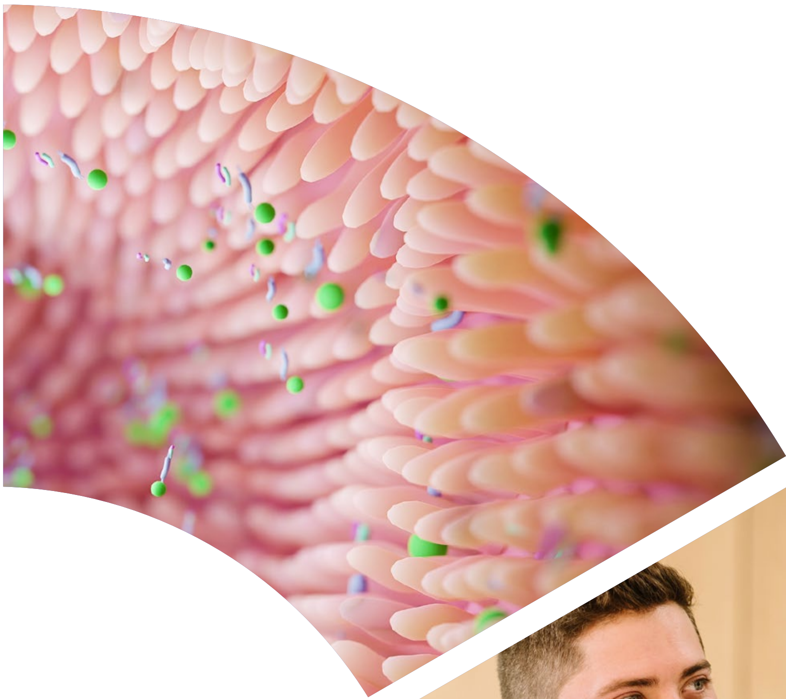

Dietary Impacts on the Gut Microbiome

Understanding the interaction between the diet and microbiome

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Diet has a significant impact on the composition of the gut microbiome.

Diet is the biggest modifiable factor impacting microbiome composition and function. The literature, along with MetaXplore data analysis, indicates the more extreme the diet, the more impact it has on the microbiome. More restrictive diets such as vegan, and ketogenic, have the most impact on the abundance of species within the microbiome. Plant-rich diets that include a variety of fruits, vegetables, legumes, grains, nuts and seeds are associated with a healthier microbiome. Understanding the interactions between the diet and microbiome can help optimise patient health outcomes.

Diets are distinct patterns of food consumption

Food group	Mediterranean	Ketogenic	Paleo	Omnivore	Vegan	Vegetarian
Meats	✓	✓✓✓	✓✓✓	✓✓	×	×
Fish	✓✓	✓	✓	✓	×	×
Eggs	✓	✓✓✓	✓✓✓	✓	×	✓
Dairy	✓	✓✓	×	✓	×	✓
Legumes	✓✓	×	×	✓	✓✓✓	✓✓
Fruits	✓	Restricted	✓✓ (non-starchy)	✓	✓✓	✓✓
Vegetables	✓✓	✓✓ (non-root)	✓✓	✓✓	✓✓✓	✓✓
Grains	✓	×	×	✓	✓	✓
Nuts	✓✓	✓✓	✓✓	✓	✓	✓

“The more extreme the diet the more impact on the microbiome”

Diet style and the gut microbiome

<table>
<tr><th></th><th>Mediterranean</th><th>Vegetarian</th><th>Vegan</th><th>Ketogenic</th><th>Paleo</th></tr>
<tr><td rowspan="7">Species</td><td>↑ Faecalibacterium prausnitzii</td><td>↓ Alistipes putredinis</td><td>↑ Prevotella copri</td><td colspan="2">↑ Hungatella_A MIC8772</td></tr>
<tr><td></td><td colspan="2">↓ Negativibacillus spp</td><td colspan="2">↑ Negativibacillus spp</td></tr>
<tr><td colspan="3">↓ Faecalicatena torques</td><td>↑ Faecalicatena torques</td><td></td></tr>
<tr><td></td><td colspan="2">↓ Bilophila wadsworthia</td><td></td><td></td></tr>
<tr><td>↓ Bifidobacterium adolescentis</td><td>↓ Bifidobacterium longum</td><td colspan="3">↓ Bifidobacterium</td></tr>
<tr><td>↓ Streptococcus thermophilus</td><td>↑ Streptococcus thermophilus</td><td colspan="2">↓ Streptococcus thermophilus</td><td></td></tr>
<tr><td>↑ Agathobacter rectale</td><td></td><td></td><td>↓ Agathobacter rectale</td><td></td></tr>
<tr><td rowspan="3">Microbial markers</td><td colspan="3">↓ TMA producing microbes</td><td>↑ TMA producing microbes</td><td></td></tr>
<tr><td></td><td>↓ BCAA producing microbes</td><td></td><td>↑ Hydrogen sulphide producing microbes</td><td></td></tr>
<tr><td></td><td colspan="2">↑ Oxalate consuming microbes</td><td colspan="2">↓ Lactate producing microbes</td></tr>
</table>

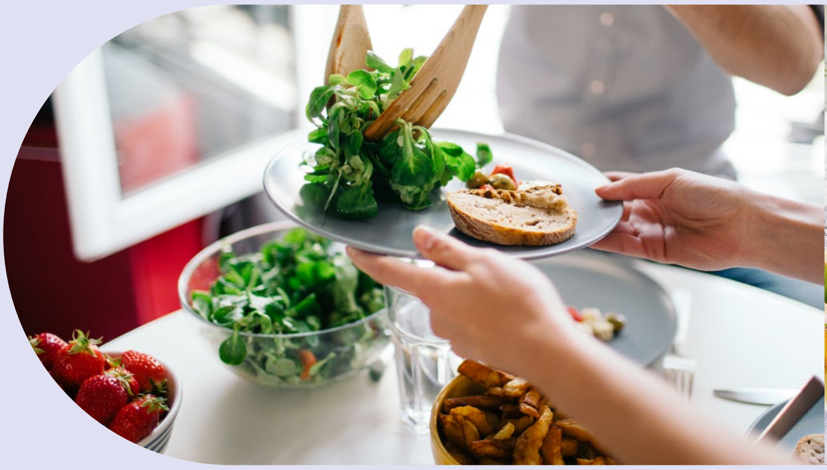
Testing reveals dietary influence on the microbiome

Testing your patients with the Co-Biome™ MetaXplore™ range can reveal your patients potential for microbial marker production or consumption, allowing you to make personalised dietary recommendations for targeted microbiome interventions.

Microbiome features

Microbiome feature	Health association	Diet association
Microbial species		
Health and disease associated species		
Prevotella copri	Commonly found in non-western populations while in Western populations it is found in fewer than 30% of individuals[1]. It is linked to both positive and negative health outcomes which may reflect the impact of diet and lifestyle on this species. *P. copri* can use both fibre and protein: - when it degrades fibre, it produces beneficial SFCAs - when it degrades protein, it produces BCAAs	Associated with vegan diets[2]. One study suggested a Mediterranean diet may provide a greater cardioprotective benefit if the microbiome does not contain *P. copri.* [3].
Alistipes putredinis	Studies have observed higher levels in patients with colon cancer[4]. However, other studies associated a low abundance of *A. putredinis* with chronic fatigue syndrome[5], irritable bowel syndrome[6,7] and liver disease[8,9].	A vegetarian diet can reduce *A. putredinis* levels[10].
Disease-associated species		
Bilophila wadsworthia	A common inhabitant of the human gut but can become problematic at high levels. Higher levels of *B. wadsworthia* have been observed in patients with colon cancer[4] and insulin resistance[11].	Increased in omnivore compared to vegan and vegetarian diets[2]. Early research suggests high fat, low fibre diets may promote *B. wadsworthia,*[12,13,14,15].
Faecalicatena torques	Previously called *Ruminococcus torques*, this is a common inhabitant of the human gut. Higher levels of *F. torques* have been observed in patients with obesity[16], insulin resistance[11,17], gut inflammation[18] and inflammatory bowel disease[19].	Decreased in vegan, vegetarian[2] and Mediterranean[20] diets and increased in ketogenic diets[21]. Increased intake of plant protein and regular fruit consumption have been associated with reduced *F. torques*[18].
Negativibacillus spp.	*N. massiliensis* and *N. sp000435195* are less common members of the human gut microbiome. They are both trimethylamine producing microbes while *N. sp000435195* can also produce hydrogen sulphide.	Both *N. massiliensis* and *N. sp000435195* are increased in ketogenic and reduced in vegetarian and vegan diets. *N. sp000435195* was also significantly increased in paleo diets[21].
Hungatella_A MIC8772	A common member of the human gut microbiome. *H. MIC8772* is a hydrogen sulphide and BCAA producing microbe.	Increased in paleo, ketogenic and low carbohydrate diets[21].
Health-associated species		
Bifidobacterium spp.	*Bifidobacterium* species are widely used in probiotic supplements, however, following the cessation of breastfeeding they are not essential for a healthy gut microbiome. Approximately, 1 in 5 samples within the MetaXplore healthy cohort contain no detectable levels of *Bifidobacterium*.	Reduced in vegan[22], low carbohydrate[18], low FODMAP[23], ketogenic[24,25] and paleo[26] diets.
Agathobacter rectale	Previously called *Eubacterium rectale*, this is a common inhabitant of the human gut. Low levels of *A. rectale* have been reported in type-1 diabetes mellitus[27], coronary heart disease[28], liver disease[8,9], chronic fatigue syndrome[29] and increased COVID-19 severity[30].	Increased in Mediterranean[20] and decreased in ketogenic diets[24,25]. Diets rich in resistant starch have been shown to increase the abundance of *A. rectale* in obese men[31]. Increased consumption of rice has been linked to increased levels of *A. rectale*[18].
Faecalibacterium praunitzii	MetaXplore detects 10 different *F. prausnitzii* species with D and G being the most common. Low levels have been linked to obesity[15], chronic fatigue syndrome[5,28], liver disease[9], inflammatory bowel disease[7,19] and irritable bowel syndrome[7].	Increased in Mediterranean diet[3,20]. Studies have shown *F. prausnitzii* can grow on FOS, inulin[32] and pectin[33] while red wine consumption has also been linked to increased *F. prausnitzii*[18].
Streptococcus thermophilus	The most widely used lactate producing bacteria for fermenting cheese and yoghurt.	Decreased in Mediterranean[20], vegan[34], and ketogenic diets[21] and increased in vegetarian[8] diets. Increased levels associated with dairy intake and frequency of yoghurt consumption[18].

Microbiome feature	Health association	Diet association
Microbial markers		
Detrimental microbial markers		
Trimethylamine producing microbes	Trimethylamine is produced by gut microbes from the breakdown of choline and carnitine. It is transported to the liver where it is converted to the compound trimethylamine-n-oxide (TMAO). Higher levels of plasma TMAO are associated with systemic inflammation, especially in patients with type 2 diabetes and cardiovascular disease[35,36,37].	Animal-rich diets (ketogenic, high protein) have higher trimethylamine producing microbes compared to plant-rich diets (Mediterranean, vegan, vegetarian)[21]. When aiming to reduce plasma TMAO, limiting dietary carnitine may be effective. Rich dietary sources of carnitine include kangaroo, beef, lamb, pork, duck, and Goat's cheese[38,39].
BCAA producing microbes	BCAAs, which include valine, leucine and isoleucine, are essential amino acids. Although BCAAs are derived from the diet, they are also produced by the gut microbiome which can contribute to elevated levels of plasma BCAAs. High levels of plasma BCAAs may be associated with systemic inflammation[40] while high levels of BCAA producing microbes may be associated with insulin resistance[17].	A vegetarian diet may reduce BCAA producing microbes[41] while a Mediterranean diet may reduce plasma BCAAs[20,42].
Hydrogen sulphide producing microbes	The gas hydrogen sulphide is produced by gut microbes when they break down sulphur-containing compounds. This gas is responsible for the rotten egg smell of flatulence. Optimal hydrogen sulphide levels may be associated with intestinal barrier integrity[43,44,45].	High protein and ketogenic diets are associated with increased hydrogen sulphide producing microbes[24]. To reduce hydrogen sulphide production, limiting or avoiding dietary and supplemental cysteine may be effective[46,47,48]. Rich dietary sources of sulphur-amino acids include cod, chicken breast, eggs, ham and minced beef[49].
Beneficial microbial markers		
Oxalate consuming microbes	Oxalate is a key component of calcium oxalate kidney stones. Decreased oxalate consuming microbes may be associated with increased urinary oxalate excretion and may be reduced in patients with recurrent kidney stones[50,51].	Oxalate consuming microbes increased in vegetarian and vegan diets[21].
Lactate producing microbes	Lactate is an organic compound produced through the microbial fermentation of carbohydrates. There is uncertainty around the role of lactate producing microbes in human health due to an emerging evidence base.	Lactate producing microbes reduced in ketogenic and paleo diets[21].



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