# Protocol Antibiotic Microbiome Tb

# Systematic Review Protocol: Antibiotic-Microbiome Interactions in Tuberculosis Treatment  
  
\*\*Title:\*\* Antibiotic-Microbiome Interactions in Tuberculosis Treatment: A Systematic Review and Meta-Analysis  
  
\*\*Registration:\*\* PROSPERO [Registration Number: Pending]  
  
\*\*Review Team:\*\*  
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## \*\*Background and Rationale\*\*  
  
### \*\*Clinical Context\*\*  
Tuberculosis (TB) treatment involves prolonged courses of multiple antibiotics that can profoundly disrupt gut microbiota composition. First-line regimens combine rifampicin, isoniazid, ethambutol, and pyrazinamide for 6 months, while multidrug-resistant tuberculosis (MDR-TB) requires 18-24 months of potentially toxic second-line drugs. These regimens can cause significant gastrointestinal toxicity, treatment interruptions, and immune dysregulation - all potentially linked to antibiotic-induced dysbiosis.  
  
### \*\*Microbiome Research Advancements\*\*  
Recent studies suggest the gut microbiome plays crucial roles in immune regulation, metabolism, and response to infectious diseases. Antibiotic exposure represents one of the most disruptive influences on microbiome composition, potentially leading to:  
  
- Loss of beneficial bacterial species and metabolic functions  
- Overgrowth of antibiotic-resistant organisms and pathogens  
- Impaired immune responses and immune reconstitution inflammatory syndrome  
- Altered drug metabolism and treatment efficacy  
- Increased risk of secondary infections and toxicity  
  
### \*\*Evidence Gaps and Research Need\*\*  
While preclinical and observational studies suggest antibiotic-microbiome interactions may influence TB treatment outcomes, systematic synthesis of this evidence is lacking. Understanding how TB antibiotics alter gut microbiome composition and function could:  
  
1. \*\*Identify potential biomarkers\*\* for treatment monitoring  
2. \*\*Inform antibiotic selection\*\* strategies for microbiom...