The colonic microbiota is likely to play an important role in health maintenance or progression to diseases. From birth, the gastrointestinal tract becomes colonised by a succession of bacterial species and the composition of the microbiota is similar to that of adults from around the time of weaning. The adult human large intestine usually contains more than 200 g of contents and is colonised by hundreds of bacterial species, reaching a total cell density of about 10^{11} bacterial cells/ml thereby outnumbering host cells about 10-fold. This complex microbial community also harbours about 100-fold more genes than the human genome. Inter-individual variation is observed for the gut microbiota but a dominant group of bacterial species has been identified in faecal samples from healthy adult individuals. Microbiota variation may be a consequence of several factors including acquisition of bacteria at birth, host immune responses, antibiotic usage and diet.

The increasing speed and decreasing cost of sequencing is now making metagenomic analysis of the whole microbial community a popular option. Metabolomics is a comprehensive and non-selective analytical chemistry approach aimed at providing a global description of all the metabolites present in a given biological sample. Although metabolic profiling has been used for decades, modern instrumentation and statistical methodology has found recent application in predicting the outcome of dietary and clinical studies. Metabolomic data provide vital information on the overall function of the gut microbiota. It is becoming increasingly important to determine which microbial-derived products are responsible for disease development and/or progression. Several diseases, including cancer, are characterised by chronic low-grade inflammation and the products of microbial metabolism have the ability to modulate these effects. Bacteria ferment dietary residues to short chain fatty acids (SCFA) eg. acetate, propionate and butyrate. In addition to being the major energy source for the colonocytes, butyrate has a role in inhibition colonic inflammation and oxidative stress. SCFA are transported across the colonic epithelium and modulate the immune response through receptors which are expressed in a wide range of host tissues. The potential impact of bacterial metabolites extends beyond gut health. Bacterial cells may also provide a source of regulatory signals that influence the maturation of the gut and the immune system. In the absence of bacteria these defense systems are likely to be weakened.

Microbial metabolites may be a key factor in regulating inflammatory and immunological responses in the host. Microbiota influences physiological functions from the maintenance of barrier homeostasis locally to the regulation of metabolism, hematopoiesis, inflammation, immunity and other functions systemically. The microbiota is also involved in the initiation, progression and dissemination of cancer both at epithelial barriers and in sterile tissues.

Recently, it has become evident that microbiota, and particularly the gut microbiota, modulates the response to cancer therapy and susceptibility to toxic side effects. Most studies in the 3-year-old scientific field investigating the modulation of cancer therapy by the microbiota have been in mice, and the translation of these experimental findings to the clinic remains a challenge. Identification of the most favorable microbiota composition in clinical situations will require a very careful analysis of the correlation of different bacterial species with clinical response. The ultimate goal is to discover a bacterial species or a combination of species that both reduces systemic toxicity and promotes anticancer therapy. Thus, targeting the microbiota in cancer and other diseases is likely to become one of the next frontiers for precision and personalized medicine.