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## Exploiting antifungal immunity in the clinical context

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### Abstract

The continuous expansion of immunocompromised patient populations at-risk for developing life-threatening opportunistic fungal infections in recent decades has helped develop a deeper understanding of antifungal host defenses, which has provided the foundation for eventually devising immune-based targeted interventions in the clinic. This review outlines how genetic variation in certain immune pathway-related genes may contribute to the observed clinical variability in the risk of acquisition and/or severity of fungal infections and how immunogenetic-based patient stratification may enable the eventual development of personalized strategies for antifungal prophylaxis and/or vaccination. Moreover, this review synthesizes the emerging cytokine-based, cell-based, and other immunotherapeutic strategies that have shown promise as adjunctive therapies for boosting or modulating tissue-specific antifungal immune responses in the context of opportunistic fungal infections.

### Keywords

fungal infections; immunogenetic risk; antifungal immunity; immunotherapy

### Introduction

Since the 1980s, the global burden of opportunistic fungal infections has dramatically increased in humans. Life-threatening fungal infections such as *Pneumocystis jirovecii* pneumonia (PJP), cryptococcal meningoencephalitis, and disseminated histoplasmosis are AIDS-defining illnesses that continue to cause significant morbidity and mortality in resource-poor settings with limited access to antiretroviral and antifungal therapies [1]. The introduction of myeloablative chemotherapy and targeted immunosuppressive therapies for patients with neoplastic and autoimmune conditions has expanded the burden of opportunistic fungal infections such as invasive aspergillosis (IA) [2, 3]. Modern advances in the clinical management of critically ill patients in the intensive care unit (ICU) has resulted in an increased frequency of invasive candidiasis in recent decades [4–6]. The advent of

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allogeneic hematopoietic stem cell transplantation (HSCT) and solid organ transplantation (SOT) has transformed the management of patients with hematological malignancies and end-organ failure but has resulted in complex iatrogenic immunosuppressive states that significantly heighten host susceptibility to opportunistic fungal infections [7].

Despite improvements over the past two decades, the clinical outcome of immunocompromised patients who develop opportunistic fungal infections remains poor despite the administration of antifungal therapy. Several factors contribute to this clinical observation. Firstly, prompt diagnosis of fungal infections remains problematic due to the suboptimal sensitivity and specificity of available culture- and biomarker-based fungal diagnostic tests [8]. Delayed diagnosis in turn results in delayed initiation of appropriate antifungal therapy, which has been shown to increase patient mortality in the setting of invasive candidiasis, IA, and mucormycosis [9–11]. Secondly, despite the discovery and introduction in the clinic of several new antifungal agents [12, 13], the *in vivo* efficacy of antifungal therapy in immunosuppressed patients remains hindered by drug-drug interactions, pharmacokinetic and pharmacodynamic challenges, and drug toxicities. The emergence of antifungal resistance such as with multidrug-resistant *Candida auris*, echinocandin-resistant *Candida glabrata*, azole-resistant *Cryptococcus neoformans*, and azole-resistant *Aspergillus fumigatus* is particularly concerning as it can underlie suboptimal treatment responses and poor patient outcomes [14–17]. Thirdly, the profound net state of immunosuppression of at-risk patients is a major driver of susceptibility to acquisition of, and poor outcomes after, fungal infection, and immune restoration is often required to control opportunistic fungal infections in spite of the administration of antifungal therapy [18–20].

Thus, alongside improving fungal diagnostic tests, developing novel, broad-spectrum, and non-toxic antifungal agents, and investigating fungal virulence traits, enhancing our understanding of antifungal host defenses is essential for improving patient outcomes. This review first outlines how the recent surge in the characterization of genetic variants (single nucleotide polymorphisms [SNPs]) in certain immune pathway-related genes (Table 1) can be exploited in the clinic with the goal to assess the individualized risk of fungal infection development and prognosis in at-risk patients and to develop personalized strategies for antifungal prophylaxis, immunotherapy, and/or vaccination that could improve patient outcomes (Figure 1). Moreover, this review briefly discusses certain cytokine-based, cell-based, and other immunotherapeutic interventions that have shown promise in mouse models of fungal disease and/or human patients for boosting or dampening antifungal immune responses to benefit the infected mammalian host.

## 1. Immunogenetic-based risk assessment for fungal disease

An important clinical observation in patients infected with pathogenic fungi (and other non-fungal pathogens) is that there is significant heterogeneity in the clinical severity and outcome of infections and that clinical and environmental risk factors alone are not sufficient to fully explain the variable patient-specific risk for acquiring these infections. For example, although the majority of ICU patients share similar clinical risk factors for invasive candidiasis (e.g., broad-spectrum antibiotic use, central venous catheters, total parenteral

nutrition), the majority of these patients do not develop the infection and when candidemia develops in a subset of them, the clinical severity varies significantly among patients who share similar clinical and microbiological risk factors for developing poor outcome [4, 18]. In addition, despite the ubiquitous environmental exposure to *Aspergillus* via inhalation and similar clinical risk factors (e.g., neutropenia, corticosteroid use) among allogeneic HSCT recipients, only ~10% of them develop IA. Moreover, <10% of HIV-infected patients with similarly decreased CD4<sup>+</sup> T cell counts develop cryptococcal meningoencephalitis despite widespread environmental *Cryptococcus* exposure [21]. Taken together, these observations indicate that individual genetic variations in immune pathway genes (either alone or in combination) may confer increased susceptibility to or protection from fungal infection.

Indeed, several studies have now demonstrated the contribution of selected immune-related gene SNPs in increasing susceptibility to opportunistic fungal infections in humans (Table 1). These studies provide genetic associations that may help us develop immunogenetic-based risk assessment in patients at-risk for opportunistic fungal infections, which could lead to individualization of antifungal prophylaxis, immunotherapy, or vaccination, and/or optimization of donor selection for recipients of allogeneic HSCT. However, these studies also have limitations. First, biases may be inadvertently introduced by imbalanced population stratification, by small patient sample sizes, by variable clinical practices between different hospitals (e.g., different antifungal prophylaxis or immunosuppressive drug regimens), by the identified SNPs being in linkage disequilibrium with SNPs in other genes that are responsible for the observed phenotype, and/or by the identified SNPs influencing the risk of fungal disease indirectly by affecting other clinical risk factors for acquisition of the fungal infection (e.g., graft-versus-host disease in the setting of allogeneic HSCT). Secondly, validation studies in independent patient cohorts are lacking for most of the reported genetic associations, which are often examined in patients from only one ethnic group (typically Caucasian). Thirdly, in most reported genetic associations, whether the SNPs are dysfunctional thereby conferring impairment in antifungal host defenses is not experimentally examined. Therefore, additional studies in large patient cohorts from multiple ethnic backgrounds with rigorous multivariate statistical analyses and corroborating functional evaluations are warranted to determine which SNPs may be ideal candidates for proceeding with formal clinical trial testing of SNP-based individualized risk stratification and antifungal prophylaxis in at-risk patients. Despite these limitations, these genetic association studies provide critical information about the role of certain immune genes and pathways in host protection against pathogenic fungi, often corroborating mouse studies that reveal the mechanisms by which these genes promote effective antifungal host defense. Although an exhaustive discussion on the role of all reported SNPs is beyond the scope of this review (see Table 1 for detailed summary), the contribution of certain key immune-related SNPs genes in antifungal immune responses is briefly presented below.

**1.1 Genetic variation in fungal-sensing pattern recognition receptor (PRR) genes**—A breakthrough in the field of fungal immunology over the past two decades has been the discovery and characterization of the role of C-type lectin receptors (CLRs) as the critical fungal-sensing molecules that drive protective antifungal immune responses [22–26]. DECTIN-1 (*CLEC7A*) is the prototypic CLR recognizing fungal  $\beta$ -glucan [27]

but a growing number of CLRs are being discovered and studied whose roles in antifungal host defense is less defined (reviewed in detail elsewhere [23]). In brief, engagement of CLRs by fungal pathogen-associated molecular patterns (PAMPs) promotes the sequential activation of Syk, protein kinase C- $\delta$  and the Vav proteins, and the CARD9/BCL10/MALT1 signalosome that in turn leads to the activation of the canonical NF- $\kappa$ B pathway [23]. DECTIN-1 engagement also promotes H-Ras/RASGRF1-mediated, CARD9-dependent ERK activation and Raf-1-mediated, CARD9-independent non-canonical NF- $\kappa$ B pathway activation [28, 29]. Collectively, CLR/Syk/CARD9 signaling drives the production of pro-inflammatory cytokines and chemokines, inflammasome activation, recruitment and effector function of myeloid phagocytes, and Th17 cell differentiation [23, 30–32]. Importantly, human CARD9 deficiency is an autosomal recessive primary immunodeficiency disorder (PID) that causes fungal infection-specific susceptibility with a particular predilection for a) chronic mucocutaneous candidiasis (CMC), associated with decreased circulating Th17 cells in some patients; b) central nervous system (CNS)-targeted candidiasis, associated with impaired neutrophil recruitment and effector function in the fungus-infected CNS; c) IA that exhibits a unique tropism for extrapulmonary tissues; d) cutaneous and CNS phaeohyphomycosis; and e) deep-seated dermatophytosis [30–37].

Not surprisingly, several studies have examined the potential role of SNPs in CLR signaling pathway genes in contributing to fungal infection susceptibility in vulnerable patients. Although *CARD9* SNPs have not been associated with candidemia in hospitalized patients [38], the *CARD9* S12N SNP, which promotes enhanced type-2 immune responses via macrophage-dependent IL-5 release, was associated with the development of allergic bronchopulmonary aspergillosis (ABPA) in humans, corroborated by investigations in a *CARD9*<sup>S12N</sup> knock-in mouse [39]. Among the CLRs, the best studied SNP has been *CLEC7A* Y238\*, which alters the carbohydrate-recognition domain of DECTIN-1 and impairs  $\beta$ -glucan-dependent pro-inflammatory cytokine production by human peripheral blood mononuclear cells (PBMCs) when present in heterozygosity or homozygosity [40–45]. In several studies, the presence of Y238\* in either donors or recipients of allogeneic HSCT has been associated with a greater risk of developing IA, indicative of a role of DECTIN-1 signaling in both myeloid phagocytes and epithelial cells for anti-*Aspergillus* protection, as also shown in mice [41, 42, 46]. The *CLEC7A* Y238\* SNP has also been associated with a greater risk of mucosal *Candida* colonization in allogeneic HSCT recipients, of recurrent vulvovaginal candidiasis (RVCC), but not candidemia, and of severe phaeohyphomycosis and disseminated coccidioidomycosis [38, 43–45, 47, 48]. Other CLRs in which SNPs have been implicated in the risk of IA following HSCT include *CLEC1A* (which encodes MelLec that recognizes fungal DHN melanin) and *CD209* (which encodes DC-SIGN) whereas a *VAV3* SNP has been associated with the risk of candidemia in hospitalized patients [46, 49–51].

Although absent Toll-like receptor (TLR) (and IL-1 receptor) signaling in humans who have inherited *MYD88* deficiency does not increase the risk of developing spontaneous fungal infections [52], genetic variation in several TLRs (i.e., TLR1, TLR3, TLR4, TLR5, TLR6, TLR9) has been associated with a greater risk of developing IA in HSCT recipients, of candidemia in hospitalized patients, and/or of cryptococcosis in HIV-infected or HIV-negative individuals [46, 53–62]. Several TLR SNPs have been reported (Table 1), with the

best studied being the dysfunctional TLR4 SNPs D299G and T399I, which have been shown to cause hyporesponsiveness to inhaled LPS challenge in humans [63]. These TLR4 SNPs have been associated with an increased risk of developing IA following HSCT, as well as developing chronic cavitary pulmonary aspergillosis and candidemia [53, 56, 58, 59, 62]. Although TLR4 has been shown to recognize PAMPs and secreted virulence factors from *Candida*, *Cryptococcus*, and *Scedosporium* species [64–66], the exact mechanisms by which genetic variation in *TLR4* heightens the risk of these infections in humans remain elusive.

Among other classes of PRRs, the NLRP3, NLRC4, and NLRP10 inflammasomes have been implicated in protective host defense against mucosal and invasive fungal infections (IFIs) in mice [26, 67–70]. A variable number tandem repeat in the *NLRP3* gene was associated with increased vaginal IL-1 $\beta$  levels and enhanced risk of recurrent vulvovaginal candidiasis (RVVC) in women, a condition characterized by maladaptive, neutrophil-driven, NLRP3/IL-1 $\beta$ -associated vaginal inflammation [71, 72]. Similarly, a SNP in the sialic acid-binding lectin *SIGLEC15* was associated with increased *IL1B* and *NLRP3* expression and enhanced the risk of RVVC in women [73]. Nod2-deficient mice are resistant to IA and the presence of the NOD2 SNP P268S affected the production of IL-1 $\beta$  by human PBMCs and was associated with the development of IA following HSCT [74].

The soluble long pentraxin 3 (PTX3) binds to bacteria, viruses, and fungi and facilitates their opsonization, uptake, and killing by immune cells. Ptx3-deficient mice are highly susceptible to IA [75] and dysfunctional *PTX3* SNPs in donors of HSCT recipients have been identified as a major risk factor for IA [46, 76]. Neutrophils from individuals carrying the *PTX3* SNPs exhibited impaired phagocytosis and intracellular fungal killing, a defect that could be restored *in vitro* by administration of recombinant PTX3 [76]. Genetic variation in *PTX3* has also been associated with the development of IA in patients with SOT and chronic obstructive pulmonary disease and with the development of cryptococcosis in HIV-negative patients [77–80]. PTX2, also known as serum amyloid P component (SAP), is another PRR of the pentraxin family that binds to *Aspergillus* conidia and facilitates phagocytosis by neutrophils [81]. Apes-deficient mice are susceptible to IA and SNPs in *APCS* (which encodes PTX2) were associated with decreased SAP levels and an increased risk of IA following HSCT [81].

### 1.2 Genetic variation in cytokine, chemokine, and their receptor genes—

Following fungal invasion, the production of pro-inflammatory cytokines and chemokines in infected tissues orchestrates the recruitment and activation of immune cells that promote fungal clearance and sterilizing immunity. Several studies have examined the potential role of SNPs in cytokine, chemokine, and their receptor genes in contributing to fungal infection susceptibility in at-risk patients. SNPs in *IFNG* and the IFN- $\gamma$ -inducible chemokine *CXCL10* have been associated with an increased risk of developing IA in HSCT recipients in independent patient cohorts [46, 82]. A *TNFA* SNP was associated with the development of intra-abdominal candidiasis in surgical ICU patients [83] and genetic variation in the TNF receptors, *TNFR1* and *TNFR2*, has been associated with an increased risk of IA in patients with HSCT or hematological malignancies [46, 84, 85], in agreement with reports of invasive candidiasis and IA in individuals receiving TNF- $\alpha$  inhibitors [18, 86].

SNPs in *IL1A*, *IL1B*, and/or *IL1RN* have been associated with an increased risk of airway colonization and invasive pulmonary infection by inhaled mold fungi in SOT recipients, chronic cavitary pulmonary aspergillosis, and/or IA in patients with hematological malignancies (Table 1) [87–89]. Genetic variation in *IL4* and *IL6* have been associated with a greater risk of developing PJP in HIV-infected patients and blastomycosis in individuals of Hmong ancestry, respectively [90, 91]. SNPs in the chemokine *IL8* and its receptor *CXCR2* in Sudanese individuals have been associated with an increased risk of developing the World Health Organization (WHO)-designated neglected tropical disease mycetoma, a chronic, progressive, and debilitating granulomatous infection that is endemic in tropical and subtropical areas and causes significant morbidity in affected individuals [92]. Genetic variation in *IL10* has been associated with the development of IA in HSCT recipients and patients with hematological malignancy [93, 94], whereas SNPs in both *IL10* and *IL12B* were shown to correlate with an increased risk of persistent candidemia in hospitalized patients [95].

Mouse neutrophils rely on the chemokine receptor CXCR1 for degranulation and non-oxidative *Candida* killing and Cxcr1-deficient mice are susceptible to invasive candidiasis [96]. The dysfunctional CXCR1 SNP S276T was associated with impaired neutrophil degranulation and fungal killing and an increased risk of disseminated candidiasis in candidemic hospitalized patients [96]. The monocyte/macrophage-targeted chemokine receptor CX3CR1 is critical for fungal clearance and host survival in a mouse model of invasive candidiasis by mediating macrophage accumulation in the infected kidney via inhibition of caspase 3-dependent apoptosis [97]. In humans, the dysfunctional CX3CR1 SNP T280M was associated with impaired ERK- and AKT-mediated monocyte survival and increased susceptibility to developing candidemia and disseminated candidiasis among candidemic hospitalized patients in independent Caucasian patient cohorts [97, 98]. In contrast, the CX3CR1 SNP T280M did not increase the risk of RVVC in women [99]. Moreover, genetic variation at the *CX3CR1* locus has been associated with the development of IA in patients with HSCT and hematological malignancies [100], although the mechanistic basis of CX3CR1-dependent anti-*Aspergillus* host defense has not been examined to date.

During murine vulvovaginal candidiasis (VVC), IL-22 is protective by dampening excessive NLRP3 activation and IL-1 $\beta$  release and ameliorating neutrophil-induced immunopathology [101]. SNPs in *IL22* and *IDO1* correlated with resistance to RVVC in women, associated with increased vaginal levels of IL-22 and decreased vaginal levels of pro-inflammatory cytokines [102]. A recent genome-wide association study (GWAS) in HIV-infected patients of African descent revealed an association between genetic variation in *CSFI* (which encodes M-CSF) and the development of cryptococcosis, which was validated in an independent patient cohort [103]. M-CSF has been shown to promote the survival and activation of resident microglia, which are thought of as critical mediators of anti-cryptococcal host defense in the infected CNS tissue [104].

**1.3 Genetic variation in other immune-related genes**—Additional genetic association studies have highlighted the importance of other immune-related genes in antifungal host defenses, although more studies are required to discern the mechanistic basis

of these findings. For example, SNPs in the Fc $\gamma$  receptors *FCGR2A*, *FCGR2B*, *FCGR3A*, and *FCGR3B* have been associated with an increased risk of cryptococcosis in HIV-infected and HIV-negative patients (Table 1) [105–107]. A GWAS in hospitalized patients uncovered an association between genetic variation in *TAGAP*, *CD58*, and *LCE4A-C1orf68* with developing invasive candidiasis [108]. SNPs in *STAT1* and other type I interferon-regulated genes also correlate with the risk of invasive candidiasis in hospitalized patients [109]. Another study performed 23 GWAS in >200,000 individuals of European descent and found an association between the risk of VVC and genetic variation in both *DSG1* (which encodes desmoglein 1) and *PRKCH* (which encodes protein kinase C  $\epsilon$ ) [110]. *DSG1* contributes to maintaining barrier function and epidermal integrity [111] and *PRKCH* regulates keratinocyte differentiation [112], thus pointing to a potential contribution of these molecules to mucocutaneous host defense against *Candida* that merits further investigation.

The role of danger-associated molecular pattern (DAMP)-associated signaling in antifungal immunity has been less studied, with a reported contribution for the receptor for advanced glycation end products (RAGE) and its ligand S100B in restraining immunopathology during murine IA [113]. In addition, a SNP in *AGER* (which encodes RAGE) in both donors and recipients of HSCT and a SNP in *S100B* in donors of HSCT have been associated with a greater risk of developing IA following HSCT [46, 114]. In addition, LC3-associated phagocytosis (LAP) has been shown to promote *Aspergillus* clearance within macrophages in a DECTIN-1/Syk-dependent, calcium/calmodulin-regulated manner and can be counteracted by *Aspergillus* conidial melanin [115, 116]. A SNP in *CALM1* (which encodes calmodulin 1) that decreases *CALM1* mRNA levels was recently shown to correlate with increased risk of IA following HSCT [116]. More studies will be needed to understand the mechanisms by which genetic variation in the *PLG* gene (which encodes plasminogen) is associated with the risk of IA in HSCT recipients [117] and by which genetic variation in the *CHIT1* gene (which encodes the chitin-degrading enzyme chitotriosidase) is associated with the risk of mycetoma caused by the fungus *Madurella mycetomatis* [118].

#### 1.4 Targeted antifungal prophylaxis based on increased immunological risk

—Since the 1990s, the introduction of fluconazole prophylaxis has significantly decreased the incidence of invasive candidiasis in high-risk patients with allogeneic HSCT [119, 120]. More recently, prophylaxis with the mold-active triazole, posaconazole, was shown to decrease the incidence of IA and other IFIs in high-risk patients with allogeneic HSCT and graft-versus-host disease or hematological malignancy and prolonged neutropenia [121, 122]. However, universal administration of antifungal prophylaxis, particularly beyond the high-risk setting of allogeneic HSCT, poses significant challenges. Specifically, the number of patients needed to administer prophylaxis to prevent one fungal infection is often quite high even when using clinical risk factors to enrich for higher-risk individuals. Moreover, in most studies there is no observed survival benefit, antifungal agents are costly and exhibit toxicities and drug-drug interactions, and drug-resistant fungal strains can emerge during antifungal prophylaxis [123–126]. Therefore, immunogenetic-based risk assessment could help individualize antifungal prophylaxis by selecting patients with a greater risk for developing IFIs, thereby decreasing the numbers needed to treat to prevent disease and

minimizing the cost, toxicities, and drug resistance risk associated with widespread use of antifungal prophylaxis.

Proof-of-concept for the beneficial use of targeted antifungal prophylaxis has been demonstrated in two high-risk groups of patients with certain immunological conditions that dramatically predispose them to IA. Firstly, patients with chronic granulomatous disease (CGD), caused by mutations in any of the subunits of the nicotinamide adenine dinucleotide phosphate (NADPH) oxidase complex that impair phagocyte-dependent oxidative burst, have a ~40% lifetime risk of developing IA, which is the leading cause of infection-associated mortality in this PID [127]. The use of itraconazole prophylaxis has dramatically decreased the incidence of IFIs in CGD patients, thereby improving their outcomes [128]. Secondly, patients with lymphoma who receive the Bruton's tyrosine kinase (BTK) inhibitor ibrutinib are at increased risk for developing IA, underscoring the role of phagocyte BTK in anti-*Aspergillus* host defense [129, 130]. The incidence of IA appears to be ~2–4% in patients receiving ibrutinib monotherapy and increases to ~5–10% when ibrutinib is co-administered with corticosteroids [131–136]. When ibrutinib was co-administered with corticosteroids and chemotherapeutic agents in patients with refractory primary CNS lymphoma (TEDDI-R), 39% of them developed IA [137]. To enable the observed high rates of durable lymphoma remissions with TEDDI-R treatment in these patients without the high rate of IA, isavuconazole prophylaxis has now been added to the TEDDI-R regimen and has thus far prevented the development of IA in an ongoing clinical trial [138].

**1.5 Targeted vaccination based on increased immunological risk**—Besides guiding targeted antifungal prophylaxis, immunogenetic-based risk assessment could also help individualize fungal vaccination strategies by selecting patients with a greater risk for developing invasive candidiasis in the ICU. While several fungal vaccine candidates have been investigated in murine models of various opportunistic fungal infections (reviewed elsewhere [139–141]), an immunogenetic risk-based, targeted vaccination strategy could now become achievable with the recent development of the NDV-3A vaccine, the first-in-human fungal vaccine to exhibit immunogenicity, tolerability, and clinical efficacy in patients [142, 143]. NDV-3A, which is based on the recombinant N terminus of the *Candida albicans* adhesin Als3 (rAls3p-N) [144] combined with an aluminum hydroxide adjuvant, improved survival of mice systemically infected with *C. albicans* by eliciting potent antibody and cell-mediated immune responses [145]. Mechanistically, vaccination induced the generation of IFN- $\gamma$ - and IL-17-producing CD4<sup>+</sup> T cells, which promoted the production of phagocyte-recruiting chemokines such as CXCL1, mediated phagocyte trafficking and activation at the site of fungal invasion, and decreased tissue fungal burden [145]. Although the eventual goal of the NDV-3A vaccination platform is to determine whether it can prevent the development of invasive candidiasis in high-risk acutely ill patients in the ICU, it was initially evaluated in the context of VVC. Thus, in a murine model of VVC, administration of the NDV-3A vaccine protected animals from vaginal fungal proliferation in a manner dependent on both B and T cells [146]. In a Phase I clinical trial, NDV-3A vaccination was safe and immunogenic in healthy adults resulting in IgA and IgG antibody responses as well as IFN- $\gamma$ - and IL-17-producing CD4<sup>+</sup> T cells [143]. In a Phase II randomized, double-blind, placebo-controlled clinical trial, NDV-3A vaccination of women with RVVC was safe,



immunogenic, and exhibited clinical efficacy by decreasing the frequency of symptomatic episodes of VVC [142]. Future clinical trials will be needed to determine whether NDV-3A protects against invasive candidiasis in high-risk ICU patients. To decrease the number of patients needed to treat to prevent fungal disease, patient selection in such a clinical trial could be based on both clinical and immunogenetic risk factors of invasive candidiasis development.

**1.6 Outlook**—Moving forward, the challenge in the field will be to determine which of the reported SNPs in several immune-related genes are ideal candidates for formal testing in clinical trials of targeted antifungal prophylaxis or vaccination, whether present alone or in combination. In that regard, the combined presence of *TLR4* and *IFNG* SNPs was shown to promote additive susceptibility to IA compared to carriage of each SNP alone [59]. Similarly, the combined presence of two or more SNPs within the *CD58*, *TAGAP*, and *LCE4A-C1orf68* loci markedly increased the risk of invasive candidiasis (~20-fold) compared to carriage of each SNP alone [108]. As mentioned earlier, ideal candidates are dysfunctional SNPs that their genetic association with increased risk of fungal disease has been validated in independent patient cohorts and across ethnic backgrounds with corroborating immunological mechanistic data in mouse models of fungal disease and primary human cells.

## 2. Immunotherapeutic modalities to boost antifungal immune responses

The suboptimal clinical outcomes and severe net state of immunosuppression of patients who suffer from opportunistic fungal disease has sparked a growing interest in the role of certain adjunctive immunotherapeutic modalities that could help augment antifungal immune responses and complement conventional antifungal treatment. These interventions can be categorized into cytokine- and cell-based and are briefly highlighted below.

### 2.1 Cytokine-based and other non-cellular interventions

**2.1.1 IFN- $\gamma$ -based interventions:** IFN- $\gamma$  was discovered in 1965 as a viral inhibitory factor in phytohemagglutinin-stimulated human leukocyte cultures [147]. Since then, IFN- $\gamma$  has been shown to exert pleiotropic effects during immune homeostasis, inflammation, autoimmunity, and host defense against intracellular pathogens including *Cryptococcus* and endemic dimorphic fungi such as *Coccidioides* [148–150].

In 1991, a randomized, double-blind, placebo-controlled clinical trial showed that recombinant IFN- $\gamma$  reduced the frequency of serious (including fungal) infections in patients with CGD resulting in its FDA approval in this patient population [151]. Although a few studies have since reported a potential beneficial role for adjunctive IFN- $\gamma$  in the management of chronic progressive pulmonary aspergillosis or of invasive candidiasis or IA in patients with critical illness, hematological malignancies, or HSCT, definite evidence for the widespread utility of this intervention in these patient populations is lacking [152–155]. Recent reports have suggested a potential role for the combination of recombinant IFN- $\gamma$  with the immune checkpoint inhibitor nivolumab in the management of mucormycosis [156, 157], highlighting the need for additional preclinical and clinical studies that will precisely

define the contribution of immune checkpoint blockade in the treatment of opportunistic (including fungal) infections [158].

The contribution of IFN- $\gamma$  in host defense against infections by intra-macrophagic pathogens is well-recognized. Thus, the role of IFN- $\gamma$  in the management of patients infected by intra-macrophagic fungi has been examined in the setting of cryptococcosis and coccidioidomycosis. Firstly, the administration of recombinant IFN- $\gamma$  was shown to accelerate *Cryptococcus* clearance from the cerebrospinal fluid (CSF) in HIV-infected patients with cryptococcal meningoencephalitis [159, 160], consistent with several studies demonstrating that impaired type-1 immune responses and decreased IFN- $\gamma$  levels are predictive of poor outcomes in this disease [161–163]. IFN- $\gamma$  may also boost immunity and help remit cryptococcal meningoencephalitis in patients with idiopathic CD4 lymphopenia (ICL) [164]. Secondly, the administration of recombinant IFN- $\gamma$  has been reported to remit severe, treatment-refractory coccidioidomycosis in some patients [165]. More recently, the co-administration of recombinant IFN- $\gamma$  with the IL-4/IL-13 receptor inhibitor, dupilumab, augmented IFN- $\gamma$  and decreased IL-4 production and resulted in rapid clinical remission in another patient with disseminated, treatment-refractory coccidioidomycosis [166]. In some patients with autosomal recessive partial IFN- $\gamma$ R1 deficiency who are at-risk for infections by intra-macrophagic pathogens, IFN- $\gamma$  (or IFN- $\alpha$ ) immunotherapy may boost immune responses and promote clinical remission [167].

Besides monogenic disorders in the IFN- $\gamma$  signaling pathway [168], cryptococcosis can also develop in patients with neutralizing autoantibodies against IFN- $\gamma$  [169]. Rituximab (which targets CD20) and daratumumab (which targets CD38) deplete B cells and plasma cells, respectively, and have shown promise as adjunctive therapies in patients with treatment-refractory non-tuberculous mycobacterial disease associated with a reduction in the titers of anti-IFN- $\gamma$  neutralizing autoantibodies [170, 171]. Future studies are warranted to define the role of these biologics in the management of infections by intra-macrophagic fungi in patients with anti-IFN- $\gamma$  autoantibodies.

**2.1.2 Colony stimulating factor-based interventions:** G-CSF and GM-CSF are FDA-approved for accelerating neutrophil reconstitution in patients with hematological malignancies and HSCT recipients and have been shown to decrease the frequency and/or duration of episodes of febrile neutropenia and associated infections, albeit without an observed survival benefit [172, 173]. In mice, both G-CSF and GM-CSF improved the survival of immunosuppressed animals with invasive candidiasis or IA [174–177]. Moreover, treatment of *Aspergillus*-infected, transplanted mice with M-CSF instructed myeloid commitment in hematopoietic stem cells via direct activation of the transcription factor PU.1, thereby decreasing tissue fungal proliferation and improving survival [178]. Mechanistically, GM-CSF primes oxidative burst and the fungicidal activity of neutrophils in the *Aspergillus*-infected mouse lung [174], whereas dendritic cell-derived IL-23 release promotes the release of GM-CSF by NK cells, which in turn primes the candidacidal activity of neutrophils in the infected mouse kidney [179, 180]. In a mouse model of antibiotic pre-exposure and subsequent invasive candidiasis, impaired lymphocyte-mediated GM-CSF (and IL-17) responses in the intestine led to systemic bacterial translocation and increased mortality, which could be partially rescued by recombinant GM-CSF immunotherapy [181].

In a Phase IV randomized clinical trial that compared the role of G-CSF and GM-CSF in prevention and treatment of IFIs in allogeneic HSCT recipients, GM-CSF demonstrated superior efficacy and significantly decreased the incidence of invasive candidiasis and fungal infection-associated mortality relative to G-CSF [182]. Another study recently reported favorable clinical responses in some patients with invasive candidiasis, IA, mucormycosis and other invasive fungal infections when adjuvant GM-CSF treatment was used together with conventional antifungal therapy [183].

Decreased GM-CSF associated with defective H-RAS/RASGRF-1/ERK responses have been documented in some *CARD9*-deficient patients with CNS candidiasis and adjunctive GM-CSF immunotherapy was associated with clinical remission in these patients [184, 185]. However, in another *CARD9*-deficient patient with CNS candidiasis caused by different missense *CARD9* mutations and intact H-RAS/RASGRF-1/ERK responses, GM-CSF immunotherapy appeared to drive eosinophil-driven CNS immunopathology and disease worsening, pointing to differential effects of various *CARD9* mutations on the H-RAS/RASGRF-1/ERK signaling axis and differing clinical responses to GM-CSF [186]. Other *CARD9*-deficient patients with invasive candidiasis were reported to achieve clinical remission with G-CSF immunotherapy [187, 188]. More studies are needed to define the optimal immunotherapeutic intervention(s) in patients with *CARD9* deficiency, a subset of whom require HSCT to control treatment-refractory invasive fungal disease [189].

**2.1.3 IL-7:** IL-7 was discovered in 1988 as a growth factor that stimulated the proliferation of lymphoid progenitors [190]. In a Phase II, randomized, double-blind clinical trial of IL-7 in septic patients, IL-7 was well-tolerated, it inhibited lymphocyte apoptosis, reversed sepsis-associated lymphopenia, and induced lymphocyte proliferation, activation, and release of IFN- $\gamma$  and IL-17 [191]. In CD4-depleted, *Pneumocystis*-infected mice, IL-7 prevented T cell apoptosis, increased lymphocyte recruitment, activation, and IFN- $\gamma$  release, and decreased tissue fungal proliferation [192]. In a two-hit experimental murine model of bacterial peritonitis caused by cecal ligation and puncture followed by *Candida* sepsis, IL-7 immunotherapy promoted lymphocyte proliferation, activation, IFN- $\gamma$  release, and expression of adhesion molecules leading to improved host survival [193, 194]. In an immunocompetent individual who developed a mixed wound infection by *Trichosporon asahii*, *Fusarium*, and *Saksena* species and had failed antifungal and surgical treatment, receipt of adjunctive IL-17 immunotherapy led to improved lymphocyte counts and function, fungal clearance, and clinical remission [195]. Another setting where IL-7 immunotherapy has shown promising clinical results is ICL, a condition that heightens the risk for cryptococcosis and other opportunistic infections such as progressive multifocal leukoencephalopathy (PML) [196]. Indeed, IL-7 immunotherapy increased the numbers of circulating and tissue-resident T cells and enhanced their function [197], and exhibited promising clinical effects in an ICL patient with PML [198]. Thus, the potential role of IL-7 immunotherapy in prevention and/or treatment of opportunistic (including fungal) infections in ICL patients warrants further study.

**2.1.4 TLR and CLR cooperative activity against chromoblastomycosis:** Chromoblastomycosis is a WHO-designated neglected tropical

disease most often caused by the melanin-bearing yeast fungus *Fonsecaea pedrosoi*, which upon traumatic skin inoculation infects the subcutaneous tissues leading to progressive, disfiguring, and often treatment-refractory disease in tropical and subtropical areas [199]. *F. pedrosoi* activates the Syk/CARD9 signaling pathway via the CLR Mincle (*Clec4e*) but it fails to activate TLR-mediated immune responses, thereby leading to impaired pro-inflammatory cytokine responses in the infected mouse skin [200]. Notably, exogenous application of the TLR7 agonist imiquimod in *F. pedrosoi*-infected mice reinstated effective pro-inflammatory immune responses and facilitated infection clearance [200]. Concordantly, topical application of imiquimod combined with antifungal therapy leads to clinical remission in patients with treatment-refractory chromoblastomycosis [201–203], highlighting the key role of fungal-sensing PRR cooperation in mounting effective antifungal responses in mice and humans [18, 65, 204].

## 2.2 Cell-based interventions

**2.2.1 Granulocyte transfusions:** Granulocyte transfusions were introduced in the clinic in the 1960s and early controlled studies showed remarkable clinical and survival benefits in neutropenic patients with invasive infections [205]. Although the advent of corticosteroid and G-CSF use has led to improved donor neutrophil mobilization, granulocyte transfusions remain challenging due to the high cost, technical difficulties in harvesting large numbers of granulocytes that are required for efficacy, short shelf-life (~24 hours), transfusion-induced pulmonary reactions, and HLA alloimmunization, which is particularly problematic in individuals anticipating HSCT [206–209]. Although granulocyte transfusions decreased lung fungal burden and improved survival in *Aspergillus*-infected neutropenic mice [210], most human studies have reported conflicting results regarding their clinical efficacy and marked variability in granulocyte transfusion practices, which collectively preclude reliable conclusions about their potential role as adjunctive therapies in immunosuppressed patients [211]. In a recent multicenter, randomized, controlled clinical trial termed RING (Resolving Infection in Neutropenia with Granulocytes) that was not completed as planned due to suboptimal patient enrollment, adjunctive transfusion of G-CSF/dexamethasone-mobilized granulocytes did not demonstrate a clinical benefit over standard antimicrobial treatment alone in neutropenic patients with invasive infections [212]. However, in a post hoc analysis, individuals who received a high granulocyte dose (i.e.,  $0.6 \times 10^9$  cells/Kg per transfusion) tended to have better clinical outcomes compared to those who received lower granulocyte doses [212]. The NIH experience with granulocyte transfusions indicates that certain patient groups may exhibit a clinical benefit such as those with hematological malignancies and refractory fusariosis or CGD patients with refractory bacterial or fungal infections [213, 214].

**2.2.2 Infusion of *Aspergillus*-specific T cells or fungus-targeted chimeric antigen receptor (CAR) T cells:** Lymphocytes are dispensable for host defense against IA as *Rag2Il2rg<sup>-/-</sup>* mice that lack innate and adaptive lymphoid cells control inhaled *Aspergillus* conidia without developing invasive infection, similarly to humans with quantitative or qualitative defects in lymphoid cells [18, 215]. However, because T lymphocytes can augment the anti-*Aspergillus* effector function of myeloid phagocytes via the production of IFN- $\gamma$ , IL-17, and/or other soluble factors [216, 217], the adoptive transfer of *Aspergillus*-

specific T cells was investigated in a mouse model of IA following HSCT and was found to confer resistance to the infection [218]. In a clinical trial, Perruccio and colleagues generated *Aspergillus*-specific T cells by limiting dilution, which requires >20 days, and infused them in 10 patients with IA following HSCT, whereas 13 additional HSCT recipients with IA did not receive this adoptive immunotherapy [219]. All 10 recipients of *Aspergillus*-specific T cells had normalization of serum galactomannan levels within 6 weeks of cell infusion, whereas serum galactomannan levels remained elevated in all 13 control patients who did not receive *Aspergillus*-specific T cells. Moreover, 9/10 patients who received *Aspergillus*-specific T cells cleared the infection and only one succumbed to IA, whereas 7/13 of control individuals who did not receive *Aspergillus*-specific T cells died from IA [219]. No infusion toxicities or graft-versus-host disease were noted in that study. The advent of more rapid methods for the clinical scale generation of *Aspergillus*-specific T cells according to good manufacturing practice conditions holds promise for the potential further clinical development of this immunotherapeutic intervention [220].

Furthermore, Kumaresan *et al.* bioengineered fungus-targeting cytotoxic T cells by enforcing expression of a CAR that recapitulates the specificity of the  $\beta$ -glucan-sensing DECTIN-1 fused to the CD28 and CD3- $\zeta$  cytoplasmic signaling domain [221]. The genetically modified DECTIN-1-CAR T cells bound specifically to  $\beta$ -glucan, expressed perforin and granzyme, exhibited a central memory phenotype, produced IFN- $\gamma$ , and were able to recognize and lyse *Aspergillus* conidia and hyphae *in vitro* and *in vivo* in the lung and skin of immunosuppressed mice [221]. Moreover, a recent study described the development of CAR T cells that recognize conserved epitopes on the surface of *A. fumigatus* hyphae, but not of other *Aspergilli* or mold species. These cells were shown to a) secrete pro-inflammatory cytokines upon exposure to *A. fumigatus*, b) prime the antifungal effector function of macrophages, and c) secrete perforin and granzyme B for direct antifungal activity. Adoptive transfer of these cells into *Aspergillus*-infected mice led to their accumulation in the lung and resulted in decreased tissue fungal burden and a survival benefit in neutropenic mice [222]. Although the cost of such a CAR T cell-based immunotherapeutic approach would be currently prohibitory in the clinic, this study provides proof-of-concept that bioengineering fungus-directed cytotoxic T cells with specificity to carbohydrates and/or other fungal epitopes can be harnessed to target life-threatening fungal infections in vulnerable patients.

### 3. Immunotherapeutic modalities to ameliorate immunopathology

Although susceptibility to fungal infections is most often driven by impaired host resistance, in certain settings, the development of opportunistic fungal disease is characterized by maladaptive immune responses that can drive local detrimental immunopathology thereby impairing host tolerance to the infection. In such conditions, treatment with anti-inflammatory agents that dampen exuberant immune responses can help control the infection. Three such examples are briefly highlighted below.

**3.1 Corticosteroids for neutrophil-mediated immunopathology during disseminated candidiasis**—Although neutrophils are critical for promoting sterilizing immunity in the setting of invasive candidiasis (and IA) in mice and humans [223], their

aberrant accumulation and activation at the site of fungal infection may also come at the cost of tissue immunopathology and damage [224]. In the mouse model of invasive candidiasis, excessive, CCR1-mediated neutrophil recruitment in the infected kidney at the late phase of the infection underlies immunopathology and renal injury [225–227]. Besides the chemokine receptor CCR1, leukotriene B<sub>4</sub>, the CLR dendritic cell natural killer lectin group receptor-1 (DNGR-1), the lectin galectin-3, the tyrosine kinase Tec, the suppressor of TCR signaling (Sts) phosphatases, the endoribonuclease MCPIP1, and IL-17C have also been implicated in neutrophil-driven immunopathology in the mouse model of invasive candidiasis [228–233].

In humans, neutrophil-mediated immunopathology can be seen in a subset of neutropenic patients with hepatosplenic candidiasis upon recovery of their neutrophil counts and manifests clinically with worsening of symptoms and persistent fever [234]. Corticosteroids are often used to ameliorate excessive inflammatory responses and improve clinical symptoms in these patients [234]. A recent study examined peripheral blood immune responses in patients with chronic disseminated candidiasis upon neutrophil recovery and found neutrophilia, increased numbers of IFN- $\gamma$ -producing T cells, enhanced T cell activation, and elevated plasma levels of pro-inflammatory molecules such as IL-1 $\beta$ , TNF- $\alpha$ , IL-6, and soluble CD25 [235]. Collectively, a better understanding of the molecular drivers of inflammation in this clinical condition may help develop targeted pharmacological strategies to inhibit excessive neutrophil-driven immunopathology, as corticosteroids significantly heighten susceptibility to opportunistic (including fungal) infections [236].

### **3.2 Treatment of cryptococcosis-associated immune reconstitution inflammatory syndrome (IRIS)**

—Although IFN- $\gamma$ -producing T cells are crucial for facilitating sterilizing immunity during cryptococcosis, their aberrant accumulation and activation at the site of infection may also promote immunopathogenic effects. Clinically, these effects can be observed in HIV-negative patients with cryptococcosis [237] and in a subset of HIV-infected patients with cryptococcosis who develop IRIS after initiation of antiretroviral therapy that promotes immune reconstitution [238, 239]. The risk of HIV-associated IRIS is greater in patients with greater HIV viremia, more severe CD4<sup>+</sup> T cell lymphopenia, and active infection at the time of initiation of antiretroviral therapy [238, 239]. In these patients, the use of corticosteroids may ameliorate excessive inflammation and improve neurological symptoms [240, 241].

In mice infected with *Cryptococcus neoformans* without CD4<sup>+</sup> T cell depletion, which models non-HIV-associated human infection, excessive accumulation of Th1 cells is mediated by the release of the chemokine CXCL10 by activated resident glial cells and promotes immunopathology in the infected CNS [242, 243]. These effects were ameliorated by inhibiting the CXCL10-targeted chemokine receptor CXCR3, which improved mouse survival [242]. In non-HIV-infected patients with cryptococcal meningoencephalitis, robust accumulation of CXCR3-expressing Th1 cells in the CNS-infected tissue and increased CSF levels of CXCL10 are also observed, yet the immune response is ineffective and is associated with neuronal damage [244].

In mouse models of *C. neoformans*-associated IRIS, increased production of IFN- $\gamma$ , TNF- $\alpha$ , and IL-6 are seen in inflamed tissue, and in one of the studies the accumulation of Th1 cells was sufficient to drive CNS immunopathology associated with induction of the expression of aquaporin-4, a molecule that regulates water influx in the brain parenchyma [245, 246]. Moreover, HIV-infected patients with IRIS have increased serum levels of IL-6, IL-7, and IFN- $\gamma$  increased CSF levels of CXCL10, enhanced frequencies of activated HLA-DR<sup>+</sup> CD14<sup>+</sup> monocytes, and enriched frequencies of effector memory IFN- $\gamma$ - and IL-17-producing CD4<sup>+</sup> T cells compared to HIV-infected patients without IRIS [239, 247–249]. A better understanding of the molecular determinants of cryptococcosis-associated IRIS could enable more targeted treatments relative to corticosteroids. For example, inhibition of exaggerated TNF- $\alpha$  responses with adalimumab or thalidomide has been reported to successfully treat a few HIV-infected patients with cryptococcosis-associated IRIS [250, 251].

**3.3 Janus kinase (JAK) inhibitors for CMC in autoimmune regulator (AIRE) deficiency**—Another important breakthrough in the field of fungal immunology over the past decade has been the discovery that the IL-17R signaling pathway promotes protective host defense against mucosal candidiasis in mice and humans [252]. Indeed, patients with complete genetic deficiencies in the IL-17 receptors IL-17RA and IL-17RC or their adaptor molecule ACT1/TRAF3IP2 develop fully penetrant CMC [252–255] and several other PIDs that underlie CMC susceptibility feature varying degrees of decreased circulating Th17 cells and/or impaired IL-17 cellular responses [18, 256]. Mild, treatment-responsive oral candidiasis, but not CMC, develops in a small proportion of patients treated with IL-17 pathway-targeting biologics (mean frequency, ~1–10%) [257].

CMC develops in ~85% of patients with autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), caused by loss-of-function mutations in the *AIRE* gene that impair central immune tolerance [258]. Many APECED patients carry neutralizing autoantibodies against IL-17A (frequency, ~35%), IL-17F (~20–80% depending on the patient cohort), and IL-22 (frequency, ~85%), yet the association between CMC and neutralizing IL-17 autoantibodies is incompletely penetrant [257, 259–262], indicating that other immunological factors also contribute to CMC susceptibility. Indeed, we recently showed that exuberant IFN- $\gamma$  production by mucosal CD4<sup>+</sup> and CD8<sup>+</sup> T cells drives oral candidiasis susceptibility in Aire-deficient mice by driving epithelial barrier disruption, which can be ameliorated by genetic deletion of IFN- $\gamma$  or pharmacological JAK-STAT inhibition with ruxolitinib [263]. Similarly, excessive IFN- $\gamma$ /JAK/STAT responses were observed in the oral mucosa of APECED patients [263], suggesting that JAK inhibition may be an effective immunomodulatory strategy for CMC in this patient population, a hypothesis that is currently being tested in an ongoing clinical trial. This finding provides a conceptual framework for classifying mucosal fungal susceptibility across a spectrum of impaired type-17 mucosal host resistance and/or immunopathology-causing type-1 mucosal inflammation.

Furthermore, patients with *STAT1* gain-of-function mutations who are universally susceptible to severe CMC, exhibit enhanced IFN- $\gamma$  cellular responses, and a subset, but not all, of them have decreased numbers of circulating Th17 cells [264–266]. Strikingly,

JAK-STAT inhibition with ruxolitinib or itacitinib leads to clinical remission of CMC in patients with *STAT1* gain-of-function mutations, in many of whom, CMC remission is seen without an increase in the frequency of circulating Th17 cells, pointing to IL-17-independent ameliorating mechanisms [267–275]. Thus, JAK inhibitor-induced dampening of excessive IFN- $\gamma$  mucosal responses may contribute to the beneficial immunotherapeutic effects of JAK inhibitors in this CMC-manifesting patient population. Importantly, the expanding number of PIDs that feature CMC in the context of autoinflammation or autoimmunity and exhibit intact or even enhanced IL-17 responses (e.g., Down syndrome, mutations in *ELF4* or *IKZF2*) may reveal additional clinical conditions in which CMC is promoted by mucosal type-1 inflammation and, therefore, could perhaps also be therapeutically targeted with benefit with JAK-STAT inhibition [276–278].

## Conclusions

Opportunistic fungal infections represent significant causes of morbidity and mortality in vulnerable patients with critical illness and various inherited and acquired immunodeficiency states. Herein, an overview was presented of how our improved understanding of the cellular and molecular determinants of fungus-, tissue-, cell type-, and context-specific antifungal immune responses could be exploited in the clinical context to benefit fungus-infected patients. Taken together, immunogenetic-based risk assessment, individualization of antifungal prophylaxis and vaccination, and targeted immunotherapies that boost inadequate immune responses or ameliorate maladaptive immunopathogenic responses hold promise for improving the clinical management and prognosis of susceptible patients who suffer from life-threatening fungal infections.

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## Abbreviations:

<b>PJP</b>	<i>Pneumocystis jirovecii</i> pneumonia
<b>IA</b>	invasive aspergillosis
<b>ICU</b>	intensive care unit
<b>HSCT</b>	hematopoietic stem cell transplantation
<b>SOT</b>	solid organ transplantation
<b>SNP</b>	single nucleotide polymorphism
<b>PRR</b>	pattern recognition receptor
<b>CLR</b>	C-type lectin receptor
<b>PAMP</b>	pathogen-associated molecular pattern
<b>PID</b>	primary immunodeficiency disorder



<b>CMC</b>	chronic mucocutaneous candidiasis
<b>CNS</b>	central nervous system
<b>ABPA</b>	allergic bronchopulmonary aspergillosis
<b>PBMCs</b>	peripheral blood mononuclear cells
<b>IFIs</b>	invasive fungal infections
<b>RVVC</b>	recurrent vulvovaginal candidiasis
<b>VVC</b>	vulvovaginal candidiasis
<b>TLR</b>	Toll-like receptor
<b>PTX3</b>	pentraxin 3
<b>SAP</b>	serum amyloid P component
<b>WHO</b>	World Health Organization
<b>GWAS</b>	genome-wide association study
<b>DAMP</b>	danger-associated molecular pattern
<b>RAGE</b>	receptor for advanced glycation end products
<b>LAP</b>	LC3-associated phagocytosis
<b>CGD</b>	chronic granulomatous disease
<b>NADPH</b>	nicotinamide adenine dinucleotide phosphate
<b>BTK</b>	Bruton's tyrosine kinase
<b>CSF</b>	cerebrospinal fluid
<b>ICL</b>	idiopathic CD4 lymphopenia
<b>PML</b>	progressive multifocal leukoencephalopathy
<b>CAR</b>	chimeric antigen receptor
<b>DNGR-1</b>	dendritic cell natural killer lectin group receptor-1
<b>STS</b>	suppressor of TCR signaling
<b>IRIS</b>	immune reconstitution inflammatory syndrome
<b>JAK</b>	Janus kinase
<b>AIRE</b>	autoimmune regulator
<b>APECED</b>	autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy

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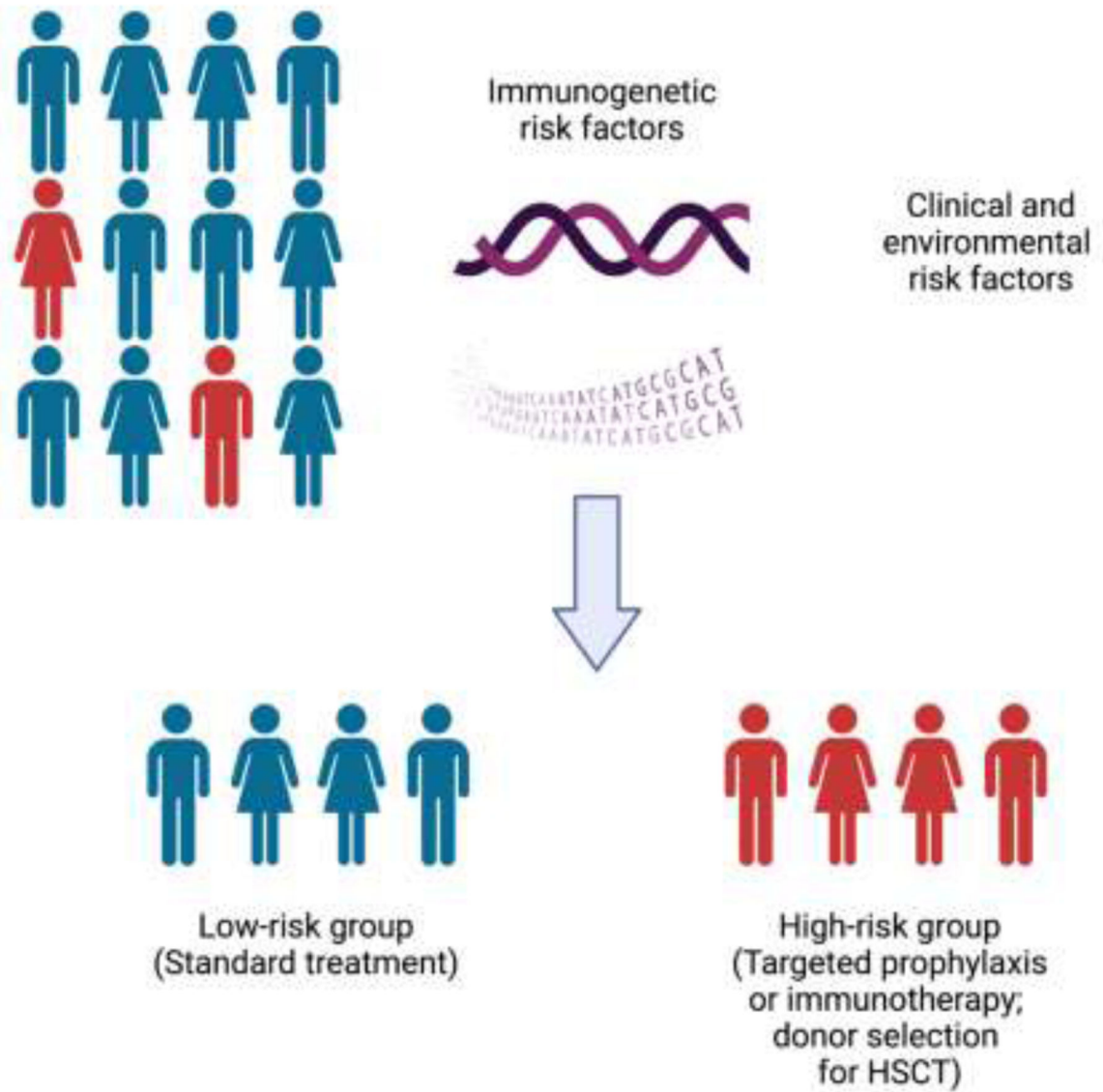
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### Highlights

- Fungal infections affect immunocompromised patients, and their outcomes remain poor despite treatment.
- Immunogenetic profiling may enable personalized risk assessment, and targeted antifungal prophylaxis and vaccination strategies.
- A *Candida albicans* Als3-based vaccine is the first-in-human efficacious fungal vaccine.
- Targeted immunotherapy holds promise for modulating antifungal immune responses in vulnerable patients with opportunistic fungal infections.



**Figure 1.** Personalized immunogenetic risk assessment in patients at risk for fungal infections. Created with [BioRender.com](https://www.biorender.com).

**Table 1.**

Key genetic variants and their reported association with the development of fungal infections in vulnerable patients.

Gene (protein when different name)	Chromosome	SNP ID (MAF)	Variant/allele	Patient population	Ethnicity	Reported risk (replication in independent patient cohorts)	Antifungal immunological or other functional defects conferred by the SNP (when known)	References
<b>Genetic variants associated with the development of aspergillosis</b>								
<i>TLR1</i>	4p14	rs5743611 (0.02)	R80T	HSCT recipients	Caucasian	Development of IA	Unknown	[61]
<i>TLR1</i> together with <i>TLR6</i>	4p14	rs4833095 (0.43) and rs5743810 (0.12)	N248S and S249P	HSCT recipients	Caucasian	Development of IA	Unknown	[61]
<i>TLR3</i>	4q35	rs3775296 (0.18)	+95C/A	HSCT donors	Caucasian	Development of IA	Impaired TLR3 expression and responsiveness in CD141 <sup>+</sup> DCs, impaired DC-induced CD8 <sup>+</sup> T cell proliferation	[57]
<i>TLR4</i>	9q33	rs4986790 (0.06) rs4986791 (0.04)	D299G T399I	Unrelated (but not related) HSCT donors	Caucasian	Development of IA, nonrelapse death post-HSCT (yes)	Unknown	[53, 59, 62]
<i>TLR4</i>	9q33	rs4986790 (0.06)	D299G	Patients with CCPA	ND	Development of CCPA	Unknown	[58]
<i>TLR5</i>	1q41	rs5744168 (0.05)	R392*	HSCT recipients	Caucasian	Development of IA	Unknown	[60]
<i>TLR6</i>	4p14	rs5743810 (0.12)	S249P	HSCT donors	Caucasian	Development of IA	Unknown	[46]
<i>CLECI1A</i> (Mel-Lec)	12p13	rs2306894 (0.33)	G26A	HSCT donors	Caucasian	Development of IA	Impaired production of IL-1 $\beta$ and IL-8 by macrophages	[50]
<i>CLECI7A</i> (DECTIN-1)	12p13	rs16910526 (0.04)	Y238*	HSCT donors and recipients	Caucasian	Development of IA (yes)	Impaired $\beta$ -glucan binding; impaired production of pro-inflammatory cytokines by PBMCs	[41, 42, 46]
<i>CLECI7A</i> (DECTIN-1)	12p13	rs7309123 (0.28)	c.375-1404C/G	HSCT donors or patients with hematological malignancy	Caucasian	Development of IA (yes)	Decreased <i>CLECI7A</i> mRNA expression in whole blood	[46, 49]
<i>CD209</i> (DC-SIGN)	19p13	rs7248637 (0.23)	*898T/C	HSCT donors or patients with hematological malignancy	Caucasian	Development of IA (yes)	Unknown	[46, 49]
<i>CARD9</i>	9q34	rs4077515 (0.37)	S12N	Patients with ABPA	ND	Development of ABPA	Increased <i>Aspergillus</i> -	[39]



Gene (protein when different name)	Chromosome	SNP ID (MAF)	Variant/allele	Patient population	Ethnicity	Reported risk (replication in independent patient cohorts)	Antifungal immunological or other functional defects conferred by the SNP (when known)	References
							induced RelB nuclear translocation and IL-5 production by PBMCs carrying the SNP in homozygosity	
<i>NOD2</i>	16q12	rs2066842 (0.10)	P268S	HSCT donors	Caucasian	Development of IA	Decreased production of IL-1 $\beta$ by <i>Aspergillus</i> -stimulated PBMCs	[74]
<i>APCS</i> (PTX2)	1q23	rs2808661 (0.10) rs3753869 (0.41)	V144V	HSCT donors	Caucasian	Development of IA	Decreased SAP levels	[81]
<i>PTX3</i>	3q25	rs2305619 (0.44) rs3816527 (0.29)	281GG 734AA	HSCT donors	Caucasian	Development of IA (yes)	Decreased PTX3 expression; decreased phagocytosis and fungicidal activity of neutrophils	[46, 76]
<i>PLG</i>	6q26	rs4252125 (0.14)	D472N	HSCT recipients	Caucasian	Development of IA (yes)	Unknown	[117]
<i>AGER</i> (RAGE)	6p21	rs2070600 (0.07)	-374T/A	HSCT donors or recipients (T cell-depleted transplant s)	Caucasian	Development of IA	Unknown	[114]
<i>S100B</i>	21q22	rs9722 (0.27)	+427C/T	HSCT donors	Caucasian	Development of IA (yes)	Unknown	[46, 114]
<i>IFNG</i>	12q15	rs2069705 (0.48)	-1616 C/T	HSCT recipients	Caucasian	Development of IA (yes)	Unknown	[46, 82]
<i>CXCL10</i>	4q21	rs1554013 (0.30) rs3921 (0.31) rs4257674 (0.31)	+11101 C/T +1642 C/G -1101 A/G	HSCT recipients	Caucasian	Development of IA (yes)	Decreased <i>CXCL10</i> mRNA expression in DCs	[46, 82]
<i>CX3CR1</i>	3p22	rs7631529 (0.05) rs9823718 (0.14)	A allele G allele	HSCT donors and patients with hematological malignancy	Caucasian	Development of IA	Unknown	[100]
<i>TNFR1</i>	12p13	rs4149570 (0.30)	-609G/T	HSCT donors and patients with hematological malignancy	Caucasian	Development of IA (yes)	Decreased <i>TNFR1</i> mRNA expression in whole blood	[46, 85]
<i>TNFR2</i>	1p36	VNTR	-322	Patients with hematological malignancy	Caucasian	Development of IA	Unknown	[84]
<i>IL1B</i>	2q14	rs16944 (0.49)	-511C/T	SOT recipients	Caucasian	Development of mold	Decreased production of	[89]

Gene (protein when different name)	Chromosome	SNP ID (MAF)	Variant/allele	Patient population	Ethnicity	Reported risk (replication in independent patient cohorts)	Antifungal immunological or other functional defects conferred by the SNP (when known)	References
						colonization and IMI	pro-inflammatory cytokines by <i>Aspergillus</i> -stimulated PBMC	
<i>IL1B</i>	2q14	rs3917354	T/-	Patients with CCPA	Caucasian	Development of CCPA	Unknown	[88]
<i>IL1RN</i>	2q14	rs4252041 (0.02)	C/T	Patients with CCPA	Caucasian	Development of CCPA	Unknown	[88]
<i>IL1A</i> together with <i>IL1B</i> and <i>IL1RN</i>	2q14	rs1800587 (0.28) and rs1143627 (0.47) and 86-bp VNTR	-889C and -511T and VNTR2	Patients with hematological malignancy	Caucasian	Development of IA	Unknown	[87]
<i>IL10</i>	1q32	rs1800896 (0.27)	-1082GG	Patients with hematological malignancy	Caucasian	Development of IA	Unknown	[93]
<i>IL10</i>	1q32	rs1800896 (0.27) and rs1800871 (0.43) and rs1800872 (0.43)	-1082G and -819C and -592A	HSCT recipients	Asian	Development of IA	Unknown	[94]
<i>IL15</i>	4q31	rs1519551 (0.38) rs6842735 (0.08) rs12508866 (0.15)	A/G G/T T/C	Patients with CCPA	Caucasian	Development of CCPA	Unknown	[88]
<i>DEFB1</i>	8p23	rs1800972 (0.14)	-44C/G	SOT recipients	Caucasian	Development of mold colonization and IMI	Unknown	[89]
<i>CALM1</i>	14q32	rs12885713 (0.30)	CC genotype	HSCT recipients	Caucasian	Development of IA	Decreased <i>CALM1</i> transcription	[116]
<i>FLOT1</i>	6p21	rs3094127 (0.27)	CC genotype	HSCT donors	Caucasian	Development of IA	Decreased production of IL-1 $\beta$ and IL-6 by <i>Aspergillus</i> -stimulated macrophages carrying the GG genotype	[279]
<b>Genetic variants associated with the development of invasive candidiasis</b>								
<i>TLR1</i>	4p14	rs5743611 (0.02) rs4833095 (0.43) rs5743618 (0.20)	R80T N248S I602S	Patients with candidemia	Caucasian (no increase d risk in African Americans)	Development of candidemia	Impaired production of pro-inflammatory cytokines by PBMC	[55]
<i>TLR4</i>	9q33	rs4986790 (0.06) rs4986791 (0.04)	D299G T399I	Patients with candidemia	Caucasian	Development of candidemia	Unknown	[56]
<i>IFIH1</i> (MDA5)	2q24	rs1990760 (0.36) rs3747517 (0.41)	A946T H843R	Patients with candidemia	Caucasian	Development of candidemia	Impaired production of pro-inflammatory cytokines by <i>Candida</i> -	[280]

Gene (protein when different name)	Chromosome	SNP ID (MAF)	Variant/allele	Patient population	Ethnicity	Reported risk (replication in independent patient cohorts)	Antifungal immunological or other functional defects conferred by the SNP (when known)	References
							stimulated PBMC	
<i>VAV3</i>	1p13	rs4914950 (0.37)	CC carriage	Patients with candidemia	Caucasian	Development of candidemia	Unknown	[51]
<i>IL10</i>	1q32	rs1800896 (0.27)	AA carriage	Patients with candidemia	Caucasian	Development of persistent fungemia in candidemic patients	Unknown	[95]
<i>IL12B</i>	5q33	rs41292470	INS/INS	Patients with candidemia	Caucasian	Development of persistent fungemia in candidemic patients	Unknown	[95]
<i>TNFA</i>	6p21	<i>rs1800629 (0.09)</i>	AA/GA carriage	Surgical ICU patients at-risk for invasive candidiasis	Caucasian	Development of intra-abdominal candidiasis	Unknown	[83]
<i>DEFB1</i>	8p23	<i>rs1800972 (0.14)</i>	GG/CG carriage	Surgical ICU patients at-risk for invasive candidiasis	Caucasian	Development of intra-abdominal candidiasis	Unknown	[83]
<i>CCL8</i>	17q12	lkg_17_29697448	N/A	Patients with candidemia	Caucasian	Development of candidemia	Unknown	[109]
<i>CXCR1</i>	2q35	rs2234671 (0.14)	S276T (CG+GG carriage)	Patients with candidemia	Caucasian	Development of disseminated candidiasis in candidemic patients	Impaired neutrophil degranulation and fungal killing	[96]
<i>CX3CR1</i>	3p22	rs3732378 (0.09)	T280M (CC+CT carriage)	Patients with candidemia	Caucasian	Development of candidemia and disseminated candidiasis in candidemic patients (yes)	Impaired monocyte survival	[97, 98]
<i>STAT1</i>	2q32	rs16833172 (0.09)	N/A	Patients with candidemia	Caucasian	Development of candidemia	Unknown	[109]
<i>PSMB8</i>	6p21	rs3198005 (0.01)	N/A	Patients with candidemia	Caucasian	Development of candidemia	Unknown	[109]
<i>SPI10</i>	2q37	rs3769845 (0.48)	N/A	Patients with candidemia	Caucasian	Development of candidemia	Unknown	[109]
<i>TAGAP</i>	6q25	rs3127214 (0.24)	N/A	Patients with candidemia	Caucasian	Development of candidemia and disseminated candidiasis in candidemic patients	Unknown	[108]
<i>CD58</i>	1p13	rs17035850 (0.24)	N/A	Patients with candidemia	Caucasian	Development of candidemia and persistent fungemia in candidemic patients	Unknown	[108]

Gene (protein when different name)	Chromosome	SNP ID (MAF)	Variant/allele	Patient population	Ethnicity	Reported risk (replication in independent patient cohorts)	Antifungal immunological or other functional defects conferred by the SNP (when known)	References
LCE4 - C1orf68	1q21	rs4845320 (0.10)	N/A	Patients with candidemia	Caucasian	Development of candidemia	Unknown	[108]
<i>CD82</i>	11p11	rs7932712 (0.36)	N/A	Patients with candidemia	Caucasian	Development of candidemia	Unknown	[281]
<b>Genetic variants associated with the development of VVC</b>								
<i>TLR2</i>	4q31	rs5743704 (0.01)	P631H	Women with RVVC	Caucasian	Development of RVVC	Decreased production of IL-17A by <i>Candida</i> -stimulated PBMC	[47]
<i>CLEC7A</i> (DECTIN-1)	12p13	rs16910526 (0.04)	Y238*	Women with RVVC	Caucasian	Development of RVVC (no)	Impaired $\beta$ -glucan binding; impaired production of pro-inflammatory cytokines by PBMC	[47, 48, 102]
<i>NLRP3</i>	1q44	rs74163773 (42-bp VNTR)	12/9 genotype	Women with RVVC	Caucasian	Development of RVVC	Increased vaginal levels of IL-1 $\beta$ and decreased vaginal levels of IL-1Ra	[71]
<i>IL4</i>	5q31	rs2243250 (0.47)	-589C/T	Women with RVVC	Caucasian	Development of RVVC	Increased vaginal levels of IL-4 and decreased vaginal level of NO	[282]
<i>IL22</i>	12q15	rs2227485 (0.48)	CC+CT carriage	Women with RVVC	Caucasian	Development of RVVC	Increased vaginal levels of IL-22 and decreased vaginal level of IL-17A, TNF- $\alpha$ , and calprotectin in women with the protective TT genotype	[102]
<i>IDO1</i>	8p11	rs3808606 (0.46)	CC+CT carriage	Women with RVVC	Caucasian	Development of RVVC	Increased vaginal levels of IL-22 and decreased vaginal level of IL-17A and TNF- $\alpha$ in women with the protective TT genotype	[102]
<i>SIGLE C15</i>	18q12	rs2919643 (0.40)	CC+CT carriage	Women with RVVC	Caucasian	Development of RVVC	Increased production of IL-17A, IL-22, and IFN- $\gamma$ by <i>Candida</i> -stimulated PBMC of	[73]

Gene (protein when different name)	Chromosome	SNP ID (MAF)	Variant/allele	Patient population	Ethnicity	Reported risk (replication in independent patient cohorts)	Antifungal immunological or other functional defects conferred by the SNP (when known)	References
							women carrying the disease-associated C allele	
<i>DSG1</i>	18q21	rs200520431 (0.01)	D/I (D the high-risk allele)	Women with VVC	Caucasian	Development of VVC	Unknown	[110]
<i>PRKCH</i>	14q23	rs2251260 (0.49)	T/C (T the high-risk allele)	Women with VVC	Caucasian	Development of VVC	Unknown	[110]
<b>Genetic variants associated with the development of cryptococcosis</b>								
<i>TLR1</i>	4p14	rs5743563 (0.18)	T/T	HIV-negative patients with cryptococcal meningitis	Asian (Chinese Han)	Development of cryptococcal meningitis	Unknown	[54]
<i>TLR1</i>	4p14	rs5743604 (0.47)	T/T	HIV-negative patients with cryptococcal meningitis	Asian (Chinese Han)	Development of cryptococcal meningitis and more severe disease	Unknown	[54]
<i>TLR2</i>	4q31	rs3804099 (0.41)	T/T	HIV-negative patients with cryptococcal meningitis	Asian (Chinese Han)	Development of cryptococcal meningitis and more severe disease	Unknown	[54]
<i>TLR6</i>	4p14	rs3796508 (0.03)	G/A	HIV-infected and HIV-negative patients with cryptococcal meningitis	Asian (Chinese Han)	Development of cryptococcal meningitis in both HIV-infected and HIV-negative patients (yes)	Unknown	[54]
<i>TLR9</i>	3p21	rs164637 (0.03)	C/T	HIV-negative patients with cryptococcal meningitis	Asian (Chinese Han)	Development of cryptococcal meningitis	Unknown	[54]
<i>TLR9</i>	3p21	rs352140 (0.42)	T/T	HIV-negative patients with cryptococcal meningitis	Asian (Chinese Han)	Development of cryptococcal meningitis	Unknown	[54]
<i>CLEC6A (DECTIN-2)</i>	12p13	rs11045418 (0.35)	CC+CT carriage	HIV-negative patients with cryptococcosis	Asian (Chinese Han)	Development of pulmonary (but not meningeal) cryptococcosis	Unknown	[283]
<i>PTX3</i>	3q25	rs2305619 (0.44)	281AA	HIV-negative patients with cryptococcosis	Asian (Chinese Han)	Development of cryptococcosis	Unknown (increased serum levels of PTX3 in individuals carrying the AA genotype)	[80]
<i>FCGR2A</i>	1q23	rs1801274 (0.44)	H131R	HIV-infected and HIV-negative patients with	Multiple	Development of cryptococcosis in HIV-negative	Unknown	[105-107]

Gene (protein when different name)	Chromosome	SNP ID (MAF)	Variant/allele	Patient population	Ethnicity	Reported risk (replication in independent patient cohorts)	Antifungal immunological or other functional defects conferred by the SNP (when known)	References
				cryptococcal meningitis		(but not HIV-infected) patients		
<i>FCGR2B</i>	1q23	rs1050501 (0.19)	I232T	HIV-negative patients with cryptococcal meningitis	Asian (Chinese Han)	Development of cryptococcal meningitis in HIV-negative patients	Unknown	[105]
<i>FCGR3 A</i>	1q23	rs396991 (0.42)	F158V	HIV-infected and HIV-negative patients with cryptococcosis	Multiple	Development of cryptococcosis in both HIV-infected and HIV-negative patients (variable validation)	Impaired antibody-dependent NK cell-mediated ADCC	[105-107]
<i>FCGR3 B</i>	1q23	N/A	NA1/NA2 alleles	HIV-negative patients with cryptococcosis	Multiple	Development of cryptococcosis	Unknown	[105, 106]
<i>CSF1 (M-CSF)</i>	1p13	rs1999713 (0.47) rs1999714 (0.46) rs1999715 (0.48)	N/A	HIV-infected patients	African descent	Development of HIV-associated cryptococcosis (yes)	Unknown	[103]
<b>Genetic variants associated with the development of PJP</b>								
<i>IL4</i>	5q31	rs2243250 (0.47)	-589C/T (CT+TT carriage)	HIV-infected patients	Caucasian	Development of PJP	Unknown	[91]
<b>Genetic variants associated with the development of blastomycosis</b>								
<i>IL6</i> locus	7p15	rs1800796 (0.31) rs1524107 (0.31) rs2066992 (0.31)	N/A	Individuals of Hmong ancestry	Asian	Development of severe blastomycosis	Decreased production of IL-6 by immortalized B cells and decreased production of IL-17A by CD4 <sup>+</sup> T cells	[90]
<b>Genetic variants associated with the development of mycetoma</b>								
<i>IL8</i>	4q13	rs4073 (0.48)	-251T/A	Patients with mycetoma	African descent (Sudanese)	Development of mycetoma	Unknown	[92]
<i>IL10</i>	1q32	rs1800872 (0.43)	-592A/C	Patients with mycetoma	African descent (Sudanese)	Development of mycetoma	Unknown	[284]
<i>CCL5</i>	17q12	rs2280788 (0.03) rs2280789 (0.19)	-28C/G -In1/I T/C	Patients with mycetoma	African descent (Sudanese)	Development of mycetoma	Unknown	[284]
<i>CXCR2</i>	2q35	rs2230054 (0.49)	+785C/T	Patients with mycetoma	African descent (Sudanese)	Development of mycetoma	Unknown	[92]
<i>TSP4</i>	5q14	N/A	A389P	Patients with mycetoma	African descent (Sudanese)	Development of mycetoma	Unknown	[92]
<i>NOS2</i>	17q11	rs1800482 (0.02)	G-954C (Lambarene)	Patients with mycetoma	African descent (Sudanese)	Development of mycetoma and	Unknown (decreased NOS activity)	[92]

Gene (protein when different name)	Chromosome	SNP ID (MAF)	Variant/allele	Patient population	Ethnicity	Reported risk (replication in independent patient cohorts)	Antifungal immunological or other functional defects conferred by the SNP (when known)	References
						more severe mycetomalesions		
<i>CR1</i>	1q32	N/A	<i>SI2</i> and <i>McC<sup>3</sup></i> alleles	Patients with mycetoma	African descent (Sudanese)	Development of mycetoma	Unknown	[92]
<i>CHIT1</i>	1q32	rs3831317	Presence of the 24-bp insertion	Patients with mycetoma	African descent (Sudanese)	Development of invasive mycetoma by <i>M. mycetomatis</i>	Unknown (decreased chitotriosidase activity)	[118]

**Abbreviations:** ABPA, allergic bronchopulmonary aspergillosis; ADCC, antibody-dependent cell-mediated cytotoxicity; AGER, Advanced glycosylation end-product specific receptor; CALM1, calmodulin 1; CCPA, Chronic cavitary pulmonary aspergillosis; CCL, CC chemokine ligand; CXCL, CXC chemokine ligand; DC, dendritic cell; DC-SIGN, Dendritic cell-specific intercellular adhesion molecule-3-grabbing non-integrin; DEF1, defensin  $\beta$ 1; DSG1, desmoglein 1; FLOT1, flotillin 1; HIV, human immunodeficiency virus; HSCT, hematopoietic stem cell transplantation; IA, invasive aspergillosis; ICU, intensive care unit; IFIH1, interferon-induced with helicase C domain 1; IFN, interferon; IL, interleukin; IMI, invasive mold infection; LCE4A, late cornified envelope 4A; MAF, minor allelic frequency (frequency of the second most frequent allele in 1000 Genomes combined population); MDA5, melanoma differentiation-associated protein 5; N/A, not available; ND, not defined; NO, nitric oxide; NOS, nitric oxide synthase; PJP, *Pneumocystis jirovecii* pneumonia; PLG, plasminogen; PRKCH; protein kinase C; PSMB8, Proteasome subunit beta type-8; PTX3, pentraxin 3; RAGE, receptor for advanced glycation end-products; RVVC, recurrent vulvovaginal candidiasis; SAP, serum amyloid P component; S100B, S100 calcium binding protein beta; SOT, solid organ transplantation; STAT1, Signal transducer and activator of transcription 1; TAGAP, T cell activation RhoGTPase activating protein; TLR, Toll-like receptor; TNF, tumor necrosis factor; VNTR, variable number of tandem repeats; VVC, vulvovaginal candidiasis.