Modulation of Gut Microbiome - from phenomenology to dietary recommendations to tackle obesity

Stoffer Loman, PhD, NutriClaim BV, The Netherlands; Work Package Leader EU FP7 project "MyNewGut".

The potential role of intestinal microbiota in the etiology of various human diseases has attracted massive attention in the last decade. Experiments in animal models have produced evidence for a causal role of intestinal microbiota in the etiology of obesity and insulin resistance. However, with a few exceptions, such causal relation is lacking for humans and most publications merely report associations between intestinal microbial composition and metabolic disorders such as obesity and type 2 diabetes.

Dietary recommendations are generally based on epidemiological evidence of an association between a food, food component or diet with the prevalence of a disease. However for microbiome-targeted dietary recommendations, little or no epidemiological evidence is available. In fact, world-wide no microbiome-related dietary recommendations have been proposed.

Nevertheless, diet-induced changes in the microbiota have been shown to be associated with insulin resistance and development of diabetes. However, it is as yet an enigma as to which extend the altered microbiota is causally related to insulin resistance and diabetes or whether these changes in the microbiota are secondary to the development of insulin resistance and diabetes, the latter two induced by non-microbiota dependent pathophysiological mechanisms. Thus, the reciprocal relationship between the gut bacteria and these metabolic disorders remains a matter of debate. In addition, and in particular with respect to fiber, the health benefits of its consumption may be conferred even without the apparent involvement of the microbiome.

In particular, e.g. studies into the role of fiber in its capacity to modify the microbiota to confer a health benefit have until now solely relied on measuring the changes in the microbiota at the start and completion of the study. Therefore, changes in the microbiota by itself are not sensitive enough to provide for a causal explanation of the observed metabolic effects. Unless multiple time points are included in the study design, kinetic of changes in the microbiota, combined with simultaneously revealing the kinetics of gene, protein and metabolome expression, applying multiple -omics techniques, microbiome-targeted dietary recommendations will remain elusive.