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Metagenomic Meta-Analysis of the Human Gut Microbiome in Sarcopenia

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The gut microbiome plays a pivotal role in maintaining human health, with dysbiosis frequently serving as an indicator of pathological states. Although numerous studies have explored its association with sarcopenia, a comprehensive mechanistic understanding remains limited and requires integration of existing findings. In this study, we analyzed six metagenomic datasets from the Southeast Asian region, comparing individuals with sarcopenia to healthy controls, to identify shared microbial signatures. Three short-chain fatty acid (SCFA)-producing genera; *Fusicatenibacter*, *Lachnospiraceae FCS020 group*, and *Lachnospira*, were consistently reduced in sarcopenic patients. As major butyrate producers, their depletion may compromise anti-inflammatory responses and perturb host energy metabolism. Functional pathway analysis further demonstrated consistent upregulation of the tricarboxylic acid (TCA) cycle in sarcopenia, suggesting mitochondrial stress in muscle and altered microbial energy utilization. Collectively, these findings highlight potential microbial and functional biomarkers of sarcopenia. Future studies incorporating experimental validation and integrative modeling that accounts for geographic and cohort-specific variability will be essential to advance biomarker discovery and clinical translation.