Changes in the gut microbiota after bariatric surgery

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The prevalence of obesity is growing worldwide and there is a concomitant increase in the prevalence of type 2 diabetes mellitus (T2D). The main therapeutic options for T2D include a change of lifestyle and/or medications. However, most patients fail to alter their lifestyles in the long run. In RYGB surgery, food is diverted to a small pouch created by restricting the stomach, bypassing the majority of the stomach, all of the duodenum and some of the jejunum. In addition to promoting weight loss, bariatric surgery has been shown to resolve diabetes in rodents and in humans. How this occurs is unclear, but weight loss itself is not the driver, since improvements in the diabetes condition occur very quickly. The possible mechanisms of diabetes resolution have been summarized as involving: (a) Metabolite shifts (systemic and local); (b) Nerve mediated effects; (c) Bile metabolism; (d) Fat metabolism and adipokines; (e) Gut hormonal changes; (f) Starvation, caloric restriction and weight loss; and (g) Intestinal gluconeogenesis and hepatoportal sensing. A potential factor mediating one or more of these putative mechanisms is a change in host-microbial interactions after anatomical rearrangement, and likely driven by changes in microbial community composition in key sections of the gut. Although effects of DJB specifically on the gut microbiota have not been reported, a few studies have addressed the effects of RYGB on the diversity of the microbiota in human and rat fecal samples, and reported fairly congruent trends. Zhang et al. characterized bacterial and archaeal 16S rRNA gene diversity (using Sanger sequencing clones and pyrosequencing) to examine the fecal microbiota of human subjects who underwent RYGB. They reported decreased levels of Firmicutes and a proportional increase in the γ-Proteobacteria compared to normal-weight and obese subjects. Furet et al. used a quantitative PCR approach to quantify levels of specific groups of bacteria in fecal samples derived from humans before and after RYGB, and reported an increase in the Bacteroides/Prevotella group and E. coli three months after surgery, and a decrease in the abundance of Bifidobacteria as well as subtypes of Firmicutes, notably the Lactobacillus/Leuconostoc/Pediococcus group. A recent study of RYGB on the fecal microbiota of non-obese rats also reported a decrease in the abundance of Firmicutes and a substantial increase in the abundance of Proteobacteria, especially of Enterobacter hormaechei (γ-Proteobacteria). These studies used stool to characterize the microbiota: stool provides an integrated view of the mucosal and luminal communities in the gut. Thus, the find-
ings raise the question of where along the gut axis the changes in diversity occur. In addition, it is not known if the changes in microbial ecology observed for RYGB are generalizable to other types of bariatric surgery such as DJB.

REFERENCE


