

Diet and the gut microbiome: from hype to hypothesis

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This manuscript is written in honour of John H. Cummings, Professor emeritus, who provided over decades seminal work on the physiology, biochemistry and diet-effects of the human large intestine.

Introduction

Bioscience has seldom seen such an acceleration in the proliferation of scientific publications in relation to human health as that for microbiome research in recent years. For the gut microbiome alone, around 20 to 30 new papers per day appear in *PubMed* and there seems to be no day where the public is not informed about “news from microbiome research”. The field is driven mainly by the ability to undertake large scale and high throughput sequencing since the costs per sample have declined rapidly allowing large sample sizes and huge cohorts to be analysed. The most recent metagenomic analysis of 11,850 human gut microbiomes from different countries and ethnicities predicted 1,952 different uncultured candidate bacterial species¹. However, in almost all individuals, the microbiota is dominated by the phyla *Bacteroides* and *Firmicutes* while *Actinobacteria*, *Proteobacteria* and *Verrucomicrobia* constitute minor phyla². And, a single strain per species usually dominates the microbiome and that “individual-specific strain” also seems to preserve the stability of the human gut microbiome over time³.

Despite ten-of-thousands of papers and huge efforts in characterising the gut microbiota of humans across the planet, science is still not able to define a “healthy microbiome” or to give specific recommendation on how to alter the microbiome to affect health outcomes. Moreover, only around 20% of the microbial diversity found in fecal samples has been associated with intrinsic and extrinsic factors⁴; leaving more than 80% of bacterial diversity in faecal samples unexplained. Very little is known about the effects of diet on the gut microbiome in humans and, particularly, on its contribution to whole body energy balance. However, diet is considered as a key environmental factor in the microbiome-health relationship and the evidence for that shall be critically

discussed here. In addition, I shall address the role of gut physiology that is usually not taken into account, when interpreting findings of faecal microbiome analysis.

How much bacterial biomass constitutes the gut microbiome?

It seems to be generally accepted that the gut microbiome makes up 1.5 to 2 kg in mass. This estimate is communicated again and again, even in scientific literature. Similarly, the number of bacteria residing in and on the human was claimed to exceed 10 times the number of human body cells. It is amazing to realize that these numbers trace back to a rough estimate provided in a paper published in 1972⁵, which has never been questioned until recently. In 2016, Sender, Fuchs and Milo analysed the evidence carefully and recalculated the ratio of bacteria to human cells and provided as the best estimate a total of 4×10^{13} of bacteria versus 3×10^{13} of human cells resulting in a close to 1:1 ratio⁶. The difference between the old and new estimate results mainly from different intestinal volumes (colonic volume) used to calculate total biomass based on bacterial density per gram or volume unit. Sender, Fuchs and Milo finally estimated a volume of 150-200 ml of colonic content by using information on the daily stool output and a mean colonic transit time and by using published estimates of bacterial numbers from stool samples. They concluded that around 200 g of total bacterial mass was residing in and on humans of which the large intestine hosts the majority⁷. This new estimate of gut microbiome mass matches quite well with data reported by John Cummings in 1990⁸ based on the weight of the total contents taken out of the large intestine at autopsy of 46 sudden death victims from Europe and Africa. In this study the mean value of the intestinal contents of colon (wet weight) was 222 g (58 to 904 g) of which 95g represented bacteria (mean value by wet weight) which, after freeze-drying, equated to 36 g dry matter (mean value) in the total colonic content. Taken

together, the best evidence currently available argues for around 200 to 250g of colonic content with around 100g of bacteria representing the gut microbiome. The amount of this biomass excreted in human stool per day accounts for around 30 to 80g of which half represents non-viable bacteria^{7,2}. It is striking to realize that the quantity of stool is seldomly reported in microbiome publications, but knowing that the daily mass excreted can vary several fold, it can be anticipated that differences in the abundance of individual bacteria species and genera may very much depend on the “dilution” from volume variation. Most recently the first studies have started using quantitative microbiome analysis to determine not only bacterial diversity (richness) derived from sequences but also number of (viable) bacterial cells in the stool sample and, consequently, it is not surprising that cell counts ranged up to 10-fold; giving a quite different picture than relative abundance only⁹. Taking these findings together, one may conclude that the quantitative aspects of gut microbiome research need much more attention. Life science without considering masses is like analysing the universe and not taking the physics into account.

A stool sample and what it can tell us

The huge differences in colonic contents in sudden death victims from Africa when compared with those from Europe mirrors the huge differences in daily stool output between individuals^{9,10}. That seems to be due to the much higher intakes of non-digestible carbohydrates/fibres in Africa compared with intake via typical European diets. But even within Europe, daily stool output varies over > 3-fold¹⁰. In addition to the wide distribution in mean stool weight across the population, there is huge day-to-day variation in stool weight for the same individual, ranging between 50 and more than 400 g¹¹. Stool also varies in appearance, by colour and consistency. That fact

has been recognized recently as a critical determinant in analysis of gut microbiome composition. Clinical diagnosis of gastrointestinal disorders associated with obstipation or diarrhoea uses the so-called Bristol stool scale (BSS) or stool chart with pictures on colouring and consistency of stool sample to classify stool on a range from 1 to 7. In various studies, the richness of the faecal microbiome as assessed by relative species abundance showed a clear association with the BSS score and, in turn, stool consistency is related to stool water content^{12,13}. Moreover, in metagenomics analyses of stool samples from cohorts, the BSS was amongst the most relevant determinants of microbiota richness and variance⁴. Consequently, the identified faecal enterotypes show also a strong clustering with moisture content of stool samples¹². Water content of stool associates with the gastrointestinal transit time and in particular with the residence time of contents in the colon and rectum¹⁴, and with stool frequency¹⁵ and all of this affects microbial diversity. Moreover, colonic and faecal water content in mammals can oscillate and that depends on circadian alterations in aldosterone concentrations that act via the colonic receptors for this mineral-corticoid to modulate electrolyte and water transport processes^{13,14}.

The mouth to anus transit time in Europeans is around 60 hours of which 7 to 24 hours is accounted for by transit through the caecum and right colon and 9 to 30 hours for the left colon. The recto-sigmoid accounts for additional 9 to 15 hours¹⁵. There are also marked gender-dependent differences in transit time with around 15 hours faster transit in men than in women¹⁰. Transit time¹⁶ and stool frequency¹⁷ are strongly associated with stool consistency and this is strongly associated with microbiota richness¹⁸. Care should thus be taken when comparing and interpreting findings on relative abundance of bacterial species or taxa variance across ethnic groups

consuming their habitual diets. In addition, care should also be taken when interpreting data obtained from a single stool sample of an individual and how its composition relates to metabolic differences and responses to diet or even disease risks. Direct-to-customer businesses based on microbiome analysis of a single stool sample are flourishing and, for the reasons outlined above, these should be viewed very critically. The huge variability in composition of the stool - day by day, or even within a day – and by variation of bacterial density in a faecal sample¹¹, makes analysis of a single sample and its interpretation questionable. Moreover, the diagnostic value of microbiome analysis for predicting metabolic health effects (see below) has been questioned recently by a study from China that revealed a major influence of the geographical region (14 districts) in which the volunteer lives on composition of the stool microbiota. This “regional effect” overruled by far all other determinants of microbiome diversity such as age, gender, BMI, BSS or diet variables¹⁹. In addition, models developed to assess metabolic disease risks based on the microbiome data obtained in one district failed to work in another district. The authors therefore recommended the models to be built for given geographical areas¹⁹.

Currently, there are no standardised and generally accepted protocols for stool sampling and processing, or for downstream analysis, nor are there any reference microbiomes that could be used as a quality assurance measure. Therefore, it is not surprising that a single stool sample analysed in different labs shows an impressive variance in composition²⁰. However, this problem of insufficient reproducibility has been recognized and some activities have been launched to standardize better current procedures^{21,22}.

The intestinal tract has longitudinal and radial compartmentation. In addition, the mucosa shows huge morphological differences from the small to the large intestine in its surface-enhancing substructures. Further, the anatomy of the gut differs between species. That becomes relevant when, for example, findings in rodents are translated to the human condition. This applies particularly to mice which as germfree animals are widely used in microbiome research. Gnotobiotic mice serve here as a host to explore the phenotypic consequences after inoculation of a microbiome from a donor, including human samples. The anatomy of the mouse large intestine is dominated by a huge cecum that serves as a fermentation chamber and that, in germfree animals, fills the abdomen almost completely (see Fig.1). That suggests that the microbiota is part of a feed-back loop that controls the growth of the tissue. Germfree mice also have a markedly increased transit time²³ and that of course has a major effect on the availability of nutrients and energy for absorption. The entire surface of the intestine is lined by mucus. In the colon, the mucus covering the epithelium is comprised of an inner firmly adherent layer of around 100 μm in thickness and a looser outer layer that ranges in thickness from 500 to 800 μm ²⁴. When the mucus layer is stained for bacteria, the inner layer appears sterile whereas the outer layer with a fluffy appearance shows the presence of bacteria in the meshwork^{25,26}. This anatomical compartmentation means that, except for tiny regions and transiently, bacteria are not directly in contact with the apical membranes of the different cells lining the epithelium. The inner mucus layer also has a distinct microenvironment that does not mix easily with the outer mucus layer and the lumen. This is seen, for example, in marked differences in ionic composition and pH but also in oxygen tension²⁷. These parameters all affect growth of different bacteria in different ways. The presence of a higher pO_2 in the mucus layer that by diffusion from the tissue into the lumen forms a

steep gradient may well explain that analysis of samples from the mucus layer show a different pattern in microbiota at the phylum and genus level than samples taken from the lumen. Although only very few studies have explored these differences in humans, studies in mice (with all restrictions for translation) suggest that the differences between luminal and mucosal (mucus-associated) microbiomes become larger in more distal segments of the intestine²⁸. When faecal samples and those taken out of the intestine by biopsy in the same individual were compared, the bacterial signatures were quite different²⁹. This means that care should be taken when extrapolating from stool data corresponding bacterial functions and the effects on the mucosa and host because i) metabolic processes that are relevant in the vicinity of the epithelium (where there is a distinct microenvironment) may be quite different from those in the lumen and ii) bacteria are mostly not in contact with the epithelial surface.

Diet effects on bacterial composition

As noted above, only around 15 to 20% of the variance in composition of the microbiome can so far be explained despite huge research efforts. What is most striking is the small effect of the host genome on the gut microbiota in humans. Both, population studies in cohorts of different ethnicity³⁰ as well as twin studies with over 1.000 twin pairs³¹ revealed that only between 2 and 9% of the taxa identified in stool samples appear to be inherited. And, except for the gene encoding in a variant lactase persistence, no significant single nucleotide polymorphisms have been found to associate with the gut microbiota³⁰. That leaves the environment as the key effector of the gut microbiome. Numerous studies have addressed individual environmental variables and determinants with significant effects on gut microbiome composition. In a comprehensive analysis of environmental and endogenous effectors in two cohorts

from Flanders (Belgium) and the Netherlands, a total of 126 factors (at a false discovery rate of <0.1) were identified as significant covariates of the gut microbiome⁴. Out of 503 variables investigated, the BSS (self-reported) ranked as number one with the most pronounced effects on microbiome composition which confirmed previous findings that moisture content of stool samples is strongly associated with bacterial diversity⁹. The 126 significant covariates of microbiome composition included gender and age, a variety of diseases, various drugs and numerous food items. However, individual dietary factors generally ranked much lower with similar effect sizes observed for e.g. energy intake, total carbohydrate content of the diet, and amounts of beer, coffee or red wine consumed⁴. Despite the comprehensive coverage of a large number of variables in these cohorts, 92.3% of microbiome composition remained unexplained.

Systematic studies addressing effects of diets or individual dietary factors on the gut microbiome in humans are sparse. David et al. investigated the impact of a plant-based when compared with an animal food-based diet (provided ad libitum) over a 5 day period in a cross-over design in healthy volunteers (6 male and 4 female) with a baseline and a wash-out period of a couple of days each³². Despite major differences in intakes of fibre, fat and protein, the α -diversity (Shannon diversity index) in stool samples did not change when microbiome composition was analysed each day. The β -diversity (Jenssen-Shannon-distance; used as a surrogate measure of the induced changes) showed significant differences when volunteers were consuming a diet based on animal products but only when compared to the respective baseline values. Marked differences were obtained for the concentration of acetate, butyrate and isovalerate and isobutyrate (based on wet weight) in stool samples. Whereas acetate and butyrate levels declined on the animal-based diet, those of the SCFA derived from

degradation of branched chain amino acids increased more than two-fold, likely as consequence of a 3-fold higher protein intake. In contrast, the plant-based diet provided around 25g of fibre per day with almost zero intake on the animal-based diet³². However, since stool output (volume) and faecal water content were not reported, the stool microbiota may also be affected by these parameters. Although feeding the two extreme diets overruled inter-individual variation in microbiome composition, the overall effects of diets in changing bacterial diversity were small. A similar finding was reported by Wu et al. in 98 individuals with recorded short term (24h recall) and long-term (food frequency questionnaire) food intake. In this study volunteers could be clustered into two distinct microbiota enterotypes with characteristic reversed compositions in *Bacteroides* and *Prevotella* taxa which were associated with long-term dietary patterns. However, a short-term dietary intervention trial in the same volunteers comparing high fat/low fibre with low fat/high fibre diets did not cause a change in the enterotype, albeit alterations in microbiome composition were found already at 24 hours after switching diets³³. In a recently published study with 34 healthy human subjects who collected stool samples each day for 17 consecutive days, faecal shotgun metagenome analysis revealed huge variability across the volunteer group but rather stable individual microbiomes despite considerable variability in the food groups consumed³⁴. Most strikingly, analysis of stool from two volunteers who consumed a meal replacement in form of a liquid diet over the observation period did not reveal any obvious differences in microbiome composition (at the genus level) when compared to volunteers consuming ordinary diets. Since differences in macronutrient intake did not associate with diversity of bacteria at the genus or functional module level, the authors³⁴ concluded that “food-based interventions seeking to modulate the gut microbiota may need to be tailored to

the individual microbiome". When taken together, studies examining effects of diet on faecal microbiomes have not delivered strong evidence that diet is a major changer of composition and even diets high in fibre content provoked rather small effects on overall bacterial diversity.

Two recent human studies have assessed the effects of two types of fermentable fibres on stool microbiome composition. In a randomized double blind placebo controlled 12 week study with 44 healthy volunteers consuming 12g per day of inulin (or placebo) for 4 weeks, microbiome analysis revealed that the variation induced by inulin consumption accounted for 0.8% of global microbiome composition whereas inter-individual variation ranged from 63.9% to 77.2%³⁵. However, significantly increased *Bifidobacterium* and decreased *Bilophila* numbers were observed during inulin intake and those changes associated weakly with softer stools. Contrary to expectations, BSS and stool frequency did not show significant alteration although inulin has been shown in numerous studies to have beneficial effects on constipation and even carries a health claim provided by EFSA for these effects. Because of their "bifidogenic" effects, galacto-oligosaccharides (GOS) were substituted for human milk oligosaccharides in cows-milk based formula diets some decades ago to provide infants with a "fermentable fibre". In a double-blinded placebo-controlled parallel intervention study with 44 obese adults given 15g GOS per day over 12 weeks, this "bifidogenic" effect was confirmed with a 5-fold increase in the abundance of *Bifidobacterium* species³⁶. Despite these specific changes, neither microbial richness in faecal samples nor overall microbiome diversity were affected by GOS intake. Comprehensive metabolic phenotyping of volunteers receiving GOS, compared with placebo, did not reveal any differences in SCFA concentrations in stool or in plasma nor any changes in gut-derived hormones or markers of inflammation in systemic circulation. In addition, there

were no significant alterations in peripheral and adipose tissue insulin sensitivity, body composition or energy/substrate metabolism³⁶. In summary, these carefully conducted fibre supplementation studies revealed that overall bacterial composition does not change significantly even with rather high daily intakes of either inulin or GOS, whereas selective effects on *Bifidobacteria* – considered to be beneficial - were found in both studies. These findings match quite well those of various other studies on effects of fibre and resistant starch in humans employing other analytical techniques such as microarray, pyrosequencing or FISH³⁷ that all revealed selective effects but rather small, or no, changes in overall bacterial composition. Factors that limit the interpretation of these studies on effects of fibre on the gut microbiome were identified in a workshop organized by the National Institutes of Health and the United States Department of Agriculture with some recommendations developed on better study designs when assessing diet/fibre effects³⁸.

Does the microbiome make you slim and obese?

One of the mysteries in microbiome research has been the contribution of the gut microbiome to overall energy homeostasis. Some studies suggest that the microbiome is an energy harvester providing net energy to the host in form of SCFA and other metabolic products and thus contributing to an obesity phenotype whereas other studies suggest that the microbiome is an energy sink. The latter are mainly studies from the animal nutrition sphere in which the use of antibiotics or other compounds that reduce the bacterial load in the large intestine of pigs or poultry have proven that less bacteria in the large intestine leads to higher weight gain^{39,40,41}. In contrast, studies that suggest that the microbiome contributes to obesity are mainly from use of gnotobiotic (germfree) mice, with or without transfer of microbiomes from lean or obese animals or even human faecal samples, and from studies with high fat diets^{42,43}.

Although some of the findings in germfree animals are remarkable, these studies may be a bit misleading when translated to the human condition because of the experimental conditions used. Rodents kept in SPF-facilities or kept sterile are fed diets that are sterilised by dry heat in autoclaves or that have been irradiated in the dry state. In either case, digestibility of the dietary constituents such as carbohydrates (starch) or protein by pancreatic enzymes is limited resulting in higher quantities of non-digested products reaching the large intestine. In mice that is predominantly the cecum with the character of a large fermentation chamber. Even in conventional animals, rather large particles from the dry, very hard food pellets can be recovered from the cecum, demonstrating that these diets *per se* have a very low digestibility in the upper small intestine. Therefore, in rodents the gut bacteria assist in extracting energy from such a diet. A lack of proper weight gain in germfree mice may be the best evidence for that. However, whereas the contents of cecum and colon constitute around 1% of total body mass in a C57BL6 mouse, in humans the colonic contents equate to only around 0.2% of total body mass. The capacity to ferment is thus considerably higher in mice than in humans and, moreover, most human diets are a mixture of raw and heat-treated foods with a much higher availability of energy by digestion and absorption in the upper small intestine. When diets for mice are heat-treated and compared with the same diets fed raw, body weight changes are more pronounced and support the notion of a loss of energy via the fermentation route^{44,45}. In humans, this issue can be exemplified with non-digestible starches and other polysaccharides which, when fermented in colon, provide an estimated 2 kcal mainly via SCFA⁴⁶ from each gram of carbohydrate (gross energy = 4 kcal) reaching the colon. That means that only 50% of the energy contained in the carbohydrate is delivered to the host and the other 50% is likely consumed by bacteria for their needs in growth and maintenance of biomass. In studies combining collection of ileostomy efflux followed by fermentation

ex vivo, it has been estimated that in humans SCFA could deliver 3-11% of total energy needs per day⁴⁷. In addition, studies comparing digestibility of raw and cooked protein suggest that fermentation of dietary protein may also contribute to energy extraction in colon. Cooked egg white has a digestibility of 91% in human's but the digestibility is reduced to 50% when the protein is given raw⁴⁸ with much more protein, and thus amino acids, reaching the colon. In summary, different quantities of fermentable/utilisable nutrients reach the large intestine from raw or heat-treated food to satisfy the energetic needs of bacteria with the delivery of some extra energy to the host that otherwise would not be available.

Studies in volunteers or patients with a stoma in the terminal ileum provide rough estimates of how much energy passes from the lower small intestine across the ileocecal valve to serve as "bacterial feed". Data compiled from various studies with analysis of ileal output reveal that around 1 to 5 g of carbohydrates, 2 to 10g of protein, 2 to 5 g of fat and some 20g of fibre per day pass from the ileum into colon^{49,50,51,52}. The quantity of non-digestible starch and non-starch polysaccharides that reach the colon seems particularly relevant since their contents in the diet vary considerably and correlate closely with the bacterial biomass⁴⁹. In addition, 2.3 g mucus per day was recovered from ileostomy effluent⁵⁰. Further, constituents of gastrointestinal secretions and epithelial cells lost by apoptosis are sources of energy for bacteria. To maintain a microbiome during fasting and starvation these sources become relevant. However, only a few bacterial species are known for their ability to utilize the glycoproteins as the major constituent of mucus. Taken together, a rough estimate is that fermentation of these substrates could yield around 250 kcal per day. This calculation comes close to the estimation of energy available for absorption in colon from a study in ileostomy patients fed diets containing different types of carbohydrates combined with an *in vitro*

digestion of the ileal effluent to quantify the SCFA produced⁵⁰. Assuming an energy intake of 2.500 kcal per day, findings from this study would translate into 75 to 280 kcal of that absorbed in colon. The daily energy output in faeces is around 140 kcal, but ranges from 50 to 450 kcal per day¹¹ and is thus almost as large as the amount that crosses the ileocecal valve to be absorbed in colon. Based on this “back of the envelope” calculation of the “caloric balance” across the human colon, one may conclude that the microbiota provides only very small energy quantities to the host – if any – compared with its own energy demands. Taken together, the energy balance in and across the human (and mouse) large intestine remains as the “dark side” and does currently not allow a final conclusion to be drawn on whether the microbiome “makes us obese or slim”. Yet, the extent to which experts in human and animal nutrition interrogate the same biology with quite opposing perceptions (as either an energy delivering or an energy consuming system) is striking. Some of the confusing views may relate to findings in rodents that need more care when translated to the human condition because of different anatomy, physiology, diets and other environmental factors. Figure 2 summarizes some of the critical physiological determinants of intestinal functions in humans that contribute significantly to microbiome quantity and diversity including the estimated nutrient/energy balance.

Evidence of different microbiome composition in obese and lean humans has been used to push the concept that net energy delivery to the host contributes to overweight and obesity⁵⁵. Predominantly changes in the ratio of *Firmicutes* to *Bacteroidetes* were found as associated with higher BMI and body fat content⁵⁴. However, more recent analysis has questioned these findings since, usually, the between-study variability in the relative abundance of *Bacteroidetes* and *Firmicutes* is far greater than the within-

study differences found in lean and obese individuals⁵⁵. Whether the reported differences between lean and obese individuals hold up, needs further studies with standardized analytical procedures and reference materials; it could well be that the gut microbiome is just another read-out of an obese phenotype rather than a cause.

The limits of models and how to better assess microbiome biology

There can be no doubt that the current methods and techniques used in microbiome research have limits and are prone to deliver misleading information. Besides the analytical constraints when it comes to characterisation of the microbiota, the importance of the microbial ecosystem as an interface between diet and host metabolism remains elusive and is quite often exaggerated. One of the most important tools to address the role of the microbiota for host and host health are gnotobiotic animals, inoculated with either faecal samples or discrete bacterial species or microbial populations. A recent critical review assessing the value of these approaches concludes that the findings are limited by conceptual flaws, limited in biological interpretation and limited in translation to the human condition⁵⁶. As addressed above, the gastrointestinal tract of a rodent is quite different on grounds of anatomy, morphology and biochemistry. And, even the very limited number of strains used is a critical constraint. Mouse strains display impressive differences in metabolic phenotype. Microbiome research should therefore preferentially use humanized mouse models in which immune and metabolic functions are made more human-like. More appropriate animals such as pigs may as well be employed. They can be fed like a human with all kind of processed food in contrast to rodents and that would also allow matrix-effects of food items to be studied which is not done or more difficult to do in mice. There is also the option to use humanized pigs⁵⁷ for those type of studies. Non-

human primates appear attractive as well, but their use has limits by both, the resources and infrastructures needed and by the much higher financial requirements.

Over the last decade various *in vitro* methods and technology platforms have been developed to simulate the human (animal) gastrointestinal tract for studying digestion and bioavailability of nutrients or assessing the effects of dietary constituents on the microbiota. Although some intestinal processes can be mimicked quite well *in vitro*⁵⁸ and data gained may be translated, others could not be confirmed *in vivo*. This was recently demonstrated by comparing the effects of inulin on the microbiome and the production of short chain fatty acids *in vitro* and in human studies⁵⁹. What currently *in vitro* models can't simulate appropriately are the autoregulatory loops that control motility and fluid handling via the enteric nervous system and the numerous gastrointestinal hormones produced in the gut that continuously adapt the physiology to the recorded status of digestion and absorption. What rarely is considered in microbiome research – and thus also not included in most *in vitro* studies – is the secretory component. Around 5 litres of endogenous fluid enter the intestine per day and are almost completely reabsorbed together with the fluids drunk and bound in food leaving around 100 ml excreted with stool. The endogenous secretions provide a continuous flow of solutes into the intestinal system comprised of electrolytes but also low molecular metabolites such as sugars, amino acids and urea. Depending on protein intake, humans produce 25 to 50g of urea per day of which around 25% cycle through the gastrointestinal system⁶⁰ with rapid hydrolysis to ammonia (mainly in colon) by bacteria possessing urease. This is associated with marked effects on pH which in turn affects the microbiota. It is thus a very interesting approach to use the effluents of volunteers with an ileostoma for *ex vivo* studies of microbiota⁴⁷. The effluent represents the “physiological substrate” that would pass into the colon for further

fermentation and when collected from volunteers consuming different diets, new insights into how diet can alter the microbiota may be gained.

Microbiome and metabolic health

Since fecal transplantation of “healthy stool” to patients with recurrent *Clostridium difficile* infections has been established as a therapy⁶¹, the principle of transferring microbiomes has also been applied to study metabolic health effects.

As an example, faecal microbiome transfer (FMT) was used very recently to study the effects of trimethylamine-oxide (TMAO) on cardiometabolic health in individuals with the metabolic syndrome⁶². TMAO is a suggested mediator of microbiome effects on the cardiovascular system since elevated plasma concentrations of TMAO associate with increased cardiovascular risk and mortality⁶³. In the gut microbiome, trimethylamine (TMA) is produced from dietary carnitine, choline and phosphatidylcholine and is then oxidized in liver to TMAO. Since a vegetarian diet delivers far less of the dietary precursors for microbial TMA production, the corresponding microbiome thus could have a much lower capacity to produce TMA resulting also in a lower cardiovascular burden. This hypothesis was tested in a FMT study using stool samples from a vegetarian donor and autologous (own) faecal samples as control provided to individuals with metabolic syndrome combined with analysis of markers for cardiovascular health⁵⁶. Although the intervention resulted in some changes in microbiome composition in the recipients, TMAO concentrations in blood and measures of vascular health remained unchanged. In addition, the TMAO-hypothesis has recently been challenged by a study that used a Mendelian randomization approach to reassess studies on TMAO in the context of cardiovascular

diseases in cohort studies⁶⁴. It was concluded that the observed TMAO levels in plasma are likely result from slight impairments in renal clearance of TMAO in the risk cohorts and that TMAO thus may not be causative but rather serve as a biomarker in the disease trajectory.

Obesity and insulin resistance (IR) appear to be associated with alterations in faecal microbiome signatures and moreover, inoculation of faecal samples from obese or lean individuals into gnotobiotic mice affected differently animal weight gain. That provided support for the hypothesis that the gut microbiome contributes to an obese phenotype and the development of the metabolic syndrome. A recent study in 22 obese individuals tested whether an FMT approach with a stool sample of a single donor of BMI 17.5 provided via capsules to 11 test volunteers can cause changes in body weight. The study period was 12 weeks with 11 other volunteers receiving placebo capsules as control. Treatment started with a dose of 30 capsules at week 4 and a second dose of 12 capsules at week 8. Each capsule contained 0.75 g stool of the donor. Careful analysis of weight changes, microbiome composition and numerous metabolic parameters revealed that the procedure *per se* was safe but failed to cause any significant alterations in the volunteers receiving stool from the lean donor⁶⁵. For the metabolic syndrome, a trial with 18 patients of which 9 received FMT with samples from lean human donors (provided as lavage via duodenal tube) and 9 obese individuals serving as control and receiving autologous FMT reported improved insulin sensitivity after 6 weeks in the group undergoing allogenic FMT⁶⁶. However, the same research group failed to show any metabolic improvements or microbiome changes after 18 weeks in a subsequent study with 26 patients undergoing allogenic FMT with 12 controls receiving autologous FMT⁶⁷. Another approach to assess the contribution of the microbiome to an IR phenotype is the treatment with antibiotics. However, a

human study with type 2 diabetic volunteers who received either amoxicillin or vancomycin for 7 days failed to provide evidence for any metabolic improvements despite significant alterations in SCFA and bile acid concentrations in stool and major changes in the microbiome⁶⁸.

A close link between microbiome composition and plasma glucose responses has been derived from a study conducted with originally 800 volunteers carrying an interstitial glucose monitor to obtain blood glucose responses to given meals and individual food items. The study revealed huge differences in glucose profiles between individuals when challenged with food items of seemingly the same carbohydrate load (but not identical in composition with respect to starch or sucrose, non-digestible starch or non-starch polysaccharide content or accompanying fat and protein content). However, the observed different responses in glucose levels were associated with microbiome signatures and the authors developed an algorithm that included some phenotypic measures and microbiome information that was able to predict blood glucose profiles in an independent cohort with an accuracy of 60 to 70%⁶⁹. This algorithm has been applied in other cohorts and proven to predict glycemic responses with similar precision^{70,71}. These findings, of course, suggest a causal link between microbiome composition, its metabolic activity and the increase in plasma glucose concentration and/or glucose clearance in response to a given food. Such a relationship may be mediated by the gastrointestinal hormone system, including the incretins, that act as central regulators of insulin secretion and thus plasma glucose concentration. However, it is more difficult to provide a mechanistic explanation for the possible role of the gut bacteria in these acute glycemic responses to foods because the bacteria reside mainly in colon. This part of the gastrointestinal tract is well equipped with a high density of enteroendocrine cells and is known to secrete

glucagon-like peptide 1 and peptide YY that contribute to upper small intestinal physiology e.g. by delaying gastric emptying and providing some satiety signals. However, the peak in blood glucose concentration after food intake occurs usually within 30 to 60 min and that is long before any food residues or digested products have reached the colon to provide via the microbiome a feed-back that could modulate glucose absorption. However, inter-individual differences in gastrointestinal motility and transit time (ITT) is an underlying phenomenon that would affect blood glucose responses and microbiome signatures in a coupled manner. ITT can be altered by drugs such as loperamide or erythromycin and agents such as senna alkaloids or magnesium citrate. These maneuvers that increase or decrease ITT have been shown to cause changes in bacterial density in stool samples⁷² and microbiome composition¹⁶. Indeed, the bacterial mass in stool (g/day) can be altered almost 3-fold by these transit time modifying agents and there is a close relationship between mass and the log of transit time⁷². In humans, colonic transit time measured by radio-opaque markers via x-ray, correlated with Shannon index or the operational taxonomic units richness as diversity markers of the fecal microbiome¹⁶. In addition, stool water content and BSS are key determinants of the 4 enterotypes that are frequently defined as core microbiome groups with distinct compositions and these are intrinsically linked to ITT¹². Further, ITT is a critical determinant of the rate of glucose absorption in the upper small intestine. For postprandial glucose profiles, compounds such as loperamide that delay gastric emptying reduce plasma glucose responses whereas prokinetic agents such as metoclopramide that increase gastric emptying lead to faster, and higher, rises in postprandial glucose concentration^{73,74}. As a consequence, gastrointestinal motility and transit through stomach and intestine that affect both upper and lower intestinal physiology link microbiome effects with individual glucose

responses. They appear as two read-outs of a common intestinal phenotype with marked intraindividual differences. Interpretation of studies of post-prandial glycemia and the microbiome should also take into account the evidence that high postprandial glucose concentrations (as observed in individuals with IR or type 2 diabetes) can alter gastric, pancreatic and intestinal responses to diet and change the ITT and that these may well be factors contributing to microbiome changes reported in these disease states^{73,74}. A direct proof of the hypothesis that the individual's ITT is a critical determinant of both, microbiome mass and diversity and postprandial glucose responses requires studies with comprehensive analysis of all related parameters.

A new quality of gut microbiome research

William Hanage in 2014 asked for a “healthy dose of scepticism” in microbiome science and proposed some key questions including whether experiments can detect differences that matter, whether studies can reveal evidence of causation and not just correlation or whether anything else could explain the findings⁷⁵. Asking these questions seems as valid today as 6 years ago despite the thousands of new papers published since then. A very recent commentary asks as well for more rigor and critique in microbiome science to avoid and prevent unrealistic expectations that may undermine the credibility of science per se⁷⁰. It all starts with better standardisation of all procedures for sampling and processing of samples and for analysis of microbiomes of which some are being addressed through activities such as *the microbiome quality control project* that was launched a couple of years ago^{22,23} and that delivered some “best practise” recommendations³⁷. The research area also needs reference materials (*stool samples* or defined mixtures of bacteria) to be included for quality control

purposes and such quality assurance measures should be made mandatory, and enforced, by funders and research journals.

Microbiome science should no longer ignore mass issues and basic intestinal (and whole body) physiology. Stool output, BSS, water content and bacterial biomass in the sample should be measured routinely. Moreover, microbiology beyond sequencing efforts needs to become quantitative by measuring the true abundance of bacteria (by numbers for at least the dominating species) and not only relative species abundance.

We need hypothesis-driven research on the effects of diet and on whether the microbiome is a net energy delivery or energy consuming biosystem. Such studies in humans, combined with studies in volunteers with ileostoma, should include careful analysis of energy going in (caloric intake) and energy excreted per day (by bomb calorimetry) of total stool and urine. Ileostomized human volunteers receiving the same diet as the healthy control would allow by collection and analysis of stoma effluent how much energy and which nutrients pass into the colon allowing to assess the energy balance across the colon in humans. Of course, some alterations in the physiology and microbiology in ileostomy patients (due to the previous disease such as colorectal cancer, Crohn's disease or colitis) may hamper the direct translation to the healthy individual, at present, there appears no better system to quantify total substrate inflow into the gut microbiome.

Although most studies with fermentable substrates showed only modest effects on overall microbiome diversity with persistent changes in a few species only³⁶, all non-digestible starches and other non-starch polysaccharides are known to cause changes in stool volume. An important question is how these changes in stool output *per se* affect the microbiome in mass and composition (diversity). For such studies, the effects of different types and quantities of carbohydrates/fibres on the microbiome should be

studied in the same volunteers combined with standardised microbiome profiling. That could well be done in pan-European/international projects with different microbiome backgrounds and with standardised diets and standardised analytical procedures. The recent study from China¹⁹ demonstrating the great importance of the geographical/regional influence on microbiome composition suggests strongly that diet effects may need to be studied at such regional levels to enable the development of generalizable conclusions and recommendations for public health.

In addition, when investigating the effects of diet, it is important to consider the technology used for food processing and whether the food is consumed raw or heat-treated. For example, in volunteers with ileostoma between 4 and 19 grams of non-digestible starch and non-starch polysaccharides (around 2 grams) were recovered from the effluent when two bananas were consumed – depending on their state of ripeness. In raw banana the starch in the granules is in a highly crystallized form and seems to resist hydrolysis by α -amylase⁵³. Starch structure in general is an important factor in digestibility, a certain fraction is always resistant to hydrolysis and that fraction is altered when food rich in starch undergo heating and cooling (or reheating). Whereas cooling can reduce digestibility of potato starch for example by around 10%, reheating does not lead to full recovery of digestibility. For many food and in particular for convenience products (frozen or microwave prepared) that may well be relevant. To date, there are no systematic studies on how food processing affects the gut microbiome and that also applies to the fundamental question on how raw versus heat-treated food in a diet affect overall energy balance and microbiome composition. Heat treatment not only changes digestibility of starch but also that of protein and fat. Using the same batch of food products and a cross-over design (and if possible with volunteers carrying an ileostoma as control for determining small intestinal

digestibility), such a study could yield interesting findings on the shift of nutrient and energy harvest from large to small intestine when early hominids employed fire and started cooking; estimated to have happened about a million years ago and considered to be a milestone in the evolution of our species and its intestinal microbiome.

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