneys of infected mice. To gain insight into the potential role of pro- and anti-inflammatory cytokines in the pathogenesis of systemic *C. glabrata* infection, the kinetics of induction of cytokine mRNAs including TNF- $\alpha$ , IL-12 p40, IL-12 p35, IFN- $\gamma$ , and IL-10 were assessed in kidneys of infected mice by real-time RT-PCR. This methodology allowed a rapid, accurate, and precise quantitation of gene transcripts (25, 29). For comparison, these cytokine mRNAs were also assessed in tissues from mice systemically infected with *C. albicans*. TNF- $\alpha$  (Fig. 3a), IL-12 p40 (Fig. 3b), IL-12 p35 (Fig. 3c), IFN- $\gamma$  (Fig. 3d), and IL-10 (Fig.



FIG. 2. Pathology in CrI:CF-1 mice systemically inoculated with *C. glabrata* or *C. albicans*. (A) Mouse kidney 4 h after infection with *C. glabrata*. Note organisms (arrows) in macrophages attached to the renal vessel endothelium. (B) Mouse kidney 72 h after infection with *C. glabrata*. Note organisms (arrow) in renal glomeruli with a mixed mononuclear cell infiltrate. (C) Mouse kidney 24 h after infection with *C. albicans*. Note organisms (arrow) in glomeruli with moderate mononuclear cell infiltrate. (D) Mouse heart 24 h after infection with *C. albicans*. Note organisms (arrow) and polymorphonuclear infiltrate. (E) Mouse brain 48 h after infection with *C. albicans*. Note organisms (arrow) with minimal inflammatory response. (F) Mouse spleen 48 h after infection with *C. albicans*. Note organisms (arrow) with mild mononuclear cell infiltrate. Magnification,  $\times 370$ .



FIG. 3. Temporal expression of TNF- $\alpha$ , IL-12, IFN- $\gamma$ , and IL-10 mRNAs in kidneys of *C. glabrata*- or *C. albicans*-infected mice. Crl:CF-1 mice were infected i.v. with virulent *C. glabrata* (10<sup>8</sup> CFU/mouse) or *C. albicans* (5 × 10<sup>6</sup> CFU/mouse). At specific time points p.i., mice were euthanized, kidneys were excised, and total RNA was extracted. Transcript levels for TNF- $\alpha$  (a), IL-12 p40 (b), IL-12 p35 (c), IFN- $\gamma$  (d), and IL-10 (e) were quantified in kidneys by real-time RT-PCR. For mRNA quantification, PCR amplification of the housekeeping ubiquitin gene was performed for each sample to control for sample loading and facilitate normalization between samples. The ubiquitin-normalized data were expressed as fold induction of gene expression in *C. glabrata*- or *C. albicans*-infected mice compared to uninfected mice. Results represent the mean ± SEM of two separate experiments, four to nine mice per treatment group. \*, significantly greater than control mice, P < 0.05.



FIG. 4. Temporal expression of TNF- $\alpha$ , IL-12, IFN- $\gamma$ , and IL-10 proteins in kidneys during *C. glabrata* and *C. albicans* infection. Crl:CF-1 mice were infected with virulent *C. glabrata* or *C. albicans* as described for Fig. 3. At specific time points p.i., the mice were euthanized, and kidneys were excised and homogenized. Levels of the immunoreactive cytokines TNF- $\alpha$  (a), IL-12 p70 (b), IFN- $\gamma$  (c), and IL-10 (d) were quantified in kidney homogenates. Results represent the mean  $\pm$  SEM of two separate experiments, 8 to 14 mice per treatment group. \*, significantly greater than control mice, P < 0.05.

3e) mRNAs were significantly enhanced in kidneys from *C. glabrata*-infected mice within 2 to 7 h p.i., with maximal induction of mRNAs for TNF- $\alpha$  and IFN- $\gamma$  at  $\leq$ 7 h p.i. and for IL-12 p40, IL-12 p35, and IL-10 at 144 h p.i. These cytokine mRNAs were also significantly enhanced in kidneys from *C. albicans*-infected mice; however, significant induction occurred later, at 4 to 24 h p.i., with maximal induction of mRNAs for TNF- $\alpha$  (Fig. 3a) at 72 h p.i., IL-12 p40 (Fig. 3b) at 24 h p.i., and IL-12 p35 (Fig. 3c), IFN- $\gamma$  (Fig. 3d), and IL-10 (Fig. 3e) at 48 to 72 h p.i.

Temporal induction of immunoreactive cytokine activity in kidneys of infected mice. In subsequent studies, the kinetics of induction of the corresponding cytokine proteins were assessed in kidneys of infected mice by cytokine-specific ELISAs. TNF- $\alpha$  (Fig. 4a), IL-12p70 (Fig. 4b), and IFN- $\gamma$  (Fig. 4c) proteins were significantly enhanced in kidney homogenates of *C. glabrata*-infected mice within 2 to 7 h p.i., with maximal induction within 4 to 24 h p.i. In contrast, IL-10 protein was not

significantly increased in kidneys of *C. glabrata*-infected mice at any time point p.i. (Fig. 4d). Immunoreactive TNF- $\alpha$  (Fig. 4a) was also significantly increased in kidney homogenates of *C. albicans*-infected mice; however, this was not apparent until  $\geq$ 48 h p.i. In contrast, IL-12 p70 (Fig. 4b) and IFN- $\gamma$  (Fig. 4c) proteins were not significantly induced in kidneys of *C. albicans*-infected mice at any time point p.i., while IL-10 protein was significantly enhanced in kidneys of similarly infected mice within 48 h p.i. (Fig. 4d).

Role of proinflammatory cytokines in host defense against systemic *C. glabrata* infection. To assess the biological relevance of TNF- $\alpha$ , IL-12 p70, and IFN- $\gamma$  in host defense against systemic *C. glabrata* infection, mice were administered cytokine-specific neutralizing MAbs prior to infection. At 3, 5, and 7 days p.i., mice were humanely euthanized, kidneys were excised, and *C. glabrata* organisms were quantified in kidney homogenates by culture. As shown Fig. 5, treatment of mice with anti-TNF- $\alpha$  MAb resulted in a significant increase in *C*.



FIG. 5. Role of endogenous TNF- $\alpha$ , IL-12, and IFN- $\gamma$  in resolution of primary systemic *C. glabrata* infection. Crl:CF-1 mice were administered control (IgGa) (ID), TNF- $\alpha$  (ID), anti-IL-12 (ID), or anti-IFN- $\gamma$  (ID) MAb (1 mg/mouse intraperitoneally) 1 day prior to infection with *C. glabrata*. At 3, 5, and 7 days p.i., mice were euthanized, kidneys were excised and homogenized, and growth of *C. glabrata* was quantified by culture of kidney homogenates. Results represent the pooled mean  $\pm$  SEM of two separate experiments, 10 to 15 animals per treatment group. \*, significantly greater than similarly infected mice administered control MAb, P < 0.05.

glabrata organisms in infected kidney at all time points p.i. compared to infected mice administered control MAb (IgG2a). In contrast, there was no significant increase in the number of organisms recovered from kidneys of similarly infected mice administered either anti-IL-12 or anti-IFN- $\gamma$  MAb compared to infected mice administered control MAb.

# DISCUSSION

Despite its increasing clinical significance, relatively little is known about the pathogenesis of systemic C. glabrata infection, and virtually nothing is known about host responses to infection with this organism (22). To gain insight into these issues, we infected immunocompetent Crl:CF-1 mice i.v. with C. glabrata and compared tissue distribution and the morphologic response and cytokine activity with those in mice similarly infected with C. albicans. Results of these studies demonstrated C. glabrata was considerably less pathogenic than C. albicans, as injection of a relatively large number of C. glabrata organisms ( $10^8$  CFU/mouse) resulted in a chronic nonfatal infection with recovery of C. glabrata from kidneys for 21 days p.i. In contrast, inoculation with approximately 100-fold-fewer C. albicans organisms (i.e.,  $5 \times 10^6$  CFU/mouse) resulted in 100% mortality within 4 days p.i., with logarithmic growth of the pathogen in infected kidneys. Our results, demonstrating persistent recovery of C. glabrata from immunocompetent mice, are in sharp contrast to a previous study by Atkinson et al. (2), who concluded that immunocompromisation was required to achieve a sustained C. glabrata infection in mice inoculated i.v. with a relatively large number of C. glabrata organisms (i.e., 10<sup>8</sup> blastoconidia). While the reason for these discrepancies in host susceptibility to infection between the

two studies is not clear, it may be due to the use of different murine and/or *C. glabrata* strains.

Subsequent morphologic examination of tissues confirmed that the kidney is the preferred target organ in systemic C. glabrata of C. albicans infections. Furthermore, both Candida species were most frequently observed in the periglomerular cortical tissue rather than in the glomerular mesangium, suggesting that the glomerular mesangium may possess more innate candicidal potential than does the surrounding cortical vasculature. In agreement with previously published studies, our morphologic studies also demonstrated that while C. albicans is dimorphic in vivo, C. glabrata is monomorphic. Likewise, the presence of hyphae in tissues of C. albicans-infected mice was associated with a significant inflammatory response, characterized by a neutrophilic infiltrate initially, followed by a mononuclear cell infiltrate composed primarily of macrophages. The minimal inflammatory cell infiltrate into tissues of C. glabrata-infected mice was composed primarily of macrophages. These results are consistent with those of previous studies (22, 49, 74, 75) and suggest that formation of pseudohyphae and/or hyphae promotes neutrophil infiltration and is key to Candida virulence. The potential role of other factors known to be important in C. albicans pathogenicity, including proteinases and phospholipases (3, 4, 8, 33, 68), have not been investigated with regard to C. glabrata.

Proinflammatory cytokines including TNF- $\alpha$ , IL-12, and/or IFN- $\gamma$  have previously been shown to play key roles in host defense against *C. albicans* infections, due to their ability enhance phagocytosis of *C. albicans* blastoconidia and increase oxygen-dependent and independent candicidal activity (45, 60). In contrast, the production of anti-inflammatory cytokines such as IL-10 impairs development of a protective immune

response to *C. albicans*, due to downregulation of phagocytic cell effector mechanisms (46, 54, 57, 67, 86). Our findings agree with those of previous studies, which demonstrate a dose-dependent induction of anti-inflammatory cytokines in response to *C. albicans* (45) and suggest that rapid induction of proinflammatory cytokines is essential for prompt control of *C. albicans* or *C. glabrata* growth and host survival. Our findings also indicate that the rapid induction of both mRNAs and corresponding proteins for proinflammatory cytokines, including TNF- $\alpha$ , IL-12 p70 and IFN- $\gamma$ , and lack of induction of immunoreactive IL-10 may play a significant role in the lack of relative pathogenicity of systemic *C. glabrata* infection.

To characterize the biological relevance of induced proinflammatory cytokines in the pathogenesis of C. glabrata infection, mice were subsequently administered cytokine-specific neutralizing antibodies, and the effect on fungal growth was assessed. Our results demonstrate a key role of TNF- $\alpha$ , rather than IL-12 and IFN- $\gamma$ , in innate resistance to systemic C. glabrata infection, as neutralization of endogenous TNF- $\alpha$  activity alone resulted in significant increase in C. glabrata growth in infected tissues. These results complement those of previous studies which have shown that murine resistance to primary C. albicans infections was dependent on TNF- $\alpha$  and independent of IFN-y and IL-12 (38, 40, 44, 45, 56, 62). The mechanism(s) by which TNF- $\alpha$  inhibits growth of *C. glabrata* has not been thoroughly investigated. However, TNF- $\alpha$  has multiple regulatory effects, exerting endocrine, paracrine, and autocrine control of inflammatory responses (37, 71). Furthermore, TNF- $\alpha$  facilitates phagocytic cell activation, resulting in altered cell functional responses including increased adherence, enhanced generation of reactive oxygen and nitrogen species, enhanced degranulation of azurophilic granules, and increased phagocytosis (21, 26, 34, 39, 42, 43, 70), all of which could facilitate control of C. glabrata replication in vivo.

Despite induction of a polarized proinflammatory cytokine response, kidneys of immunocompetent Crl:CF-1 mice remained persistently infected with C. glabrata, while the organism was cleared from the brain, heart, lungs, liver, and spleen. Mechanisms by which C. glabrata selectively resists destruction by innate immune responses in the kidney are incompletely understood. However, our morphometric examination of infected tissues demonstrated that neutrophils, which are essential for resolution of C. albicans infections, are much less numerous in tissues from C. glabrata-infected mice. Previous studies have demonstrated that leukocytes are recruited from the bloodstream into infected tissues at least in part by chemotactic cytokines and leukocyte adhesion molecules expressed by the vascular endothelium (11, 23, 50). Recent studies have demonstrated that while both chemotactic cytokines and leukocyte adhesion molecules are induced in cultured vascular endothelium in response to endocytosis of C. albicans, neither are expressed by similar cells following endocytosis of C. glabrata (23). The relative absence of these mediators likely contributes to the minimal inflammatory cell response in tissues from C. glabrata-infected mice. Furthermore, because chemotactic cytokines facilitate release of azurophilic granules, thereby contributing to phagocytic cell candicidal activity (19), a potential lack of these mediators may also contribute to persistent C. glabrata infection. Our results also support conclusions of previous studies which demonstrate that C. albicans

and *C. glabrata* differ phenotypically, as *C. albicans* is dimorphic whereas *C. glabrata* is monomorphic in vivo. Because phenotypic differences profoundly influence the efficacy of phagocyte fungicidal responses (13, 85), it is likely that these different *Candida* species differ in both their capacities to trigger phagocytic cell activation and their susceptibilities to fungicidal activity. Future studies to identify interactions between *C. glabrata* and host cells including endothelial cells and phagocytic cells are warranted.

In summary, we have demonstrated that immunocompetent mice following systemic inoculation with *C. glabrata* develop chronic nonfatal renal infections which are associated with rapid induction of proinflammatory cytokines including TNF- $\alpha$ , IL-12, and IFN- $\gamma$ . Furthermore, endogeneous TNF- $\alpha$  plays a dominant role in controlling growth of *C. glabrata* in vivo, as neutralization of TNF- $\alpha$  activity resulted in enhanced tissue burden. Future in vivo studies to elucidate the role of endogenous cytokines in host resistance to *C. glabrata* are warranted, as manipulation of cytokine gene expression may provide an important adjuvant therapy for prevention and/or treatment of systemic candidiasis in immunocompromised patients.

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