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Gut microbes and obesity in adolescents

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The composition of the gut microbiota has been associated with obesity in animal models and considered to be a potential environmental factor involved in this disorder⁽¹⁾. In the present preliminary study the composition of the faecal microbiota of obese and overweight adolescents (aged 14.8 (SD 1.3) years) was investigated initially and after following a nutritional intervention strategy based on an energy-restricted diet (30–40%) and a physical activity programme (energy expenditure 3762–11 286 kJ/week) for 3 months. Eight obese and overweight individuals were identified according to the International Obesity Task Force criteria⁽²⁾ in the frame of the EVASYON project. The microbiological analyses were carried out by fluorescent *in situ* hybridization, using oligonucleotide probes targeting the main microbial groups colonizing the human distal gut (*Archaea*, *Bacteroides*, *Bifidobacterium*, *Clostridium coccoides*–*Eubacterium rectale*, *Clostridium leptum*, Enterobacteriaceae, *Enterococcus*, *Fusobacterium prausnitzii*, *Lactobacillus*, *Roseburia*–*Eubacterium*, *Ruminococcus* and sulphate-reducing bacteria). Enterobacteriaceae and sulphate-reducing bacterial counts were significantly reduced ($P < 0.05$) in faecal samples of individuals ($n = 5$) showing remarkable reductions in their weight (4–7 kg) but not in those ($n = 3$) showing minor weight losses (<2 kg) after the intervention. In contrast, this last group of children showed significantly lower ($P < 0.05$) counts of *Roseburia*–*Eubacterium* populations. These gut microbes could play a role in obesity by affecting either the energy harvest from the diet⁽³⁾ or the signalling pathways that link inflammation with obesity⁽⁴⁾. Overall, the present preliminary study shows that modifications in the gut microecology are associated with corporal weight in adolescents under a similar energy-restricted diet. Investigations are in progress to confirm this trend and assess whether the intentional manipulation of the gut microbiota could be envisaged as a strategy to combat obesity and immune disorders resulting from obesity.

Table 1. Microbial composition of faeces from overweight and obese adolescents

Weight reduction ...	4–7 kg				<2 kg			
	Initial		3 months		Initial		3 months	
	No. of cells/g faeces ($\times 10^8$)							
Microbial group	Mean	SE	Mean	SE	Mean	SE	Mean	SE
Enterobacteriaceae	9.61	1.23	4.95*	0.96	7.44	2.97	6.78	1.28
<i>Roseburia</i> – <i>Eubacterium</i>	16.5	10.23	9.88	5.76	21.3	4.39	12.4*	5.96
Sulphate-reducing bacteria	3.53	3.24	1.09*	0.58	3.21	2.49	1.62	0.37

Mean values were significantly different from initial values (Student's *t* test): * $P < 0.05$.

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