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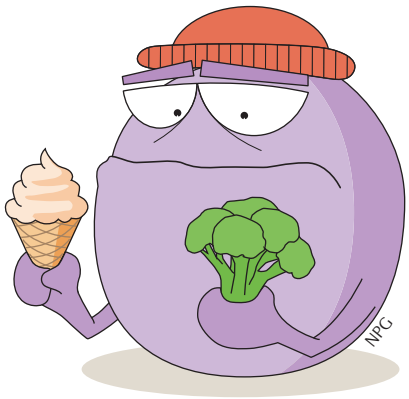
MICROBIOME

Microbiota-based nutrition plans

Blood glucose levels after a meal (clinically termed postprandial glycaemic response, or PPGR) are determined by the dietary intake of an individual in combination with additional factors, including the gut microbiota. Importantly, elevated PPGRs are linked to the development of type 2 diabetes mellitus and metabolic syndrome. The links between diet, the gut microbiota and PPGRs are still being elucidated, but a new study has shown that PPGRs to standardized meals are highly variable between individuals and are dependent on multiple factors, including the gut microbiota. Furthermore, monitoring individual responses to different foods and integrating this information with health parameters and microbiome composition in a machine-learning algorithm enabled the elaboration of individualized nutrition plans that improved PPGRs and resulted in consistent alterations in the composition of the gut microbiota.

Zeevi, Korem, Zmora and Israeli *et al*. began by measuring glucose levels in an 800-person cohort, every 5 minutes for 7 days, during which participants followed their normal routine except for the consumption of standardized meals as the first meal of the day. These data were used to calculate PPGRs and revealed that the PPGRs to the same meal were reproducible within the same person, but varied between individuals. Notably, the variability in PPGRs correlated with different clinical parameters and with the composition of the gut microbiota, which were determined prior to the start of the study. For example, the authors found a positive correlation between the abundance of Proteobacteria, Enterobacteriaceae and Actinobacteria and elevated



PPGRs to some of the standardized meals, whereas the presence of Clostridia and Prevotellaceae correlated with lower PPGRs.

To validate these findings, the authors tested whether the clinical and microbiome parameters could be used to predict individual PPGRs. Indeed, a machine-learning algorithm that incorporated these factors enabled accurate prediction of PPGRs, and a subsequent analysis of the algorithm predictions revealed that the composition of the gut microbiota predicted individual PPGRs. For example, the growth of *Eubacterium rectale* was associated with low PPGRs and the abundance of *Parabacteroides distasonis* was associated with high PPGRs.

Finally, the authors examined whether the algorithm could be used to design individualized nutrition plans that improve PPGRs. To do so, they recruited 26 participants who underwent the same 7-day monitoring as the initial cohort, followed by two 1-week diets: one week participants were fed a 'good diet' (predicted to induce low PPGRs in the specific individual); and a different week they were fed a 'bad diet' (predicted to induce high PPGRs in the same individual). Notably, the PPGRs during the 'good diet' week were lower than during the 'bad diet' week. Furthermore, daily profiling of the microbiome composition in these participants revealed that the abundance of specific bacterial taxa changed during the diet interventions, consistently across participants. For example, the abundance of *Bifidobacterium adolescentis* increased following the 'bad diet' and decreased following the 'good diet', whereas the abundance of *Roseburia inulinivorans*, *Eubacterium eligens* and *Bacteroides vulgatus* increased following the 'good diet' and decreased following the 'bad diet'.

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Collectively, these data demonstrate that PPGRs are highly variable between individuals, even when they consume the same meal, and that individual PPGRs are multifactorial, with differences in the gut microbiota being associated with these processes. Furthermore, this study identified multiple correlations between standardized meals, specific microbial taxa and PPGRs, which open the door for future studies addressing the mechanistic details that underlie the complex link between diet, the gut microbiota and metabolic diseases.

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