

Host response to *Candida albicans* bloodstream infection and sepsis

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Candida albicans is a major cause of bloodstream infection which may present as sepsis and septic shock - major causes of morbidity and mortality world-wide. After invasion of the pathogen, innate mechanisms govern the early response. Here, we outline the models used to study these mechanisms and summarize our current understanding of innate immune responses during *Candida* bloodstream infection. This includes protective immunity as well as harmful responses resulting in *Candida* induced sepsis. Neutrophilic granulocytes are considered principal effector cells conferring protection and recognize *C. albicans* mainly via complement receptor 3. They possess a range of effector mechanisms, contributing to elimination of the pathogen. Neutrophil activation is closely linked to complement and modulated by activated mononuclear cells. A thorough understanding of these mechanisms will help in creating an individualized approach to patients suffering from systemic candidiasis and aid in optimizing clinical management.

Candida Bloodstream Infection and Sepsis

Severe sepsis and septic shock are major causes of death and morbidity world wide,¹ and several studies have suggested that the problem is increasing due to growing numbers of patients at risk.^{1,2} Epidemiological analyses show a shift in the classes of microorganisms causing sepsis. The incidence of Gram-positive organisms has increased for several years, and drawn equal with Gram-negative bacteria in some studies.¹ However, with the global spread of Gram-negative multi-resistance, Gram-negative pathogens continue to pose a major threat. In addition to bacteria, fungi—mainly *Candida albicans* and other *Candida spp.*—can cause sepsis and this entity has increased over the last decades, now causing significant impact and health care-associated costs.^{2,3} In addition, fungal sepsis is associated with a higher mortality than bacterial sepsis.^{2,4–8} *Candida* bloodstream infection

frequently arises from either gastrointestinal colonization and transmigration of the pathogen through the mucosal barrier, or from colonization of foreign material for example, intravenous (i.v.) catheters.³ Colonized i.v. catheters may account for as much as 25–40% of cases of candidemia.^{9–11} In the EPIC-II study, a 1-day point prevalence study involving 13,796 analyzed patients in 1,265 intensive care units, fungi accounted for 19% of all infections.¹² A retrospective analysis of this patient cohort revealed that 12.6% of all positive blood cultures were either positive for *Candida spp.* alone or detected mixed bacterial and fungal infection.¹³ This is in line with other data showing that in the United States, *Candida spp.* account for 8–10% of all positive blood cultures.^{14,15} However, despite being a frequent cause of nosocomial infection, *Candida spp.* generally account for only ~5% of sepsis cases.¹⁶ This is related to the fact that *Candida* bloodstream infections—although showing a high mortality—do not fulfill classical diagnostic criteria for sepsis and septic shock in most cases.^{5,17,18} (Table 1). This suggests that classical diagnostic criteria for sepsis may be inadequate to fully account for the clinical implication of systemic fungal infection.¹⁹ In addition to primary *Candida* sepsis, invasive *Candida* infection frequently occurs as a complication of bacterial sepsis due to concomitant immune paralysis. These secondary *Candida* infections have been shown to prolong ICU stay, increase mortality and generate additional costs.²⁰

In recent years, our understanding of early immune activation processes during systemic *Candida* infections has advanced considerably. On the one hand, this has been achieved by combining insights from different infection models. Most importantly however, modern genomic technologies have allowed researchers to elucidate mechanisms of immune activation and response based on the analysis of genetic variation in human patients.²¹ In this review, we summarize our current understanding of early immune response to *Candida* during bloodstream infections which includes mechanisms that govern protective immune reaction to *C. albicans* invasion as well as harmful immune responses resulting in *Candida* induced sepsis and septic shock.

Analyzing Systemic *Candida* Infections

Various model systems have been employed in *C. albicans* research to date, including the fruit fly, nematode, wax moth and zebrafish. The latter has been particularly useful due to the presence of innate and adaptive immune systems, transparent tissues

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Table 1. *Candida* BSI and sepsis

	<i>Candida</i> BSI	<i>Candida</i> Sepsis
Frequency	5–15% of all BSI	2–5% of sepsis cases, only a minority of <i>Candida</i> BSI proceed to severe forms of sepsis (see below)
Diagnostic criteria	Positive blood-culture for <i>Candida</i> ^a	Systemic inflammatory response syndrome (SIRS) with 2 or more of the following symptoms: temperature <36°C or >38°C; heart rate >90/min; respiratory rate >20/min or PaCO ₂ <32 mmHg; WBC <4×10 ⁹ /L or >12×10 ⁹ /L or ≥10% bands due to an infection with <i>Candida</i> ^c
Pathology	Dissemination of <i>Candida</i> in the bloodstream with/without affection of (multiple) organs presenting as “acute disseminated candidiasis” or “chronic disseminated candidiasis” with the latter mainly occurring in neutropenic patients.	Clinical presentation is dominated by severe dysregulation of immunity, coagulation and circulation. In progressive disease this results in organ failure (“severe sepsis”) and cardinal decompensation (“septic shock”).
Associated mortality	< 30–40% ^{b, 6–8}	~70% ⁵ septic shock complicating <i>Candida</i> BSI is “a near fatal condition” ¹⁸

Note: ^aOther diagnostic tests may also be indicative, e.g., PCR based detection in blood, β -glucan testing. ^bThese are mortality rates from case series of *Candida* BSI including patients with sepsis, severe sepsis or septic shock; so fatality rates for *Candida* BSI without sepsis will be lower. ^cCurrently, several authors suggest to rephrase sepsis definitions and restrict sepsis to cases with resulting organ failure.¹⁹

and comparative intra-species transcriptional responses of *C. albicans*.^{22–24} Notably, the roles of NADPH oxidase in response to *C. albicans* hyphae have been expanded upon with the help of non-invasive imaging of spacio-temporal macrophage responses in this model.²⁴ The most commonly used infection model is the mouse, and murine models have been developed to mimic both major routes of *C. albicans* dissemination.^{25–27} In the i.v. murine infection model, fungal cells are administered directly into the bloodstream and rapidly disseminate, evoking a strong inflammatory reaction.²⁸ The major target organs are the kidneys, and both systemic inflammation as well as rapid deterioration of the animals resembles hyper-inflammatory sepsis. However, exclusive kidney involvement is rare in human systemic candidiasis and kidney manifestation typically only occurs in disseminated candidiasis affecting multiple organs.^{29,30} Despite this, the murine infection model enables the analysis of rapid immune activation induced by systemic *Candida* dissemination and has undoubtedly revealed important insights into host responses to fungal infection.^{31,32}

Unlike humans, mice are intrinsically *Candida* naïve and establishing colonization of the gastrointestinal tract in adult mice requires anti-microbial therapy and oral application of *Candida*.³² A murine model of *C. albicans* gastrointestinal colonization and systemic spread has been described by Koh et al.^{25,32,33} Concomitant introduction of immuno-suppression and mucosal damage after colonization resulted in translocation and dissemination by *C. albicans*. This model is particularly useful for studying virulence factors and immune mechanisms involved in translocation and dissemination. A major advance in our technological portfolio to study host-pathogen interaction during systemic infection is the development of *in vivo* imaging systems.^{34,35} Recently, these tools have been used for *in vivo* imaging of *Candida* infection.³⁶ This allows monitoring of dissemination and systemic infection over time in living animals with considerable sensitivity. Furthermore, it reduces animal tolls and offers the possibility to shift from end-point data toward

kinetic analyses. Initial experiments already revealed the gall-bladder as an unexpected site of *C. albicans* persistence during anti-microbial therapy.³⁶

As for all murine infection models, it has to be kept in mind that peripheral blood components in mice differ, both in numbers and function, from their human counterparts^{37,38} and conclusions from defined animal models are not necessarily transferable to human patients. To overcome some of these limitations, human whole blood infection models can be used to analyze host-pathogen interactions in a situation which closely mirrors that *in vivo*.³⁹ Such infection models have successfully been used to identify microbial virulence factors,⁴⁰ to analyze early immune responses,⁴¹ to determine the influence of genetic polymorphisms on immune response⁴² or to test potential therapeutic approaches or vaccine efficacy.^{43–46} With regard to activation of host immunity, whole blood infection assays can provide time-resolved data on cell activation, localization and physiological state of the pathogen. Most importantly whole blood infection assays require minimal pre-analytical handling of the cells. Therefore these assays avoid modulation of immune cell function by the isolation procedure that inevitably occurs when using purified primary human immune cells^{47–49} (see Fig. 1). However, purified primary cells provide an important tool to analyze specific contributions of receptors and signaling pathways in defined cell populations^{50,51} and patterns of activation observed in the whole blood model do not necessarily reflect those observed in organ tissue. Furthermore, immune cell activation in blood *in vivo* is also determined by tissue derived mediators which are absent in *ex vivo* blood. In contrast, in the whole blood model, many parameters of immune cell function remain inaccessible to direct quantification due to experimental limitations. We have shown recently that bio-mathematical modeling can provide tools to partially overcome these limitations. Using such a virtual infection model, it was for the first time possible to prove the dominant role of neutrophils in the immune response to *Candida* in human blood.³⁹





	 Cell culture	 Primary cells	 Whole blood	 Mouse
PRO	<p>easy, cost effective and scale-up possibility</p> <p>well developed molecular and functional tools, imaging possible</p>	<p>system allows dissection of human cell functions</p> <p>human and murine comparisons and analyses of patient samples possible</p> <p>live-cell imaging possible</p>	<p>multi-faceted system allowing interaction of different immune mechanisms</p> <p>independent of media and serum, “no-touch” isolation</p> <p>human and murine comparisons and analyses of patient samples possible</p>	<p>complexity of an intact living mammal</p> <p>genetic modification possible</p> <p>disease progression study possible</p>
CON	<p>receptors, signalling cascades and effector mechanisms may be lost</p> <p>physiological relevance difficult to prove</p>	<p>limited molecular and functional tools</p> <p>function can be altered by isolation procedure</p> <p>donor variation depending on uncontrollable environmental factors</p>	<p>only short-term analyses, live-cell imaging currently not possible</p> <p>limited possibilities to study genetic influences</p> <p>limitations to dissecting single cell-type interactions</p>	<p>immune cell distribution and function different from human</p> <p>not a natural host for <i>Candida</i></p> <p>animal sacrifice</p>

Figure 1. Advantages and disadvantages of *C. albicans* infection models. The most commonly employed *C. albicans* infection models are immortalized cell culture, primary immune cells, whole blood and mice. Each method bears both limitations and advantages, a thorough knowledge of which can be applied to determining the most suitable model.

Finally—with all models being but models—it is encouraging to see that modern technologies allow the analysis of molecular pathways determining the outcome of host–pathogen interaction directly in human infection. Genetic analyses in patients suffering from chronic mucocutaneous candidiasis have generated unprecedented insight into the role of STAT1 signaling and Th17 response in anti-fungal immunity.^{3,52,53} These findings have been extended to other fungal infections and significantly advanced our knowledge of antifungal immunology.⁵⁴ By integrating transcriptional analysis and functional genomics, Smeeckens et al. identified a prominent role of the type I interferon pathway in anti-*Candida* host defense. They confirmed these analyses by showing that polymorphisms in type I interferon genes modulated *Candida*-induced cytokine production and were correlated with susceptibility to systemic candidiasis.⁵⁵ Genetic analyses of patients at risk for non-*Candida* fungal infections have also identified other important regulators of anti-fungal immunity.^{3,21,56} Together, these model systems have

generated important insight into mechanisms governing immune responses against *Candida* and established a repertoire of receptors and signaling cascades relevant for fungal recognition.⁵⁷ In the next sections, we will put a focus on immune effector mechanisms that are relevant for systemic *Candida* infections.

Complement in *Candida* Sepsis

Considerable evidence shows that complement activation plays a central role in systemic infection and sepsis.^{58,59} The interaction of *C. albicans* with complement has recently been reviewed in detail and we refer to the review of Luo et al.⁶⁰ Although patients suffering from genetic defects in complement do not show increased risk for fungal infections, evidence from both murine and *in vitro* experiments indicates an important role of complement in antifungal responses. However, even in patients with chronic granulomatous disease – a severe functional

defect of neutrophils - numbers of invasive *Candida* infections are surprisingly low, (Winkelstein et al.^{60b} and Falcone and Holland^{60c}). This may reflect both redundancy of immune effector functions or the fact that intestinal barrier integrity may be at large protective against *Candida* invasion.^{25,60a}

Aside from multiple functions in the immune response against invading pathogens, complement activation also modulates other signaling events during systemic infection. Several studies have shown that Toll-like receptor (TLR) activation can occur by way of complement, and multiple nodes of interaction between complement and coagulation have been identified.^{61,62} The surface of *C. albicans* is a strong trigger inducing all 3 pathways of complement activation⁶³ (Fig. 2). This results in rapid formation of C3 convertase, generation of

chemotactic cleavage fragments and subsequent fungal opsonization by C3b, which facilitates phagocytosis.⁶⁴⁻⁶⁶ Of major importance during sepsis is the generation of high levels of the complement activation products C3a and C5a, which act as anaphylatoxins.⁵⁹ Mice lacking the C5a precursor molecule C5 or the C3a precursor C3 are highly susceptible to invasive *C. albicans* infection.⁶⁷⁻⁶⁹ Moreover, C5 deficiency is associated with increased levels of pro-inflammatory cytokines, including TNF- α and IL-6, and rapid fungal replication in many organs.^{60a,70,71} The prominent effects of C5 deletion are most likely related to the lack of its activation product C5a, which has been shown to be critical for activation of human monocytes by *C. albicans* and which significantly enhances the release of pro-inflammatory cytokines, e.g., IL-6 and IL-1 β .⁷²

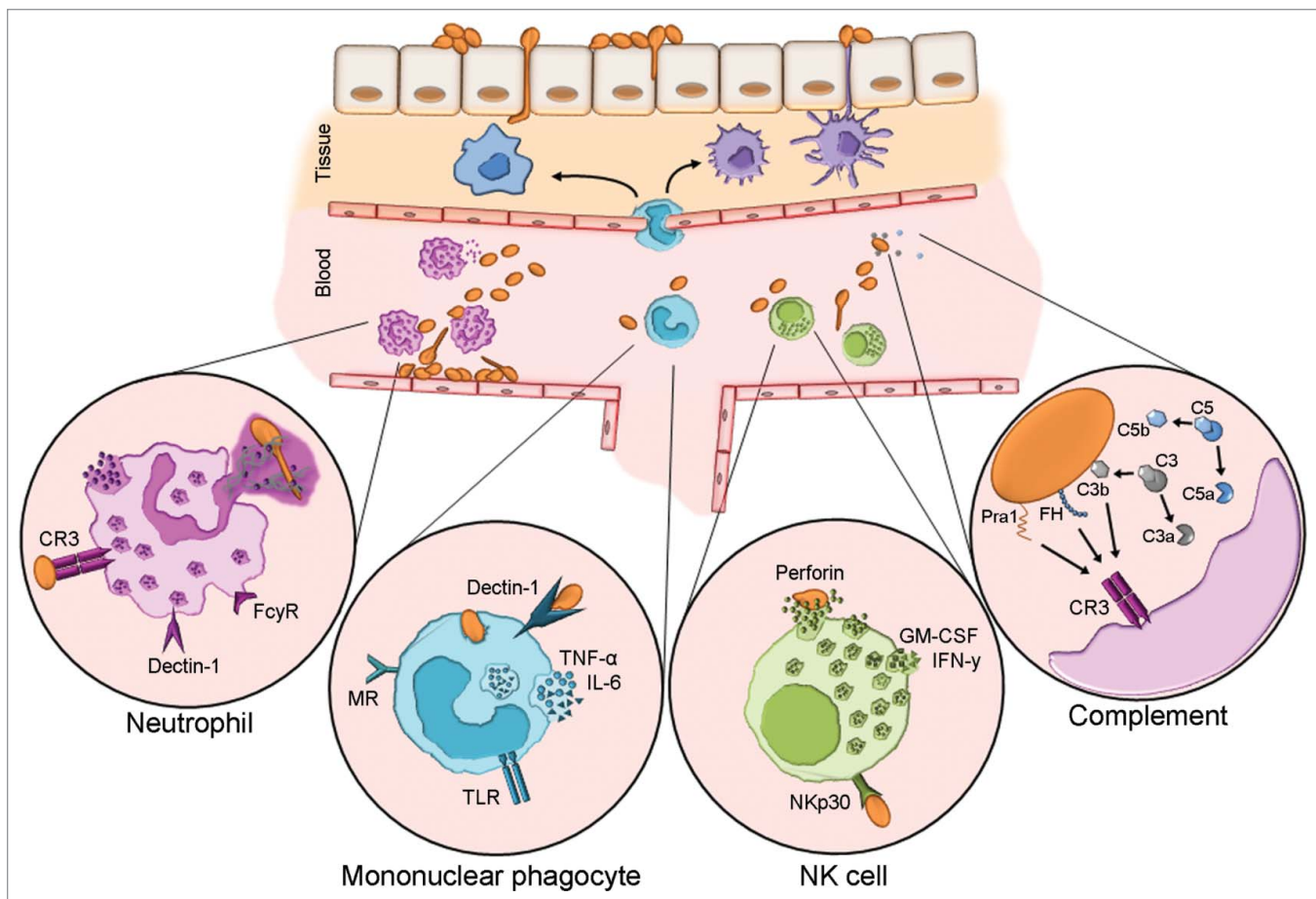


Figure 2. Host innate immune responses to *C. albicans* blood stream infection. Upon transmigration of skin/mucosal barrier and entry to the blood stream, *C. albicans* will activate the complement system and encounter circulating and resident leukocytes. Neutrophils are considered the forerunners of innate responses to *C. albicans* due to their efficient recognition and clearance of the fungus. Complement receptor 3 (CR3) and Fc γ R are the paramount human neutrophil receptors capable of recognizing *C. albicans*. Contact to the fungus initiates various signaling cascades, which in turn instigate effector mechanisms e.g. phagocytosis, oxidative burst and neutrophil extracellular trap (NET) formation. Mononuclear phagocytes include circulating monocytes as well as macrophages and dendritic cells residing in various tissues. These cells recognize *C. albicans* principally via dectin-1 which acts in concert with other pattern recognition receptors. They are a dominant source of IL-6 and TNF- α , both of which can exert direct effects on the fungus and also influence other immune cells. Although NK cells harbor many PRR capable of *C. albicans* recognition, NKp30 is the principal mediator of NK cell anti-*Candida* activity. NK cell-released perforin is directly candidacidal. Additionally, NK cells secrete GM-CSF and IFN- γ which both potentially modulate other immune cells. *Candida* is a potent activator of human complement. Complement activation results in opsonization by deposition of C3b and release of anaphylatoxins C5a and C3a which influence immune cell recruitment and effector mechanisms. In addition to C3b, recognition of the fungal protein Pra1 and surface-recruited Factor H, a major regulator of complement activation, mediate recognition by immune cell CR3.

Furthermore, C5a can influence neutrophil function during sepsis and even induce paralysis of neutrophils.^{73,74} Thus, early and pronounced activation of complement is also a critical determinant in the activation of cellular responses toward *Candida* and directly triggers activation of major innate immune cell populations involved in anti-fungal immunity while at the same time potentially contributing to adverse effects of fulminant immune activation.

The Various Roles of Neutrophils in *C. albicans* Sepsis

Polymorphonuclear leukocytes (PMN) represent the majority of circulating leukocytes in humans. The sheer number of this cell type in circulation, as well as their aggressive and successful elimination of invading pathogens,⁷⁵ advocates them as forerunners of innate defense. In the murine system, early availability of neutrophils has been shown to be essential for protection.⁷⁶ Both clinical and experimental evidence has confirmed that neutrophils are integral components of the innate immune system during *C. albicans* infection. Most importantly, human neutrophils are the only immune cell which can prevent the transition from yeast to filamentous growth—a key virulence trait of *C. albicans*,^{37,77} and dominate the transcriptional response of *C. albicans* in whole blood.⁷⁸ PMN control the elimination of *C. albicans* from the bloodstream³⁹ and as such, these professional phagocytes are considered primary effector cells in *C. albicans* infection prevention and neutropenia is a clear risk factor for mortality in human systemic candidiasis.^{79,80} However, it must be noted that in systemic *Candida* infection, PMN can also exert adverse effects which are linked to their potent pro-inflammatory activity and bystander damage to host tissues inflicted by antimicrobial effector mechanisms. In line with this, neutropenic patients with invasive candidiasis may require corticosteroid therapy after neutrophil reconstitution to avoid adverse effects of hyper-inflammation.⁸¹ Circulating PMN are recruited rapidly to sites of *Candida* infection and upon activation IL-8 is the major cytokine released by *C. albicans* activated PMN which promotes the further recruitment of PMN.⁷⁷ Consequently, the IL-8 – IL-8R signaling axis is essential for protective immunity.⁸² However, several other cytokines contribute to PMN recruitment and function. In the murine model system for example type 1 interferon (INF-1) signaling mediates neutrophil recruitment by stimulating early release of inflammatory cytokines, e.g., IL-6.⁸³ IL-17 can be produced by T cells, but also neutrophils during *Candida* sepsis, when it promotes early and sustained recruitment of neutrophils into the *C. albicans* infected kidney.⁸⁴ While IFN-1 and IL-17 are important at early stages, chemokine receptor CCR1 is necessary for PMN trafficking from the blood to the kidney during later stages of infection,⁸⁵ which is correlated with neutrophil-mediated immunopathology and mortality. While other myeloid cells constantly expressed CCR1, neutrophils were found not to express the receptor until days after *C. albicans* infection. Independent of CCR1 expression, neutrophils were able to mount normal effector mechanisms, demonstrating that

the immunopathology related to the quantity of infiltrating neutrophils and not their activity.⁸⁵ Aside from recruiting PMN, cytokines and chemokines are involved in activating these cells during *Candida* infection. Murine knock-out strains of several cytokines display a decrease in PMN anti-*C. albicans* activity due to an impaired intrinsic pre-stimulation of PMN.⁸⁶ Cell types that secrete factors modulating PMN anti-fungal activity include antigen-presenting cells, epithelial and endothelial cells as well as antigen-specific T cells.⁸⁶⁻⁸⁸ In addition to this, NK cell-PMN cross-talk may be immunologically relevant^{89,90} (see later).

Neutrophil receptors involved in *Candida* recognition

PMN express various pattern recognition receptors as well as receptors for opsonizing antibodies and complement components.⁹¹ Thus, interaction with *Candida* as well as concomitant activation is mediated by a set of closely interlinked interactions and signaling events and cannot be contributed to a single receptor. However, several lines of evidence suggest that complement receptor 3 (CR3; also known as $\alpha_m\beta_2$ integrin; Mac-1, CD11b/CD18) is a major receptor for *C. albicans* yeast and hyphae on human neutrophils.^{50,92,93} CR3 is expressed on circulating neutrophils and may be rapidly recruited from intracellular compartments to the cell surface upon activation.⁹⁴ Van Bruggen and co-workers found that phagocytosis of unopsonized *C. albicans* by human PMN was mainly mediated by CR3, while no explicit role for neutrophil expressed dectin-1 was observed⁹⁵ (Fig. 2). Multiple possibilities for the interaction of *C. albicans* with this receptor have been described: CR3 is the major receptor for C3b and its cleavage product iC3b and can therefore recognize *C. albicans* after complement mediated opsonization.⁹⁶ Furthermore, the *C. albicans* surface protein Pra1 as well as the cell-wall component β -glucan can directly bind to CR3.⁹⁷ Finally, *C. albicans* harbors a set of proteins known as CRASPs (complement regulator surface acquiring proteins) that can recruit the complement regulator factor H (CFH) and related complement regulators to its surface.^{60a} After recruitment to the surface of *Candida*, CFH family proteins CFH, CFH-like protein 1 (CFHL1) and CFH-related protein (CFHR) 1 can bind to CR3 and increase attachment of neutrophils to *C. albicans*.⁹⁸ Thus, CR3 is able to mediate both uptake of both (C3b-)opsonized and non-opsonized *C. albicans*. In contrast to CR3, human dectin-1, a major human receptor for β -glucan,⁹⁹ seems to play a minor role in phagocytosis of *Saccharomyces cerevisiae* or zymosan by human PMN.⁹⁵ In addition, neither generation of reactive oxygen intermediates (ROI) nor secretion of IL-8 in response to zymosan required dectin-1 signaling in human PMN.⁹⁵ These data may indicate a less pronounced role for dectin-1 in PMN-*Candida* interaction, contrary to the dominant role of dectin-1 signaling in other cell types (see below). This is further confirmed by recent findings showing that killing of *C. albicans* by human PMN occurs independently of dectin-1⁵⁰. In contrast, loss of caspase-associated recruitment domain 9 (CARD9), the intracellular adapter molecule downstream of dectin-1 signaling,^{100,101} has been shown to significantly impair unopsonized anti-*Candida* immunity in human neutrophils.⁵¹ However, this function seems to be independent of dectin-1 and is known to act downstream

of several receptors, including other C-type lectin receptors.⁵⁰ It should be noted that dectin-1 may be more important for the activation of murine PMN by *Candida*.¹⁰² In the murine system, dectin-1 has been shown to induce and activate CR3 after ligand binding to also recognize fungal components.^{103,104} This cross-activation was found to be required for murine neutrophil cytotoxic responses.¹⁰⁴ CR3 activation and neutrophil effector functions in murine neutrophils also required exchange factors for RhoGTPases Vav1 and Vav3.¹⁰⁴

Neutrophils also express a range of Toll-like receptors (TLR). In mice, TLR2 expression is required for optimal neutrophil chemotaxis, pro-inflammatory cytokine production and MPO activity in response to murine *C. albicans* infection.¹⁰⁵ However, TLR signaling is not essential for anti-*Candida* activity of human PMN as shown by testing PMN from patients with IRAK4 deficiency, a central component in TLR signaling.¹⁰⁶ Finally, neutrophils constitutively express FcγR; specifically, FcγRIII (CD16) activation can initiate characteristic neutrophil activation mechanisms, e.g., degranulation and respiratory burst.^{107,108} In summary, while CR3 seems to play a central role multiple receptors may contribute to the interaction of PMN with *C. albicans*.

Anti-candida effector mechanisms of neutrophils

Once they recognize the pathogen, PMN have a range of weapons they can unleash against *C. albicans*. Among the most prominent mechanisms is the rapid formation of reactive oxygen intermediates (ROI) termed 'oxidative burst'. Upon activation, the neutrophilic NADPH oxidase-complex is assembled on the cytoplasmic membrane to release superoxide into the extracellular space, or on the phagosomal membrane to release oxidants into phagosome.^{109,110} PMN isolated from NADPH (and MPO) deficient mice show reduced *C. albicans* killing *ex vivo*.^{111,112} Aside from inducing oxidative stress,^{113,114} ROI are required for the formation of the so-called neutrophil extracellular traps (NETs).^{115–117} However, this may only be the case in the blood stream as NET formation seems to be CR3 dependent and ROI independent in tissues.⁹³ NETs provide a barrier past which a pathogen cannot easily pass, and instead becomes entangled in a mesh of cytotoxic compounds. These are structures formed of released neutrophil chromatin decorated with anti-microbial substances, principally calprotectin,¹¹⁷ which are normally stored within neutrophilic granules and can be formed within 10 minutes of activation.¹¹⁸ NETs have been shown to entrap free bacteria in the bloodstream and therefore prevent dissemination in an *Escherichia coli* model of sepsis.¹¹⁹ They may form simply from the plasma of septic patients,¹²⁰ as well as upon direct contact with a pathogen. *C. albicans* induces NET formation, after which both filamentous and yeast forms are trapped and killed.¹¹⁶ The relevance of NETs to *Candida* sepsis may be suggested by increased susceptibility of mice deficient in calprotectin, a key component of NETs, to systemic candidiasis. However, with additional immunomodulatory effects of calprotectin well established in the literature, this is not formal proof for a role of NET-formation in anti-*Candida* immunity.¹¹⁷ In addition to oxidative burst and NET formation, neutrophils contain an arsenal of anti-microbial

peptides and proteins, many of which also have anti-fungal activity. Furthermore, they can release cytokines, which recruit other immune cells and potentially induce damage in *Candida* and induce carbohydrate and nitrogen starvation.^{113,121} However, it is still relatively unclear exactly how PMN kill *C. albicans*. Most likely, a combination of different stresses forms the basis for their fungicidal activity.^{122,123} In a recent study, 2 distinct mechanisms for killing of *C. albicans* dependent on how PMN recognize either opsonized or unopsonized fungus have been described.⁵⁰ Unopsonized *C. albicans* is recognized via CR3 and killing is CR3 and CARD9 dependent, whereas dectin-1 was not required. In contrast, opsonized *C. albicans* was recognized via FcγR, and PKC and NADPH oxidase activity were the principal killing machinery.⁵⁰ The latter studies demonstrate that in the complex environment of the host, combinations of killing mechanisms are in play which occur independent of pattern recognition receptors like TLR and dectin-1 dominating the activation of monocytic cells and can compensate for each other under deficiency conditions. Thus, redundancy of anti-fungal mechanisms is most likely a major contributor to the potent fungicidal activity of PMN.

Linking Innate and Adaptive Immune Responses: Monocytes, Macrophages and Dendritic Cells

Relative to neutrophils, monocytes—the second most abundant innate immune cell population in human blood—may play a smaller role in the initial response to *C. albicans* blood stream infection and are in fact less effective in *C. albicans* killing in whole blood.³⁹ Nevertheless, monocytes as well as macrophages and dendritic cells (DC) are crucial in establishing protective immunity and monocyte deficient mice suffer quick dissemination into organs and higher mortality following *C. albicans* infection,¹²⁴ although monocytopenia alone does not confer susceptibility to candidiasis.^{125,126} Monocytes may also play an integral role in anti-*Candida* defense in locations of dissemination, e.g., the kidney, where early and organ specific innate responses have recently been demonstrated in the murine model.¹²⁷ Abrogation of inflammatory monocyte trafficking into the kidneys impaired fungal clearance and decreased survival. Migration of these cells was mainly mediated by CCR2 and depletion of CCR2-expressing cells led to uncontrolled fungal growth in the kidneys and brain.¹²⁸ Similarly, the promotion of macrophage survival and accumulation in tissues by CX3CR1-dependent mononuclear cells is a critical mechanism by which the early innate response can protect against candidiasis.¹²⁹ DC are the most potent antigen presenting cells in the human body and play a crucial role in inducing and modulating adaptive immune responses. Recently the role of DC in anti-fungal immune responses has been reviewed (see ref¹³⁰). The spectrum of receptors used for recognition of *Candida* in these cells is broad and includes C-type lectin receptors (CLR) including dectin-1, dectin-2, Macrophage Mannose Receptor (MMR) and DC-SIGN, as well as TLRs, namely TLR2, TLR4, TLR7 and TLR9.^{91,130} Aside from these, several other receptors can contribute to recognition of *Candida*, including complement receptors CR3, CR4 and Fc-receptors. Despite this plethora of potential

receptors, dectin-1 seems to play a prominent role in the recognition of *C. albicans* and activation of DC by *C. albicans* occurs via dectin-1 recognition of β -glucan, and involving, to a lesser extent, recognition of other surface structures by TLR.¹³¹ Similarly, dectin-1 is central for recognition of *A. fumigatus*.¹³² Dectin-1-triggered CARD9 signaling then drives cytokine production, through an NF- κ B and NFAT-dependent pathway.¹³³ The central importance of CARD9 signaling to the DC response to *C. albicans* is highlighted by the finding that mice deficient in the dectin-1-CARD9 pathway are unable to mount normal DC cytokine secretion, for example IL-6 and TNF- α , and neither are they able to generate Th17 cells upon confrontation with *C. albicans*.^{101,134} In addition, IFN- β production by DC induced by *C. albicans* is largely dependent on dectin-1 and dectin-2 mediated signaling and plays a crucial role in the defense against *C. albicans* infection.^{83,135,136} The prominent role of CLR signaling in murine *Candida* infection has recently been confirmed by a study showing that the selective loss of spleen tyrosine kinase Syk but not the TLR adaptor protein MyD88 in DC abrogates innate resistance to systemic *C. albicans* infection in mice. Syk is recruited by dectin-1 and other CLR and can trigger NF- κ B activation via CARD9¹⁰¹ as well as other signaling cascades e.g., NFAT, MAPK and PI3K.^{137,138} Engagement of dectin-1 with *C. albicans* leads to Syk expression and CARD9 complex assembly. This was found to be essential for *C. albicans* induced IL-23p19 release, which in turn mediates GM-CSF secretion by natural killer (NK) cells at the site of infection. As NK cell-derived GM-CSF sustains the anti-*Candida* activity of neutrophils, the authors conclude that DC mediated an innate response to *Candida* sepsis, dependent on SYK signaling.^{139,140}

Natural Killer Cells

Although traditionally studied in the context of anti-viral and anti-tumor immunity, NK cells have recently gained prominence as key players in various fungal infections. These cells form a population of innate lymphocytes, accounting for 5–10% of circulating blood lymphocytes. Most of the blood NK cells express high levels of CD56 (CD56bright) and produce high levels of perforin.¹⁴¹ Early on, activity of NK cells was reported against *Cryptococcus neoformans*.^{142,143} Anti-fungal roles for NK cells in aspergillosis and cryptococcosis are attributed to cytokine and perforin release, respectively.^{144–146} Whereas patients with inherited NK cell deficiencies are generally not more susceptible to candidiasis than the healthy population, in a murine model of invasive oropharyngeal candidiasis, combined T and NK cell deficiencies were detrimental to outcome, while T cell deficiency alone exerts no discernible phenotype.¹⁴⁷ Recently, several studies have addressed the role of NK cells in systemic *Candida* infection. NK cells are activated by *C. albicans* and can wield direct perforin mediated cytotoxic effects on the fungus.⁹⁰ Interestingly, human NK cells have been found to ingest *C. albicans* by phagocytosis and elicit pro-inflammatory responses.⁹⁰ NK cells harbor a range of receptors capable of recognizing *C. albicans* such as TLR, mannose,

scavenger, FC γ receptor and NK cell activating receptors.^{148,149} However, the principal *C. albicans* recognition receptor was recently shown to be NKp30.¹⁵⁰ NKp30 was responsible for recognition and killing of *C. albicans* and also *C. neoformans*. Recognition of fungi via NKp30 resulted in PI3K signaling and perforin release, which has been shown to exert anti-fungal activity. Using NK cells from HIV infected patients, which exhibit a diminished expression of NKp30, the authors showed that reduced levels of NKp30 are associated with defective anti-fungal activity.¹⁵⁰ NK cells can also indirectly affect *C. albicans* via modulation of other immune cells.^{90,140} Several cytokines released by *Candida*-activated NK cells, including GM-CSF and IFN- γ , may directly trigger anti-fungal effector mechanisms in other immune cells.^{140,151,152} NK cells have been shown to exert immuno-modulatory functions,^{128,153–155} influence PMN survival¹⁵⁶ and expression of neutrophil activation markers.¹⁵⁷ In a murine model for *C. albicans* sepsis in immuno-competent mice, NK cells have a detrimental influence on the course of disease by promoting hyper-inflammation, which resulted in reduced survival time.¹⁵⁸ In contrast, in immuno-compromised animals deficient in B and T cells, NK cells were found to be beneficial in recruiting and activating other immune cells, aiding in eventual clearance of the fungus.¹⁵⁸

Conclusion and Outlook

Immune responses in systemic *Candida* infection and sepsis are complex and involve several rapidly acting players. More importantly, the balance between protective immunity and harmful hyper-inflammation is hard to define and several protective inflammatory reactions have been shown to also contribute to sepsis pathology. A future thorough understanding of these mechanisms may offer new insight into the pathophysiology of these infections, as well as open new avenues for tests allowing early discrimination of bacterial and fungal sepsis and targeted anti-microbial therapy. With individualized approaches to clinical management of infections rapidly developing and a pressing need for stratification of the broad clinical entity sepsis being increasingly recognized, this research forms the basis for translational approaches to fungal sepsis.¹⁵⁹ To get meaningful insight into the underlying mechanisms, a combination of models has to be used, taking into account the strengths and weaknesses of each of them. Thus, although the murine system clearly provides the model of the highest complexity, it is not necessarily always superior. Finally, the field of infection genetics has provided major advances to our understanding of anti-*Candida* immunity. With molecular tools rapidly evolving and sequencing approaches becoming more and more feasible, it is likely that new findings will arise from in-depth studies of individuals suffering from well characterized diseases. Clearly, these studies will pave the way toward optimized and individualized clinical management of infectious diseases.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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