

As we face a global metabolic disease epidemic, the investigation of more detailed and personalised interventions is becoming increasingly important. Extensive research has revealed a strong understanding of the role of the microbiome in metabolic diseases, such as:

- Cardiovascular disease
- Type 2 diabetes
- Non-alcoholic fatty liver disease (NAFLD)
- Obesity.

The webinar, <u>Managing Metabolic Health through the Gut Microbiome</u> reviewed scientific literature with a focus on evidence-based strategies to modify clinical interventions centred around the following microbial risk factors for metabolic disease:

- Trimethylamine (TMA)
- Branched Chain Amino Acids (BCAA)
- Hexa lipopolysaccharides (Hexa LPS).

Summarised below are key evidence-based interventions for each microbial risk factor.

Red meat intake drives microbial trimethylamine production		
Test	The <i>Insight</i> [™] test identifies individuals whose microbiomes have a high potential to produce trimethylamine (TMA) which the liver then converts into trimethylamine oxide (TMAO).	
Evidence	Meta-analyses have shown that high blood levels of TMAO are associated with significant increased risk of metabolic disease, including:	
	 47% increased risk of all cause mortality (Farhangi, 2020), 	
	 62% increased risk of cardiovascular events (Heianza et al, 2017), 	
	89% increased risk of diabetes (Zhuang et al, 2019), and	
	 12% increased risk of hypertension (Ge et al, 2020). 	
	Dietary carnitine drives microbial TMA production but response is highly individual (Wang et al, 2019).	
	Red meat is the richest dietary source of carnitine (Knuttel-Gustavsen and Harmeyer 2007).	
	Cruciferous vegetables contain indoles known as I3C and DIM which have been shown to inhibit the conversion of TMA to TMAO (Cashman <i>et al</i> , 1999).	
Intervention	Personalised interventions to target a high microbial potential to produce TMA include limiting red meat consumption and increasing intake of cruciferous vegetables.	

High incrobial beach production is predictive of insulin resistance		
Test	The Insight [™] test identifies individuals whose microbiomes have a high potential to produce branched chain amino acids (BCAAs).	
Evidence	Increased microbial production of BCAAs have been associated with the development of insulin resistance and type 2 Diabetes Mellitus (Wu <i>et al</i> , 2020; Pederson <i>et al</i> , 2016).	
	If the blood levels of BCAAs exceed the capacity of the muscle to utilise them it results in the accumulation of toxic compounds which ultimately leads to insulin resistance (Shou <i>et al</i> , 2019).	
	Physical activity increases the muscles capacity to utilise BCAAs and reduces the risk of insulin resistance (Shou <i>et al</i> , 2019).	
	Low fibre western style diets are associated with increased plasma BCAAs levels (Merz <i>et al</i> , 2018; Dhakan <i>et al</i> , 2019; DeFillipis <i>et al</i> , 2019).	
Intervention	Personalised interventions to target high microbial potential to produce BCAA include increasing fibre intake to prevent microbial BCAA production and increasing physical activity to increase muscle capacity to utilise BCAAs.	

High hexa LPS indicates a pro-inflammatory microbiome		
Test	The Insight [*] test identifies individuals whose microbiomes have a high potential to produce hexa lipopolysaccharides (Hexa LPS).	
Evidence	Hexa LPS are pro-inflammatory compounds produced by some species of bacteria within the Proteobacteria phylum (Di Lorenzo <i>et al</i> , 2019).	
	Blood LPS levels have been shown to be elevated in obesity, type 2 diabetes and non-alcoholic fatty liver disease and Alzheimer's disease (Cani <i>et al</i> , 2008).	
	Saturated fat increases postprandial blood LPS levels while omega 3 fatty acids decrease postprandial blood LPS levels (Lyte <i>et al</i> , 2016).	
	Increasing fibre intake protects the gut barrier which prevents LPS crossing the gut barrier and reduces inflammation. (Kopf <i>et al</i> , 2018).	
Intervention	Personalised interventions to target high microbial potential to produce hexa LPS include limiting saturated fat intake and maximising omega 3 fatty acid and fibre intake.	

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References

Cani PD, Bibiloni R, Knauf C, Waget A, Neyrinck AM, Delzenne NM, Burcelin R. **Changes in gut microbiota control metabolic** endotoxemia-induced inflammation in high-fat diet-induced obesity and diabetes in mice. *Diabetes*. 2008; 57(6):1470-81. doi: 10.2337/db07-1403.

Cashman JR, Xiong Y, Lin J, Verhagen H, van Poppel G, van Bladeren PJ, Larsen-Su S, Williams DE. In vitro and In vivo inhibition of human flavin-containing monooxygenase form 3 (FMO3) in the presence of dietary indoles. *Biochemical Pharmacology*. 1999. 58: 1047-1055.

De Filippis F, Pasolli E, Tett A, Tarallo S, Naccarati A, De Angelis M, Neviani E, Cocolin L, Gobbetti M, Segata N, Ercolini D. **Distinct genetic and functional traits of human intestinal prevotella copri strains are associated with different habitual diets.** *Cell Host Microbe*. 2019;25(3):444-453.e3. doi: 10.1016/j.chom.2019.01.004.

Dhakan DB, Maji A, Sharma AK, Saxena R, Pulikkan J, Grace T, Gomez A, Scaria J, Amato KR, Sharma VK. **The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches.** *Gigascience*. 2019;8(3):giz004. doi: 10.1093/gigascience/giz004.

Di Lorenzo F, De Castro C, Silipo A, Molinaro A. **Lipopolysaccharide structures of gram-negative populations in the gut microbiota and effects on host interactions.** *FEMS Microbiol Rev.* 2019;43(3):257-272. doi: 10.1093/femsre/fuz002.

Farhangi MA. Gut microbiota-dependent trimethylamine N-oxide and all-cause mortality: Findings from an updated systematic review and meta-analysis. *Nutrition*. 2020;78:110856. doi: 10.1016/j.nut.2020.110856.

Ge X, Zheng L, Zhuang R, Yu P, Xu Z, Liu G, Xi X, Zhou X, Fan H. **The gut microbial metabolite trimethylamine N-oxide and hypertension risk: A systematic review and dose-response meta-analysis.** *Adv Nutr.* 2020;11(1):66-76. doi: 10.1093/advances/nmz064.

Heianza Y, Ma W, Manson JE, Rexrode KM, Qi L. **Gut microbiota metabolites and risk of major adverse cardiovascular disease events and death: A systematic review and meta-analysis of prospective studies.** *J Am Heart Assoc.* 2017; 6(7):e004947. doi: 10.1161/JAHA.116.004947.

Knuttel-Gustavsen S and Harmeyer J. **The determination of L-carnitine in several food samples.** *Food chemistry.* 2007. 105: 793-804

Kopf JC, Suhr MJ, Clarke J, Eyun SI, Riethoven JM, Ramer-Tait AE, Rose DJ. **Role of whole grains versus fruits and vegetables in reducing subclinical inflammation and promoting gastrointestinal health in individuals affected by overweight and obesity: a randomized controlled trial.** *Nutr J.* **2018;17(1):72. doi: 10.1186/s12937-018-0381-7.**

Lyte JM, Gabler NK, Hollis JH. **Postprandial serum endotoxin in healthy humans is modulated by dietary fat in a randomized, controlled, cross-over study.** *Lipids Health Dis.* 2016;15(1):186. doi: 10.1186/s12944-016-0357-6.

Merz B, Frommherz L, Rist MJ, Kulling SE, Bub A, Watzl B. **Dietary pattern and plasma BCAA-variations in healthy men and women-results from the KarMeN Study.** *Nutrients*. 2018;10(5):623. doi: 10.3390/nu10050623.

Pedersen HK, Gudmundsdottir V, Nielsen HB, Hyotylainen T, Nielsen T, Jensen BA, Forslund K, Hildebrand F, Prifti E, Falony G, Le Chatelier E, Levenez F, Doré J, Mattila I, Plichta DR, Pöhö P, Hellgren LI, Arumugam M, Sunagawa S, Vieira-Silva S, Jørgensen T, Holm JB, Trošt K; MetaHIT Consortium, Kristiansen K, Brix S, Raes J, Wang J, Hansen T, Bork P, Brunak S, Oresic M, Ehrlich SD, Pedersen O. **Human gut microbes impact host serum metabolome and insulin sensitivity.** *Nature*. 2016;535(7612):376-81. doi: 10.1038/nature18646.

Shou J, Chen PJ, Xiao WH. **The effects of BCAAs on insulin resistance in athletes.** *J Nutr Sci Vitaminol (Tokyo).* 2019;65(5):383-389. doi: 10.3177/jnsv.65.383.

Wang Z, Bergeron N, Levison BS, Li XS, Chiu S, Jia X, Koeth RA, Li L, Wu Y, Tang WHW, Krauss RM, Hazen SL. **Impact of** chronic dietary red meat, white meat, or non-meat protein on trimethylamine N-oxide metabolism and renal excretion in healthy men and women. *Eur Heart J.* 2019;40(7):583-594. doi: 10.1093/eurheartj/ehy799.

Wu H, Tremaroli V, Schmidt C, Lundqvist A, Olsson LM, Krämer M, Gummesson A, Perkins R, Bergström G, Bäckhed F. **The gut microbiota in prediabetes and diabetes: A population-based cross-sectional study.** *Cell Metab.* 2020;32(3):379-390.e3. doi: 10.1016/j.cmet.2020.06.011.

Zhuang R, Ge X, Han L, Yu P, Gong X, Meng Q, Zhang Y, Fan H, Zheng L, Liu Z, Zhou X. **Gut microbe-generated metabolite trimethylamine N-oxide and the risk of diabetes: A systematic review and dose-response meta-analysis.** *Obes Rev.* 2019;20(6):883-894. doi: 10.1111/obr.12843.