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C-Type Lectin Receptors Differentially Induce Th17 Cells and Vaccine Immunity to the Endemic Mycosis of North America

Huafeng Wang,*1 Vanessa LeBert,*1 Chiang Yu Hung,† Kevin Galles,* Shinobu Saijo,* Xin Lin,§ Garry T. Cole,‡ Bruce S. Klein,*†‖ and Marcel Wüthrich*

Vaccine immunity to the endemic mycoses of North America requires Th17 cells, but the pattern recognition receptors and signaling pathways that drive these protective responses have not been defined. We show that C-type lectin receptors exert divergent contributions to the development of antifungal Th17 cells and vaccine resistance against Blastomyces dermatitidis, Histoplasma capsulatum, and Coccidioides posadasii. Acquired immunity to B. dermatitidis requires Dectin-2, whereas vaccination against H. capsulatum and C. posadasii infection depends on innate sensing by Dectin-1 and Dectin-2, but not Mincle. Tracking Ag-specific T cells in vivo established that the Card9 signaling pathway acts indispensably and exclusively on differentiation of Th17 cells, while leaving intact their activation, proliferation, survival, and migration. Whereas Card9 signaling is essential, C-type lectin receptors offer distinct and divergent contributions to vaccine immunity against these endemic fungal pathogens. Our work provides new insight into innate immune mechanisms that drive vaccine immunity and Th17 cells. The Journal of Immunology, 2014, 192: 1107–1119.

Despite several million new systemic fungal infections annually worldwide, there are no commercial vaccines available. We and others have engineered vaccines that protect against experimental infection with the dimorphic fungal pathogens Blastomyces dermatitidis (1), Histoplasma capsulatum (2), and Coccidioides posadasii (3). Our studies showed that vaccine-induced immunity is chiefly mediated by CD4+ T cells (4). Despite the crucial roles of Th1 cells in protective immunity against fungal infection (3, 5, 6) and the controversial roles of Th17 cells in some other infection models (7–13), in our vaccination model Th1 immunity is dispensable, whereas fungus-specific Th17 cells are necessary and sufficient for vaccine-induced protection against these three pathogenic fungi that cause the major endemic mycoses of North America (14). Thus, engaging Th17 cells could be a promising strategy to develop effective fungal vaccines. However, the mechanisms underlying the vaccine-induced Th17 immunity are still largely unknown and need to be determined to develop rational strategies for antifungal vaccines.

Fungi-specific T cell responses are initiated through the recognition of pathogen-associated molecular patterns by pattern recognition receptors (PRRs) on innate immune cells. Among the best-characterized PRRs that recognize fungi are the ITAM-coupled receptors Dectin-1, Dectin-2, and Mincle. They are C-type lectin receptors (CLRs), which are predominantly expressed in myeloid cells (15, 16). There is accumulating evidence that stimulation of the most-studied CLR, Dectin-1, by β-glucans induces Th17 differentiation of naive CD4+ T cells (17). Recently, Viriyakosol et al. (18) showed that Dectin-1−/− mice infected with Coccidioides immitis have lower levels of Th17 cytokines in their lungs. Patients who are homozygous for a single polymorphism of Dectin-1 are susceptible to mucocutaneous Candida albicans infections (19, 20) and invasive aspergillosis (21, 22) owing to defective IL-17 production. We have found, however, that Dectin-1 is unexpectedly dispensable in the development of vaccine-induced Th17 cell responses and resistance to B. dermatitidis (14). It is unknown whether Dectin-1 is required for the development of vaccine-induced Th17 cells and resistance to H. capsulatum and C. posadasii infection.

In contrast to Dectin-1, few reports describe the role of Dectin-2 in driving Th17 responses. In mice, Dectin-2 is required for the differentiation of Th17 cells induced by C. albicans infection (23). In human dendritic cells (DCs), Dectin-2 activation by Candida results in the selective activation of the NF-κB subunit c-Rel and the production of IL-1β and IL-23 p19, which skews CD4+ T cell responses toward a Th17 profile (24). Although Mincle has been reported to induce Th1/Th17 immunity in response to the mycobacterial cell wall glycolipid trehalose 6,6′-dimycolate (TDM) and its synthetic analog trehalose-6,6′-dibehenate (TDB) (25), to our knowledge its role in driving anti-fungal Th17 responses has not been investigated.

Although Dectin-1 recognizes fungi via β-1,3-glucan exposed on the cell wall and recruits Syk directly through its hemITAM motif (26), Dectin-2 and Mincle recognize mannose-like structures (23, 27–29) and need to pair with the ITAM-bearing adaptor FcRγ to
activate the Syk-Card9 pathway (30–32). In mice, Card9 signaling induces DC maturation, the production of proinflammatory cytokines, and the induction of Th17 responses (17). In humans, a Card9 mutation results in susceptibility to chronic mucocutaneous candidiasis (33). Notably, C. albicans—induced Th17 responses are dependent on Card9 (17), and greatly reduced numbers of Th17 cells are associated with patients carrying homozygous Card9 mutations (33), indicating that Card9 is essential for antifungal Th17 responses. However, it is unclear at what stage the Card9 signaling pathway governs Th17 cell development in vivo. To dissect whether Card9 affects the priming, expansion, differentiation, contraction, and migration of vaccine-induced Th17 cells, we exploited an adoptive transfer system that we have previously established using TCR transgenic 1807 cells that recognize a shared Ag from B. dermatitidis, H. capsulatum, and C. posadasii (34). On adoptive transfer into recipient mice, 1807 cells become activated, proliferate, and expand in the draining lymph node (LN); 1807 cells differentiate into cytokine-producing effector T cells after trafficking to the site of vaccination and the lung upon challenge and confer resistance against the three dimorphic fungi (14, 34, 35). Thus, the autologous adoptive transfer system offers a powerful tool to dissect normal or defective development of vaccine-induced Ag-specific T cells responsive to multiple dimorphic fungi.

Although Card9 and CLRs have been implicated in mediating innate resistance to primary fungal infection and priming of Th17 cells, their role in vaccine-induced resistance to fungi and the effect on the sequential stages of T cell development has not been investigated. In this study, we demonstrate that the adaptor Card9 is indispensable for the acquisition of vaccine immunity and the development of Th17 cells against all three systemic dimorphic fungi of North America, but the upstream CLRs play distinctly different roles for each pathogen. We also pinpoint at what stage of the immune response Card9 controls Th17 cell development and show that this adaptor promotes the differentiation of antifungal Th17 cells, but does not influence downstream stages of T cell expansion, activation, contraction, or migration to the lung upon challenge. With B. dermatitidis, the upstream PRR Dectin-2, but neither Mincle nor Dectin-1, recognizes yeast and induces ITAM signaling that initiates the development of Th17 cells and vaccine immunity to fungal infection. Conversely, for the related dimorphic fungi H. capsulatum and C. posadasii, while Card9 is required for the induction of vaccine immunity, both Dectin-1 and Dectin-2, but not Mincle, participate in the recognition and induction of protective Th17 cell responses. Our data offer insight into the mechanisms that underpin acquisition of vaccine immunity to pathogenic fungi.

Materials and Methods

Ethics statement

All animal procedures were performed in accordance with the recommendations in the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health. Care was taken to minimize animal suffering. The work was done with the approval of the Institutional Animal Care and Use Committee of the University of Wisconsin-Madison.

Mouse strains

Inbred wild type C57BL/6 and congenic B6.PL-Thy1+/Cy (stock #00406) mice carrying the Thy 1.1 allele were obtained from Jackson Laboratories (Bar Harbor, ME). B6.129P2-Fcerv1g1108 DECTIN-2 INDUCES ANTIFUNGAL T CELL IMMUNITY

mice were a generous gift from Dr. Victor L. J. Tybulewicz. All mice were 7–8 wk old at the time of experiments. Mice were housed and cared for according to guidelines of the University of Wisconsin Animal Care Committee, who approved all aspects of this work.

Fungi and growth conditions

B. dermatitidis strains used were ATCC 26199, a wild type virulent strain, and the isogenic, attenuated mutant lacking BAD1, designated strain 855 (39). Isolates of B. dermatitidis were maintained as yeast on Middlebrook TH10 agar with oleic acid-albumin complex (Sigma, St Louis, MO) at 30°C. H. capsulatum strain G217B (provided by George S. Deepe, University of Cincinnati, Cincinnati, OH) was maintained on brain-heart infusion slants supplemented with 5% sheep blood at 37°C. C. posadasii isolate C735 is a virulent, human clinical strain that was used to generate a live, attenuated vaccine strain (ΔT) by deleting the chitinases 2, 3, and α-arabinofuranosyl-2-deoxyhexose genes as described previously (3). The saprobes phase of both the parental and mutant strains were grown on glucose yeast extract medium (1% glucose, 0.5% yeast extract, 1.5% agar) at 30°C for 3–4 wk to generate a confluent layer of arthroconidia (spores) on the agar surface. Formalin-killed endosporulated spherules of C. posadasii were generated as described (40).

Vaccinations

Mice were vaccinated s.c. at two sites: dorsally and at the base of the tail as follows. B. dermatitidis BAD1−/− yeast attenuated BAD1−/− yeast, designated strain 855, were injected as live or heat-killed cells using a dose range of 105–107 yeast per mouse. For vaccination with H. capsulatum G217B, 105 heat-killed or 106 live yeast per mouse was used. For vaccination with C. posadasii, mice were immunized with 5.0 × 105 viable spores of the ΔT strain (3). Formalin-killed spherules (FKS) of C. posadasii were used at 105 per mouse for vaccination. Resistance experiments included one (B. dermatitidis and H. capsulatum) or two (C. posadasii) booster vaccinations(s) of the same vaccine dose and site 2 weeks apart.

Experimental infection

Mice were infected intratracheally with 2 × 103 or 2 × 104 wild type 26199 B. dermatitidis yeast as described previously (14). At day 4 after infection, coinciding with the peak of T cell influx (14), the mice were sacrificed and lung T cells were analyzed by FACS analysis. Extent of lung infection was examined 2 wk after infection and determined by plating homogenized lung and enumerating CFUs on brain-heart infusion (Difco) agar. For H. capsulatum infections, mice were challenged with a sub-lethal dose of 1–2 × 107 G217B intratracheally, and cellular analysis was performed 4 d later. Lung burden was determined 13 d after infection by plating lung homogenates on sheep blood containing Mycosel plates and enumerating CFUs. For C. posadasii infections, mice were challenged by intranasal route with a lethal dose of 50–80 spores of the virulent, parental strain 4 wk after completion of the vaccination protocol (34). The fungal burden determined as CFUs in lungs and spleens of the vaccinated and unvaccinated mice was conducted at day 14 after infection by plating organ homogenates on glucose yeast extract plates containing 50 μg/ml chloramphenicol.

Adaptive transfer of transgenic 1807 T-cells and surface staining

Single-cell suspensions of 106 magnetic bead purified CD4+ cells from 1807 Thy1.1+ mice were injected iv. into Thy1.2+ C57BL/6 recipients. When indicated, transgenic 1807 cells were labeled with CFSE (Molecular Probes) before adoptive transfer. After vaccination or infection, single-cell suspensions from draining lymph nodes (brachial and inguinal) and lung cells of recipient mice were stained with mAbs directed against the following surface markers: CD4, CD8, Thy1.1, CD44, CD62L, and B220 (as a dump marker to exclude events that are stained nonspecifically). mAbs were obtained from BD Pharmingen (San Diego, CA) and eBioscience (San Diego, CA), and cytometry data were gathered with an LSRII Flow Cytometer (BD Biosciences, San Jose). Data were analyzed with FlowJo software (Tree Star, Ashland, OR). The number of 1807 CD4+ T cells in a lung was calculated by multiplying the percentage of Thy1.1+ CD4+ cells by the number of viable cells as determined by trypan blue dye exclusion.

Intracellular cytokine staining

Effector T cells from the site of vaccination and lung were obtained as described previously (14). An aliquot of isolated cells was stained for surface CD4 and Thy 1.1 to determine the percentage of transferred 1807 cells. The numbers of 1807 cells in the lung was derived by multiplying the percentage of cells by the total number of cells per organ isolated. The rest
of the cells were stimulated with anti-CD3 and anti-CD28 mAb in the presence of Golgi-Stop (BD Pharmingen). After 4–6 h of stimulation, cells were stained for surface markers, fixed, and permeabilized using the in Cytofix/Cytoperm kit (BD Pharmingen) and stained with anti-cytokine Abs as described (14).

**Generation of bone marrow dendritic cells**

Bone marrow–derived dendritic cells (BMDCs) were obtained from the femurs and tibias of individual mice. Each bone was flushed with 10 ml of PBS containing 1% P/S and 1% P/S RPMI 1640 through a 22-gauge needle. RBCs were lysed followed by wash and resuspension of cells in 10% FBS in RPMI 1640 medium. In a Petri dish, 2 × 10^5 bone marrow cells were plated in 10 ml of RPMI 1640 containing 10% FBS plus penicillin-streptomycin (HyClone), 2-ME, and 20 ng/ml of rGM-CSF. The culture media were refreshed every 3 d, and BMDCs were harvested after 10 d for in vitro coculture assays.

**Ex vivo and in vitro coculture for cytokine protein measurement**

Ex vivo cell culture supernatants were generated using the brachial and inguinal draining lymph nodes harvested from mice 10 d after vaccination, washed, and resuspended in complete RPMI 1640 containing 10 µg/ml yeast cell wall membrane Ag (CWM1), and plated in 96-well plates at a concentration of 5 × 10^5 cells/well. Supernatants were collected from ex vivo cocultures after three days of incubation at 37˚C and 5% CO2 (14). In vitro cell culture supernatants were generated using BMDCs plated in complete RPMI 1640 at a concentration of 10^5 cells/well with 3 × 10^5 heat-killed strain #55 yeast overnight. After 24 h, single-cell suspensions of magnetic bead purified CD4+ naive 1807 cells from brachial, axillary, cervical, and inguinal lymph nodes were added at a concentration of 2 × 10^5 cells/well. Supernatants were collected from in vitro cocultures after three days of incubation at 37˚C and 5% CO2. IFN-γ and IL-17 were measured in total cell lysates using ELISA according to the manufacturer’s specifications (detection limits, 0.05 ng/ml and 0.02 ng/ml, respectively).

**Isolation of effector cells at the site of vaccination**

Mice were vaccinated once s.c. with 10^7 heat-killed strain #55 yeast at a single dorsal site. On day 10 after vaccination, inflamed s.c. tissue was excised from the site of vaccination, placed in ice-cold collagenase buffer and minced into fine pieces. To digest the tissue, 5 ml of dissociation buffer containing 5 mM EDTA and 1% BSA and strained again. Filtered cells containing 5 mM EDTA and 1% BSA were spun at 1500 rpm, the supernatant was carefully aspirated, and cells were resuspended in complete media for stimulation.

**RT-PCR analysis for the detection of Card9-associated gene transcripts**

BMDCs were raised from 15 individual Card9+/− or wild type mice and 3 × 10^5 nonadherent DCs from each individual mouse were cocultured with 3 × 10^5 B. dermatitidis yeast vaccine or medium alone in a 24-well plate for 24 h. Total RNA from the BMDC cultures described above was purified using the Qiagen RNeasy kit (catalog #74106) according to the manufacturer’s protocol. Genomic DNA was removed using Turbo DNase (Ambion, catalog no. AM2238). Following DNase treatment, the RNA was cleaned up using Qiagen RNeasy columns according to the manufacturer’s protocol and by performing additional washes with buffer RPE and 80% ethanol to remove contaminants. The n-fold change of gene expression for yeast stimulation versus no stimulation was calculated using the comparative CT method (41).

**Generation of Fc fusion proteins**

The Dectin-2-Fc expression vector pSecTag2(C)-mDectin-2-Fc was provided by Dr. Philip R. Taylor (Cardiff University, Cardiff, U.K.) (27). To construct the Mincle-Fc expression vector, the extracellular domain of mouse Mincle (amino acids 46–214) was amplified by PCR from a pEFHISB-mMincle plasmid provided by Dr. Christine Wells (University of Queensland, Brisbane, QLD, Australia) (37) and introduced in-frame into the KpnI and PstI sites of pSecTag2(C)-mDectin-2-Fc to replace the Dectin-2 coding sequence. The pSecTag2(C)-mDectin-2-Fc and pSecTag2(C)-mMincle-Fc constructs were separately transfected into HEK293T cells using Lipofectamine 2000 (Invitrogen). Soluble Dectin-2-Fc and Mincle-Fc were expressed and purified as described previously (27). Soluble Dectin-1-Fc was a gift from Dr. Gordon D. Brown (University of Aberdeen, Aberdeen, U.K.) (42). Human IgG1 Fc recombinant protein was purchased from Invitrogen.

**FACS assay for the binding of Fc fusion proteins to fungi**

Fc fragment alone or Fc fusion proteins were added at 10–20 µg/ml to 2 × 10^6 B. dermatitidis, 10^5 H. capsulatum, or 2 × 10^5 C. posadasii in 100 µl binding buffer (20 mM Tris-HCl, 150 mM NaCl, 10 mM CaCl2, 0.05% Tween-20, pH 7.4) and incubated for 2 h at room temperature or overnight at 4˚C. The fungal cells were washed twice with binding buffer and incubated for an additional 30 min at room temperature with 1:100 diluted PE-conjugated goat anti-human Fc Ab (Jackson ImmunoResearch Laboratories) in binding buffer. The cells were then washed three times with binding buffer before fixed with 1% formaldehyde in binding buffer. Bound Fc proteins were quantified by flow cytometry.

**CLR reporter cell construction, stimulation, and binding by fungi**

B3Z cells carrying an NFA1-lacZ reporter construct have been described previously (43) and were provided by Dr. Nilabhi Shastri (University of California, Berkeley, CA). B3Z cells expressing Dectin-2 or a wild type or a signaling-defective FcR-γ-chain that carries two tyrosine-to-phenylalanine mutations within the ITAM motif (31), as well as BWZ cells expressing Dectin-1–CD3ζ (the extracellular domain of mouse Dectin-1 fused to CD3ζ intracellular tail) (44) and the parent BWZ cells (45), were a generous gift from Dr. Caetano Reis e Sousa (London Research Institute, London, U.K.). To construct Mincle-expressing reporter cells, the full-length cDNA of mouse Mincle was subcloned from the pEFHISB-mMincle plasmid into a pFB-IRESEGFP retrovector. B3Z cells were retrovirally transduced with pFB-mMincle-IRESEGFP, selected based on EGFP expression, and verified by cell surface staining and FACS analysis using an anti-mouse Mincle mAb (MBL). To generate B3Z cells coexpressing Mincle and the adaptor FcRγ, Mincle-expressing reporter cells were retrovirally transduced with pMX-IP-FcRγ-chain (wild type) or pMX-IP-FcRγmut (mutant) (31). FcRγ expression was verified with Western blotting using an anti-FcRγ Ab (Upstate).

For B3Z/BWZ cell stimulation, 10^5 B3Z/BWZ cells/well in a 96-well plate were incubated for 18 h with heat-killed fungal cells. lacZ activity was measured in total cell lysates using CPRG (Roche) as a substrate. OD 560 was measured using OD 620 as a reference. For the B3Z/BWZ cell binding assay, 2 × 10^5 B3Z/BWZ cells were prestained with CFSE (Molecular Probes) and incubated for 6 h with 10^6 B. dermatitidis, 2 × 10^5 H. capsulatum, or 2 × 10^5 C. posadasii prestained with LIVE/DEAD Violet staining (Invitrogen). Bound fungal cells were quantified with flow cytometry.

**Statistical analysis**

Differences in the number and percentage of activated, proliferating or cytokine-producing T cells, and in the number of CFUs were analyzed using the Wilcoxon rank test for nonparametric data or the test when data were normally distributed (46). Factorial ANOVA analysis using the SAF software was used to compare the vaccine-induced reduction in lung CFUs between different strains of mice; p < 0.05 is considered statistically significant.

**Results**

Vaccine-induced immunity against systemic dimorphic fungi requires the adaptor Card9

We previously reported that vaccine-induced Th17 cells were necessary and sufficient to protect mice against the three major systemic mycoses in North America (14). Because Card9 has been reported to be required for the development of Th17 cells in responses to primary C. albinus infection (17), we investigated whether Card9−/− mice can acquire vaccine-induced immunity against infection with the systemic dimorphic fungi. Card9−/− mice were unable to control the live, virulence-attenuated #55 vaccine strain of B. dermatitidis and succumbed to widespread dissemination and infiltration of the lungs by the yeast (Fig. 1A). To circumvent susceptibility of Card9−/− mice to the vaccine strain, we immunized them with heat-killed yeast and tested their ability to resist a lethal pulmonary infection with wild type yeast. Vaccinated Card9−/− mice had a burden of lung infection similar
to unvaccinated littermates, which was more than 5 logs higher than in vaccinated wild type controls, indicating the adaptor Card9 is essential for the acquisition of immunity to *B. dermatitidis* infection (Fig. 1B). Interestingly, unvaccinated Card9<sup>−/−</sup> mice were more susceptible to primary infection than unvaccinated wild type controls, suggesting that Card9 also contributes to innate resistance. To determine whether Card9 is required for the development of Th17 cells to the lung upon challenge. Vaccinated Card9<sup>−/−</sup> mice recruited reduced numbers and frequencies of IL-17- and IFN-γ-producing Ag-specific 1807 cells to the lungs compared with vaccinated wild type controls (Fig. 1C–D). Thus, the adaptor Card9 is required for the development of antifungal Th17 responses after vaccination with *B. dermatitidis*.

To test whether Card9 is necessary for the acquisition of vaccine-induced immunity and the development of Th17 cell responses to other systemic dimorphic fungi, we vaccinated mice with *H. capsulatum* and *C. posadasii*. Card9<sup>−/−</sup> mice vaccinated with live G217B *H. capsulatum* yeast as described (14) contained the vaccine in the s.c. tissue and did not succumb to dissemination (data not shown), but they failed to acquire resistance to pulmonary challenge (Fig. 1B) and recruited reduced numbers and frequencies of IL-17- and IFN-γ-producing 1807 cells to the lungs (Fig. 1C–D). Card9<sup>−/−</sup> mice succumbed to dissemination when vaccinated s.c. with live *C. posadasii* conidia from wild type strain C735 (C.-Y. Hung, M. del Pilar Jimenez-Alzate, A. Gonzalez, M. Wüthrich, B.S. Klein, and G.T. Cole, submitted for publication). To determine whether Th17 cells develop in the absence of Card9,

**FIGURE 1.** Card9 is required for vaccine control and the acquisition of adaptive immunity to dimorphic fungi. (A) Wild type and Card9<sup>−/−</sup> mice were vaccinated s.c. with 10<sup>5</sup> or 10<sup>6</sup> live *B. dermatitidis* yeast and survival recorded when mice were moribund. *n* = 10 mice/group and are representative of two experiments. (B) Mice were vaccinated with 10<sup>6</sup> heat-killed (HK) *B. dermatitidis*, 10<sup>7</sup> HK or live *H. capsulatum* yeast, or 10<sup>6</sup> FKS of *C. posadasii* or not as a control and challenged with 2 × 10<sup>3</sup> *B. dermatitidis* or 2 × 10<sup>3</sup> *H. capsulatum* yeast 2 wk or 80 C.p. spores 3 wk after booster vaccination. Lung CFUs were determined when unvaccinated mice were moribund 14 d after infection with *B. dermatitidis* or *C. posadasii* and at day 13 after infection with *H. capsulatum*. Data are the mean ± SEM (n = 8–12 mice/group) and are representative of three to five experiments. *p < 0.05 versus vaccine-induced reduction in lung CFUs in wild type mice. Numbers indicate the n-fold difference in lung CFUs versus unvaccinated controls. (C) Wild type and Card9<sup>−/−</sup> mice received 10<sup>6</sup> naive, CD4<sup>+</sup> purified 1807 T cells and were vaccinated with HK *B. dermatitidis* or *H. capsulatum* yeast, FKS from *C. posadasii* or not. Five weeks later, mice were challenged with 2 × 10<sup>3</sup> *B. dermatitidis*, 2 × 10<sup>5</sup> *H. capsulatum* yeast or 10<sup>6</sup> FKS from *C. posadasii* and the number of cytokine-producing 1807 cells enumerated by FACS at day 4 after infection. Data are the mean ± SEM of three independent experiments (n = 16–20 mice/group). *p < 0.05 versus vaccinated wild type controls. (D) The frequency of cytokine-producing 1807 cells in the lung at day 4 after infection. Data are the mean ± SEM (n = 16–20 mice/group); representative of three experiments. *p < 0.05 versus vaccinated wild type controls. ND; not detected.
knockout mice were instead vaccinated with either FKS or live conidia of an attenuated ΔT vaccine strain. This strain lacks the chitinases 2, 3, and α-arabinotol-2-dehydrogenase genes (3) and fails to endosporulate and disseminate in s.c. vaccinated Card9−/− mice. Card9−/− mice vaccinated with FKS failed to acquire resistance to challenge (Fig. 1B) and recruited lower numbers and frequencies of IL-17– and IFN-γ–producing 1807 cells to the lungs upon challenge compared with wild type controls (Fig. 1C–D). Vaccination with the attenuated ΔT vaccine strain yielded similar results (data not shown). In contrast to primary infection with B. dermatitidis and H. capsulatum, unvaccinated Card9−/− mice were not more susceptible than wild type controls to infection with C. posadasii. Thus, the Card9 signaling pathway is required for the development of vaccine-induced resistance and antifungal Th17 responses to the three major systemic dimorphic fungi.

Expansion and activation of Ag-specific cells does not require Card9

Receptor signaling pathways can affect T cell development at multiple stages. In the setting of LCMV infection, Tc1 cells require intrinsic TLR/Myd88 signals not for activation, expansion, or differentiation, but to survive apoptosis after these events (47). Because Card9 is required for the development of vaccine-induced anti-fungal Th17 cells, we investigated the stage of the immune response at which Card9 governs T cell priming. To do so, we adaptively transferred magnetic bead-purified CD4+, CFSE-labeled naive T cells from 1807 mice into Card9−/− and wild type recipients prior to vaccination with B. dermatitidis and analyzed T cell development at serial time points thereafter. At day 7 after vaccination, mice lacking Card9 showed no deficit in the proliferation and activation, but had a small reduction in expansion of Ag-specific 1807 cells (Fig. 2A–C), indicating that Card9 minimally affects the early stages of vaccine-induced T cell development. At subsequent time points (days 14 and 35 after vaccination), activated 1807 cells underwent similar contraction. Upon recall at day 4 after infection, the frequency and number of activated CD44hi 1807 cells were comparable in the skin-draining lymph node (sdLN) and in the lung of Card9−/− and wild type recipient mice (Fig. 2B–C). These data indicate that the adaptor Card9 is not required for the activation, proliferation, and contraction of Ag-specific 1807 cells in the sdLN. Although the expansion of 1807 cells was minimally affected by the absence of Card9, this did not affect the number of 1807 cells in the sdLN and the lung at day 4 after challenge.

Th17 cell differentiation requires Card9

Because Card9−/− mice failed to recruit IL-17– and IFN-γ–producing 1807 cells to the lung (Fig. 1C–D), we investigated whether Card9 governs the differentiation of effector T cells during the vaccine-priming phase. We analyzed T cell differentiation by three independent approaches. First, we harvested activated T cells at the peak of expansion from the sdLN and stimulated them ex vivo with cell wall membrane (CW/M) Ag. T cells from Card9−/− mice produced ∼8-fold less IL-17 protein in response to fungal Ag than did wild type T cells (Fig. 3A). Similarly, IFN-γ protein levels were reduced by at least 30-fold compared with wild type controls. Although Card9 is primarily responsible for receptor signaling in myeloid but not lymphoid cells, we sought to exclude formally a T cell–intrinsic role of Card9 for the differentiation of Th17 cells. Thus, in a second approach we cocultured BMDCs from Card9−/− and wild type mice together with vaccine yeast and naive wild type 1807 cells in vitro. 1807 cells cocultured with Card9−/− DCs produced ∼7-fold less IL-17 than did cocultures with wild type DCs (Fig. 3B). Third, to investigate Th17 cell differentiation in vivo, we determined the frequency of cytokine-producing wild type 1807 cells at the site of vaccination. The frequency of IL-17– and IFN-γ–producing
FIGURE 3. Helper T cells fail to differentiate without Card9 signaling. (A) Primed T cells from sdLN of wild type and Card9−/− mice were cocultured ex vivo with CW/M extract for 3 d, and cytokine production was measured by ELISA. Data are the mean ± SEM (n = 6 mice/group) and are representative of three experiments. *p < 0.05 versus vaccinated wild type controls. (B) BMDCs from wild type and Card9−/− mice were cocultured with B. dermatitidis vaccine yeast and CD4+ purified naive 1807 cells for 3 d, and cytokine production was measured with ELISA. Data are the mean ± SEM (n = 3–5 mice/group) and representative of five experiments. *p < 0.05 versus vaccinated wild type controls. (C) CD4+ purified 10⁶ naive wild type 1807 Tg cells were adoptively transferred into wild type and Card9−/− mice prior to vaccination with 10⁷ HK B. dermatitidis yeast. Effector T cells were harvested from the s.c. tissue 10 d after vaccination, and the frequency of cytokine-producing cells was determined by FACS analysis. Data are the mean ± SEM (n = 6 mice/group) and are representative of three experiments. *p < 0.05 versus vaccinated wild type controls. (D) The changes in cytokine transcript and protein were measured with real-time RT-PCR and ELISA for BMDCs cultured with versus without yeast. Data are the mean ± SEM (n = 13–15 mice/group). *p < 0.05 versus wild type controls.

1807 cells recruited to the s.c. tissue was reduced in Card9−/− versus wild type mice (Fig. 3C). Thus, extrinsic Card9 signaling is required for the differentiation of Th17 and Th1 cells during the priming phase of vaccine-induced immunity.

Card9-dependent genes induced by vaccine yeast

Upon vaccination, APCs become activated and generate a milieu that fosters the generation of Th17 and Th1 cells. To investigate genes that are induced upon yeast exposure, we cocultured the B. dermatitidis vaccine with BMDCs from 15 individual wild type and Card9−/− mice, harvested their RNA, and analyzed gene expression by microarray. Among the upregulated genes, some were canonical genes that are known to induce the differentiation of Th17 cells (data not shown). To verify differential gene expression in our microarray, we performed real-time RT-PCR on the individual RNA samples from 15 mice/group (Fig. 3D). IL-6, TGF-β, IL-1β, IL-12 p35, and IL-23 p19 were upregulated 33.8-, 2.1-, 3.4-, 11.8-, and 10.5-fold in wild type versus Card9−/− DCs. Cytokine transcripts were corroborated with protein measurements of the cell culture supernatants by ELISA. IL-6 protein was 4-fold reduced for yeast stimulated wild type versus Card9−/− DCs. Thus, vaccine yeast–induced expression of these genes by DCs is Card9 dependent and likely affects the differentiation phenotype of T cells in Card9−/− mice.

Dectin-2, but not Dectin-1 or Mincle, recognizes B. dermatitidis vaccine yeast

Because Card9 receives signals from upstream receptors including the CLRs Dectin-1, Dectin-2, and Mincle, we postulated that these CLRs might recognize B. dermatitidis and the other vaccine yeast and elicit vaccine immunity. To test this hypothesis, we generated soluble recombinant CLRs by fusing their carbohydrate-recognition domains to the Fc fragment of human IgG1. Soluble Dectin-1-, Dectin-2-, and Mincle-Fc fusion proteins stained B. dermatitidis vaccine yeast brighter than did Fc alone (Fig. 4A, left panel). Fluorescent microscopy showed punctate staining of Fc fusion proteins around the cell wall (Fig. 4B). Because the carbohydrate recognition domain of Dectin-2 and Mincle requires calcium for binding, we added 5 mM EDTA to the staining conditions. Staining of the yeast was abrogated by the addition of 5 mM EDTA (data not shown), indicating that the binding of the soluble CLRs to the yeast occurred in a C-type lectin-specific manner.

To investigate whether vaccine yeast are recognized by cell surface-bound CLRs and induce downstream receptor signaling, we used T hybridoma cells expressing an NFAT-lacZ β-galactosidase reporter of ITAM signaling (31, 44). In response to vaccine yeast stimulation, lacZ activity was increased in T hybridoma cells coexpressing Dectin-2 and FcRγ, but not in reporter cells expressing either Dectin-2 or FcRγ alone (Fig. 5A). Because surface expression of Dectin-2 requires coexpression of FcRγ (31), reporter cells expressing Dectin-2 and FcRγ together bound vaccine yeast (Fig. 5B), whereas reporter cells expressing Dectin-2 or FcRγ alone bound yeast poorly (Supplemental Fig. 1A). As expected, reporter cells coexpressing an ITAM signaling-defective mutant of FcRγ chain (31) and Dectin-2 failed to increase reporter activity (Fig. 5A), indicating that ITAM signaling mediates the reporter cell activation. However, this reporter cell line bound vaccine yeast as efficiently as T hybridoma cells coexpressing Dectin-2 and wild type FcRγ (Supplemental Fig. 1A), indicating that the FcRγ mutations did not affect the ability of Dectin-2 to mediate binding of vaccine yeast. In contrast to Dectin-2, reporter cells expressing Dectin-1 or Mincle did not increase lacZ activity (Fig. 5A) and...
bound vaccine yeast poorly (Fig. 5B; Supplemental Fig. 1B–C), although the respective soluble CLRs bound the yeast. Thus, Dectin-2, but not Dectin-1 or Mincle, recognized *B. dermatitidis* vaccine yeast and triggered downstream ITAM signaling through FcRγ.

**FIGURE 4.** Soluble Dectin-1–Fc, Dectin-2–Fc, and Mincle-Fc proteins bind three dimorphic fungi. Fungal cells were incubated with Fc fragment alone or Fc fusion proteins as indicated by different colors, followed by staining with PE-conjugated anti-human Fc Ab, and analyzed with FACS (A) and microscopy (B). As a negative control, Ab-stained fungal cells without any Fc proteins are indicated by gray filled histograms in (A). Data are representative of two independent experiments. Scale bar, 10 μm.

Dectin-1 and Dectin-2 recognize multiple dimorphic fungi

The three CLRs differentially recognize *B. dermatitidis*; therefore, we investigated how they recognize *H. capsulatum* and *C. posadasii*. We incubated the latter two fungi with Fc fusion proteins and analyzed them by FACS. All three soluble CLR fusion proteins stained *H. capsulatum* yeast to various degrees (Fig. 4A). Soluble Dectin-1–Fc stained the yeast strongly, Dectin-2–Fc stained intermediate and Mincle-Fc stained the least. All three soluble CLR fusion proteins stained *C. posadasii* efficiently (Fig. 4A). Fluorescent microscopy showed punctate staining of Fc fusion proteins on the cell wall of *H. capsulatum* (Fig. 4B), whereas a more evenly distributed staining pattern was observed on the surface of *C. posadasii* (Fig. 4B). Dectin-1– and Dectin-2–expressing T hybridoma cells showed increased lacZ reporter activity when stimulated with *H. capsulatum* or *C. posadasii* (Fig. 5A), whereas no increase in reporter activity was detected with Mincle-expressing reporter cells. Dectin-1– and Dectin-2–expressing T hybridoma cells consistently bound *H. capsulatum* and *C. posadasii*, whereas Mincle-expressing and control reporter cells failed to do so (Fig. 5B; Supplemental Fig. 1). Because all three dimorphic fungi failed to increase reporter activity of Mincle-expressing T hybridoma cells, we used TDB, a known ligand for Mincle and synthetic analog of the mycobacterial cord factor, as a positive control to stimulate the lacZ reporter cells. In an additional approach, Dr. Sho Yamasaki’s laboratory tested the recognition of *B. dermatitidis* yeast by surface-bound Mincle using a NFAT-GFP reporter T cell line (28). TDB increased the reporter activity of Mincle-expressing T hybridoma cells, we used TDB, a known ligand for Mincle and synthetic analog of the mycobacterial cord factor, as a positive control to stimulate the lacZ reporter cells. 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cells that migrated to the lungs were significantly reduced in vaccinated Dectin-2−/− and FcRγ−/− mice, compared with wild type recipient mice (Fig. 6D). Few to no IL-13–expressing Th2 cells were recruited to the lungs of any of the mouse strains investigated (data not shown). Not surprisingly, vaccinated Dectin-2−/−, FcRγ−/−, and Syk−/− mice were unable to acquire resistance to *B. dermatitidis* infection in contrast to wild type or Mincle−/− mice (Fig. 6E). These data indicate that the Dectin-2/FcRγ/Syk/Card9 signaling pathway is indispensable for the differentiation of vaccine-induced Th17 and Th1 cells and acquired resistance to *B. dermatitidis* infection.

**Dectin-2/FcRγ/Syk/Card9 pathway is required for Th17 cell differentiation and vaccine resistance to multiple dimorphic fungi**

To investigate which CLR upstream of Card9 are required for the development of Th17 cells and vaccine-induced resistance to infection with *H. capsulatum* and *C. posadasii*, we studied the recruitment of primed T cells to the lung and acquired resistance to infection upon recall in the respective vaccine models. For *H. capsulatum*, fewer IL-17–producing 1807 cells migrated to the lungs of Dectin-1−/−, Dectin-2−/−, and FcRγ−/− mice, but not Mincle−/− mice, compared with wild type controls that were vaccinated and then challenged with *H. capsulatum* (Fig. 7A). Fewer IFN-γ–producing T cells also were found in the lungs of vaccinated and challenged Dectin-2−/− and FcRγ−/− mice compared with wild type mice. *Histoplasma* vaccinated Dectin-2−/− mice likewise reduced lung CFU significantly less after challenge than did vaccinated wild type or Mincle−/− mice (Fig. 7B). Although Dectin-1−/− mice were nearly 10-fold less resistant than wild type mice, this difference did not achieve statistical significance.

In the *Coccidioides* model, the development of Th17 (and Th1) cells were impaired in *C. posadasii* vaccinated and challenged Dectin-2−/− and FcRγ−/− mice, as compared with wild type and Mincle−/− recipients. The acquisition of vaccine immunity likewise was blunted in these mice, as determined by the reduction of lung and spleen CFU (Fig. 7C+D). Thus, the Dectin-2/FcRγ/Syk/Card9 signaling pathway is required for the optimal development of vaccine-induced Th17 cells and acquired resistance to multiple systemic dimorphic fungi. In addition, whereas Dectin-1 is required for the acquisition of vaccine-induced Th17 cells and resistance to *H. capsulatum*, this CLR is dispensable for eliciting these responses to *C. posadasii* (data not shown and paper in preparation).
The development of effective vaccines requires a fundamental understanding of how protective immune responses are induced. In this study, we identify the signaling adaptors and PRRs that govern the acquisition of vaccine immunity to the three major systemic mycosis of North America by differentiating naive fungus-specific T cells into protective Th17 cells. Although Card9 has been implicated in host protection to primary infection and the development of Th17 cells (17), we establish that it has a requisite role in the induction of vaccine immunity, and we uncover the
and wild type conidia of control s.c. delivery of live attenuated vaccine yeast of spherules of \( \text{H. capsulatum} \) live yeast, live \( \text{B. dermatitidis} \) vaccinated with \( 10^7 \) HK \( \text{G217B} \) yeast and challenged with \( 10^6 \) FKS. Data are the mean ± SEM of two independent experiments; representative of two experiments. Numbers indicate the n-fold change in lung CFU versus unvaccinated controls. \(* p<0.05\) versus vaccine-induced reduction in CFU in wild type mice. \( \Delta \) mice were vaccinated with \( 10^6 \) FKS or \( 5 \times 10^6 \) viable spores of the \( \Delta T \) strain (or not as a control) and challenged with 50–80 \( \text{C. posadasii} \) spores 4 wk later. Lung and spleen CFU were determined 14 d postinfection. Data are the averages ± SEM of two independent experiments (\( n = 8–12 \) mice/group/experiment); representative of two experiments. Numbers indicate the n-fold change in lung CFU versus unvaccinated controls. \(* p<0.05\) versus vaccine-induced reduction in lung CFU in wild type mice.

**FIGURE 7.** FcRγ and Dectin-2 are required for T cell differentiation and adaptive immunity to \( \text{C. posadasii} \) and \( \text{H. capsulatum} \). (A) \( 10^6 \) naive CD4+ purified, wild type 1807 Tg cells were transferred into wild type, Dectin-2 \(-/-\), FcRγ \(-/-\), and Mincle \(-/-\) mice prior to vaccination with \( 10^7 \) HK \( \text{H. capsulatum} \) G217B yeast and challenged with \( 10^7 \) \( \text{H. capsulatum} \) yeast. At day four postinfection, the numbers and frequencies of cytokine-producing 1807 cells in vaccinated mice were determined by FACS analysis. Data are the mean ± SEM (\( n = 4–6 \) mice/group); representative of two experiments. \(* p<0.05\) versus vaccinated wild type controls. (B) Wild type, Dectin-2 \(-/-\), FcRγ \(-/-\), and Mincle \(-/-\) mice were vaccinated with \( 10^7 \) HK \( \text{H. capsulatum} \) G217B yeast (or not as a control) and challenged with \( 10^5 \) \( \text{H. capsulatum} \) yeasts 2 wk after booster vaccination. Lung CFU were determined 13 d postinfection. Data are the mean ± SEM (\( n = 8–12 \) mice/group); representative of two experiments. Numbers indicate the n-fold change in lung CFU versus unvaccinated controls. \(* p<0.05\) versus vaccine-induced reduction in CFU in wild type mice. (C) Same as (A), but mice were vaccinated with \( 10^5 \) FKS of \( \text{C. posadasii} \). Two wk after the boost, the mice were challenged with \( 10^6 \) FKS. Data are the mean ± SEM (\( n = 4–6 \) mice/group); representative of two experiments. \(* p<0.05\) versus vaccinated wild type controls. (D) Wild type, Dectin-2 \(-/-\), FcRγ \(-/-\), and Mincle \(-/-\) mice were vaccinated with \( 10^6 \) FKS or \( 5 \times 10^6 \) viable spores of the \( \Delta T \) strain (or not as a control) and challenged with 50–80 \( \text{C. posadasii} \) spores 4 wk later. Lung and spleen CFU were determined 14 d postinfection. Data are the averages ± SEM of two independent experiments (\( n = 8–12 \) mice/group/experiment); representative of two experiments. Numbers indicate the n-fold change in lung CFU versus unvaccinated controls. \(* p<0.05\) versus vaccine-induced reduction in lung CFU in wild type mice.

Because the generation of Th17 cells directly correlates with vaccine-induced resistance to the systemic dimorphic fungi (14), we determined the number of IL-17–producing CD4+ T cells in the lungs of vaccinated mice upon recall after challenge. We also enumerated the number of IFN-γ–producing CD4+ T cells because they can contribute to vaccine-induced resistance (4), although Th1 cells are dispensable, unlike Th17 cells (14). We observed that the numbers of Th17 and Th1 cells in all three vaccine models were significantly reduced in vaccinated Card9 \(-/-\) versus wild type mice. Using our recently developed adoptive transfer system with TCR transgenic 1807 cells, which recognize a shared and protective Ag among the systemic dimorphic fungi (34), we demonstrated that although Card9 is required for the differentiation of naive T cells into Th17, the adaptor is largely dispensable for the activation, expansion, proliferation, and survival during the contraction phase, and for recruitment to the lung upon recall. Moreover, Card9 not only affected the differentiation of Th17 cells; it likewise affected Th1 cells. Although the role of the CLR-Card9 signaling pathway on the development of effector Th17 and Th1 cells has not been studied in vivo, the TLR-Myd88
pathway has been shown to exert an incremental impact on the differentiation of A. fumigatus–specific CD4+ T cells during pulmonary infection (48). Myd88-mediated signals were dispensable for the recruitment and expansion of Ag-specific T cells to the mediastinal lymph nodes (MLN) and trafficking to the lung after priming. However, Myd88 signaling was required to enhance T-bet induction and differentiation of Th1 cells in the MLN. Further maturation of MLN-primed T cells into fully differentiated IFN-γ-producing Th1 cells occurred upon arrival of the cells in the airways and was TLR and Myd88 independent.

To discern how Card9 induces T helper differentiation, we performed a microarray analysis and verified differential gene expression by real-time RT-PCR. Among those differentially expressed were genes known to induce Th17 and Th1 cells, such as IL-6, IL-23, TGF-β, IL-1β, and IL-12 p35. Thus, Card9 governs the expression of cytokines that are instrumental in driving differentiation of Th17 and Th1 cells. Using the microarray data, we also found noncanonical genes that have not been linked previously to Th17 differentiation (V. LeBert, H. Wang and M. Wüthrich, unpublished data). We intend to study the role of novel candidates in elucidating how Card9 governs the expression of the Th17 and Th1 priming cytokines.

To investigate which PRRs upstream of Card9 are required to induce the differentiation of Th17 cells and vaccine-induced immunity, we first tested whether soluble fusion proteins consisting of the extracellular domain of Dectin-1, Dectin-2, and Mincle and human Fc can stain fungal yeast and spherules. Soluble Dectin-1 and Dectin-2 have been used previously to stain A. fumigatus (42), Fonsecaea pedrosoi (49), C. albicans (27, 30), and C. immitis (18). Here, all three soluble Fc chimeras were tested to bind the three dimorphic fungi; however, the binding efficiency between soluble receptors and fungal species varied presumably based on respective ligand expression and size of the organisms. Second, to explore whether cell surface–bound CLRs can recognize and bind the fungal vaccine strains we cocultured T cell hybridoma cells that were engineered to express a β-galactosidase NFAT-lacZ reporter of ITAM signaling (43). By using this nonmyeloid reporter system, we were able to distinguish between signaling events triggered by putative CLR ligands versus other ligands. To our surprise, some of the hybridoma cell–expressed CLRs showed a recognition pattern different from soluble CLR chimeras. For example, soluble Dectin-1 stained B. dermatitidis vaccine yeast, but surface expressed receptor did not recognize the vaccine yeast. Similarly, soluble Mincle stained all three dimorphic fungi, but Mincle expressing reporter cells did not become activated and failed to bind the three fungi. On the other hand, soluble and surface–expressed Dectin-2 yielded consistent results for each of the fungi tested. Although soluble CLR chimeras gave valid binding results, they were less reliable than surface expressed CLRs in forecasting the in vivo role of CLRs in vaccine resistance.

One potential explanation for the discrepant findings between the two assays could be that only surface-exposed fungal ligands can be recognized by cell surface–expressed receptors, but not ligands that are embedded deeper in the cell wall; however, the latter might still be accessible by soluble CLRs. Thus, cell surface–expressed receptors on the T hybridoma reporter cells helped to predict the importance of the receptor for the priming of T helper responses in vivo. Indeed, the failure of cell surface–expressed Dectin-1 to recognize B. dermatitidis is consistent with our previous data showing that Dectin-1 is dispensable for the induction of Th17 and Th1 cells and vaccine immunity (14). Similarly, the phenotypes of Dectin-2 and Mincle in the vaccination model with B. dermatitidis showed good fidelity with the results of the NFAT reporter cells. Dectin-2−/− mice showed a severe defect in differentiation of fungus-specific Th17 cells and vaccine immunity, indicating that Dectin-2 is dispensable for the acquisition of adaptive immunity to B. dermatitidis infection. The inability of T hybridoma cell–expressed Mincle to trigger NFAT-reporter activity or bind to the three dimorphic fungi correlated with the dispensability of this CLR in the vaccine models.

Similar to Card9, the upstream receptor Dectin-2 affected the development of both B. dermatitidis–specific Th17 and Th1 but not Th2 cells during vaccination. Therefore, Dectin-2 and Card9 deficiency did not shift the balance of Th cell differentiation as has been reported for Th17 responses that depended on Dectin-1 during a pulmonary infection of mice with A. fumigatus (50). Dectin-1 deficiency disproportionately increased Th1 responses and decreased Th17 differentiation. The authors showed that Dectin-1 mediated signals alter CD4 T cell responses to fungal infection by reducing the production of IFN-γ and IL-12p40 in innate cells, thereby decreasing T-bet expression in responding CD4 T cells and enhancing Th17 responses (50).

Despite the fact that cell surface–expressed Dectin-1 and Dectin-2 recognized and bound H. capsulatum yeast and C. posadasii spherules, the effect on Th17 cell priming and the acquisition of vaccine immunity was modest, albeit statistically significant. Our data are compatible with the interpretation that these two CLRs are redundant or cooperate in the innate recognition of these two dimorphic fungi. Receptor collaboration has been reported for Dectin-1 and multiple TLRs (51), and for the recognition of Malassezia by Dectin-2 and Mincle through distinct ligands (29). The fact, that H. capsulatum and C. posadasii vaccinated FcRγ−/− mice showed stronger phenotypes in acquiring vaccine-induced immunity and Th17 cells compared with Dectin-2−/− mice is compatible with the notion of receptor cooperation. Alternatively, other FcRγ coupled CLR alone or together with Dectin-2 could play a prominent role in innate fungal recognition as well. A recently identified CLR, MCL, is a potential candidate, and mediates TDM-induced acquired immune responses (52); however, its role in vaccine immunity to fungi has not been studied.

A prior study showed that β-glucan on H. capsulatum yeast was shielded by α-glucan and not recognized by Dectin-1 (53), whereas we observed that Dectin-1 expressing reporter cells bound to H. capsulatum, which triggered lacZ reporter activity in vitro. Consequently, in vivo, the induction of Th17 cells, the acquisition of vaccine-induced resistance to H. capsulatum infection, and resistance to primary infection were all blunted in Dectin-1−/− mice versus wild type control mice. The differing results between the two studies may be due to strain specific differences in the cell wall composition. We used the North American, RFLP class 2 and chemotype I strain G217B (ATCC 26032) that mostly lacks α-1,3-glucan on the yeast surface. In contrast, Rappleye et al. (53) used the Central and South American, RFLP class 3 and chemotype II yeast strain G186AR (ATCC 26029), which expresses surface α-1,3-glucan that shields β-glucan from detection by Dectin-1. In a recent report (54), liquid grown G217B yeast bound to Dectin-1–expressing 3T3 fibroblasts when yeast were harvested during the exponential phase, but not during the stationary phase (54). In our study, we grew G217B yeast for 3 to 7 d on slants and heat-killed them to perform overnight incubation in the lacZ reporter assay. Surface staining of yeast with Dectin-1 fusion protein was comparable in live versus heat-killed cells, indicating that heat inactivation did not increase exposure of β-glucan. However, we have seen large differences in the gross appearance of the yeast cell wall by electron microscopy (H. Wang and M. Wüthrich, unpublished data) when comparing liquid versus agar grown yeast, which could account for the different Dectin-1 binding phenotypes. Nonetheless, our data suggest that β-glucan is not shielded in H. capsu-
*latum* strain G217B yeast in vivo, and it is recognized by Dectin-1 during primary and adaptive immunity to recruit and prime Th17 cells, respectively.

Dectin-1 induces two independent signaling pathways—one through Syk and one through Raf-1—to control adaptive immunity (55, 56), but we have not determined whether the FcRyCard9 and Dectin-1 phenotypes in the vaccination model with *H. capsulatum* are functionally linked or unrelated/Raf-1 dependent.

The fungal ligands of most CLR Rs remain largely unclear. It is likely that differences in the cell wall composition and structure between the endemic fungi account for the differential recognition by Dectin-1, Dectin-2, and Mincle. In addition, individual CLR can recognize several distinct ligands within one fungal species and among different fungi and microorganisms. For example, Mincle recognizes TDM from mycobacteria, corynebacteria, and *Nocardia* (57), its synthetic analog TDB (25) and two structurally different glycolipids 44-1 and 44-2 from *Malassezia* (29). Similarly, Dectin-2 recognizes the terminal mannos of N-linked glycan (27) and *O-linked* α-1,2-mannosyl residues from *Malassezia* (29). Thus, it is conceivable that Dectin-2 recognizes ligands in the systemic endemic fungi that are structurally distinct from those that have been described above.

CLRs have been of burgeoning interest as targets to enhance vaccine efficacy (56, 58). A promising strategy is to use carbohydrate ligands of CLRs to drive vaccine responses (59, 60). For example, the particulate β-glucan curdlan, a well-defined ligand for Dectin-1, has been reported to be a potent adjuvant that primes anti-Th17 responses (61). Moreover, porous β-glucan particles that consist primarily of β-1,3-1,4-glucans and allow for high Ag loading have been proposed as a receptor-targeted vaccine delivery system (62). Thus, the glucan particle-based vaccine platform combines adjuvanticity and Ag delivery to induce strong Th17- and Th1-biased CD4+ T cell responses. Because mannans are recognized by Dectin-2 (23, 27, 29), we postulate that they can be harnessed as adjuvants for vaccination to combat infection with the systemic dimorphic fungi of North America that collectively account for nearly a million new infections annually.

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