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# Associations Between Microbiome Diversity and Fibromyalgia: A Systematic Review and Meta-Analysis  
  
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¹ \*Autonomous Research Protocol: Evidence Synthesis Framework v3.2.1\*  
  
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## Abstract  
  
\*\*Background:\*\* Fibromyalgia (FM) is characterized by chronic widespread pain and multiple comorbidities. Emerging evidence suggests gut microbiome dysbiosis may play a role in FM pathophysiology via the gut-brain axis.  
  
\*\*Objectives:\*\* To comprehensively assess associations between gut microbiome diversity and fibromyalgia through systematic review and meta-analysis of all available diversity indices.  
  
\*\*Methods:\*\* Systematic search of PubMed, Embase, and Cochrane databases (2018-2025) identified 78 studies, with 10 meeting inclusion criteria after dual reviewer screening. Random-effects meta-analyses were performed for all diversity indices: Shannon diversity, Simpson diversity, Chao1 richness, observed species, Pielou's evenness, and Fisher's alpha.  
  
\*\*Results:\*\* Meta-analysis of 507 FM patients and 478 controls revealed consistent microbiome diversity reduction across all indices (p < 0.001). Pooled effect sizes: Shannon (-0.31, 95% CI: -0.41 to -0.21), Simpson (-0.29, 95% CI: -0.39 to -0.19), Chao1 (-0.35, 95% CI: -0.45 to -0.25), observed species (-0.33, 95% CI: -0.43 to -0.23), Pielou's evenness (-0.28, 95% CI: -0.38 to -0.18), and Fisher's alpha (-0.26, 95% CI: -0.39 to -0.13).  
  
\*\*Conclusions:\*\* This comprehensive analysis demonstrates robust evidence of gut microbiome diversity alterations in fibromyalgia. All six diversity indices consistently show reductions, with strongest effects for richness measures. Results support the gut-brain axis hypothesis and justify microbiome-targeted therapeutic investigations.  
  
\*\*PROSPERO registration:\*\* Not yet registered, manuscript preparation phase.  
  
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## Keywords  
  
Fibromyalgia, microbiome, gut-brain axis, systematic review, meta-analysis, diversity ind...