HMT OMEGA Metabolomic Profiling

At HMT, our OMEGA Suite CEMS/LCMS profiles over 900 metabolites in human plasma. A subset of these metabolites appear to be influenced or generated by the gut microbiome reflecting biodiversity and the status of the biome-host relationship.

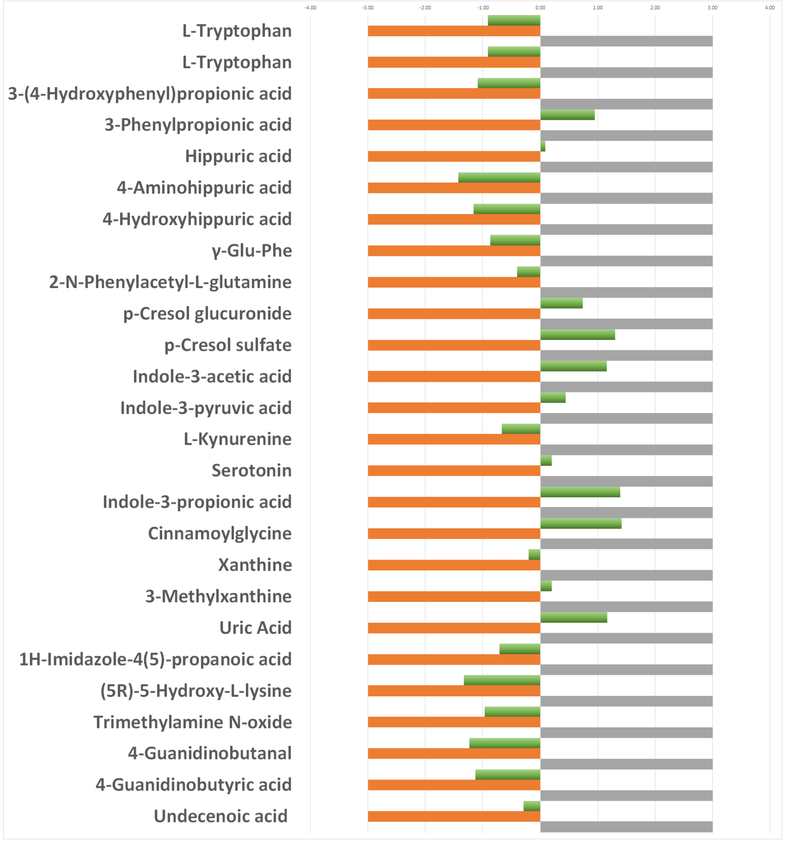
Despite the hundreds of associations between the gut microbiome and disease that have been identified over the past decade, we still do not yet understand what constitutes a 'healthy' microbiome–host relationship. It is likely that the connection between microbiome community structure and human health is highly contextual and complex, depending on diet, behavior, exposure to pathogens, history of antibiotic exposure, genetics and other factors. Understanding this interplay in a metabolomic context will enable future experimental work and the development of personalized multimodal interventions aimed at promoting wellness and treating disease (1).

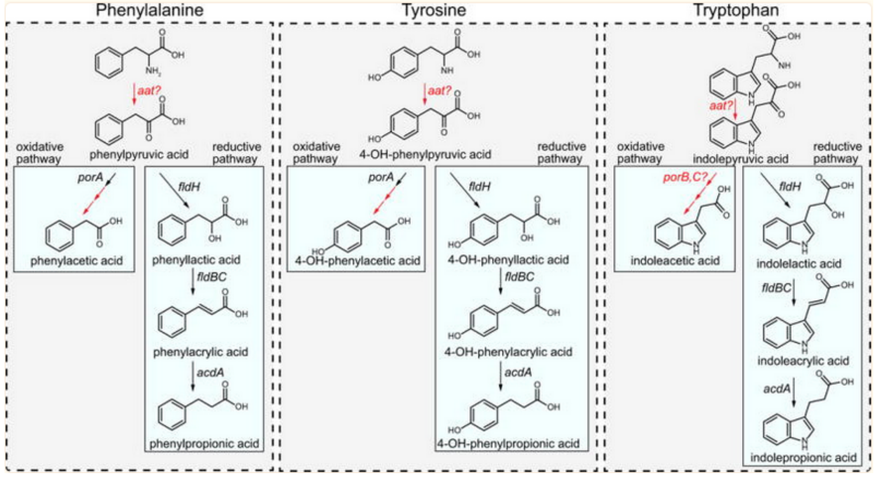
The human gut microbiota produces an unknown number of metabolites that accumulate in the bloodstream , where they can have systemic effects on the host. Among these metabolites are those from aromatic amino acid transformations. The gut symbiont *Clostridium sporogenes* generates aromatic amino acid metabolites. This pathway produces twelve compounds, nine of which are known to accumulate in host plasma. All three aromatic amino acids (tryptophan, phenylalanine and tyrosine) serve as substrates for this pathway, and it involves branching and alternative reductases for specific intermediates. Phenylalanine, tyrosine and tryptophan are all metabolized through the reductive pathway by the same enzymes.Gut bacteria-driven modulation of these plasma metabolites are thought to alter host immune activation and intestinal permeability(2).

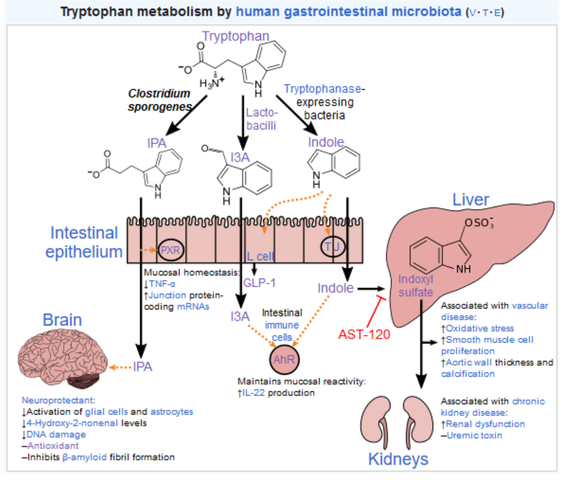
*Clostridium sporogenes*colonizes thehuman gastrointestinal tract, where it uses tryptophanto synthesize indoleand subsequently 3-indolepropionic acid(IPA)– a type of auxin (plant hormone)– which serves as a potent neuroprotective antioxidant within the human body and brain. IPA is an even more potent scavenger of hydroxyl radicals than melatonin. Similar to melatonin but unlike other antioxidants, it scavenges radicals without subsequently generating reactive and pro-oxidant intermediate compounds.*C. sporogenes* is the only species of bacteria known to synthesize 3-indolepropionic acid *in vivo* at levels which are subsequently detectable in the blood stream of the host (3).

(1)Dodd D, Spitzer MH, Van Treuren W, Merrill BD, Hryckowian AJ, Higginbottom SK, Le A, Cowan TM, Nolan GP, Fischbach MA, Sonnenburg JL. A gut bacterial pathway metabolizes aromatic amino acids into nine circulating metabolites. Nature. 2017 Nov 30;551(7682):648-652. doi: 10.1038/nature24661. Epub 2017 Nov 22. PMID: 29168502; PMCID: PMC5850949.
(2) Wilmanski, Tomasz & Rappaport, Noa & Earls, John & Magis, Andrew & Manor, Ohad & Lovejoy, Jennifer & Omenn, Gilbert & Hood, Leroy & Gibbons, Sean & Price, Nathan. (2019). Blood metabolome signature predicts gut microbiome α-diversity in health and disease. 10.1101/561209.
(3) From Wikipedia, the free encyclopedia

Biodiversity Metabolite Z- SCORE







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Profiling Metabolic Biodiversity