In vivo inhibition of tryptophan catabolism reorganizes the tuberculosis and augments immune-mediated control of *Mycobacterium tuberculosis*

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*Mycobacterium tuberculosis* continues to cause devastating levels of mortality due to tuberculosis (TB). The failure to control TB stems from an incomplete understanding of the highly specialized strategies that *M. tuberculosis* utilizes to modulate host immunity and thereby persist in host lungs. Here, we show that *M. tuberculosis* induced the expression of indoleamine 2,3-dioxygenase (IDO), an enzyme involved in tryptophan catabolism, in macrophages and in the lungs of animals (mice and macaque) with active disease. In a macaque model of inhalation TB, suppression of IDO activity reduced bacterial burden, pathology, and clinical signs of TB disease, leading to increased host survival. This increased protection was accompanied by increased lung T cell proliferation, induction of inducible bronchus-associated lymphoid tissue and correlates of bacterial killing, reduced checkpoint signaling, and the relocation of effector T cells to the center of the granuloma. The enhanced killing of *M. tuberculosis* in macropaths in vivo by CD4+ T cells was also replicated in vitro, in cocultures of macaque macrophages and CD4+ T cells. Collectively, these results suggest that there exists a potential for using IDO inhibition as an effective and clinically relevant host-directed therapy for TB.

There is an urgent need to improve antitubercular treatment strategies. Tuberculosis (TB) continues to result in close to two million deaths worldwide on an annual basis, and is the single biggest killer of AIDS patients (1). Additionally, ∼10% of newly diagnosed patients exhibited disease with some resistance to anti-TB drugs, ranging from multidrug-resistant to extensively drug-resistant TB (2). The failure to control TB stems from the lack of relatively poor understanding of both pathogenesis and the host factors that contribute to the susceptibility of TB disease. However, nonhuman primates (NHPs) recapitulate the complete breadth of the lung pathology and granulomatous responses that are emblematic of human disease (3). The granuloma is the site of host–*Mycobacterium tuberculosis* interactions, which either result in acute infection or the control of infection in a latent state (4). *M. tuberculosis* modulates immune interactions to inhibit mycobacterial killing and therefore promote long-term survival of the bacilli.

The expression of indoleamine 2,3-dioxygenase (IDO) is dramatically enhanced in macaque granuloma (5). IDO catabolizes tryptophan (Trp) to kynurenine (Kyn) and other metabolites, and acts to suppress the immune response, particularly the CD4+ T cell production of IFN-γ (6). Induction of host IDO is a nascent strategy to starve pathogens of Trp, an essential amino acid (7). However, *M. tuberculosis* can synthesize its own Trp de novo (8), potentially an adaption for its survival during Trp catabolism by IDO in host phagocytes. Therefore, IDO production has little effect on mycobacterial metabolism and yet impacts protective host immune responses.

Here we demonstrate that increased IDO1 expression correlates with higher bacterial burden. Furthermore, IDO is particularly enriched in the macrophage-rich inner layer of the granuloma (5). This spatial expression may prevent lymphocytes, which are predominant in the external layers of the granuloma, from reaching the infected phagocytes, and this inhibition may further promote bacterial survival. We therefore hypothesize that the highly organized granulomas seen in NHPs and humans may be advantageous to *M. tuberculosis* due to this spatial exclusion of immune cells.

**Significance**

*Mycobacterium tuberculosis* induces the expression of the indoleamine 2,3-dioxygenase (IDO) enzyme, which catabolizes tryptophan. Tryptophan metabolites potently suppress host immunity. The present study demonstrates that blockade of IDO activity reduces both clinical manifestations of tuberculosis (TB) as well as microbial and pathological correlates of the human TB syndrome in macaques. In granulomas, T cells localize in the periphery, and are unable to access the core, where bacilli persist. Inhibiting IDO activity altered granuloma organization such that more T cells translocated to the lesion core and exhibited highly proliferative signatures. Our results identify a highly efficient immunosuppressive mechanism at play in the granuloma environment that aids in *M. tuberculosis* persistence. The ability to modulate this pathway with safe and approved compounds could, however, facilitate chemotherapy-adjunctive host-directed therapy approaches for the control of TB.
of immune-protective lymphocytes. As such, the IDO pathway represents a potential target for host-directed therapy (HDT) to augment the control of TB.

Inhibitors of IDO activity [e.g., 1-methyl-tryptophan (1-MT, D-1MT)] are being evaluated as anticancer drugs. In this study, we demonstrated that D-1MT–mediated IDO inhibition resulted in somewhat increased M. tuberculosis killing, improved clinical signs of disease, increased lymphoid follicles and proliferation of pulmonary lymphocytes, and was associated with a drastic reorganization of the granuloma that allowed lymphocyte trafficking into the macrophage-tropic internal layers. These results lend significant credence to the utilization of IDO inhibitors as an HDT strategy adjunctive to anti-M. tuberculosis chemotherapy (9).

**Results**

**IDO1 Is Expressed in a M. tuberculosis Burden-Dependent Manner in Infected Phagocytes and Experimental Hosts.** We first studied whether IDO levels are induced in a M. tuberculosis burden-dependent manner. We found that IDO expression is induced in M. tuberculosis-infected murine (C3HeB/FeJ) bone marrow-derived macrophages (BMDMs) (Fig. 1A) and rhesus macaque BMDMs (Fig. 1B and Fig. S1) in vitro and in lungs of M. tuberculosis-infected C3HeB/FeJ mice (Fig. 1C and D). Furthermore, IDO expression levels were highly correlated with lung CFUs (P = 0.02, r² = 0.68) (Fig. 1E). We have recently shown that most animals with latent TB infection (LTBI) that were subsequently coinfected with simian immunodeficiency virus (SIV), reactivated (10). In coinfected animals, IDO levels largely
correlated with \textit{M. tuberculosis} burdens (Fig. 1 F and G). Animals with TB exhibited an ~20- to 40-fold IDO induction relative to baseline, whereas the expression was unperturbed in animals that did not reactivate (Fig. 1 F and G) with high degree of concordance \((P < 0.0001, r^2 = 0.48)\) (Fig. 1F). To effectively demonstrate IDO induction as a correlate of \textit{M. tuberculosis} burden, we measured its expression in macaques receiving chemotherapy. Daily oral administration of mixofloxacin, ethambutol, and pyrazinamide, a multidrug-resistant regimen in humans, reduced IDO1 expression relative to untreated controls (Fig. 1 F and G). Consistent with the above findings, low IDO expression was observed in animals infected with nonpathogenic \textit{M. tuberculosis} (\textit{Mtb}) strains \textit{Mtb}\textit{ΔsigH} and \textit{Mtb}\textit{ΔdosR} (11–13) (Fig. 1 F and G). Lungs of animals infected with a high dose of \textit{Mtb}\textit{ΔsigH} mutant had reduced IDO levels (Fig. 1 F and G), which again demonstrates that IDO levels were driven by uncontrolled \textit{M. tuberculosis} replication. Unlike \textit{Mtb}\textit{ΔsigH}, \textit{Mtb}\textit{ΔdosR} exhibits only partial attenuation, and adaptive immune responses are required for its control (13), likely explaining the intermediate expression of IDO in animals infected with \textit{Mtb}\textit{ΔdosR} (Fig. 1G). Hence, IDO is expressed in an \textit{M. tuberculosis} burden-dependent manner. Concomitantly, the expression of the \textit{M. tuberculosis} \textit{trpA}, \textit{trpB}, \textit{trpD}, and \textit{trpY} genes was induced in macaques with active TB (ATB) relative to LTBI (Fig. 1I). Thus, Trp biosynthesis is switched on in \textit{M. tuberculosis} in vivo and correlates with host expression of IDO (Fig. 1J).

\textbf{D-1MT Treatment Improves the Clinical Outcomes and Reduces Lung Tissue Pathology.} Macaques recapitulate several aspects of human TB including ATB and LTBI (5, 11–26), HIV coinfected-mediated reactivation TB (10, 15), as well as immune protection (5, 21). We tested the importance of IDO signaling in vivo in acutely infected macaques by treating the animals with D-1MT, a specific inhibitor of IDO activity. Treatment was initiated 1 wk after \textit{M. tuberculosis} infection (Fig. S2). The progression of TB was significantly altered in treated macaques, as reflected by clinical outcomes (Fig. 2). Whereas all of the control animals had to be killed within 5 wk of \textit{M. tuberculosis} infection, D-1MT–treated animals survived until 8 wk, exhibited significantly delayed kinetics, and lower levels of serum C reactive protein (CRP) compared with controls (Fig. 2A). Similarly, treated animals exhibited limited weight loss over time compared with control animals (Fig. 2B). This finding was consistent with the low bacterial burdens detected in treated animals (Fig. 2 C–E). CFUs were determined from bronchoalveolar lavage (BAL) in two groups each at week 1 (the time when treatment was initiated), week 3 (i.e., 2 wk after treatment), and at the end point, at which time \textit{M. tuberculosis} CFUs were also assessed in the lung tissues. The control animals exhibited significantly higher \textit{M. tuberculosis} burdens \((P < 0.05)\) in BAL at week 3 and in the terminal lung samples compared with the D-1MT–treated animals. BAL data are shown for at least three animals (Fig. 2C). However, the CFU levels in the BAL did not differ between the two groups at week 1, before initiating treatment, indicating that the initial infections were similar (Fig. 2C). The total bacterial burdens in terminal lungs (Fig. 2D) and bronchial lymph node (BLN) (Fig. 2E) were significantly lower in D-1MT–treated animals than in the control animals \(\left(\text{log}_10 \text{CFU} < 0.05\right)\). The bacterial burdens were also lower in liver, kidney, spleen in D-1MT–treated animals than controls (Fig. 2E). D-1MT–treated animals presented with fewer granulomas (Fig. 2F) relative to control animals (Fig. 2G) and exhibited significantly lower \((P < 0.005)\) lung pathology (Fig. 2H). Hence, animals treated with D-1MT not only had better clinical outcomes (Fig. 2 A and B) and reduced pathology (Fig. 2 F and H), but also exhibited reduced bacterial burdens (Fig. 2 C–E).

Together, these results underscore our contention that, although active TB developed in all animals, the disease in D-1MT–treated animals progressed more slowly and to a lesser extent.

\textbf{D-1MT Treatment Reduces the IDO Enzymatic Activity.} The central area of the BAL cytospin that contained regular, monolayer-distributed cells, as confirmed by H&E staining (Fig. S2), was used for Kyn staining on samples obtained from D-1MT–treated and control animals at week 3. Kyn is one of the end products of IDO enzymatic activity. Numerous studies have implicated it in the immunosuppressive function of this signaling pathway (27). It is also known to be a ligand for the aryl hydrocarbon receptor signaling pathway (28).

Confocal microscopy revealed greater levels of Kyn accumulation in controls, relative to D-1MT–treated animals (Fig. 3A). Furthermore, quantitative analysis revealed a highly significant \((P = 0.0001)\) reduction in the average number of Kyn⁺ cells in D-1MT–treated animals (Fig. 3B). We also quantified absolute levels of Kyn and Trp in the plasma, a second measure of IDO activity by ELISA using pure standards, and calculated the Kyn/Trp ratio as an indirect measure of IDO activity (Fig. 3C). The two groups had virtually indistinguishable Kyn/Trp ratios at week 1 (i.e., before the initiation of treatment). In week 3 plasma samples, however, a significantly different \((P < 0.0001)\) Kyn/Trp ratio was observed between two groups. Both results suggest that D-1MT treatment inhibits IDO enzyme activity (>95% reduction) (Fig. 3C). The effect of D-1MT on IDO enzymatic activity could also be observed in the treated group of animals at later stages (up to week 8) during the infection (Fig. S2B). These results establish that the changes in disease progression in D-1MT–treated animals were correlated with inhibition of IDO.

\textbf{Effect of the in Vivo Modulation of IDO Signaling on T Cell Phenotype.} We phenotyped mononuclear cells isolated from dematricized lung and BAL from the end point. Using these samples, we assessed temporal changes in both T cell numbers and T cell phenotypes in the lungs. BAL data at the end point was compared between two groups (Fig. 3 D–H), as previously described (10–13, 16, 20–23). The quantification of memory subsets was established for T cell populations based on CD28 and CD95 coexpression for which a representative flow cytometry plot and
We assessed if IDO inhibition improved the function of granulomas in effectively controlling M. tuberculosis infection. We next analyzed the potential effects of D-1MT treatment on inducible bronchus-associated lymphoid tissue (iBALT) formation. The presence of granuloma-associated iBALT is correlated with protection from M. tuberculosis infection (13). Paraffin-embedded lung samples collected at the time of necropsy were assayed for iBALT by histopathology and immunofluorescence staining with CD3 (detects T cells) and CD20 (detects B cells) antibodies, followed by confocal microscopy and image analysis (13). The presence of B cells and their follicular organization were greater in D-1MT-treated animals (Fig. 3I) relative to control animals (Fig. 3I). The total number of B cells enumerated in multiple lesion sections of lung was significantly higher (P = 0.0013) for D-1MT-treated animals compared with controls (Fig. 3K). These results further support our previous observations that protection from M. tuberculosis infection directly correlates with the presence of granuloma-associated iBALT (10, 13, 19, 22).

IDO Inhibition in Vivo Causes Broad-Spectrum Improvement in Granuloma Function. We assessed if IDO inhibition improved the function of granulomas in effectively controlling M. tuberculosis infection.
(Fig. 4 and Figs. S6 A–D and S7 A and B). Host genes involved in the proinflammatory cytokine storm and especially the NF-kB network were induced to higher levels in controls relative to D-1MT-treated animals, highlighting the acute nature of infection in that group (Fig. 4G, two leftmost heat maps). The expression of a majority of type I IFN signaling/neutrophil response genes, which are well-characterized biomarkers of active TB (35), was also higher in controls (Fig. 4H). Supervised analyses further revealed signatures of elite granuloma performance in D-1MT-treated animals. These responses were associated with a reduction in T cell inhibitory signaling, including the immune checkpoint inhibitors LG3, CTLA4, IDO1, CD27, and CD244, and so forth, all of which exhibited lower expression in D-1MT–treated animals (Fig. 4I). LG3 expression was detected in CD3ε as well as CD3ε+ T cells (Fig. S7 A and B). LG3 is expressed in populations of activated T cells, such as Tregs and NK cells (23, 36), and in the lymphocyte-rich outer layer of the granulomata during ATB (23), and contributes to the reprogramming of the Th1 response (37). Such an environment is likely to be supportive of M. tuberculosis persistence rather than its clearance. Concomitantly, the lungs of treated animals presented with a signature of enhanced T cell stimulation and function: for example, increased CCR5 (involved in cross-talk between T cells and macrophages via its ligands CCL16 and CCL8 (38, 39)), CCL25 (involved in the migration of activated T cells), CCL7 and CCL8 (40) cytokine expression. This was accompanied by increased growth receptor and calcium signaling, signifying a rapidly proliferating thymocyte population (Fig. 4J). In contrast, the lungs of control animals exhibited correlates of T cell dysfunction and exhaustion (Fig. 4A), in agreement with other recent work (42). These results indicate that T cell dysfunction and exhaustion in control animals leads to better M. tuberculosis survival than in treated animals (P < 0.05) (Fig. 2E).

The lungs of D-1MT–treated animals concomitantly also expressed more intense antimicrobial responses, characterized by induction of certain CD8ε+ T cell genes: for example, CTSB (involved in killing of the pathogen) and other antimicrobial genes, such as CD8ε cytotoxic function (43). In the B cell module, BTK, which is involved in promoting B-cell development and maturation (44), was enhanced 3.3-fold by D-1MT treatment. On the other hand, ETS1, which is involved in down-regulating B cell differentiation (45), was induced by 21-fold in controls compared with D-1MT–treated lungs. Thus, the robust expression of antimicrobial genes, such as cathelicidin antimicrobial peptide, cathepsin B, lysosomal vATPase, and RAB39, in D-1MT–treated animals (Fig. 4G) further underscored our hypothesis that expression of IDO is a strategy utilized during infection. Most of these genes were either down-regulated or their expression was reduced in control animals.

Several other genes that have positive effects on T cells, either by differentiation or activation, were also induced in D-1MT–treated animals relative to controls (Fig. 4H). On the other hand, genes that negatively affect T cells, either through regulating effector function or survival, were more highly expressed in control animals. The higher expression of genes in the apoptosis module in the treated group was particularly interesting; despite higher T cell proliferation (~46% in D-1MT–treated animals compared with ~12% in control animals) (Fig. 3), the total T cell counts were indistinguishable between the two groups (Fig. S4 E–G). The expression of NR4A1, which encodes a regulator that promotes T cell apoptosis (46, 47), was induced in the lungs of D-1MT–treated animals (Fig. 4I). These microarray results suggest that the highly proliferative thymocytes being recruited to the lungs of D-1MT–treated animals exhibited apoptosis-mediated turnover.

In addition to several pathways related to T cell proliferation, differentiation, and apoptosis, the induction of type I IFNs (Fig. 4J) in BAL confirms the lung data (Fig. 4B) from D-1MT–treated animals. Selected results were validated by qRT-PCR (by ~50%) in the BAL (Fig. S6B) and lungs (Fig. 4B) of D-1MT–treated animals compared with control animals. Whereas the expression of IDO2 and IFN-γ was not statistically different in both BAL (Fig. S6C) and lungs (Fig. 4B) of D-1MT–treated animals compared with control animals. Whereas the expression of IDO2 and IFN-γ was not statistically different in both BAL (Fig. S6C) and lungs (Fig. 4B) of D-1MT–treated animals compared with control animals.

Inhibition of IDO Permits the Reorganization of the TB Granuloma and Allows CD4ε+ T Cells Access to the Lesion Core. The expression of IDO in M. tuberculosis–infected macaques primarily occurred in the myeloid (inner half) of the granuloma and colocalized with the CD68ε+/CD163ε signal. This result reinforced our belief that antigen-presenting cells (APCs) in the lung express IDO in response to acute M. tuberculosis replication. We hypothesized that this may lead to the reorganization of the tuberculoma, such that the CD4ε+ T cells in the lymphoid (outer half) ring are excluded from the pathogen-rich regions, thereby facilitating greater survival and persistence of M. tuberculosis.

Next, since the expression of IDO specifically occurs in the inner myeloid compartment of the tuberculoma and we suspected the translocation of T cells to the center of the lesion (neecrotic center) in lung granuloma of D-1MT–treated and control animals (Fig. 5). Toward this end, we studied if the demarcation between the necrotic center and the lymphocytic layer was more disrupted in the lesions derived from IDO-inhibitor–treated animals relative to untreated animals where it was well defined (Fig. 5 C and D). We found drastic and significant differences (P < 0.05) in the number of CD4ε+ T cells present in the inner half of the center of the lesions derived from D-1MT–treated relative to untreated animals (Fig. S5 D and E). This led to demarcation of T cells and their migration from the lymphocytic layer to the necrotic center of granuloma were higher in D-1MT–treated animals (Fig. 5E). These results clearly indicate that IDO signaling affects T cell infiltration into the necrotic centers of granulomas. However, quantification of cells staining positive for IDO indicated that the numbers in the macrophage layer were indistinguishable between the groups (Fig. S7). Additionally, anti-M. tuberculosis staining revealed a higher number of bacilli in the lung lesions derived from control- in comparison with D-1MT–treated animals (Fig. 6). Greater bacillary signal was present in the necrotic center in the treated animals compared with the macrophage-rich layer in control animals (Fig. 6). The effector role of CD8ε+ T cells in the control of M. tuberculosis infection has recently been described (10). In the present study, we determined that the proliferation of central and effector memory CD8ε+ T cells was significantly enhanced in D-1MT–treated animals than controls (Figs. 3 and 6). Therefore, we sought to better characterize the phenotype of the lymphocytes migrating toward necrotic lesions (Fig. 5E). Approximately 60% of these cells in lesions from D-1MT–treated animals were found to be positive for granzyme B, which was significantly greater than in controls (Fig. 6). A correlation between the frequency of granzyme-expressing T cells and control of human pulmonary TB has been previously described (50). Granzyme B expression on lymphocytes migrating to the lesion core upon IDO inhibition suggests that the latter controls tissue remodeling events. We speculate that IDO
Inhibition permits lymphocytes with cytotoxic phenotype to migrate to the center of the tuberculoma and assist in the control of *M. tuberculosis* replication. It is possible that some of these cells may be classic CD8$^+$, but the role of other CD3$^+$ populations, such as NKT cells and mucosal-associated invariant T cells, cannot be ruled out. These results indicate that intragranulomatous T cell function is radically altered by D-1MT-mediated inhibition of IDO activity.

We conclude that blockade of IDO signaling leads to significantly better control of *M. tuberculosis* infection and reduces the signs of TB disease by promoting the proliferation of memory T cell subtypes and by enhancing the ability of granulomas to kill *M. tuberculosis*. Because of the possibility that disruption of granuloma following D-1MT treatment might lead to increased dissemination of *M. tuberculosis* to extrapulmonary tissues, we performed CFU assays in BLN, liver, kidney, and spleen at the time of necropsy. The CFU counts in these organs revealed lesser bacterial burdens than controls; however, these numbers were statistically insignificant in liver, kidney, and spleen but drastically reduced in BLN in
comparison with controls (Fig. 3F). Thus, CFU measurements ruled out that disruption of granuloma by D-1MT treatment does not cause an increase in bacterial dissemination to extrapulmonary tissues, but indeed, these animals have overall lesser bacterial burdens.

**Inhibition of IDO Signaling in Macrophage: CD4+ T Cell Cocultures Restricts Mycobacterial Growth.** We cocultured *M. tuberculosis*-infected rhesus macrophages where IDO expression had been silenced, with *M. tuberculosis*-specific CD4+ T cells in vitro, and measured bacterial burden (Fig. S1) used were from rhesus macaques with acute TB infection. The siRNA specifically affected IDO1 (Fig. S1 F and J) and not IDO2 (Fig. S1 F and K) expression. IDO1 silencing resulted in a greater control of *M. tuberculosis* replication when macrophages were cocultured with CD4+ T cells but not in macrophages alone (Fig. S1E). The silencing of IDO1 resulted in increased levels of IFN-β (Fig. S1 F and K).

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**Fig. 5.** Extensive relocalization of T cells to the internal regions of the macaque granulomata after inhibition of IDO-signaling. H&E staining of a representative lesion from D-1MT–treated (Left) and control (Right) groups is shown (A). A schematic representation of the granulomata shown in A is drawn in B, distinctly differentiating the lymphocytic and macrophage layers from the necrotic center. The expression of IDO was measured as a function of its presence in either of the three intragranulomatus compartments (necrotic, macrophage, or lymphocytic layer) by immunostaining: IDO (green), CD3 (red), and nuclei (blue) (C). A magnification of the white square area in C is shown in D, with white arrowheads pointing to CD3+ cells in red. The number of CD3+ cells (E, Upper) as well as total nuclei (E, Lower) in multiple granulomata in D-1MT-treated (orange with circular data points) and control (gray with triangle data points) animals enumerated in the lymphocytic, macrophage, and necrotic center compartments are shown. For quantification, 10 fields from each compartment were counted under a fixed magnification (corresponding to an area of 0.05 mm²) using a multispectral imaging camera (CRI Nuance). The data are means ± SEM, *P < 0.05, **P < 0.01, ***P < 0.001 using a Student’s t test. [Scale bars, 20 μm (C, also applies to A and B); 5 μm (D).]
and L), while the expression of IFN-γ (Fig. S1 F and M) and the internal control GAPDH (Fig. S1F) was not perturbed.

**Discussion**

*M. tuberculosis* utilizes the host granulomatous response to persist in the face of strong immunity (51), by modulating both innate (52) and adaptive (53) immune responses. The fate of *M. tuberculosis* infection is decided in the granuloma; some lesions affect elite control of *M. tuberculosis* replication via enhanced killing, but others fail, resulting in uncontrolled replication and spread. Therefore, the potential to modulate granulomatous responses in favor of bacterial killing by enhancing natural immunity using HDT exists (54, 55). These HDT approaches can channel the chronic immune dysregulation displayed by granulomas that fail, resulting in counterproductive lung pathology, into productive responses characterized by sterilization of granulomas.

*M. tuberculosis* can overcome the restriction imposed by IDO and the resulting Trp insufficiency, by biosynthesizing this amino acid (8). IDO potently suppresses CD4+ T cells via a variety of mechanisms, including limiting their proliferation (56), induction of immunoregulatory APCs, and by promoting the differentiation of Th0 cells into Tregs (57, 58). Thus, high IDO activity has been correlated with pathogen burden and sepsis during infection (59), especially with intracellular pathogens (60), including *M. tuberculosis* (61). Here, inhibition of IDO activity by a potent yet safe inhibitor in macaques led to a slightly better control of *M. tuberculosis* replication, and somewhat reduced pathology and disease severity, accompanied by increased proliferation of CD4+ and CD8+ memory and effector populations, and the inhibition of lung marker T cell exhaustion and dysfunction. This was associated with reorganization of the granuloma, with T cells otherwise present in the peripheral region of lesions being able to gain greater access to the core region. It has recently been shown that mycobacterial infection results in the reprogramming of macrophages in the granuloma to a flattened, epithelial phenotype (62). This results in macrophage interdigitation and tighter granulomas. Inhibition of canonical epithelial pathways in the zebrafish model of *Mycobacterium marinum* infection resulted in the dysregulation of the granuloma, along with immune cell access to the lesion core, and reduced bacillary burdens (62). These results, taken together with our study, suggest that the ability of pathogenic mycobacteria to replicate within host lungs is intricately linked to lesion organization, and disruption of this process represents an attractive future strategy for the control of TB.

Our results have implications both for the fundamental understanding of why granulomas are unable to achieve their full potential during *M. tuberculosis* infection and for providing clues to

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**Fig. 6.** Granuloma performance in D-1MT–treated and control animals. Immunohistochemistry staining of lung sections for CD3+ T cells; (A) Ki67 (red), (B) granzyme B (red) with CD3 in green and nuclei (TOPRO3) stained in blue (A and B) and *M. tuberculosis* (red) staining (C). Multiple granzyme B+ cells can be observed in the necrotic center of granuloma from D-1MT-treated animals and are marked with white arrowheads. The far-right images in each panel are close-ups of the boxed region. (Scale bars, 150 μm.) The total number of cells positive for both CD3 and Ki67 as well as CD3 and granzyme B in A and B, respectively, as well as total nuclei in each panel were counted in multiple granulomata for each group and plotted. The graphs (far right in each panel) show percentages of cells positive for Ki67 (A) and granzyme B (B). The H&E staining of a representative lung lesion from D-1MT–treated (Upper) and control animals (Lower). (Scale bars, 20 μm (C, H&E); 150 μm (C, immunostaining).) A schematic representation of the granulomata and demarcation (L, lymphocytic layer; M, macrophage layer; N, necrotic center) in C is shown as described and is also applicable to A and B. The far-right image in C is the close-up of the boxed region and the graph shows the enumeration of bacilli in both groups (C). ***P < 0.001, ****P < 0.0001 using a Student’s t test. Data are means ± SEM, D-1MT treated (orange circle), controls (gray circle).
likely targets of productive HDT against TB, including IDO. These results suggest that the complex and highly ordered architecture of the primate (and human) lung tuberculosis may in fact be beneficial to the pathogen by preventing contact between T cells and pathogen-containing APCs. It may, however, be possible to alter granuloma architecture by inhibiting IDO signaling, and thereby allowing T cells access to the lesion core while also fostering the development of the follicular organization of B cell-containing iBALT. Such lesions appeared to overcome checkpoint inhibition and T cell dysfunction, greatly promoting bacterial killing.

Inhibition of IDO signaling in vivo, as well as in vitro, enhanced the expression of the type I IFNs, although the expression of all type I downstream genes (e.g., IFIT1, IFIT2, IFIT3, and IFITm) was reduced. The genes not surprisingly given that both IFN-α as well as type I IFN. This regulation of IDO by type I vs. type II interferons is context- and cell-type–dependent (63). It appears that type I IFN plays a major role in triggering IDO expression in primate alveolar macrophages in the context of M. tuberculosis infection, and therefore, inhibition of IDO enzymatic activity likely causes induction of type I IFN gene expression via feedback (63, 64). Whereas type I IFN is an important antiviral mechanism (65), its induction correlates with increased lung pathology and exacerbated disease upon M. tuberculosis infection (66). As such, approaches targeting type I IFN signaling have been successfully attempted in experimental models of TB (66). Our data suggest that the concurrent silencing of IDO signaling and type I IFN signaling could lead to a more profound control of TB in macaque (and human) lungs. Furthermore, testing the potential of such HDT alone, as well as concurrently with anti-TB chemotherapy, could pave the way for future clinical applications. Our results suggest that therapeutic strategies aimed at eliminating or reducing the levels of cells with IDO induction following M. tuberculosis infection, such as mycobacteria, could suppress cells in the lung, may also result in a reduction of TB. Finally, we have not discussed as part of this report the conundrum that IDO expression on nonhematopoetic cells following M. tuberculosis infection may indeed have a protective effect for the host, as has been shown in the murine model (67). Moreover, several novel IDO inhibitors are being generated (e.g., Indoximod), and it may be possible in future studies to test if they are preclinically superior to D-1MT in suppressing IDO activity.

Materials and Methods

In Vivo. Ten rhesus macaques were infected with a high dose of M. tuberculosis CDC1565 (~200 CFU) via the aerosol route, as described previously (10–16, 23). Five animals were randomly chosen to be in the treatment group and were D-1MT–treated daily, via the oral route with an IDO enzymatic activity inhibitor, D-1MT (45 mg/kg body weight) 1 wk after M. tuberculosis infection. The remaining animals served as controls.

NHPs, Infection, Sampling, Killing, and Clinical Pathology. All 10 animals were negative for tuberculin skin test (TST) before infection, but tested positive 3 wk after M. tuberculosis infection. Blood and BAL were collected before and after M. tuberculosis infection and during the time course of D-1MT treatment till necropsy. CFUs were measured in BAL 1 wk after M. tuberculosis infection and every 2 wk thereafter until the end point. Lung pathology was determined as described previously (11, 15). Tissues were washed in cold PBS and weighed. Tissues were either fixed in formalin or snap-frozen and stored at −80 °C for future analysis.

Flow Cytometry. Flow cytometry was performed on whole blood, BAL, and lung samples from all animals, as previously described (10–13, 20, 21, 23, 26). Briefly, memory subsets were established for T cell populations based on CD28 and CD95 coexpression (72), as previously described (11), and subdivided based on CD3+, CD28+, CD95– subsets being defined as central memory, and CD3+, CD28–, CD95+ being defined as effector memory. Various antibodies and their amount used for staining are described in Table S2.

Cytokine Assay. Cytokine assays were performed in lung samples derived at time of necropsy from D-1MT–treated and control animals, as well as from naïve (not infected with M. tuberculosis and untreated) lungs (as baseline) following the procedures described earlier (11, 23, 68–71).

Quantitative Real-Time RT-PCR and Transcriptomics. Total RNA from BAL obtained at baseline and 3 wk after M. tuberculosis infection of two representative animals from each group, was amplified using MessageAmp II aRNA Amplification Kit (Thermo Fisher Scientific) and processed for microarray and qRT-PCR, as described previously (11, 13).

In Vitro Culturing. Monocyte derived macrophages (MDMs) were generated from macaque blood and cocultured with CD4+ T cells, as described previously (71). A subset of MDMs was treated with IDO1-specific siRNA 24 h before M. tuberculosis infection (multiplicity of infection = 10∶1) (Table S1) to inhibit IDO1 expression, as described previously (71). Samples were collected at 0 and 24 h post-infection (71) and used for CFU assay, qRT-PCR, and immunocytochemistry.

Statistics. Unless otherwise stated, statistical analyses were performed with Prism v7 (GraphPad). For statistics, either Mantel–Cox (log-rank) survival analysis or Student’s t test was used with replication for more than one group. Log-rank test was performed after one-way ANOVA with Bonferroni multiple comparisons was performed. When required, a goodness-of-fit in linear regression was performed for the statistical analysis between two groups.

More details can be found in SI Materials and Methods.

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