

The metabolic activity of gut microbiota in obese children is increased compared to normal weight children and exhibits more exhaustive substrate utilization

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The gut microbiota contribute otherwise impossible metabolic functions to the human host. Shifts in the relative proportions of gut microbial communities in adults have been correlated with intestinal disease and have been associated with obesity. The aim of this study was to elucidate differences in the microbial composition and metabolic activities of gut microbiota from obese versus normal-weight children. Fecal samples were obtained from obese (n=15; mean BMI SDS score= 1.95) and normal-weight (n=15; mean BMI SDS score= -0.14) Swiss children aged 8-14. Composition and diversity of gut microbiota were analyzed by qPCR and temporal temperature gradient electrophoresis (TTGE). No significant quantitative differences in gut microbiota communities of obese and normal-weight children were identified. Microbial community profiling by TTGE revealed a high degree of both intra- and intergroup variation. Intergroup comparison of TTGE profiles failed to identify any distinct populations exclusive to either obese or normal-weight children. HPLC analysis identified significantly higher ($P < 0.05$) concentrations of short-chain fatty acids (SCFA) butyrate and propionate in obese versus normal-weight children. Significantly lower concentrations of intermediate metabolites were detected in obese children, suggesting exhaustive substrate utilization by obese gut microbiota. Our results indicate that a metabolic dysbiosis may be involved in the etiology of childhood obesity. In turn, aberrant and overactive metabolic activity within the intestine could dictate survival or loss of individual microbial communities, leading to the alteration in population ratios previously identified in adults.