

Euro Herbal Medicine 2020: Importance of the gut microbiome for optimal health outcomes in metabolic diseases- Faryal Luhar- Pinnacle of Health-Naturopathic Wellness Centre

Faryal Luhar

Pinnacle of Health-Naturopathic Wellness Centre, Canada & SA

Microbes existed on earth long before humans. Single-celled bacteria living in or on the human body outnumber human cells; the American Academy of Microbiology putting human cells at 37 million, compared to 100 trillion cells of the microbiome. This co-existence between the human self and his/her intestinal microbiota is significant for optimal health; the extensive population and variety of the microflora playing an important role in one's genetic expression, immune function, body weight and composition and even mental health. Ongoing research on the human microbiome reinforces the notion that humans live in symbiosis with a diverse microbial population; how this affects health and disease is an important question. The microbiome composition varies between healthy individuals and those afflicted with numerous diseases. A flurry of scientific research has implicated these microbes as having a significant role in digestive disorders as well as the development of obesity, diabetes, cardiovascular disease and even cancer. The role of inflammation within the pathogenesis of those diseases is well recognized. Inflammatory markers and metabolic endotoxemia are increased in obesity, diabetes and insulin resistance, and cardiovascular disease and the gut is the primary point of entry for modifying these inflammatory states. The gut microbiota is being recognized as a separate endocrine organ capable of crosstalk with the host, thereby influencing health or disease. The human microbiome is now viewed to be a counterpart to the human genome. Developing a healthy gut flora begins with vaginal childbirth and breastfeeding. A healthy diet to scale back inflammation and oxidative stress, stress management and therefore the use of probiotics are other essential factors that beneficially influence the interior ecology to enhance health outcomes. The loss of microbial diversity is also linked to urbanized living and reconnecting with nature may play a significant role in health and disease outcomes.

The human intestinal tract harbours a diverse and complex microbial community which plays a central role in human health. It has been estimated that our gut contains within the range of 1000 bacterial species and 100-fold more genes than are found within the human genome. This community is usually mentioned as our hidden metabolic 'organ' thanks to their immense impact on human wellbeing, including host metabolism, physiology, nutrition and immune function. It is now apparent that our gut microbiome coevolves with us which changes to the present population can have major consequences, both beneficial and harmful, for human health. Indeed, it has been suggested that disruption of the gut microbiota (or dysbiosis) can be significant with respect to pathological intestinal conditions such as obesity and malnutrition, systematic diseases such as diabetes and chronic inflammatory diseases such as inflamma-

tory bowel disease (IBD), encompassing ulcerative colitis (UC) and Crohn's disease (CD).

The importance of the gut microbiome in human health and disease is becoming clear because of high throughput sequencing technologies (HTS) also as parallel recent nongenomics techniques developments. The aim of this review is to summarize the very significant major developments that have occurred with reference to revealing the microbial diversity of the human gut and the way this intestinal microbiota impacts on gastrointestinal (GI) disease.

In recent years a number of large funding initiatives were undertaken with a view to understanding the complexity of the human microbiome, including the gut environment. The European Metagenomics of the human intestinal tract and the US human Microbiome Project (HMP) have both, through large-scale sequencing, worked towards establishing the baseline healthy gut microbiota and how this is altered in a disease state.

We are focused on investigating the correlation between the gut microbiome and intestinal pathologies, particularly obesity and IBD. In one instance, this consortium sequenced faecal DNA from a cohort of 124 individuals, including healthy subjects and those with IBD or obesity, to establish a catalogue of nonredundant genes from the intestinal tract. This project indicated that 40% of genes were shared among the majority of individuals and therefore represented a core metagenome. It was also found that 99.1% of genes were of bacterial origin, with the majority of the remaining genes belonging to the archeal kingdom, with a relatively small number of eukaryotic and viral genes also being detected.

The large-scale sequencing for meta-analyses has produced 16S rRNA data from 690 samples from 300 subjects and across 15 body sites. The HMP also generated a catalogue of microbial genomes from the human microbiome, which consists of approximately 800 reference genomes from multiple body sites to date. Both consortia provided a hugely valuable microbial catalogue that highlights the substantial variation in microbial species and genes in the gut. In addition, together with others, this work helps our understanding of what constitutes a 'healthy' gut microbiota while revealing novel potential associations between the gut microbiota and GI diseases.

As the volume of knowledge concerning the composition and functional potential of the gut microbiota increases, the amount of diseases that are linked with alterations in our gut microbial

community has also expanded. Indeed, the various instances of such potential associations are too great to summarize during this review and thus here the main target is on associations that are the main target of greatest attention, that is, the likelihood of a link between the gut microbiota and chronic GI diseases, including irritable bowel syndrome and IBD, systemic diseases like type 2 diabetes and obesity, as well as the onset of colorectal cancer.