

Review Article

The Human Microbiome in the Fight against Tuberculosis

Madeleine R. Wood,^{1†} Elaine A. Yu,^{1†} and Saurabh Mehta^{1,2*}

¹Division of Nutritional Sciences, College of Human Ecology, Cornell University, Ithaca, New York; ²Institute for Nutritional Sciences, Global Health, and Technology, Cornell University, Ithaca, New York

Abstract. The human microbiome is an intriguing potentially modifiable risk factor in our arsenal against *Mycobacterium tuberculosis*, the leading infectious disease killer globally. Previous studies have shown associations between the human microbiome and pulmonary disease states; however, etiological links between the microbiome and tuberculosis (TB) infection or disease remain unclear. Immunomodulatory roles of the microbiome may prove to be a critical asset in the host response against TB, including in preventing TB infection, reducing progression from latency, mitigating disease severity, and lowering the incidence of drug resistance and coinfections. This review examined the associations between TB and the gut and lung microbiome. Eight studies were identified through a PubMed database search, including one animal study ($N = 1$), case report ($N = 1$), and case–control studies ($N = 6$). TB infection and disease were associated with reduced gastrointestinal microbial diversity in a murine model and human case report. Sputum microbial diversity differed by TB status in case–control studies, although some reported heterogeneous findings. Current evidence suggests that the gut and lung microbiome are associated with TB infection and disease. However, as studies are limited, etiological and longitudinal research is needed to determine clinical relevance.

INTRODUCTION

Mycobacterium tuberculosis caused 1.5 million deaths in 2014,¹ and one-third of the global population has latent tuberculosis (TB) infection.² The scourge of TB infection and disease has been documented since early human history, and highlights the substantial remaining challenges of TB control and eradication efforts. In addition to current strategies, successfully addressing TB infection and disease may require targeting other modifiable risk factors, including host microbiota.

The number of host cells comprising the human body is vastly outnumbered by the number of symbiotic microorganisms,³ and therefore interactions between host cells and microbes occur constantly. The microbiome refers to “the ecological community of commensal, symbiotic, and pathogenic microorganisms that literally share our body space.”⁴ Previous studies have highlighted potential roles of the gastrointestinal and lower respiratory tract’s microbiome in the immunological response against TB infection and disease. Generally, bidirectional linkages between the gut microbiome and immune system have been well documented.^{5,6} Gut microbiota have been associated with a number of disease states, including asthma, autoimmune disorders, cardiovascular diseases, and nonalcoholic fatty liver disease.^{5–7}

This review assessed the association between TB infection and disease and the gut and lung microbiome. The microbiome may have important implications for addressing major challenges to effective TB control, including through immunomodulation, to reduce and address TB transmission, progression from latency, disease severity, and drug resistance.

TB pathology and immune response. *Mycobacterium tuberculosis* bacilli are transmitted from patients with active TB through airborne droplets.² In lungs, the innate host response includes the detection (by Toll-like receptors) and elimination (via alveolar macrophages and dendritic cells inducing antimicrobial peptides [cathelicidin] and autophagy)

of *M. tuberculosis*.⁸ Gamma-interferon and tumor necrosis factor-alpha activate the antimycobacterial capacity of macrophages, through producing nitric oxide, reactive oxygen, and nitrogen intermediates.⁸ Immune cells (macrophages, fibroblasts, T and B cells) accumulate to form granulomas, surrounding *M. tuberculosis* and restricting growth.⁸ Despite these host defenses, survival mechanisms of *M. tuberculosis* (including inhibiting phagolysosome fusion) allow some bacteria to persist within granulomas.⁸

In terms of adaptive immunity, cell-mediated responses by cluster of differentiation (CD)4+ and CD8+ T cells are critical to successfully address *M. tuberculosis*.⁸ Primary effector functions of CD4+ and CD8+ T cells include producing gamma-interferon and cytokines to activate macrophages, and lysing infected macrophages.⁸ The T helper (Th₁) cytokine expression pattern is important to eliminate *M. tuberculosis*⁹; conversely, Th₂ and regulatory T (T_{reg}) cell responses support *M. tuberculosis* survival.^{8,10} However, an enhanced Th₁ response simultaneously causes inflammation and host tissue damage,¹¹ which suggests a balanced Th₁/Th₂ immune response is ideal for patient health outcomes. In summary, the dynamic interplay between host immune response and *M. tuberculosis* survival mechanisms (such as T cell homeostasis) is modulated through numerous factors, potentially including the microbiome.

The gut and lung microbiome. Gut bacteria play important roles in nutrient metabolism, intestinal homeostasis (through preventing overgrowth of intestinal pathogens), and immunity.^{5,12,13} Several studies have examined the associations between altered gut microbiota and clinical pathologies including inflammatory bowel disease, diabetes, and obesity.^{5,6,14}

Historically, the lower respiratory tract has been considered sterile in healthy individuals, but recent culture-independent studies have shown evidence to the contrary.^{15,16} Given the limited available studies focusing on the lung microbiome, one key research gap is determining whether the observed microbiota are simply a continuation of the upper respiratory tract or separate. Preliminary findings corroborate that microbial populations present in the lung are distinct from the upper respiratory tract,¹⁷ and show intra-lung heterogeneity.¹⁶

*Address correspondence to Saurabh Mehta, Cornell University, 314 Savage Hall, Ithaca, NY 14853. E-mail: smehta@cornell.edu
†These authors contributed equally to this work.

Immunomodulation of microbiota. Murine studies involving gut microbiota have provided evidence of the modulation of microbiota by the immune system. In one study, transgenic mice with expression of human defensin 5, antimicrobial polypeptides secreted by Paneth cells in the small intestine, received a virulent *Salmonella typhimurium* challenge.¹⁸ The transgenic mice had lower bacterial burden in their terminal ilea, compared with wild-type controls.¹⁸ In addition, mice lacking specific proteins involved in innate immunity (Toll-like receptor 5, nucleotide-binding oligomerization domain-like receptor family pyrin domain-containing 6 inflammasome) had intestinal dysbiosis and associated pathologies, including colitis or insulin sensitivity.^{19,20} Subsequently, the transfer of altered microbiota to wild-type mice was observed to lead to disease.²⁰ Based on preliminary data, hypotheses include that immune responses (including against *M. tuberculosis*) facilitate cross talk between microbial populations (e.g., between the lung and gut microbiome); and dysbiotic microbiota may adversely influence some clinical pathologies.

Microbial diversity is hypothesized to affect the growth of particular opportunistic pathogens, due to resource competition. Krishna and others (2016) observed that opportunistic pathogens (*Rothia mucilaginosa*) were associated with increased complexity and diversity of sputum microbiota among patients with active TB.²¹ Iwai and others (2014) reported that lower bacterial burden was associated with increased community richness (taxa per sample) and phylogenetic diversity among Ugandans with human immunodeficiency virus and acute pneumonia.²²

Influence of the microbiome on immunity. Conversely, specific commensal gut microorganism species have been observed to modulate the immune system.^{23–26} Gut bacteria species (*Bacteroides fragilis* species, *Clostridium* genus) were associated with altered T_{reg} cell counts, function, and development.^{23,24} Previous studies have reported the influence of bacteria on respiratory health, including 1) airway inflammation and 2) lung damage (in the context of influenza and probiotic supplementation). In germ-free mice, increased airway inflammation was rescued by the administration of certain bacterial species (*Faecalibacterium*, *Lachnospira*, *Rothia*, and *Veillonella*).²⁶ Similarly, greater abundance of bacteria species (*Veillonella*, *Prevotella*) in the supraglottic-characteristic taxa were associated with higher indicators of airway inflammation.²⁷

Moreover, two studies showed links between gut bacteria and lung damage. Disrupted gut microbiota (decreased *Bifidobacterium* and *Lactobacillus*) was associated with altered immune response to influenza A infection and increased lung damage in a murine model.²⁸ Separately, probiotic supplementation of *Bifidobacterium* was associated with improved Toll-like receptor 7 response and reduced lung damage.²⁸ One hypothesis is that probiotics are protective against pneumococcal disease through modulating the upper respiratory tract microbiome.²⁹

In summary, given these dynamic bidirectional interactions between the microbiome and host immunity, commensal bacteria could have a role in the immunological response to pulmonary TB infection and disease. Specific commensal microorganisms may facilitate the cell-mediated immune response to TB infection and disease, and modulate inflammation and lung damage through functional changes of the metagenome and metabolite production.^{12,13}

TB AND THE MICROBIOME

In this review, eight studies examined the association between pulmonary TB infection and disease and the microbiome, including an animal study,³⁰ a case report,³¹ and 6 case-control studies (Table 1).^{21,32–36} Key study findings are highlighted in the following two sections (regarding TB and the gut or lung microbiome, respectively), and study methodology is compared in the third section.

TB and the gut microbiome. Low bacterial species richness and abundance were found in gastrointestinal tract samples from mice and a patient with active TB (Table 1).^{30,31} Five female BALB/c mice were infected with aerosolized *M. tuberculosis* (CDC1551 strain).³⁰ Pre- and postinfection samples differed, in terms of bacterial abundance (among 88 operational taxonomic units [OTUs]; $q < 0.01$) and composition (beta-diversity indices of weighted and unweighted UniFrac distances by Principal Coordinate Analysis [PCoA]; both $P \leq 0.005$).³⁰ In a second experiment, mice were infected with a different strain of *M. tuberculosis* (H37Rv; $N = 5$), and compared with 1:1 age-matched controls.³⁰ Fecal samples from a single time point postinfection similarly showed differential clustering and bacterial abundance among 73 OTUs; $q < 0.01$, compared with uninfected samples.³⁰ In the case report, Dubourg and others (2013) obtained stool samples from a patient with multidrug-resistant active TB who previously received multiple oral antibiotic regimens.³¹ Gut microbiota were severely depleted (39 bacterial species, 18 phylotypes, and 19 OTUs).³¹

Other studies have corroborated the potential role of intestinal microbiota in TB. Perry and others (2010) reported that individuals with latent TB and *Helicobacter pylori* had more interferon gamma and Th₁-like cytokines, compared with those without *H. pylori*.³⁷ *Actinobacteria* in infant stool samples was associated with increased T cell responses to vaccination, including Bacille Calmette–Guérin vaccination for TB.²⁵ Furthermore, cynomolgus macaques with *H. pylori* infection were less likely to develop active TB if inoculated with *M. tuberculosis*.³⁷ Another murine study demonstrated how specific enteric bacteria (*Helicobacter hepaticus*) modulated the immune system to alter susceptibility to *M. tuberculosis* and vaccine response in a mouse model.³⁸ One hypothesis was that activation of the innate immune system facilitates an enhanced response to other pathogens, such as *M. tuberculosis*.

Several recent studies have provided evidence of the immunomodulatory mechanism of the gut microbiome, which produces short-chain fatty acid (SCFA) metabolites that may affect the host response against *M. tuberculosis*.³⁹ Intestinal microbiota produce SCFAs through the fermentation of resistant starches and dietary fiber.⁴⁰ SCFAs have roles in host metabolism (as substrate for de novo lipid and glucose synthesis) and immunomodulation (through downregulating pro-inflammatory cytokines and T_{reg} cells).⁴¹ In a study involving *M. tuberculosis* stimulation of human peripheral blood mononuclear cells, physiological concentrations of the SCFA butyrate significantly decreased pro-inflammatory cytokine production.³⁹ Given the importance of the cell-mediated response (including T_{reg} cells⁴²) against TB infection, SCFA production is one hypothesized mechanism of the link between the microbiome and TB infection and disease.

Overall, the gut microbiome of TB samples had lower bacterial abundance and composition, relative to controls.

TABLE 1
Studies assessing the association between TB and the lung and gut microbiome*

Study design	Sample size		Location	Exposure	Assessment	Biological specimen	Outcome		Reference
	Cases	Controls					Microbial assessment method(s)	Hypervariable region†	
Murine model	5 female BALB/c mice	–	Maryland	TB infection (aerosolized <i>Mycobacterium tuberculosis</i> CDC1551 strain)	Bacterial diversity‡	Stool	16S rRNA sequencing	V1–V2	30
								Pre- vs. postinfection	
								<ul style="list-style-type: none"> • Alpha diversity (Shannon diversity index): postinfection decrease (in all mice) • Beta diversity (PCoA; UniFrac): $P < 0.001$ • 88 OTUs more abundant preinfection: $q < 0.01$ 	<ul style="list-style-type: none"> • Majority of differential OTUs: Firmicutes phyla • Relative species abundance of Lachnospiraceae and Ruminococcaceae and Bacteroidales order greater preinfection and among controls
5 female BALB/c mice	5 mice (1:1 age-matched)			TB infection (aerosolized <i>M. tuberculosis</i> H37Rv strain)					
Case study	Patient with multidrug-resistant TB	–	Marseille, France	–	Microbial diversity	Stool	16S and 18S rRNA sequencing; culture	V6	31
								<ul style="list-style-type: none"> • Differential clustering (PCoA; UniFrac distances): $P < 0.001$ • 73 different OTUs: $q < 0.01$ • Depleted gut microbiota: 39 bacterial species, 18 phylotypes, 19 OTUs • Most phyla (from pyrosequencing) confirmed with culture (Firmicutes, Actinobacteria, Proteobacteria), except Fusobacteria species (only culture) and Cyanobacteria/Chloroplast (only pyrosequencing) 	

(continued)

TABLE 1
Continued

Study design	Sample size		Location	Exposure	Assessment	Outcome			Key findings	Reference
	Cases	Controls				Biological specimen	Microbial assessment method(s)	Hypervariable region(s)		
Case control	31 patients with pulmonary TB	24 controls	Shanghai, China	TB status	Bacterial diversity	Sputum (cases); saliva / pharyngeal secretions (controls)	16S rRNA sequencing	V3	<ul style="list-style-type: none"> New species detected by culture (<i>Candidatus 'Paenibacillus antibioticophila'</i>) and 18S rRNA sequencing (3 fungal species) TB vs. control Greater phyla and genera richness among patients with TB (24 phyla; 564 genera) vs. controls (17 phyla; 235 genera) Most prevalent phyla: Firmicutes, Proteobacteria, Bacteroidetes, Crenarchaeota, and Actinobacteria Lower Bacteroidetes and higher Actinobacteria prevalence Certain genera (<i>Stenotrophomonas</i>, <i>Cupriavidus</i>, <i>Pseudomonas</i>, <i>Thermus</i>) and phyla (Aquificae, Planctomycetes) only in TB samples Differential clustering (PCoA; UniFrac distances) 	32

(continued)

TABLE 1
Continued

Study design	Sample size			Location	Exposure	Assessment	Outcome			Reference
	Cases	Controls	Biological specimen				Microbial assessment method(s)	Hypervariable regions†	Key findings	
32 patients with unilateral pulmonary TB	24 healthy controls	Jiangsu, China	TB status	Bacterial diversity	Bronchoalveolar lavage (cases); saliva, pharyngeal secretions (controls)	16S rRNA sequencing	V3	TB vs. control	36	
22 patients with TB	14 controls with TB-like coughing	Hong Kong SAR, China	TB status	Bacterial diversity	Sputum	16S rRNA sequencing	V1-V2	TB vs. control	33	

Key findings:

- Clustering (PCoA; UniFrac distances): distinct
- Genus: most abundant genus differed
- TB (uninfected vs. infected lungs)
- Clustering (PCoA; UniFrac distances): similar
- Genus: *Mycobacteria* and *Porphyromonas* abundances greater inside TB lesions
- Shannon diversity index: higher in bronchoalveolar lavage fluid from lungs with lesions, compared with controls
- TB vs. control
- Phyla: lower Firmicutes, and higher Proteobacteria and Bacteroidetes abundance
- Genus: lower *Streptococcus*, and higher *Neisseria* and *Prevotella*
- OTUs: 8 more prevalent, 2 less prevalent

(continued)

TABLE 1
Continued

Study design	Sample size		Location	Exposure	Assessment	Biological specimen	Outcome		Key findings	Reference
	Cases	Controls					Microbial assessment method(s)	Hypervariable region(s)		
									<ul style="list-style-type: none"> No differences in clustering (PCoA; UniFrac distances) <p>Overall</p> <ul style="list-style-type: none"> 98% of identified sequences accounted for 5 phyla (Proteobacteria, Firmicutes, Bacteroidetes, Fusobacteria, Actinobacteria) Most prevalent bacterial genera: <i>Neisseria</i>, <i>Prevotella</i>, <i>Streptococcus</i> 	34
Group 1: Newly diagnosed pulmonary TB (N = 25)	Group 4: Healthy controls (N = 20)		Shanghai, China	TB status	Bacterial diversity	Sputum (cases); throat swabs (controls)	16S rRNA sequencing	V1-V2	<ul style="list-style-type: none"> Clustering (PCoA; UniFrac distances) differed between Groups 1 and 3 vs. 4; similar between Groups 1 and 3 Relative species abundance (phyla, genera): heterogeneous between groups Some genera (<i>Bergeyella</i>, <i>Sharpea</i>) only in Groups 1-3 	
Group 2: Recurrent TB (N = 30)										
Group 3: Treatment failure (N = 20)										
6 patients with TB	6 controls without TB		Medellin, Colombia	TB status	Bacterial and fungi diversity	Sputum, oropharyngeal, nasal samples	16S rRNA sequencing (bacteria); fungi [fungal nuclear ribosomal internal transcribe spacer 1 regions])	V1-V2	<ul style="list-style-type: none"> Bacteria: TB vs. control 	35

(continued)

TABLE 1
Continued

Study design	Sample size			Exposure	Assessment	Outcome			Key findings	Reference
	Cases	Controls	Location			Biological specimen	Microbial assessment method(s)	Hypervariable region†		
									<ul style="list-style-type: none"> • Shannon diversity index: bacterial diversity (in nasal samples) less diverse • Clustering (PCoA; UniFrac distances): sputum and oropharyngeal samples clustered together, distinct from nasal samples • Oropharyngeal: <i>Streptococcaceae</i> more abundant 	
									<ul style="list-style-type: none"> • Phyla: relative abundance differed across sample type (bacterial diversity higher in sputum and lower in nasal samples) 	
									<ul style="list-style-type: none"> • Genus: <i>Cryptococcus</i> (in oropharyngeal samples) significantly lower 	
									<ul style="list-style-type: none"> • Shannon diversity index: fungal diversity greatest in nasal samples • Phyla: 90% sequences in Ascomycota and Basidiomycota; Ascomycota significantly differed between study participants 	

(continued)

TABLE 1
Continued

Study design	Sample size		Location	Exposure	Assessment	Outcome			Key findings	Reference
	Cases	Controls				Biological specimen	Microbial assessment method(s)	Hypervariable region†		
25 patients with pulmonary TB	16 controls		Madhya Pradesh, India	TB status	Bacterial diversity	Sputum	16S rRNA sequencing	V6–V7	TB vs. control	21

- Clustering (PCoA): distinct
- Phyla: higher Firmicutes and Actinobacteria, lower Proteobacteria and Fusobacteria
- Most prevalent genera (cases): *Streptococcus*, *Neisseria*, *Veillonella*; controls: *Gammaproteobacteria*, *Streptococcus*, *Neisseria*, *Haemophilus*
- Species: *Veillonella dispar* and *Rothia mucilaginosa* greater
- Shannon diversity index: lower for TB (3.88; 602 OTUs) than controls (4.13; 490 OTUs)

HIV = human immunodeficiency virus; OTU = operational taxonomic units; PCoA = principal coordinate analysis; rRNA = ribosomal RNA; SAR = Special Administrative Region; TB = tuberculosis.
 *PubMed search strategy was based on the following terms: "(microbiota[mesh] OR microbiota[ti] OR microbiome[ti] OR virome[ti] OR gut bacteria[ti] AND (tuberculosis[ti] OR TB[ti]))" and restricted by publication date (before June 6, 2016). Exclusion criteria included 1) not primary data source (including reviews, editorials); 2) no whole microbiome sequencing techniques; and 3) not among patients or animals with TB or exposure to TB (including assessing vaccine response among healthy volunteers, microbiome among patients with HIV, or reproductive tract inflammation). Among the 44 studies initially identified, eight studies were within the scope of this review and included.
 †Assessed by 16S rRNA sequencing.
 ‡First experiment: baseline (preinfection) to 179 days (postinfection). Second experiment: 0–46 days.

However, given the limited data and heterogeneous study designs, preliminary evidence suggests the need for further studies to confirm etiology through mechanistic and clinical studies. Potential next steps include improving our understanding of the role of metabolites in mediating the association between the gut microbiome and TB disease and infection.

TB and the lung microbiome. Several case-control studies in this review showed that bacterial diversity (richness, abundance, OTU clustering, Shannon index) in the respiratory tract differs between individuals with active TB, compared with controls (Table 1).^{21,32-34,36} Based on PCoA, four studies found distinct OTU clustering of sputum samples from study participants with TB disease, compared with controls.^{21,32,34,36} However, one study observed no differences in OTU clustering.³³ All case-control studies identified differences in bacterial richness or relative abundance, based on taxonomic categorizations (phyla, genus, species), in sputum from individuals with and without active TB. However, the specific differential taxonomic groups were inconsistent and not replicated across studies, which may reflect the relatively small and diverse sample populations.

In five case-control studies, sputum was considered an indicator for the microbiome of the lung and lower respiratory tract among study participants with active TB. Given that sputum is likely to be contaminated by the upper respiratory tract during expectoration, the continued use of sputum reflects the challenge of directly obtaining samples from the lung.

Sample collection methods for referent groups varied, including samples from deep coughing of healthy individuals,^{32,36} throat swabs,³⁴ bronchoalveolar lavages,³⁶ and sputum from individuals with TB-like coughing.³³ Botero and others (2014) reported that the microbial compositions of sputum and oropharyngeal samples were similar, which supports the use of throat swabs from controls.³⁵ Limitations include deep cough, throat swab, and sputum samples may represent the upper respiratory tract (instead of the lung and lower respiratory tract microbial composition); TB-like coughing could be caused by other diseases that affect the microbiome; and the invasiveness of bronchoalveolar lavages. Thus, interpretations of study findings need to account for potential sample contamination and the appropriate selection of controls.

As a brief summary, several studies showed distinct bacterial richness or relative abundance of the lung microbiome among patients with active TB, compared with controls. Further studies are needed, particularly in light of differences in study designs and discrepant observations.

Comparison of study methods. Strengths of studies in this review included the consistent use of next-generation platforms for 16S ribosomal RNA (rRNA) sequencing to assess the bacterial microbiome in all eight studies. Seven studies used 454 instruments (GS FLX, GS FLX-Titanium [Roche Diagnostics, Base, Switzerland]), and one study used an Ion Torrent PGM (Thermo Fisher Scientific, San Jose, CA). Two studies additionally evaluated fungal species,^{31,35} and one study compared 16S rRNA results with culture and 18S rRNA sequencing.³¹ In all studies, sequence analyses were conducted through software (including Quantitative Insights Into Microbial Ecology,⁴³ Mothur⁴⁴), and OTUs were identified through aligning sequences with reference databases (Ribosomal Database Project,⁴⁵ Greengenes⁴⁶), to eliminate chimeras. Some studies considered differences (including sociodemographic characteristics) of sample populations,

which are supported by previous literature. In addition, the eight studies included study participants from several geographic locations, which allowed for comparison and confirmation of similar findings across diverse populations.

Available studies had several limitations, in addition to aforementioned challenges. Compared with Sanger sequencing (such as with ABI 3730 Genetic Analyzer [Applied Biosystems, Foster City, CA]), 454 sequencing has been reported to have higher error rates due to greater insertion and deletion rates.⁴⁷ Importantly, methodological heterogeneity in data analyses rendered comparisons across studies difficult; these included differences in hypervariable regions (V1-V3, V6, V7), diversity indices (including alpha- [Shannon index, Chao1] and beta-diversity [unweighted and weighted UniFrac, Jaccard]), and additional analyses (PCoA, hierarchical clustering heatmap).

Separately in the case-control studies, the sample sizes (12-95) and geographic locations (Asia [China, Hong Kong, India], South America [Colombia]) ranged widely. Therefore, results were difficult to generalize to other countries. In addition, numerous other potential confounding factors (antibiotic use [including anti-TB treatment], comorbidities, environmental factors, diet) were either unaccounted for or considered differently across study populations. Standard anti-TB medications are a combination of antibiotics, which are expected to alter the microbiome, and therefore need to be considered while interpreting study results. Four of the six case-control studies excluded participants with recent antibiotic use (1 or 3 months before baseline).^{32,33,35,36} However, two studies did not report the exact length of time that participants did not receive antibiotics before sample collection,²¹ or prior antibiotic use.³⁴ In the case report, the patient was receiving anti-TB treatment of multidrug-resistant TB at the time of sample collection.³¹

DISCUSSION

In this review, there is limited evidence regarding the key question of the bidirectional associations between TB infection and disease and the lung and gut microbiome. Potential mechanistic pathways need to be considered through epidemiological and mechanistic studies, including immunological, nutritional, metabolic, and endocrine factors (Figure 1). Furthermore, there are a number of other research gaps and related questions that have not been directly addressed by studies to date. One of these overarching knowledge gaps involves inter individual variability, which is a key focus area of the Human Microbiome Project.⁴⁸ What is the extent that a core set of human microbiome genes or species is shared between individuals?⁴⁸ In addition, what are the temporal changes of lung and gut microbiota (including throughout TB disease progression and treatment)? Separately, to what extent does cross talk occur between the lung and gut microbiome, particularly in response to TB infection and disease-related perturbances? Followingly, do these interactions between the respiratory and gastrointestinal microbiome modulate immune responses to TB infection and disease?

CONCLUSION

Based on preliminary evidence from studies in this review, the lung and gut microbiome were associated with TB infection and disease. The microbiome is a potential modifiable

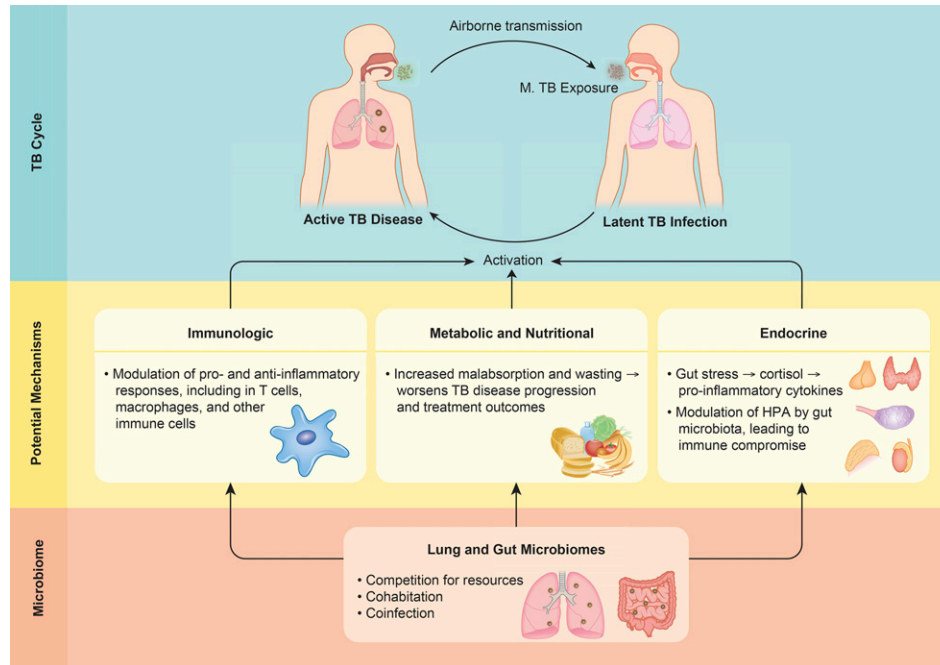


FIGURE 1. Potential mechanistic pathways between the microbiome and tuberculosis (TB).

risk factor for TB infection and disease; however, the number of available studies is limited. Most studies have focused on characterizing the microbial profile among individuals with and without active TB disease. Future studies are necessary to further elucidate etiology, key mechanisms, and potential clinical significance. Specifically, it is important to assess 1) the sputum and gut microbiome as risk factors for TB infection and disease susceptibility, disease progression, and treatment outcomes and 2) the effects of TB infection and disease on the sputum and gut microbiome, which can subsequently impact health via alteration of immune responses.

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Authors' addresses: Madeleine R. Wood and Elaine A. Yu, Division of Nutritional Sciences, College of Human Ecology, Cornell University, Ithaca, NY, E-mails: mrw245@cornell.edu and eay27@cornell.edu. Saurabh Mehta, Division of Nutritional Sciences, College of Human Ecology, Cornell University, Ithaca, NY, and Institute for Nutritional Sciences, Global Health, and Technology, Cornell University, Ithaca, NY, E-mail: smehta@cornell.edu.

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