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Dysbiosis of the adolescent gut microbiota: implications for immune modulation in inflammatory bowel disorders and obesity

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Recent studies have increasingly focused on the association between the gut microbiome and obesity or inflammatory diseases in adults, yet there remains a paucity of research examining this relationship in adolescents with gastrointestinal (GI) diseases. To address this gap, we conducted a comprehensive analysis of 16S rRNA-seq datasets obtained from 202 adolescents, encompassing ulcerative colitis (UC), Crohn's disease (CD), obesity (Ob), and healthy controls (HC). Utilizing Quantitative Insights Into Microbial Ecology (QIIME) and Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt), we identified Operational Taxonomic Units (OTUs) and subsequently analyzed Kyoto Encyclopedia of Genes and Genomes (KEGG) Orthology (KO) terms and pathway enrichment. Our findings revealed distinct distributions of six primary gut microbiota taxa (unclassified *Dorea*, unclassified *Lachnospiraceae*, unclassified *Ruminococcus*, *Faecalibacterium prausnitzii*, *Prevotella copri*, unclassified *Sutterella*) across obesity and inflammatory disease states. Notably, dysbiosis within *Lachnospiraceae* was observed in adolescents with inflammatory diseases (UC and CD), while alterations in *Prevotella* and *Sutterella* were evident in obese adolescents. Specifically, the relative abundance of *Faecalibacterium prausnitzii* and unclassified *Lachnospiraceae* was significantly elevated in the UC group compared to CD, Ob, and HC groups, while the Ob group exhibited markedly higher levels of *Prevotella copri* and unclassified *Sutterella*. Further investigation of associations between these six specific microbiota and KO terms revealed a connection with NOD-like receptor signaling, suggesting potential impacts on the immune system and inflammatory response during critical adolescence. This study elucidates the differential influence of microbial community dysbiosis on inflammatory and immune response pathways in adolescents with inflammatory diseases and obesity, contributing valuable insights to the growing body of literature on gut microbiome-host interactions in this understudied population.