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Associations between gut microbiota and weight loss in an energy-restricted dietary intervention trial in adults with elevated adiposity

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A relationship between characteristics of gut microbiota and obesity are now well-established⁽¹⁾. However, less well-understood is the extent to which these microbiological features change during periods of weight loss. This study aimed to investigate the relationship between gut microbiota and weight loss in adults (aged 25 to 65 years, BMI of 27.5 to 34.9 kg/m²) enrolled in a 9-month randomised controlled trial⁽²⁾. Participants were randomised to consume an energy-restricted diet that was either almond-enriched (30–50 g/daily) or nut-free (carbohydrate-rich snack foods). Data were collected at baseline (BL, n = 108), 3 months (3M, weight loss, n = 87) and 9 months (9M, weight maintenance, n = 82) for body weight, diet composition (weighed food diaries) and faecal microbiota composition (16S rRNA V4 amplicon sequencing). Paired data were analysed using mixed-effects models adjusted for baseline BMI, age, sex, dietary fibre. As reported previously, significant weight loss occurred for both diet groups to an equal extent⁽³⁾. Significant inverse relationships were observed at BL between BMI and both microbiota richness (number of unique bacterial taxa detected) (estimate = −6.56, 95% CI = −9.9 to −3.19, p = 0.0002) and diversity (Shannon's index) (−0.06, −0.1 to −0.02, p < 0.001). The strongest relationship at BL involved members of the Christensenellaceae bacterial family, which negatively correlated with BMI (r = −0.26, p = 0.007), consistent with prior studies^(3,4). Microbiota richness (8.79, −0.73 to 18.34, p = 0.024) and diversity (0.08, −0.01 to 0.18, p = 0.019) were significantly higher at 9M compared to BL but not at 3M (p > 0.05). Compared to BL, microbiota composition (the taxa detected and their relative abundance) was significantly at 3M (p < 0.001) and 9M (p = 0.007). Following weight loss at 3M, significant increases in the relative abundance of members of the Christensenellaceae and Ruminococcaceae families were observed (log2 fold change > 1, FDR p < 0.05). Positive associations between weight loss and an increase in the relative abundance of Christensenellaceae family was evident at 3M (0.001, 0.0002 to 0.002, p = 0.010), but did not remain significant at 9M. Additionally, weight loss at 3M (0.0002, 1.3 × 10^{−5} to 0.0005, p = 0.038) and at 9M (0.0002, 4.6 × 10^{−6} to 0.0005, p = 0.045) was positively associated with an increase in the relative abundance of *Lachnospiraceae ND3007*, a bacterial genus associated with improved diet quality⁽⁵⁾. Our findings demonstrate that the abundance of specific bacterial populations within the gut microbiota change in a manner that is proportionate to weight loss resulting from an energy-restricted diet. The extent to which these microbes are simply markers of altered diet, or whether they contribute in a causal manner to weight loss, as suggested by emerging preclinical data⁽³⁾, is yet unknown.

References

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