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The Goldilocks model of immune symbiosis with *Mycobacteria* and *Candida* colonizers

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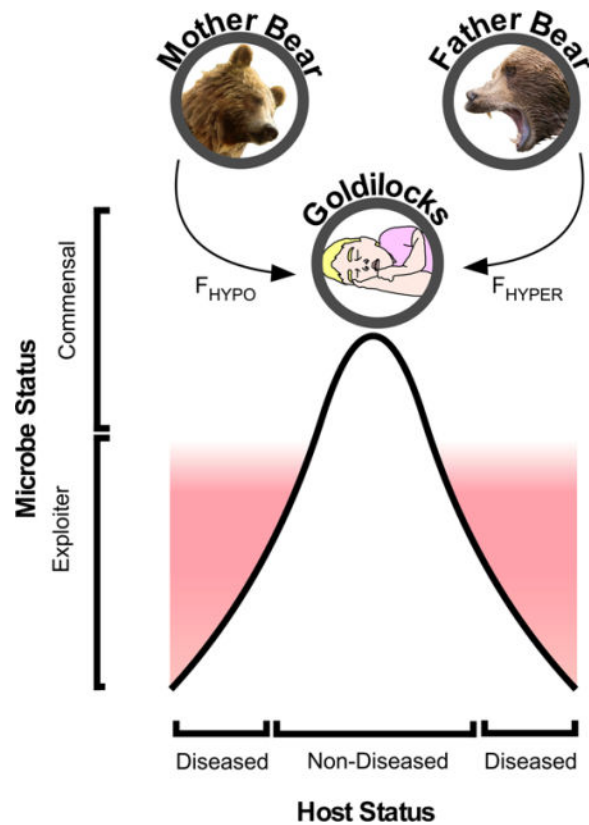
Abstract

Mycobacteria and *Candida* species include significant human pathogens that can cause localized or disseminated infections. Although these organisms may appear to have little in common, several shared pathways of immune recognition and response are important for both control and infection-related pathology. In this article, we compare and contrast the innate and adaptive components of the immune system that pertain to these infections in humans and animal models. We also explore a relatively new concept in the mycobacterial field: biological commensalism. Similar to the well-established model of *Candida* infection, *Mycobacterial* species colonize their human hosts in equilibrium with the immune response. Perturbations in the immune response permit the progression to pathologic disease at the expense of the host. Understanding the immune factors required to maintain commensalism may aid with the development of diagnostic and treatment strategies for both categories of pathogens.

Graphical abstract

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1. INTRODUCTION

Species in the genera *Mycobacteria* and *Candida* include etiological agents of globally significant diseases, as well as non-pathogens that live in either soil and aquatic environments (i.e. *Mycobacteria*) or on the surface of animals, plants and insects (i.e. *Candida*). *Candida* and *Mycobacteria* species (spp) have very little in common from a strictly biological perspective: *Candida* spp are eukaryotes with a diploid genome that is sensitive to external stress and extensively heterozygous¹, replicate primarily via asexual cell division and hyphal extension, and have polysaccharide-rich cell wall. *Mycobacteria* are prokaryotes with a haploid genome that is relatively stable, divide asymmetrically², and have a multilayered hydrophobic cell wall. However, despite their biological differences *Candida* and *Mycobacteria* spp share something in common: both are chronic colonizers of large numbers of humans, but elicit disease in a relative minority of colonized humans. Specifically, an estimated >30% of the world population is colonized with *Candida* and/or *Mycobacteria* spp, ~90% of whom show no clinical signs of disease.

Several flavors of disease can occur following *Candida* or *Mycobacteria* infection. *Candida* infections are categorized as mucocutaneous or disseminated candidiasis. Mucocutaneous candidiasis is typified by the hallmark infection of oropharyngeal candidiasis, also known as thrush. This disease form can also present as an invasive infection on barrier surfaces of the skin, nails, esophagus, or vulvovaginal mucosa. Disseminated candidiasis includes bloodstream infections (candidemia) and infection of normally sterile organs including liver,

spleen, kidney, heart, and brain. The case-fatality rates for disseminated candidiasis are high, with reports of 30–50%, while mucocutaneous candidiasis carries high morbidity for patients^{3,4}. Globally, there are an estimated 400,000 cases of candidemia, 10 million cases of thrush, and 2 million cases of esophageal candidiasis annually³. Mycobacterial infections similarly impact large portions of the globe, and include nontuberculous mycobacterial infection (NTMI), leprosy, swimming pool granuloma, buruli ulcer, and tuberculosis (TB). TB is particularly significant at the global level, and is caused by aerogenic transmission of *Mycobacterium tuberculosis*, which primarily infects macrophages in the lung alveoli⁵. In its active form, TB is associated with “consumption” of the lung tissue and dissemination of *M. tuberculosis* to other organs; in its latent form, TB is asymptomatic and not infectious. Improved public health practices and the use of effective drug treatment have reduced exposure and disease rates in many countries. However, the efforts to control TB in many other countries are not optimal, casting doubt on the World Health Organization’s goal of halving TB incidence by 2050⁶. For these reasons, it is important to have a data-informed framework for understanding the relationship between humans and *Candida* and *Mycobacteria* pathogens.

Here we will introduce a novel concept regarding the biological relationship between immune cells and *Mycobacterial* pathogens that is modeled on established concepts regarding the host relationship with *Candida* spp. Namely, we advocate that humans’ relationship with *Candida* and *Mycobacteria* spp is best described in terms of biological commensalism, and that most individuals maintain the human:commensal equilibrium via innate and T cell-associated cytokines. In a relative minority of individuals, too little or too much of select cytokines offsets this equilibrium and leads to a diseased state. We term this model the “Goldilocks Model.” To support this model, we will review data demonstrating that recognition of *Candida* and *Mycobacteria* spp by overlapping pattern recognition receptors (PRRs) leads to similar innate cytokine profiles, which consequently direct T cell differentiation. We also review data concerning how the T cells govern *Candida* and *Mycobacterial* disease outcome, as well as the polymorphisms in PRR and cytokine response genes that associate with disease susceptibility.

2. HUMAN COLONIZATION AS A SURVIVAL STRATEGY FOR CANDIDA AND MYCOBACTERIA

Natural selection is the force behind both prokaryotic and eukaryotic evolution, and is the process whereby heritable traits that increase a species likelihood of survival become more common over successive generations. We can therefore assume that during human history the ancestors of what are now *Candida* and *Mycobacteria* pathogens found the human niche to give them a selective advantage. Their adaptation to humans is understandable, as the human niche is stable relative to many other environments, with a regulated temperature and wealth of nutrients from the food we ingest. Competition with other bacteria is also limited in the human niche: while a common microbial environment such as soil may contain up to $\sim 3 \times 10^8$ CFU per gram of soil⁷, the human niche is relatively sterile (the gut being an exception, with $\sim 3 \times 10^{11}$ CFU per gram⁸). For several *Mycobacterial* and *Candida* spp, co-evolution has led to humans now being their only niche. Since most individuals fail to

develop disease following initial *Mycobacteria* or *Candida* colonization, *Mycobacteria* and *Candida* spp are best described in ecological terms as *commensals* in the majority of chronically colonized individuals, and *exploiters* in the minority of chronically colonized individuals (FIG 1A).

Candida and *Mycobacteria* spp use of chronic colonization as a survival strategy contrasts with pathogens that solely cause acute disease. FIGURE 1B depicts the life cycle of two human pathogens that employ distinct survival mechanisms: *Yersinia pestis* and *Mycobacterium tuberculosis*. *Y. pestis* caused the Black Death of the 14th century, and passages between rodents and fleas until infecting a human via a flea bite. Human to human transmission of pneumonic plague can also occur. *Y. pestis* employs a rapid bacterial replication rate at the expense of host survival, and is best described in ecological terms as an exploiter of humans (FIG 1A). By the time its human host dies (a matter of days), *Y. pestis* will have replicated N times (N being an arbitrary number). Contrasting with the life cycle of *Y. pestis* is that of *M. tuberculosis*, which does not have a non-human host and passes between humans via aerosolization of infected sputum. In most infected individuals, *M. tuberculosis* enters a slowly replicating, dormant state that does not cause clinical disease. By the time it's latently infected host dies (a matter of years and/or decades), *M. tuberculosis* will have also replicated N times. A minority of infected individuals (~10%) develop active disease and produce the infected sputum that allows for *M. tuberculosis* transmission to a new generation of hosts. For these reasons, we propose that *M. tuberculosis* is best described in ecological terms as a commensal of most infected individuals, and an exploiter in the minority of infected individuals (FIG 1A). In contrast to the relative novelty of the commensal status of *Mycobacteria* spp, it is well-established that *Candida* spp live primarily as commensals. The ecological niche for *Candida* spp is primarily on animal or plant hosts, and the relationship is generally benign to the host. Certain species are commensals in humans that transmit via physical contact (e.g. the touch of caregivers), which correlates with the species that can act as the most common opportunistic pathogens in humans (including *C. albicans*, *C. glabrata*, *C. parapsilosis*, *C. tropicalis*, *C. lusitanae* and *C. krusei*). *Candida* spp colonize the majority of humans in the oral cavity, gastrointestinal tract or genital tract. Colonization usually precedes invasive infection and is a key predictor of subsequent disease⁹. In spite of this and the moderate replication rate of *Candida* spp, the majority of colonized humans never develop invasive infection and do not require anti-fungal treatment to maintain normal health. Invasive infection occurs with breaches in normal host immune or barrier function. Thus, through three distinct survival strategies *Y. pestis*, *M. tuberculosis* and *C. albicans* will have both replicated the same N times. However, we consider the strategy of *M. tuberculosis* and *C. albicans* to be more successful in the long term (a matter of millennia) given that neither species cause the rapid, deleterious effects on their host population that were characteristic of the Black Death.

The concept of *Mycobacteria* spp being human commensals may initially seem to conflict with the fact that *Mycobacteria* spp also cause significant global mortality. Historical perspective is needed to reconcile this dissonance. Using *M. tuberculosis* as an example: the relationship between *M. tuberculosis* and humans is ancient, having evolved alongside humans for the past 10K–70K years¹⁰. The organism's ability to enter latency is important

for this long relationship, allowing it to infect an individual without impacting her/his evolutionary fitness until she/he becomes immunocompromised with age¹¹. While latent TB is asymptomatic and not infectious, active TB is associated with “consumption” of the lung tissue and dissemination of *M. tuberculosis* into the airways; the extensive coughing that ensues can then spread *M. tuberculosis* into the air and enable its infection of a new generation of hosts¹². The organism’s need to balance between activity versus latency not only ensures the survival of *M. tuberculosis*: it has also selected against *M. tuberculosis* variants that are more pathogenic and, thus, more capable of killing its only natural reservoir¹⁰. Whatever equilibrium may have existed between *M. tuberculosis* and its human hosts was altered in the 1970s, the beginning of the HIV/AIDS pandemic¹³. HIV is a retrovirus that is transmitted through sexual intercourse (via semen or vaginal fluid), blood contamination (via shared needles), or from mother to child perinatally (intrauterine, intrapartum or via breastmilk). The ability of HIV to infect and affect immune lineages that keep *M. tuberculosis* in latency, including T cells and macrophages¹⁴, results in HIV-positive (HIV⁺) individuals being more likely to develop active TB than HIV-negative (HIV⁻) individuals^{15–18}. The HIV/AIDS pandemic has also allowed for the outgrowth of more pathogenic clinical isolates since selective barriers are diminished^{10,19}. Thus, whereas the organism’s transition from latency to active disease may take decades in HIV⁻ individuals (a phenotype consistent with the ecological commensals), the recent evolution of HIV and its ability to accelerate the loss of T cells and macrophage lineages results in higher rates of active disease (a phenotype consistent with ecological exploiters).

In many respects, our immune symbiosis with *M. tuberculosis* mirrors that we have with non-tuberculous mycobacteria (NTM). NTM include species that colonize human epithelia, as well as species that are ubiquitous in soil and aquatic environments^{20,21}. NTM spp that colonize human epithelia are rarely pathogenic, include constituents of the healthy microbiota, and can be found along the urogenital tract (*M. smegmatis*, *M. lentiflavum*)^{22–24}, gastrointestinal tract (*M. lentiflavum*)²⁴, mouth or respiratory tract (*M. confluentis*, *M. branderi*, *M. bohemicum*, *M. interjectum*, *M. intermedium*, *M. conspicuum*)^{25–31}, and skin (*M. smegmatis*, *M. bohemicum*, *M. intermedium*)^{32–34}. NTM spp that are found primarily in soil and aquatic environments include *M. vaccae*, the *M. avium* complex (MAC, *M. avium* and *M. intracellulare*), and *M. abscessus* complex (MABSC, *M. abscessus* subspecies *abscessus*, *massiliense*, and *bolletii*). *M. vaccae* is unique among soil NTM inasmuch that it is also a transient human colonizer³⁵, and benefits the host in a manner that resembles ecological mutualism (FIG 1). Specifically, ingested *M. vaccae* inhibits pulmonary allergic inflammation in mice³⁶, and decreases anxiety in both mice³⁷ and humans³⁸ via an as-yet-undefined gut-brain-microbiota axis³⁹. MAC was first isolated from wood pigeons⁴⁰, but is now known to be ubiquitous in the environment and found in freshwater and salt-water, soil, food, dust, domestic and wild animals^{41–44}. In both water and soil, MAC and MABSC species (MAC/MAB) can be free-living, biofilm-associated, or amoeba-associated^{45,46}. Infection with MAC/MAB can follow exposure to aerosols of MAC/MAB-containing water while bathing^{47,48}, or to aerosols of MAC/MAB-containing soil while gardening⁴⁹ or during a natural disaster⁵⁰. The first case of human disease due to MAC/MAB was reported in 1943, in a patient with underlying lung disease⁵¹. After an incubation period suspected to be weeks to months, infection of humans with

MAC/MAB can lead to three basic forms of disease: pulmonary disease, lymphadenitis and disseminated disease. However, as with *M. tuberculosis*, most individuals infected with MAC/MAB do not develop disease, but instead contain or resolve infection within histiocytic infiltrates or granulomas^{52–56}. Whether MAC/MAB colonizes healthy individuals is debatable, as there is little primary science literature testing for their presence on healthy individuals. Winthrop et al⁵⁷ demonstrated that among 283 Oregon residents with respiratory NTM isolates, 53% of participants did not have NTM lung disease and could be considered healthy, colonized individuals. A recent survey of the healthy human microbiome at 18 body habitats failed to detect MAC via 16S rRNA sequencing, but did detect MABSC in the vaginal posterior fornix⁵⁸. Regardless of whether MAC/MAB colonizes healthy individuals, the frequency of individuals who have unknowingly been infected with MAC/MAB is likely high. This is best illustrated by the work of von Reyn et al^{59–62}, who demonstrated that 40% of US-born health care workers have a positive delayed type hypersensitivity (DTH) response to *M. avium* Sensitin without previously experiencing mycobacterial disease, and that NTM are responsible for most positive Mantoux reactions in the same study population⁶¹. Rather than affecting the immunocompetent, individuals who are immunocompromised due to either an inherited or acquired immunodeficiency are most likely to develop MAC disease. Prior to antiretroviral therapy, disseminated MAC infection was the most frequent bacterial complication of AIDS, constituting 45% or more of AIDS-defining infection in the USA, Japan and Europe⁶³. When these MAC/MAB infection data are considered along with TB incidence data in HIV/AIDS communities, they indicate that intact innate and T cell responses are necessary to maintain *Mycobacteria* spp in a commensal state and limit their transition to becoming ecological exploiters.

In summary, clinical and microbiological data support a model wherein most individuals infected with *Candida* and *Mycobacteria* spp do not develop disease, and that instead these species function as commensals. Their commensal status is kept in check by innate and adaptive immune lineages, which when absent (due to either an acquired or inherited immunodeficiency) predispose humans to *Candida* and *Mycobacteria* disease. Given their biological divergence, it is remarkable that *Candida* and *Mycobacteria* spp both elicit similar innate and adaptive immune responses. In the following sections, we will review the bases of these overlapping innate and adaptive responses, as well as literature demonstrating the deleterious impact of hyporesponsive innate and adaptive cells. Importantly, we will also review literature demonstrating that hyperresponsive innate and adaptive cells are also deleterious to the host. Collectively, these literature support a model wherein *Mycobacteria* and *Candida* spp are kept in a commensal state when there is a balance of two opposing forces: immune hyporesponsiveness and immune hyperresponsiveness.

3. INNATE RESPONSES TO *CANDIDA* AND *MYCOBACTERIA* SPECIES

Overview of innate responses to *Candida* and *Mycobacteria* spp

Cells of the innate immune response are at the interface of *Candida* and *Mycobacterial* colonizers and the human host. The best-characterized innate responses are those of phagocytic lineages: monocytes, macrophages/dendritic cells (DCs) and neutrophils, which each respond to prokaryotic and eukaryotic colonizers following the physical interaction of

pattern recognition receptors (PRRs) with pathogen associated molecular patterns (PAMPs). *Candida* and *Mycobacteria* spp relationship to innate immune cells has been described as both “immune-evasive” and “immunostimulatory”⁶⁴, and the immunogenicity of *Candida* and *Mycobacteria* PAMPs varies depending on their environmental conditions^{65–70}. *C. albicans* and most pathogenic *Candida* spp are pleomorphic fungi that grow as yeast, pseudohyphae or hyphae forms, and have an outer membrane comprising a lipid bilayer and polysaccharide-rich cell wall that promotes adherence to epithelial cells⁷¹. The majority of *Candida* PAMPs reside within the cell wall of the yeast form, and include mannose-rich *O*- and *N*-linked glycoproteins, chitin and β -glucans⁷² (FIG 2A). The relative abundance of these PAMPs declines with *Candida* spp transition to hyphal form^{73,74}; the greater abundance of PAMPs in *Candida* spp yeast form may influence the relative pro-inflammatory capacity compared to that of hyphae. However, the transition to the hyphal form has been shown to be required for virulence⁷⁵. Recent evidence indicates that a *Candida* hyphal-derived cytolytic peptide damages epithelial membranes and initiates the epithelial immune response⁷⁶. In addition to differences in PAMPs and virulence factors, the hyphal form of, *C. albicans* can physically escape phagocytosis by DCs⁷⁰. Mycobacterial PAMPs are similarly enriched in the cell wall (FIG 2B), and their immunogenicity is also influenced by environmental conditions^{77–80}. For example, when *M. tuberculosis* grows at an air-liquid interface (resembling the lung environment) it produces and accumulates high levels of trehalose-6,6′ dimycolate (TDM), which is pro-inflammatory and a regulator of *M. tuberculosis*-elicited pathology in animals⁸¹.

Remarkably, despite their biological differences and distinct membrane compositions, *Candida* and *Mycobacteria* PAMPs activate similar host PRRs (FIG 2C). The PRRs activated by *Candida* and *Mycobacteria* spp include membrane-associated Toll-like receptors (TLRs) and C-type lectin receptors (CLRs), as well as cytosolic NOD-like receptors (NLRs) and RIG-I-like receptors (RLRs). The PRRs that recognize *Candida* and *Mycobacteria* spp are listed in FIG 2C, alongside their cognate PAMPs. Because of their recognition by similar PRRs, *Candida* and *Mycobacteria* spp also trigger overlapping signal pathways in innate lineages. After Dectin-1 recognition of *Candida* spp, both spleen tyrosine kinase (SYK) and the serine/threonine kinase RAF1 are independently activated; downstream targets of SYK activity include PKC δ , which integrates with RAF1 to activate NF κ B^{82–85}. The activities of AKT, PI3K and MTOR are also triggered by β -glucan, albeit independent of Dectin-1 and Complement Receptor (CR)^{86,87}. *Candida* PAMP stimulation of Dectin-1, NLRP3 and NLRC4 each cause activation of the canonical caspase-1 containing inflammasome^{67,88,89}, whereas Dectin-1 can also activate a non-canonical caspase-8 containing inflammasome⁹⁰. MAPK activity in macrophages varies depending on whether they have encountered *Candida* spp in either their yeast or hyphal form^{91,92}. The extent to which neutrophil extracellular traps (NETs) are released by PMNs is also governed by *Candida* and *Mycobacteria* spp aggregation⁹³.

Phagocytic innate cells’ secretion of cytokines is an important consequence of *Candida* and *Mycobacteria* spp recognition. As anticipated based on their activating similar PRRs, *Candida* and *Mycobacteria* spp stimulate secretion of similar cytokines at disease sites in humans^{94–101}. Among the more genetically important are the *IL12B*-dependent cytokines IL12 and IL23 (IL12/23), which positively-regulate the differentiation of human T helper

(T_H) cells into T_H1 and T_H17 lineages^{102–104}. Reflecting the multi-faceted influence of IL12/23, individuals who are insensitive to IL12/23 are susceptible to numerous intracellular pathogens^{105,106}; paradoxically, IL12/23 also contributes to mycobacteria-driven pathology, as repeat BCG-immunization of tuberculous mice causes IL23-dependent lung damage¹⁰⁷. IL23 is required to prevent mucosal *Candida* infection. Mice deficient in the p19 subunit of IL23 are susceptible to oropharyngeal candidiasis with a phenotype similar to humans with chronic mucocutaneous candidiasis (CMC)¹⁰⁸. Not surprisingly, a subset of humans with CMC are deficient in IL23 or its receptor. When the deficiency is in the subunits shared with IL12 signaling (p40 subunit of IL23 or IL12Rβ1 receptor subunit), patients are susceptible to both *Candida* and mycobacterial diseases^{109,110}. These inborn errors of IL12/IL23 comprise a portion of patients with Mendelian susceptibility to mycobacterial diseases (MSMD)¹¹¹. The IL23 pathway is also involved in control of disseminated candidiasis. Mice deficient in IL17 signaling (downstream of IL23) have increased mortality, higher fungal kidney fungal loads and lower neutrophil recruitment in a model of disseminated candidiasis than wildtype mice¹¹².

Non-phagocytic innate cells at barrier surfaces also respond to *Candida* and direct the phagocytic response. Specifically, γδ T cells and innate TCRαβ⁺ cells are essential to the initial control of *Candida* in the oral cavity and/or skin^{113,114}. γδ-T cells are a minor subset (~1–5%) of T cells whose receptors are distinct from the αβ-TCRs found on the majority of human T cells. In mice γδ-T cells can be classified into two subsets based on their TCR diversity¹¹⁵. The first subset is found in lymphoid tissues and, like αβ-T cells, displays a highly diversified TCR repertoire¹¹⁶. The second γδ-T cell subset is intraepithelial and expresses a more restricted TCR repertoire^{117,118}. This is particularly true in the skin and the female reproductive tract of mice, where the γδ-T cells are essentially homogeneous^{115,119}. The TCR diversity of human peripheral blood γδ-T cells is also limited, as the predominant γδ-T cell subset in the peripheral blood expresses Vγ9 Vδ2¹¹⁵. Human γδ-T cells are nevertheless activated by a diverse range of antigens, including non-peptide antigens¹²⁰, isoprenoid pathway intermediates¹²¹, alkylamines derived from numerous bacteria and plants¹²², mycobacterial ligands¹²³, heat shock proteins¹²⁴, nucleotide conjugates¹²⁵ and prenyl pyrophosphates¹²⁶. However, unlike αβ-T cells which must be activated by antigen in the context of MHC, the mechanism by which γδ-T cells recognize antigen remains obscure¹²⁷. The oral cavity also has a resident population of innate TCRαβ⁺ cells, also termed “natural T_H17 cells” or nT_H17, that expand in the face of oropharyngeal *Candida* infection¹¹³. Both γδ-T cells and innate TCRαβ⁺ cells secrete IL17 in response *Candida* challenge without requiring previous priming. Similar to the adaptive immune response, innate IL17-producing cells direct immune clearance of *Candida* through neutrophil recruitment and the promotion of antimicrobial peptide production by epithelial cells. In contrast to *Candida* infection, the precise role of γδ-T cells and their effector mechanisms during mycobacteria infection remains to be completely defined. Following intravenous administration of *M. tuberculosis*, γδ-T cell deficient mice are more susceptible to infection than wild type controls¹²⁸; however after respiratory infection with the same organism the absence γδ-T cells had no effect on bacterial burden¹²⁹. Nevertheless, increased numbers of neutrophils are observed in the granulomas of *M. tuberculosis*-infected γδ-T cell deficient

mice¹³⁰, suggesting that $\gamma\delta$ -T cells may regulate immunopathology during chronic infection.

Innate hyporesponsiveness to *Candida* and *Mycobacteria* spp is detrimental to the host

Candida and *Mycobacteria* disease can occur in any tissue, and can be exacerbated by either ablation of innate responses in experimental disease models, or the inheritance of human alleles that confer innate hyporesponsiveness. Neutrophils are among the first recruits to an infected site^{131–135}. Neutrophils, or polymorphonuclear cells (PMNs), are the most abundant leukocyte in the circulation; following bacterial infection of the lung, alveolar epithelial cells near the infected site express several PMN-attractants (e.g. IL8) and PMN-growth factors (e.g. GCSF) that promote the recruitment of PMNs from proximal capillaries into the infected space¹³⁶. Once in the infected space, they are capable of killing pathogens via a variety of effector mechanisms¹³⁷. These mechanisms include NADPH oxidase-dependent production of reactive oxygen species (ROS), myeloperoxidase (MPO)-dependent production of hypochlorous acid (HOCl), elastase (ELA2)-dependent proteolysis and gelatinase B (MMP9)-dependent proteolysis¹³⁷. These and other effector enzymes are held within one of three PMN granule types (azurophilic, specific and gelatinase granules); upon recruitment and activation of PMNs to an infected site, degranulation results in their release to the extracellular space¹³⁸. An additional mechanism by which PMNs kill bacteria is by attracting monocytes¹³⁹, which release even greater amounts of ROS than PMNs when normalized for cellular content¹⁴⁰. For both mucocutaneous and disseminated candidiasis, disease susceptibility is induced with neutrophil depletion in animal models^{135,141,142}. Neutropenia is a well-described risk factor for disseminated candidiasis in humans¹⁴³. Phagocytosis of *Candida* by macrophages is also key to control of disseminated candidiasis¹⁴⁴. People with dysfunctional neutrophils, such as with chronic granulomatous disease, are susceptible to fungal infections including candidiasis¹⁴⁵. High frequency of TH17 cells and associated cytokines does not compensate for the abnormal phagocytes¹⁴⁶. In contrast to PMNs' protective role in mucocutaneous and disseminated candidiasis, PMNs' contribution to mycobacterial control in immunocompetent animals is nil to modest depending on the model system used¹⁴⁷. Specifically, while neutrophils can kill *M. tuberculosis in vitro*¹⁴⁷, and are capable of promoting DC presentation of *M. tuberculosis* antigens¹⁴⁸, their depletion from immunocompetent mice results in either no or modest changes to standard disease readouts¹⁴⁷.

In humans, the inheritance of genomic polymorphisms that decrease innate responsiveness can increase *Candida* and/or *Mycobacteria* disease susceptibility, either by causing a change in the amino acid sequence of immune signals and their receptors, or altering the mRNA expression levels via *cis*- or *trans*-factors. A consequence of this sequence polymorphism is variation in disease susceptibility. Non-HLA genes with alleles that associate with *Candida* and/or *Mycobacteria* disease susceptibility or severity are listed in FIG 3, and can be broadly categorized as regulators of pattern recognition, cytokine responsiveness, and antimicrobial effectors. For most of the genes in FIG 3, the strength of an association between a given allele and disease susceptibility is strongly influenced by ethnicity and gender, as well as the presence or absence of a comorbidity¹⁴⁹. Although the mechanism by which a polymorphism influences disease susceptibility is not always known, those for which the

mechanism is known influence innate responsiveness do so by either introducing a nonsense mutation (Dectin-1¹⁵⁰) a missense mutation (MDA5¹⁵¹), absent protein expression (CARD9¹⁵²), altered PAMP affinity (TLR3¹⁵³), impaired transcription factor activity via a disruption in DNA binding (IRF8¹⁵⁴), decreased mRNA expression (DC-SIGN¹⁵⁵), lowered protein expression (MBL2¹⁵⁶; TLR2¹⁵⁷; CD14¹⁵⁸; SP-A and SP-D¹⁵⁹), disrupted association with accessory host molecules (MRC1¹⁶⁰), attenuated TLR2 signal transduction (TIRAP¹⁶¹), and altered signal peptide sequence (TLR8¹⁶²). Importantly, animal models of *Candida* and *Mycobacteria* infection demonstrate that the PRRs that respond to *Candida* and *Mycobacteria* PAMPs are genetically redundant, and a deficiency in one PRR allele is often insufficient to confer disease susceptibility. Rather, disease susceptibility is conferred by the combinatorial impact of multiple hyporesponsive PRR alleles.

Innate hyperresponsiveness to *Candida* and *Mycobacteria* spp is detrimental to the host

Paradoxically, just as innate hyporesponsiveness promotes *Candida* and *Mycobacterial* disease susceptibility, so too can innate hyperresponsiveness. PMNs' contribution to host defense from *Candida* spp is tissue-specific and varies with stage of infection. Although the PMN response is required for *Candida* clearance and control of infection in the oral cavity, PMNs appear to be responsible for the pathology and symptoms associated with vulvovaginal candidiasis¹⁶³. The influx of PMNs also does not reduce fungal burden during vulvovaginal candidiasis. In the context of disseminated candidiasis, the protective effectiveness of neutrophils early in infection is reversed later in infection¹⁶⁴. Regarding *Mycobacteria* spp, clinical and experimental data demonstrate that PMNs are detrimental in the context of TB with comorbid immunodeficiency, and contribute to the latent-to-active TB transition. In individuals with active TB/AIDS, the number of BAL PMNs is elevated relative to HIV-seropositive TB patients without previous AIDS-defining illnesses¹⁶⁵⁻¹⁶⁷. PMNs are also present at high frequencies in the BAL of HIV⁻ individuals with advanced TB¹⁶⁸, as well as in the cerebrospinal fluid of individuals with disseminated, tuberculosis meningitis¹⁶⁹⁻¹⁷¹. High frequencies of circulating PMNs at the time of TB diagnosis associates with a poor prognosis¹⁷², and a PMN-driven, IFN-inducible transcript signature in adult whole blood correlates with clinical TB severity and distinguishes between those with active and latent TB¹⁷³. Lung PMN infiltrations are prominent in genetically susceptible strains of mice infected with *M. tuberculosis*¹⁷⁴⁻¹⁷⁷. Importantly, the survival of *M. tuberculosis*-infected, genetically susceptible DBA/2 mice is extended following depletion of PMNs using anti-Ly6G, or neutralization of the PMN growth factor G-CSF¹⁷⁴. Similar to genetically susceptible strains, engineered TB-susceptible strains also have prominent PMN-associated pathology, and can be rescued by PMN-depletion. For example, in the absence of the IFN γ R, *ifngr*^{-/-} mouse neutrophils fail to apoptose and accumulate in large numbers in the lung¹⁷⁸; PMN depletion extends the life of *ifngr*^{-/-} mice, without affecting *M. tuberculosis* burden¹⁷⁸. PMN-depletion also extends the life of *M. tuberculosis*-infected *card9*^{-/-} mice¹⁷⁹. Collectively, these clinical and experimental data demonstrate that immunodeficiency, whether acquired or inherited, results in an environment where PMNs become a significant source of tissue pathology during active mycobacterial disease.

4. ACQUIRED IMMUNITY TO CANDIDA AND MYCOBACTERIAL SPECIES

Acquired immunity to *Candida* and *Mycobacterial* spp is that which develops following activation of *Candida* or *Mycobacteria* antigen-specific T cells and B cells. Having first arisen in jawed vertebrates, cells of the adaptive immune system are activated by the evolutionarily older innate immune system, and express surface receptors that are specific to non-self antigens. The enormous diversity of surface receptors is brought about through V(D)J recombination and somatic hypermutation. Adaptive immunity to *Candida* or *Mycobacteria* is an essential compliment to innate immunity, as deficiencies in various aspects of adaptive immunity confer fungal- and mycobacterial-disease susceptibility. The T cell subsets that respond to *Candida* and/or *Mycobacteria* spp include CD8+ $\alpha\beta$ -T cells, CD4+ $\alpha\beta$ -T cells, and CD1-restricted T cells. Below we will review those aspects of *Candida* and *Mycobacteria*-specific T cell activation and effector mechanisms that prevent disease. Although antibody responses to *Candida* and *Mycobacteria* are measurable in infected individuals, B cells' influence on fungal and mycobacterial disease outcome is not reviewed here, but has been recently reviewed elsewhere^{180,181}.

Overview of T cell responses to *Candida* and *Mycobacteria* spp

CD8+ $\alpha\beta$ T-cells—Pathogen clearance by CD8+ $\alpha\beta$ -T cells has historically associated with viral infections, since the MHC Class I pathway samples and presents proteins that are present in the cell cytosol (viral components typically localize to cytosol, whereas bacterial components typically localize to the phagolysosome and are thus accessible to the MHC Class II pathway). However, CD8+ T cells contribute the control of chronic *M. tuberculosis* infection¹²⁹, and mycobacterial antigens can escape into the cytosol and access the MHC Class I pathway¹⁸². CD8+ T cells are protective in vivo, and direct cytolytic activity toward *M. tuberculosis* infected cells in a manner that is perforin-dependent and promoted by IL12^{183–185}. In children, the frequency of circulating IFN γ -producing *M. tuberculosis*-specific CD8+ T cells is cellular biomarker of primary TB¹⁸⁶. In adults, *M. tuberculosis*-specific CD8+ T cells are found in high frequency in infected individuals and recognize antigen both in the context of classical human leukocyte antigen (HLA) alleles¹⁸⁷ and the major histocompatibility complex class I-related gene protein (MR1)¹⁸⁸. MR1-restricted CD8+ cells are enriched in mucosal sites, have a limited TCR diversity, and are “innate-like” inasmuch as they rapidly respond to pathogens soon after thymic egress¹⁸⁹. MR1-restricted CD8 cells are also referred to as Mucosal Associated Invariant T (MAIT) cells, and are also negatively impacted by HIV infection¹⁹⁰.

CD4+ $\alpha\beta$ T-cells—CD4+ $\alpha\beta$ -T cells, or T_H cells, play an important role in maximizing the capabilities of the adaptive immune response. Unlike CD8+ $\alpha\beta$ -T cells, CD4+ $\alpha\beta$ -T cells have limited bactericidal, fungicidal or cytotoxic abilities; rather, they manage and direct other adaptive and innate cells to perform these tasks. CD4+ $\alpha\beta$ -T cells express TCRs that recognize antigen bound to Class II MHC molecules. The activation of a naive CD4+ $\alpha\beta$ -T cell causes it to release cytokines, which influences the activity of many cell types, including the APC that activated it. Several types of effector CD4+ $\alpha\beta$ -T cell responses can be induced by APCs, with each influencing the host's response to pathogens through secretion of cytokines; these types of effector CD4+ $\alpha\beta$ -T cell responses are designated as T_H1, T_H2,

T_{H17} , T_{FH} and T_{H9} . T_{H1} cells secrete $IFN\gamma$ and $TNF\alpha$, both of which are critical for the eradication of chronic intracellular pathogens such as *M. tuberculosis*. T_{H2} cells produce the cytokines IL4, IL5, IL6, and IL13, which are essential for optimal antibody production and for the elimination of extracellular organisms including helminthes and nematodes. T_{H17} cells produce IL17 (also known as IL17A), IL17F and IL22 and, on initial characterization, were broadly implicated in autoimmune disease; a more natural role for T_{H17} cells is suggested by studies that have demonstrated preferential induction of IL17 in cases of host infection with various bacterial and fungal species including *C. albicans*¹⁰⁸. T_{FH} cells are a subset of CD4+ T cells that migrate to B cell follicles after activation and promote germinal center formation and B cell Ig isotype switching. Finally, T_{H9} cells secrete IL9 and IL10 and are a relatively recent addition to the list of known CD4+ $\alpha\beta$ -T cell responses; while their transfer into a lymphopenic host results in autoimmune colitis, a role for T_{H9} cells during the course of a bacterial infection has yet to be demonstrated. Like CD8+ $\alpha\beta$ -T cells, most of the CD4+ $\alpha\beta$ -T cells apoptose upon resolution of infection, with a few remaining as CD4+ memory cells.

In oropharyngeal candidiasis, antigen-specific IL17 producing CD4+ cells (T_{H17} cells) are induced in response to repeated exposure to *Candida*¹⁹¹. T_{H17} cells confer protection to susceptible mice. In the absence of CD4+ cells, IL17 production is transferred to CD8+ cells or CD3+CD4-CD8- cells with similar protective function. As mentioned above, CD4+ T cells are critical for the control the chronic bacterial pathogen *M. tuberculosis*. In the absence of CD4-expressing cells at the initiation of *M. tuberculosis* infection typical mononuclear granulomatous lesions do not form; depletion of CD4+ T cells from mice that have controlled infection results in the recrudescence of *M. tuberculosis* growth, resulting in increased bacterial numbers in various organs, increased lung pathology and decreased survival. Reflecting the requirement for CD4+ T cells, the cessation of bacterial growth correlates with their arrival into the infected lung. Despite the abundant evidence that CD4 T cells play in protecting against bacterial growth, we've yet to fully define the mechanisms by which they mediate immunity. Of the various CD4 T cell subtypes mentioned above, T_{H1} cells are considered most often to be necessary for control of *M. tuberculosis*. The T_{H1} response results in the production of $IFN\gamma$, a cytokine that is critical for activation of bactericidal mechanisms in infected macrophages (i.e. production of NO and O^- radicals).

NKT cells

CD1-restricted T-cells (referred to as NKT cells) are a heterogeneous group of T cells that recognize the non-polymorphic CD1 molecules, antigen-presenting complexes that binds self- and foreign lipids and glycolipids. They constitute a small fraction of all peripheral blood T cells, but are found in abundance in the liver. NKT cells express an $\alpha\beta$ -TCR and sometimes co-express a variety of molecular markers typically associated with NK cells such as NK1.1. They differ from conventional $\alpha\beta$ -T cells in that their TCR repertoire is far more restricted and that they recognize lipids and/or glycolipids instead of peptides. Upon activation, NKT cells rapidly down-regulate their TCR and produce large quantities of $IFN\gamma$, IL4, GM-CSF and multiple other cytokines and chemokines. Although CD1 is dispensable for host defense from oropharyngeal candidiasis and experimental TB^{113,192}, the activation of NKT cells via α -galactosylceramide affords some protection from

subsequent *M. tuberculosis* infection¹⁴³. Human CD1 can present mycobacterial mycolic acid to human NKT cells *in vitro*¹⁹³, and human CD1 transgenic mice present mycobacterial lipids *in vivo*¹⁹⁴. Antigen-specific human NKT cell lines can lyse *M. tuberculosis*-infected macrophages, as well as kill mycobacteria directly via release of the antimicrobial peptide granulysin¹⁹⁵. Circulating NKT cells are dysfunctional in active TB patients relative to non-diseased controls¹⁹⁶, further suggesting that generation of NKT cells is part of protective immune response that occurs in most infected individuals.

T cell hyporesponsiveness to *Candida* and *Mycobacteria* spp is detrimental to the host

When T cells are either absent or functionally-impaired, *Candida* and *Mycobacteria* infections are almost universally detrimental to the host, and best described in ecological terms as exploitive (FIG 1A). The importance of T cells to mycobacterial resistance was established in the 1980s at the Trudeau Institute (Saranac Lake, NY). During that period, Orme and Collins demonstrated that thymectomized mice were susceptible to infection with *Mycobacteria* spp, and that resistance could be restored by adoptive transfer of spleen T cells^{197,198}. In the absence of thymus-derived cells, mycobacterial growth in multiple organs is unrestricted and mice quickly become moribund. The essential nature of T cells is also true in the guinea pig TB model¹⁹⁹. Sadly, in humans the detrimental effect of T cell hyporesponsiveness is demonstrated by the morbidity and mortality associated with TB/HIV co-infection, as HIV depletes the T cells that are needed to limit *M. tuberculosis* growth and dissemination. Recent studies of HIV-infected humanized mice demonstrate that acquired T cell deficiency causes an increase in proinflammatory cytokine expression, which in turn attract PMNs that cause tissue destruction²⁰⁰. This immunological chain of events is supported by histological studies of granuloma composition in TB/HIV+ individuals, which are enriched in PMNs relative to those of TB/HIV- individuals²⁰¹. Acquired and inherited forms of T cell hyporesponsiveness also result in susceptibility to CMC in humans and mice. Inherited defects range from autoimmune diseases with antibodies directed against the T-cell derived cytokines (Autoimmune polyendocrinopathy syndrome-I or APS-I) to deletions along the IL23/IL17 signaling pathway. CMC is nearly universal in APS-I patients, but they are not prone to other infections^{202,203}. Defects in the signaling pathway that result in CMC susceptibility include mutations or deficiency in the IL17 receptor (*IL17RA*), IL17, IL17F, signal transducer and activator of transcription 3 (STAT3), dedicator of cytokinesis 8 (DOCK8), Tyrosine kinase 2 (TYK2), IL-12R β 1, IL12p40, Caspase recruitment domain-containing protein 9 (CARD9), and I κ B α . (FIG 3). Susceptibility to oropharyngeal candidiasis is universal in untreated HIV/AIDS²⁰⁴, solid organ transplant recipients and those undergoing cancer chemotherapy²⁰⁵, again highlighting the importance of normal T_H cell responses.

T cell hyperresponsiveness to *Candida* and *Mycobacteria* spp is detrimental to the host

At the interface of *Candida* and *Mycobacteria* susceptibility are cytokine signaling pathways that influence disease by either directing or inhibiting T_H cell differentiation. For example, signaling through STAT1 results in a T_H1 phenotype characterized by IFN α / β , IFN γ and IL27 secretion under normal conditions. With a gain-of-function *STAT1* mutation, this phenotype is further skewed resulting in deficient Th17 signaling and susceptibility to CMC^{206,207}. The impact of T_H cell cytokine signaling on *Candida* and *Mycobacteria* disease

susceptibility is also illustrated by the fact that most susceptibility alleles encode regulators of T_H cell differentiation (FIG3). When inhibition of T_H1 and T_H17 responses is absent – either due to repeated mycobacterial stimulation (e.g. Koch’s phenomenon)¹⁰⁷ or a genetic deficiency in inhibitory ligands²⁰⁸ – T cell hyperresponsiveness develops and leads to pathology at sites of infection. In humans, the detrimental impact of T cell hyperresponsiveness is observed in TB patients with immune reconstitution inflammatory syndrome (TB-IRIS). IRIS is an inflammatory response in *Mycobacteria*/HIV co-infected individuals that develops after commencing anti-retroviral therapy (ART): concomitant with declines in HIV viral loads, there is a rapid expansion of T_H cells specific to *M. tuberculosis* or nontuberculous mycobacteria (NTM)²⁰⁹. Accompanying this expansion are high circulating levels T_H1 - and T_H17 -associated cytokines^{210–212}, which contribute to progressive organ dysfunction in animal models of TB-IRIS²⁰⁹.

Among animal models of TB, the negative impact of T cell hyperresponsiveness is most notable in *M. tuberculosis* infected IL27 knockout mice. IL27 is a heterodimeric cytokine of the IL12 family that consists of the Epstein-Barr virus-induced gene 3 (EBI3) and IL27p28 proteins that are expressed from distinct genes²¹³. IL27 is primarily produced by macrophages and DCs following activation, but the repertoire of cells that secrete the cytokine is expanding. IL27 signals through a receptor that is a heterodimer of WSX-1 and gp130 expressed on monocytes, macrophages, DCs, NK cells and lymphocytes^{214,215}. IL27 is unique in that it can both activate and suppress immune responses. IL27 was originally described as a cytokine that promotes differentiation of T_H1 cells and production of IFN γ ²¹⁶. However, WSX-1-deficient animals mount T_H1 responses suggesting that IL27 is compensated for in this regard^{217–220}. The anti-inflammatory effects of IL27 have been documented in animal models of infectious and chronic disease, including tuberculosis^{217–223}. WSX-1 deficient mice exhibit improved control of mycobacterial growth^{218,219}. However, these mice are also susceptible to severe immunopathology during chronic infection that compromises survival. This includes enhanced T cell proliferation, T cell activation, and heightened IFN- γ production^{217–220}. IL-27 is involved with both the generation of anti-inflammatory T cells (Tr1) that produce large amounts of IL-10^{224,225}, and suppression of T_H17 cells that mediate inflammation^{218,219}. IL-27 also has anti-inflammatory activity toward human macrophages with consequences to control of bacterial growth, including *M. tuberculosis* and *M. bovis* BCG^{226–229}.

6. THE GOLDILOCKS MODEL OF IMMUNE SYMBIOSIS WITH *CANDIDA* AND *MYCOBACTERIA* COLONIZERS

In one telling of the fairy tale “Goldilocks and the Three Bears”, Goldilocks is an innocent young girl who wanders into a forest, and happens upon the house and home of three bears (a Father Bear, Mother Bear and Child Bear). The three bears were not home, and Goldilocks enters the home to discover – among other items – three beds which vary in softness. Having grown tired from her wanderings, Goldilocks settles into the bed of Child Bear, which is neither too hard (as was Father Bear’s bed and demeanor) nor too soft (as was Mother Bear’s bed and demeanor). The three bears return home to discover the sleeping Goldilocks, who upon waking reacts to sight of Father Bear and Mother Bear by jumping

out a window, falling to her death. The tale of Goldilocks has been used by multiple academic fields to model how homeostasis or maintenance of an ideal state (represented by the sleeping Goldilocks) is maintained by a balance of two opposing forces (represented by the hardness of Father Bear and softness of Mother Bear), and that a detrimental outcome happens upon an imbalance of these opposing forces (represented by the death of Goldilocks). Academic fields that have applied a “Goldilocks Model” include materials science²³⁰, evolutionary biology²³¹, auditory development²³², visual development²³³, vaccinology²³⁴ and workplace safety²³⁵.

Based on our above review of literature regarding innate and adaptive responses to *Mycobacteria* and *Candida* spp, we propose a “Goldilocks model of immune symbiosis” (FIG 4). In most infected individuals, *Candida* and *Mycobacteria* spp are best described as *commensals*, since they benefit from a second species (i.e. the human host) without damaging the host. In a relative minority of individuals, *Candida* and *Mycobacteria* spp transition from being biological *commensals* to being biological *exploiters*. The percentage of individuals in whom this commensal-to-exploiter transition occurs is ~12% of *M. tuberculosis* infected individuals²³⁶, and virtually no *C. albicans* infected individuals in the absence of an immune or barrier defect. The commensal state of *Mycobacteria* and *Candida* spp is represented by the sleeping Goldilocks at the curve maximum in FIG 4, while the commensal-to-exploiter transition is represented by red curve minima. *Mycobacteria* and *Candida* spp are kept in a commensal state when there is a balance of two opposing forces: immune hypo-responsiveness (represented by Mother Bear) and immune hyper-responsiveness (represented by Father Bear). The *commensal-to-exploiter* transition occurs when there is an imbalance between these two forces, such as that caused by acquired immunodeficiency (e.g. HIV) or reoccurring immune stimulation (e.g. Koch’s phenomenon). As depicted by the steep slope on either side of sleeping Goldilocks (FIG 4), the commensal-to-exploiter transition is irreversible in the absence of medical intervention.

Based on our model we can make several predictions that impact upon *Candida* and *Mycobacteria* disease prevention and treatment. First, we would predict that boosting immune responses in hypo-responsive individuals will maintain *Mycobacteria* and *Candida* spp in a commensal state and prevent disease. This prediction is supported by clinical data in children, whose immune system is hypo-responsive to mycobacterial stimuli relative to adults. Specifically, BCG-vaccination increases resistance to mycobacterial disease in children²³⁷. Similarly, infants less than 6 months of age are unable to maintain oral *Candida* in a commensal state and are therefore prone to thrush. A second and more surprising prediction is that immunosuppression would be effective in some individuals to prevent *Candida*- and *Mycobacteria*-related pathology. Vitamin D₃ suppresses human T_H1/T_H17 differentiation, yet promotes resolution of TB pathology in humans and experimental models^{238,239}. There are also situations in which steroidal and non-steroidal anti-inflammatory drugs are effective adjuncts to TB chemotherapy^{238,239}, as well as host directed therapy for treating TB-IRIS²⁰⁹. In terms of *Candida* infection, there is a surprising disconnect between the severity of immune dysfunction in HIV/AIDS infection and the susceptibility and/or severity of vulvovaginal candidiasis. The discrepancy along with the association of exuberant neutrophil responses with this form of candidiasis again suggests a role for dampening the immune response to treat symptomatic infection²⁴⁰. While using

anti-inflammatory drugs in any infected patient should of course be done cautiously, their documented value in some individuals supports the model depicted in FIG 4.

In conclusion, despite the obvious differences between *Candida* and *Mycobacteria* spp, there is remarkable overlap in the pattern recognition pathways that respond to these species, which in turn lead to similar innate and adaptive responses. *Candida* and *Mycobacteria* spp include pathogens that can cause localized or disseminated infections in a relative minority of colonized individuals. However, since the majority of colonized individuals are asymptomatic, *Candida* and *Mycobacteria* spp are best described in ecological terms as commensals which can transition to an exploitive state following immune perturbations. These perturbations can be either hyporesponsive or hyperresponsive in nature, and can originate from innate and adaptive lineages. Although the commensal status of *Mycobacteria* spp is a newer concept in the field of mycobacterial immunology, the commensal status of *Candida* spp is a well-accepted concept in the field of fungal immunology. Based on this model, understanding the immune factors that maintain *Candida* and *Mycobacteria* spp in a commensal state may aid the development of diagnostic and treatment strategies for both categories of pathogens.

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A

Type of Ecological Interaction	Effect on Humans	Effect on Species	Example Species
Competition	Detrimental	Detrimental	<i>Panthera leo</i> , <i>Panthera tigris</i> , <i>Ursus arctos</i> On 1 Mu
Amensalism	Detrimental	No effect	<i>Physalia physalis</i> , <i>Toxicodendron radicans</i>
Mutualism	Beneficial	Beneficial	<i>Bacteroides thetaiotaomicron</i> , <i>Lactobacillus acidophilus</i>
Neutralism	No effect	No effect	<i>Methanopyrus kandleri</i> , <i>Pyrolobus fumarii</i>
Commensalism	No effect	Beneficial	<i>C. albicans</i> and <i>M. tuberculosis</i> (majority of humans)
Exploitation	Detrimental	Beneficial	<i>C. albicans</i> and <i>M. tuberculosis</i> (minority of humans)

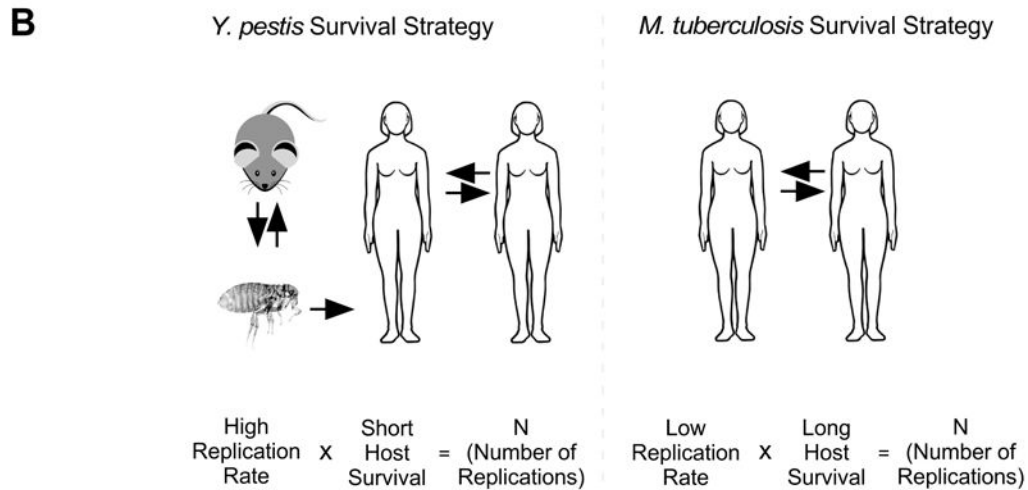
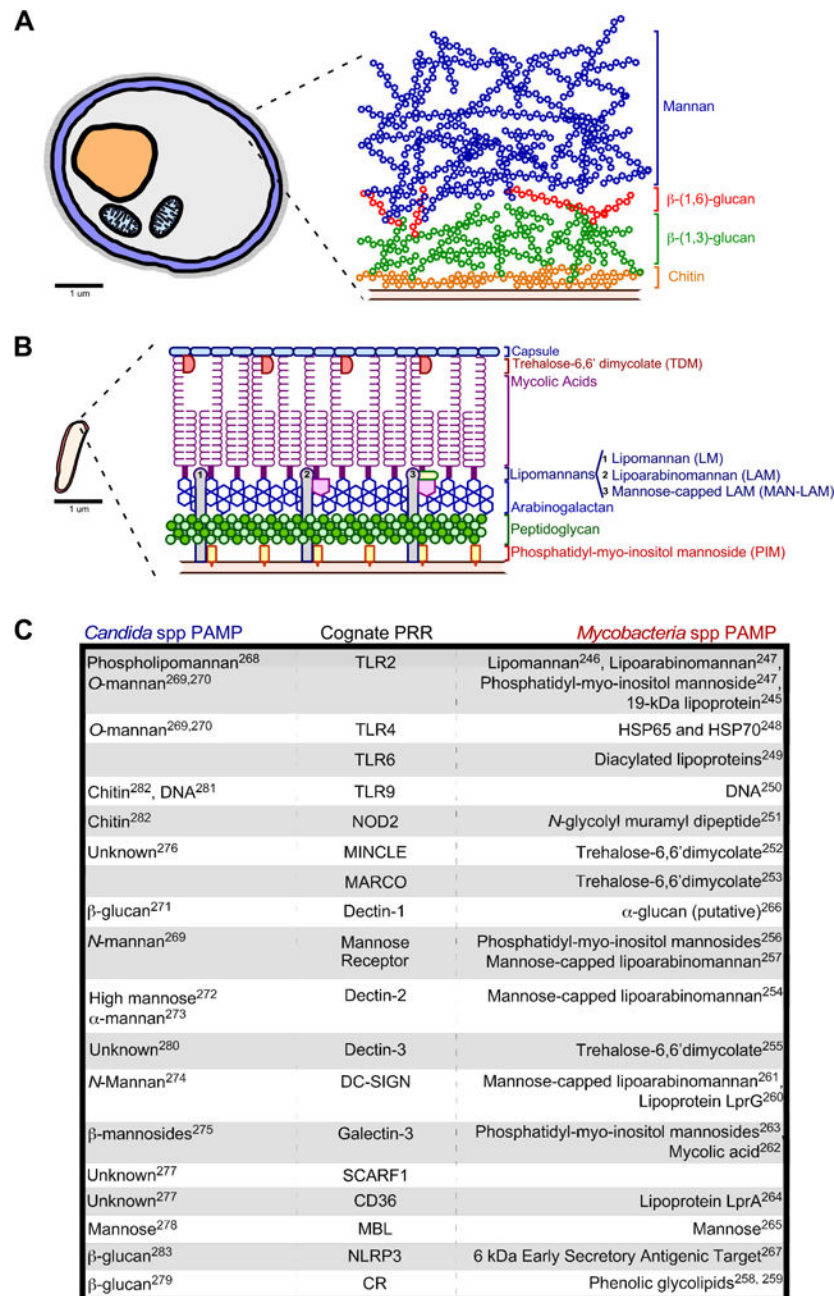


FIGURE 1.

Candida and *Mycobacteria* species exist as commensals in the majority of infected individuals. **(A)** A table listing the six types of ecological relationships that can exist between two biological species, as well as examples of such species in relation to human. **(B)** A comparison of the survival strategies of two human pathogens: *Yersinia pestis* and *Mycobacterium tuberculosis*. *Y. pestis* can transmit via flea bite to rodents or a human, in whom disease disseminates and can then spread to other humans via cough. *Y. pestis* has a high replication rate at the expense of the human host, whose post-infection survival is short; in this manner, *Y. pestis* reaches an arbitrary number (N) of replications. In most individuals, *M. tuberculosis* survive via a different approach. Namely, *M. tuberculosis* combines a low replication rate with long prolonged host survival. In this manner, *M. tuberculosis* can reach the same N replications without causing disease in most individuals.

**FIGURE 2.**

(A–B) *Candida* and *Mycobacteria* spp. differ substantially in morphology and size: *Candida* spp (A) are eukaryotes that have fimbriae, a cell wall, cell membrane, intracellular organelles (e.g. nucleus and mitochondria), and a large size relative to *Mycobacterial* spp (B) that are prokaryotes with an extracellular hydrophobic cell wall, cell membrane and intracellular compartment. The depiction and relative sizes of *Candida* and *Mycobacteria* spp are based on the electron microscopy studies of Fekete et al²⁴¹ and Shoonmaker et al²⁴², respectively. (A) Depiction of *Candida* spp cell wall and the relative localization of common *Candida* PAMPs. (B) Depiction of *Mycobacteria* spp cell wall and the relative localization of common *Mycobacteria* PAMPs, based on recent reviews of the cell wall structure^{243,244}. (C)

Listed are the human PRRs activated by *Candida* and *Mycobacteria* spp, alongside their cognate PAMPs from each pathogen class. The superscript number(s) next to each mycobacterial PAMP indicates a corresponding reference that documents its association with or activation of TLR2^{245–247}, TLR4²⁴⁸, TLR6²⁴⁹, TLR9²⁵⁰, NOD2²⁵¹, MINCLE²⁵², MARCO²⁵³, Dectin-2²⁵⁴, Dectin-3²⁵⁵, Mannose Receptor^{256,257}, CR^{258,259}, DC-SIGN^{260,261}, Galectin-3^{262,263}, CD36²⁶⁴, MBL²⁶⁵, Dectin-1²⁶⁶, NLRP3²⁶⁷. The superscript number(s) next to each *Candida* PAMP indicates a corresponding reference that documents its activation of either TLR2^{268–270}, TLR4^{269,270}, Dectin-1²⁷¹, Mannose Receptor²⁶⁹, Dectin-2^{272,273}, DC-SIGN²⁷⁴, Galectin-3²⁷⁵, MINCLE²⁷⁶, SCARF1²⁷⁷, CD36²⁷⁷, MBL²⁷⁸, CR3²⁷⁹, Dectin-3²⁸⁰, TLR9^{281,282}, NLRP3²⁸³, NOD2²⁸².

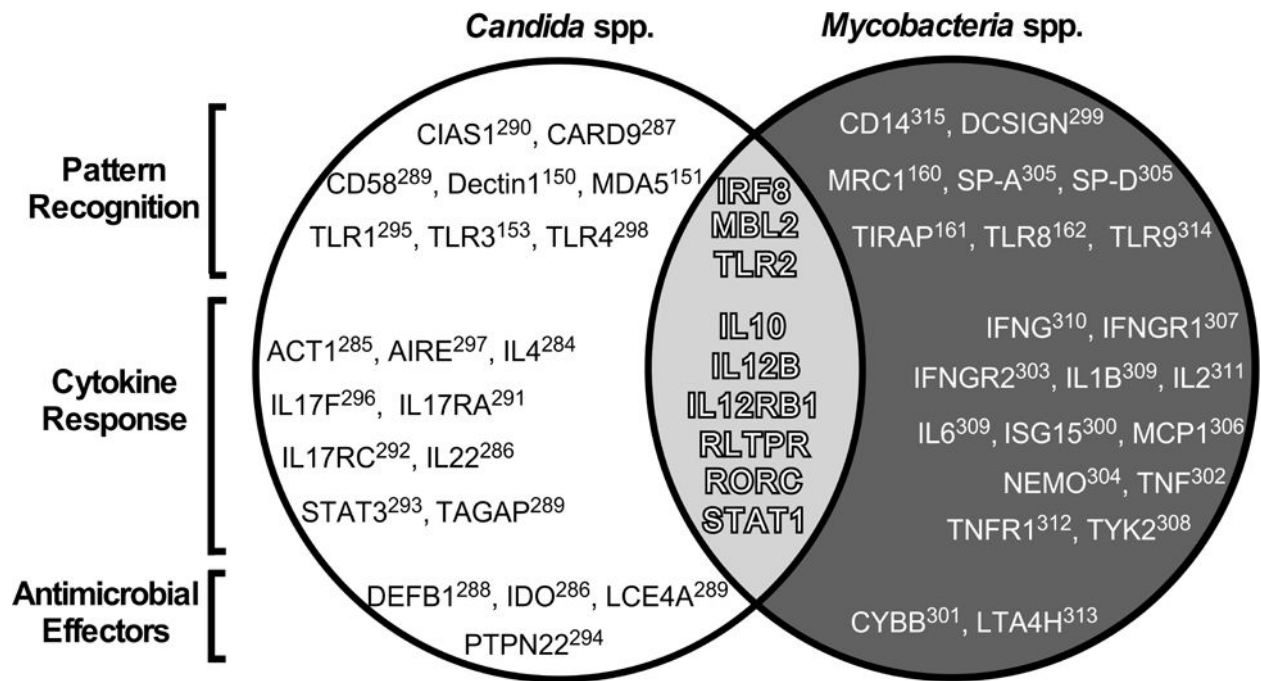


FIGURE 3.

Human susceptibility to *Candida* and *Mycobacteria* disease associates with polymorphic alleles of genes involved in pathogen recognition, cytokine responsiveness, and antimicrobial effector mechanisms. Listed in the white portion of the Venn diagram are non-HLA genes with alleles that associate with *Candida* disease susceptibility^{150,151,153,284–298}. Likewise, listed in the black portion are non-HLA genes with alleles that associate with *Mycobacteria* disease susceptibility^{160–162,299–315}. Listed in the gray overlap are nine genes with alleles that associate with both *Candida* and *Mycobacteria* disease susceptibility: *IRF8*¹⁵⁴, *MBL2*^{156,316,317}, *TLR2*^{157,314,318}, *IL10*^{319–321}, *IL12B*^{110,320}, *IL12RB1*^{322–325}, *RLTPR*³²⁶, *RORC*³²⁷ and *STAT1*^{206,207,328–332}. As indicated by labels on the left, each gene is further classified as being a regulator of either pathogen recognition (top row), cytokine responsiveness (middle row) or antimicrobial effector mechanisms (bottom row).

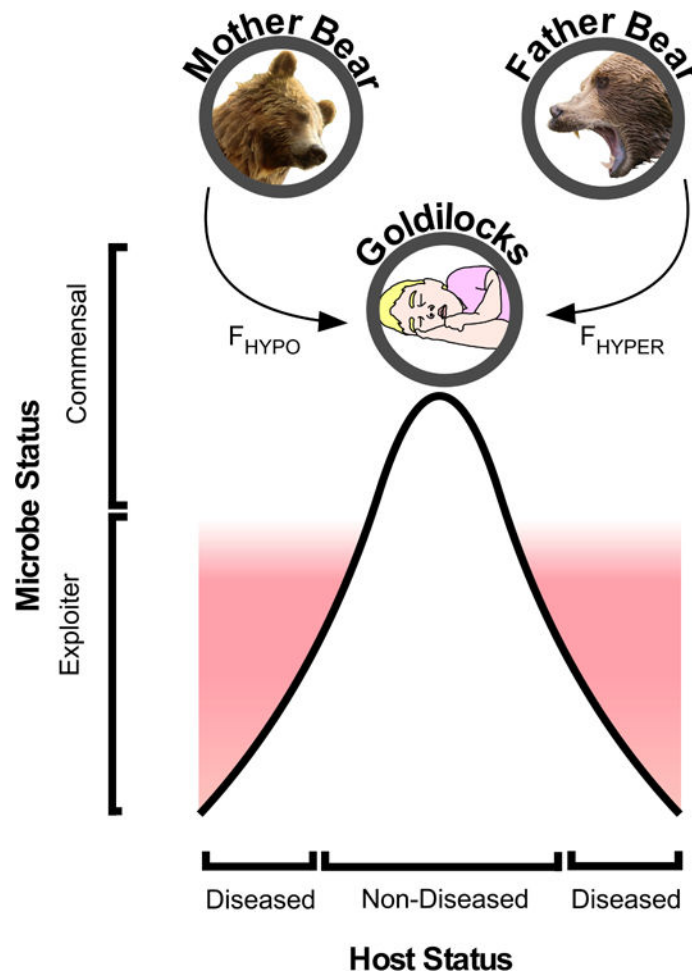


FIGURE 4.

Goldilocks model of immune symbiosis with *Candida* and *Mycobacteria* Colonizers. Depicted by Mother Bear and Father Bear are two equally important but opposing forces: immune-hyporesponsiveness (F_{HYPO}) and immune-hyperresponsiveness (F_{HYPER}). In the majority of humans these two forces are balanced, a consequence of which is maintenance of *Candida* and *Mycobacteria* spp in a commensal state (represented by sleeping Goldilocks). Depicted below sleeping Goldilocks is a bell curve, the maxima of which represents those individuals in whom *Candida* and *Mycobacteria* spp remain in perfect equilibrium with the forces of immune-hyporesponsiveness and immune-hyperresponsiveness. Proximity to this equilibrium is a characteristic of most individuals infected with *Candida* or *Mycobacteria* spp, and is not associated with disease. In a relative minority of individuals, an imbalance exists between the forces of immune-hyporesponsiveness and immune-hyperresponsiveness (examples of which are provided in our review for both innate and adaptive immune cells), leading *Candida* and *Mycobacteria* spp to transition from a commensal to exploitive state. This transition from commensal to exploiter leads to disease, and is irreversible in absence of medical intervention.