

ASC20264944



Abstract ID

Title

Microbiome Patterns Differ Between Simple & Complicated Pediatric Appendicitis: A Systematic Review

Authors and Affiliations

Primary Author - **Daniela A. Armella Tangarife** ¹
Additional Author - **James G. Verner**, BS,RN ¹
Additional Author - **Elaina J. Vitale**, MLIS ^{1,3}
Additional Author - **Heather B. Blunt**, MSLIS ^{1,3}
Senior Author - **Reto M. Baertschiger** ^{1,2}

1. Geisel School of Medicine
Dartmouth College
Lebanon, NH USA
2. Dartmouth Hitchcock Medical Center, Dartmouth Health Children's Hospital
Section Of Pediatric Surgery, Department Of Surgery
Lebanon, NH USA
3. Geisel School of Medicine
Health Sciences And Biomedical Libraries, Dartmouth College
Lebanon, NH USA

Classifications

Type Clinical/Outcomes
Clinical Area Pediatrics

Conflict of Interest Declarations

Off Label Use: No

Disclosures

Introduction: Acute appendicitis represents a leading cause of pediatric surgical emergencies, especially in middle to high income countries. Research exploring gut microbiome differences between complicated and uncomplicated pediatric appendicitis remains sparse. Current research falls short explaining how microbial composition relates to disease severity. This systematic review hypothesized that gut microbiome influences severity of appendicitis and aims to evaluate microbiome patterns that could provide evidence towards tailored treatments with consideration of geographic differences.

Methods: This systematic review is registered in PROSPERO (CRD420251076665). The search was conducted utilizing Ovid MEDLINE, Cochrane Library, Global Index Medicus, and Scopus on July 9, 2025. No language or date restrictions were applied. Included studies examined gut/fecal/appendiceal microbiome composition in children <18

Abstract

years with confirmed acute appendicitis, distinguished complicated from uncomplicated cases, and provided separate microbiome data by severity group. Cross-sectional, cohort, case-control studies, and RCTs using culture-based methods, 16S rRNA sequencing, metagenomics, or microbiological techniques were eligible. Utilizing PRISMA guidelines, 443 abstracts were screened by two independent reviewers, 32 disagreements were resolved by a third reviewer, and 90 abstracts were selected for full-text screening. Data extraction included study characteristics, demographics, microbiome methods, and compositional findings.

Results: After full-text review, we identified 21 predominantly prospective studies (81%) that met criteria, describing 2,191 pediatric patients (1,375 simple, 816 complicated appendicitis). Eighteen studies were from high-income countries, 3 from middle-income countries. Eleven studies identified *Fusobacterium*, showing significantly higher complication rates (53.1% vs 32.3%, RR=1.64, 95% CI: 1.48-1.83). *Fusobacterium* was associated with complicated appendicitis in 11 of 18 high-income countries, whereas none of 3 middle-income countries reported *Fusobacterium*. Analysis revealed complicated appendicitis showed increased bacterial diversity, higher prevalence of pathogenic organisms (particularly *P. aeruginosa* and *Enterococcus*), and greater antibiotic resistance.

Conclusion: This systematic review provides the first comprehensive synthesis of gut microbiome differences between complicated and uncomplicated pediatric appendicitis. By identifying bacterial taxa associated with appendicitis severity, this work reveals specific bacterial strains for risk-assessment that may contribute to personalized pediatric appendicitis management, loco-regional differences, and improved risk stratification and patient outcomes.