

**MODULATION OF THE GUT MICROBIOME AND ANTIMICROBIAL RESISTANCE  
MECHANISMS IN THE GASTROINTESTINAL TRACT INDUCED BY PROLONGED  
CONSUMPTION OF *Trachyspermum roxburghianum***

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The gut microbiome, a complex ecosystem of bacteria, fungi, and viruses, plays a very important role in human health, influencing metabolic, immune, and neurological functions. Dysbiosis and antimicrobial resistance (AMR) are growing global health challenges, necessitating innovative approaches to understand and mitigate these issues. *Trachyspermum roxburghianum*, a medicinal plant with potent antimicrobial and anti-inflammatory properties, is widely used in Ayurveda and traditional medicine. However, its long-term effects on gut microbiota composition and AMR mechanisms remain inadequately investigated. This study conducted a comprehensive review of literature published between 2017 and 2024, utilizing Google Scholar as the search engine and ScienceDirect as the primary database, while adhering to PRISMA-P 2020 guidelines for screening and selection. After rigorous screening and eligibility assessment, 24 relevant articles were included for full analysis. Inclusion criteria focused on studies examining *T. roxburghianum*'s impact on gut microbiota and AMR pathways, while exclusion criteria were applied using a structured approach, eliminating studies that lacked molecular or microbial analysis, were unrelated to gut microbiota or AMR, or were non-English publications. Findings indicate that prolonged *T. roxburghianum* consumption modulates gut microbial diversity, potentially inducing both probiotic and dysbiotic effects. Key AMR mechanisms, including efflux pump activation, quorum sensing, biofilm formation, and horizontal gene transfer, were identified as critical contributors to resistance development. Clinically, these changes may increase susceptibility to opportunistic infections while offering therapeutic benefits for gastrointestinal disorders. However, current evidence is limited by small sample sizes, variable methodologies, and a lack of long-term human studies. Emerging technologies, such as metagenomics, transcriptomics, and CRISPR-based gene editing, hold promise for further elucidating these mechanisms and developing targeted interventions. This study underscores the dual role of *T. roxburghianum* in gut health modulation and AMR. Future research should focus on controlled clinical trials, omics-based exploration, and AI-driven microbiome analysis to optimize its therapeutic use while minimizing AMR risks.

**Keywords:** Antimicrobial Resistance (AMR), *Trachyspermum roxburghianum*