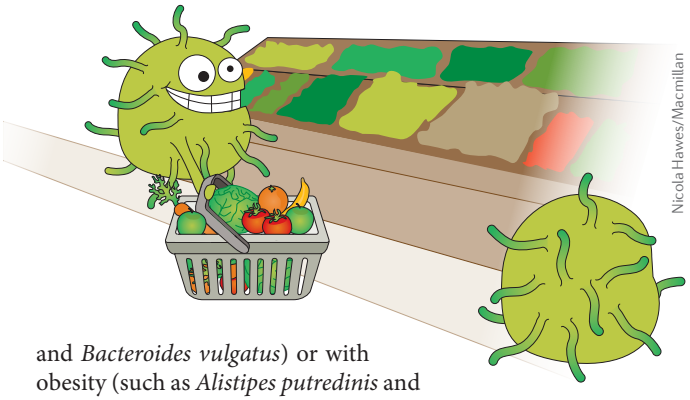
GENOME WATCH

Carpe diet

Elisa Viciani



This month's Genome Watch examines how coupling deep sequencing of the gut microbiome with metabolic profiles can advance the development of microbiota-focused personalized precision nutrition.

Obesity is considered one of the most important health challenges of the 21st century. Overweight occurs when energy intake through diet exceeds the amount of energy used by the body, and it is a major risk factor for type 2 diabetes, cardiovascular diseases and various types of cancer.

Diet has been shown to modulate both the composition and function of the gut microbiota. However, owing to the unique nature of the gut microbial community of a particular person, the same diet can have variable effects on different individuals.

Postprandial hyperglycaemia has been shown to be associated with obesity, but the increase in blood glucose levels after a meal (postprandial glycaemic response) cannot be easily predicted using current methods. Zeevi *et al.*[1] monitored the levels of blood glucose after a meal in 800 individuals and integrated those data with their gut microbiome profiles, life style information and nutrient intake using a machine learning approach. To test whether the response of an individual to a given food could be predicted using this approach, the authors designed a personally tailored diet to modify the postprandial blood glucose levels. Indeed, the personalized diets decreased the postprandial glycaemic response of the participants and caused several consistent alterations in their intestinal microbiota. For example, the relative abundance of *Bifidobacterium adolescentis*, high levels of which are associated with obesity, decreased, whereas other bacterial species that are found at low levels in individuals with type 2 diabetes mellitus (such as *Roseburia inulinivorans*, *Eubacterium eligens* and *Bacteroides vulgatus*) or with obesity (such as *Alistipes putredinis* and members of the Bacteroidetes phylum) were present at high levels. Thus, the predicted individualized beneficial diets seemed to modify the composition of the gut microbiota of the participants, and had a consistent effect on postprandial blood glucose levels.

Together with diet, the gut microbiota is an important factor that contributes to obesity by altering energy harvest and storage in the host. *Akkermansia muciniphila* is a mucin-degrading bacterium that is present at low levels during obesity and diabetes[2], and its administration to mice has been shown to decrease fat mass gain[3]. Given the recent insights that have been gained into the importance of the gut microbiota in obesity and metabolic disorders, it is crucial to better define its composition and function at the species level in individuals with obesity. Liu *et al.*[4] recently used shotgun sequencing of 257 faecal samples that included samples from obese and lean individuals, and individuals with obesity undergoing weight loss treatment by sleeve gastrectomy. *A. muciniphila* and *Faecalibacterium prausnitzii* were found to be highly enriched in lean individuals together with *Bacteroides thetaiotaomicron* and other *Bacteroides* species. Moreover, they observed a lower Bacteroidetes-to-Firmicutes ratio and changes in the gut microbiome of individuals with obesity, which suggested a state of microbial dysbiosis in the group with obesity. The functional characterization of the microbiome of individuals with obesity showed that their microbiota may have a higher ability to utilize carbohydrates and to produce pro-inflammatory factors, aromatic amino acids and branched-chains amino acids. Consistent with this, the administration of live *B. thetaiotaomicron* to mice fed a high-fat diet protected them against diet-induced obesity and decreased the concentration of circulating amino acids. Finally, weight loss in individuals with obesity subjected to sleeve gastrectomy partially restored intestinal microbiome and metabolic profiles that were similar to those observed in lean individuals within 3 months.

In light of this evidence, microbiota-focused precision nutrition could enable the design of personalized diet interventions, which might improve the control of postprandial blood glucose levels and their effect on the metabolism of the host. Although still in its infancy, this line of research shows that the microbial species associated with lean individuals can interact with the resident microbiota to help control energy supply to the host. Further research will enable better predictions that could be applied to design longer-term personalized dietary interventions and extended to address other clinically relevant issues related to metabolic disorders.

Elisa Viciani is at the Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK.
e-mail: microbes@sanger.ac.uk

doi:10.1038/nrmicro.2017.123
Published online 3 Oct 2017

1. Zeevi, D. *et al.* Personalized nutrition by prediction of glycemic responses. *Cell* **163**, 1079–1094 (2015).
2. Everard, A. *et al.* Cross-talk between *Akkermansia muciniphila* and intestinal epithelium controls diet-induced obesity. *Proc. Natl Acad. Sci. USA* **110**, 9066–9071 (2013).
3. Plovier, H. *et al.* A purified membrane protein from *Akkermansia muciniphila* or the pasteurized bacterium improves metabolism in obese and diabetic mice. *Nat. Med.* **23**, 107–113 (2017).
4. Liu, R. *et al.* Gut microbiome and serum metabolome alterations in obesity and after weight-loss intervention. *Nat. Med.* **23**, 859–868 (2017).

Competing interests statement
The author declares no competing interests.