Cutting Edge: Vitamin D Regulates Lipid Metabolism in *Mycobacterium tuberculosis* Infection

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Cutting Edge: Vitamin D Regulates Lipid Metabolism in Mycobacterium tuberculosis Infection

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Vitamin D has long been linked to resistance to tuberculosis, an infectious respiratory disease that is increasingly hard to treat because of multidrug resistance. Previous work established that vitamin D induces macrophage antimicrobial functions against Mycobacterium tuberculosis. In this article, we report a novel, metabolic role for vitamin D in tuberculosis identified through integrated transcriptome and mechanistic studies. Transcriptome analysis revealed an association between vitamin D receptor (VDR) and lipid metabolism in human tuberculosis and infected macrophages. Vitamin D treatment of infected macrophages abrogated infection-induced accumulation of lipid droplets, which are required for intracellular M. tuberculosis growth. Additional transcriptomics results showed that vitamin D downregulates the proadipogenic peroxisome proliferator–activated receptor γ (PPARγ) in infected macrophages. PPARγ agonists reversed the antiadipogenic and the antimicrobial effects of VDR, indicating a link between VDR and PPARγ signaling in regulating both vitamin D functions. These findings suggest the potential for host-based, adjunct antituberculosis therapy targeting lipid metabolism. The Journal of Immunology, 2014, 193: 000–000.

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effective treatment of tuberculosis, a global infectious disease that kills almost two million people a year, can only be achieved with a protracted, multituberculosis regimen; the rapid emergence of antibiotic resistance has been eroding even these less-than-optimal treatment options (1). A hallmark of infection with Mycobacterium tuberculosis, the causative agent of tuberculosis, is the differentiation of infected macrophages into lipid-rich foam cells (2). These cells accumulate lipid droplets, lipid storage organelles (3) that are required for intracellular bacillary growth (4), presumably because they provide nutrients (2). Foam cells are located in the tuberculous granuloma at the interface between the caseous center and the lymphocytic cuff; there they contribute to an environment permissive for mycobacterial dormancy (5). Thus, the remodeling of macrophage lipid metabolism that occurs during M. tuberculosis infection is likely associated with infection outcome. Finding ways to prevent infection-induced dysregulation of macrophage lipid metabolism might help control infection.

In the present study, we asked whether the protective role of vitamin D during infection with M. tuberculosis (6–8) involves an effect on macrophage lipid metabolism, in addition to its well-known induction of macrophage antimicrobial functions (9), because vitamin D can have lipid-altering effects (10), and the vitamin D receptor (VDR) interacts with lipid-sensing regulatory molecules affecting macrophage functions (11).

Materials and Methods

Cell growth and infection

In vitro infections were performed with M. tuberculosis H37Rv and with the human monocytic cell line THP-1, essentially as previously described (12). Briefly, PMA-differentiated cells were infected with mid-log bacterial cultures at the indicated multiplicity of infection (MOI). Wells were washed three times to remove extracellular bacteria at 4 h postinfection, at which time any compound(s) was added with fresh culture medium, as required, and maintained for the duration of the experiment. All manipulations with viable M. tuberculosis were performed under approved biosafety level 3-containment protocols.

Analysis of bacterial growth and lipid droplets

Bacterial CFU were enumerated on 7H10 agar plates. For detection of lipid droplets using flow cytometry, cells were fixed with 4% paraformaldehyde and stained with LipidTOX Deep Red (Molecular Probes, Life Technologies, Grand Island, NY). Data were collected with an Accuri 6 flow cytometer, and data analysis was performed using CFlow Plus software.

RNA extraction for transcriptomics and quantitative RT-PCR

Gene expression profiles for THP-1 cells were determined using Affymetrix Human Gene 2.0 ST, following the vendor’s protocols. For measurement of
individual gene expression levels, RNA was extracted, oligonucleotide primers and molecular beacon probes were designed, and quantitative RT-PCR was performed as described (13). Gene expression was normalized against that of the reference gene GAPDH.

Gene expression analysis

Transcriptome data were obtained from Gene Expression Omnibus accession no. GSE19491 for clinical samples (14) and from GSE17477 for THP-1 cells (15). Data from the current study have been deposited to the Gene Expression Omnibus under accession no. GSE57028 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE57028). Statistical analysis was performed in R. One-sided and two-sided t tests were performed to compare measurements of transcript levels between sample groups, and the resulting p values were calculated. To evaluate gene sets defined by Reactome (http://reactome.org/), Gene Ontology (http://www.geneontology.org/), or by transcriptional modulators (16), each set was tested for extreme ranks of differential expression among all measured genes in each comparison by coincident extreme ranks in numerical observations, and multiple transcript measurements were combined as described (17). The Benjamini–Hochberg method was used to calculate the false discovery rate (FDR).

Results and Discussion

We used transcriptomics to explore associations among VDR signaling, tuberculosis, and lipid metabolism. When we analyzed the transcriptome of M. tuberculosis–infected THP-1 cells (15), we found that VDR was highly represented among DNA-binding proteins associated with upregulated genes (Fig. 1A). Reanalysis of human whole-blood transcriptome data from Berry et al. (14) identified altered expression of VDR-bound genes associated with latent M. tuberculosis infection and bacillus Calmette–Guérin (BCG) vaccination compared with controls, as well as with pulmonary tuberculosis compared with latent infection or treated disease (Fig. 1B). Thus, mycobacterial infection leaves a significant fingerprint of VDR-regulated gene expression in leukocytes, and this fingerprint is recapitulated in THP-1 cells. Next, we investigated the link between the VDR signal and the cellular functions associated with infection. Upregulated gene pathways in THP-1 cell infection included “metabolism of lipids and lipoproteins” (and its subsets “cholesterol biosynthesis” and “sphingolipid metabolism”), in addition to well-studied immune responses, such as IFN-α/β signaling and TLR cascades (Supplemental Fig. 1). Further analysis revealed that VDR was the DNA-binding protein most significantly associated with upregulation of “metabolism of lipids and lipoproteins” (Fig. 1C, Supplemental Fig. 1). VDR was also significant within upregulated lipid metabolism pathways in some of the clinical comparisons in Fig. 1B, including pulmonary tuberculosis versus controls (FDR = 5e−06) and BCG vaccination versus controls (FDR = 2.3e−03). Collectively, the transcriptomics data strongly implicate VDR in the regulation of lipid metabolism in M. tuberculosis–infected THP-1 cells and in human tuberculosis.

To assess the mechanistic implications of the transcriptomic results, we experimentally investigated the connection between macrophage lipid metabolism and VDR signaling in the context of M. tuberculosis infection. Because lipid droplets form in M. tuberculosis–infected macrophages (2), we measured lipid droplet content as a readout for altered lipid metabolism in infected THP-1 cells. We found that addition of vitamin D (1,25-dihydroxyvitamin D3) to the infected cells prevented induction of lipid droplets (Fig. 2A) but had no effect on lipid droplets in uninfected cells (Supplemental

FIGURE 1. Transcriptomic analyses of in vitro THP-1 infection and clinical data. (A) DNA-binding proteins implicated by genes upregulated in M. tuberculosis–infected THP-1 cells. Gene sets were defined as genes annotated as bound by each transcriptional modulator (16). Differential expression between sample classes for these gene sets was determined by a nonparametric test (coincident extreme ranks in numerical observations) (17). The resulting p values were plotted onto the x-axis. Of 60 gene sets at FDR < 0.05, the top five are shown (IRF8, n = 607; IRF1, n = 326; VDR, n = 161; STAT4, n = 896; SUZ12, n = 2812). To represent effect size, sets with fewer genes were given greater bar height than were larger sets that yielded similar p values. (B) Statistical significance of VDR-bound genes in clinical comparisons, as indicated. Primary data were from a previous study (14). The p values were calculated as in (A). (C) DNA-binding proteins implicated by analysis of upregulated genes annotated for “metabolism of lipids and lipoproteins” (n = 348) in infected THP-1 cells. Gene sets were defined by the overlap between the pathway genes and genes annotated as bound by a transcriptional modulator (Supplemental Fig. 1). Each overlap set was tested for differential expression as in (A). Of 29 gene sets at FDR < 0.05, the top five are shown (VDR, n = 23; SOX2, n = 165; RUNX1, n = 126; ERG, n = 64; FOXA2, n = 93), plotted as in (A).
Moreover, vitamin D did not concurrently reduce bacterial CFU (Fig. 2B), but it did limit bacillary growth at later times postinfection (Supplemental Fig. 2B). Together, the data show that inhibition of lipid droplet induction by vitamin D was dependent on infection and was not merely secondary to reduced bacterial burden.

To explore the underlying mechanisms, we obtained transcriptome data from infected THP-1 cells with and without vitamin D treatment and from corresponding controls. Analysis of lipid-annotated gene sets showed that, in most cases, vitamin D treatment did not alter the direction of the infection-induced changes (Fig. 3A). However, the gene set “lipid binding” and its subset “phospholipid binding” were significantly upregulated by infection alone but were downregulated by vitamin D treatment of infected cells (Fig. 3A). This expression pattern mirrors the effect of infection and vitamin D treatment of infected cells on the formation of lipid droplets (Fig. 2A).

Further analysis of the downregulated “lipid-binding” genes for DNA-binding protein annotations identified a strong signal associated with peroxisome proliferator–activated receptor γ (PPARγ) in vitamin D–treated, infected cell transcriptomes (Fig. 3B). This result agrees with a role for PPARγ in VDR inhibition of adipocyte differentiation (18).

The downregulation of PPARγ-bound genes in the response of infected cells to vitamin D led us to test relationships between PPARγ and VDR signaling. We found that macrophage infection with M. tuberculosis induced PPARγ expression and activity (the latter assessed as expression of the sentinel PPARγ target gene CD36) and that vitamin D abrogated this induction (Fig. 4A). We then tested whether PPARγ agonists reversed the vitamin D inhibition of lipid droplet induction. When M. tuberculosis–infected THP-1 cells were treated with vitamin D and with two PPARγ agonists, rosiglitazone (a thiazolidinedione) and GW1929 (a non-thiazolidinedione), lipid droplets returned to levels comparable to those seen with M. tuberculosis infection alone (Fig. 4B) [lipid droplets were unaffected by agonists alone in uninfected (data not shown) or infected cells (Fig. 4B)]. Moreover, the PPARγ agonists also reversed the antimicrobial effect of vitamin D while having very little, if any, effect on bacterial growth when tested alone (Fig. 4C). Thus, PPARγ agonism counteracts both antiadipogenic and antimicrobial effects of vitamin D. These results agree with proadipogenic
and bacterial growth–promoting effects of PPARγ in *M. tuberculosis*–infected macrophages (Supplemental Fig. 2A, 2C) (19). Taken together, our findings show that VDR signaling decreases lipid droplet formation in *M. tuberculosis*–infected macrophages by limiting the adipogenic function of another nuclear hormone receptor protein, PPARγ, and the antimicrobial and antiadipogenic effects of VDR both involve reduction in PPARγ signaling.

In conclusion, integrated data from transcriptomic and mechanistic analyses provide evidence for 1) a connection between VDR signaling and lipid metabolism in human tuberculosis, BCG vaccination, and macrophage response to *M. tuberculosis* infection in vitro, 2) an antiadipogenic effect of vitamin D in *M. tuberculosis*–infected macrophages, and 3) cross-talk between PPARγ and VDR in both *M. tuberculosis*–induced dysregulation of macrophage lipid metabolism and macrophage antimicrobial activity. The observed cross-talk is consistent with the integration of VDR- and PPARγ-signaling pathways seen in other cell types and contexts (20). Because VDR does not appear to regulate PPARγ directly (21), the cross-talk might involve effects on interactions with the common heterodimerization partner, retinoid X receptor, which is required for DNA binding and transcriptional activity of either heterodimer (11), and/or on intracellular levels of the cognate lipid ligands required for transcriptional activity (11). The finding that VDR and PPARγ exert divergent effects on lipid metabolism and bacillary growth in *M. tuberculosis*–infected human macrophages points to opposing roles of the corresponding signaling pathways on macrophage activation state and permissivity for *M. tuberculosis* infection. Although the data clearly indicate that inhibition of lipid droplet formation by vitamin D occurs in the absence of concurrent antimicrobial effects, mechanistic links might exist between antiadipogenic and antimicrobial functions of vitamin D. These remain to be elucidated.

The present findings have clinical relevance. For example, they point to a need for reinterpretation and de novo investigation of epidemiological links among tuberculosis risk, vitamin D levels, and metabolic abnormalities, including diseases such as diabetes. Moreover, identification of drug-targetable host factors involved in lipid metabolism might lead to treatments that enhance host resistance to *M. tuberculosis* infection and serve as adjuncts to antituberculosis chemotherapy.

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**Disclosures**

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