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# Obesity-associated fecal microbiota from human modulates body mass and metabolites in mice

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Obesity has become a worldwide epidemic, and a possible role of gut microbiota in its etiology has been uncovered. Fecal microbiota transplantation from humans to mice allows identification of specific microbiota configurations that are causally related to obesity. However, microbial communities vary considerably among individuals, causing a possible limitation in previous works based on a few human donors. The aim of this study was to investigate the transmissibility of metabolic phenotypes with fecal microbiota using a considerably higher number of human donors.

We transplanted the microbiotas from 16 obese juveniles (6-18 years old, BMI z-score median 2.84 range 1.84-3.98) and 16 controls (7-18 years old, BMI z-score median 0.095 range -0.58-0.88) separately into 64 germ-free male Swiss Webster mice caged in pairs and fed standard chow. Average body weight gain of mice with microbiotas from obese donors started to be significantly higher than the control group 7 days post colonization (dpc), ending with a difference of  $8.6 \pm 4.3\%$  of initial body weight at 51 dpc ( $p=0.02$ ). Total feeding efficiency was also higher in mice with "obese microbiota". Cecal concentrations of butyric acid and iso-butyric acid were significantly lower in the obese group, showing an altered microbial activity. No differences in serum leptin, serum lipids (triglycerides, total cholesterol, free fatty acids) or glucose homeostasis (HOMA-IR, HbA1c) were detected.

These results establish the gut microbiota as a causal factor for altered weight gain and changes in cecal levels of short chain fatty acids. This is promising given size of the donor groups, thus accounting for individual variations in the microbiota. 16S rRNA gene sequencing and qPCR of butyrate-related genes/bacteria are ongoing to reveal the structural and functional microbiota configurations as well as their dynamics; serum bile acids will be analysed to further understand the effect of microbial metabolites on obesity development.