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Role of gut microbiota in gastrointestinal health

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Abstract

The combined gut microbiota (the community of micro-organisms in the gastrointestinal tract), exerts powerful and diverse effects on physiology. It plays a role in synthesizing useful biologically active molecules, modulating immune responses, behavior, and mood. Dysbiosis, where the balance of the microbiota is disrupted, is associated with increased risk of certain diseases, conditions and autoimmune reactions. This article examines the gut microbiota and its role in the body.

Keywords: Gastrointestinal tract; Dysbiosis; colonization; gut microbiome; Escherichia coli; Bifidobacteria

Introduction

The human GI tract has a massive total surface of 250-400m^2. This enhances the processes of digestion and absorption, and functions as a surface substrate for microbial attachment and colonization [1]. Larger numbers of microbes are also found suspended and replicating within the nutrient-dense medium of the gastrointestinal secretions and partially digested food. An estimated 100 trillion micro-organisms, including bacteria, viruses, fungi and protozoa, colonize the GI tract, with microbes outnumbering human cells between three and 10 to one.

The combined microbial genome is thought to comprise over 3 million genes, which dwarfs the 23,000 genes present in the human genome [2]. This huge microbial genome is collectively known as the gut microbiome and codes for a multitude of microbial metabolites, which are released into the gut and subsequently absorbed and distributed throughout the body. The combined gut microbiota is often referred to as a 'super-organism', which, as it releases biologically active molecules, can be thought of as a 'virtual endocrine organ' that exerts powerful and diverse effects on human physiology. With an estimated collective weight of 2kg, the gut microbiota has a larger mass than the liver, which is the largest internal organ [3]. For many years it has been understood that bacteria living in the gut, such as *Escherichia coli* (E coli), perform vital functions, such as the biosynthesis of vitamin K (a key co-factor in the blood clotting cascade), but it is only in the last decade that the complex interplay between the micro-organisms of the gut microbiota and human tissues is gradually being understood. Today it is recognized that not only does the microbiota play a role in synthesizing useful biologically active molecules, it is intimately involved in modulating immune responses and also influences behavior and mood. Of particular interest is the observation that dysbiosis, where the normal balance of species within the microbiota is disrupted, is associated with increased risk of certain diseases and medical conditions, including Parkinson's disease, autism, obesity, diabetes and certain autoimmune reactions. Microbial species forming the gut microbiota is a major challenge in trying to identify the microbes that live within the human GI tract is that many cannot be grown using the standard microbiological culturing techniques [4].

However, the advent of modern genome sequencing has allowed rapid identification of micro-organisms without the need for culturing. The bacterial species of the gut have been the most heavily researched, while knowledge of the viral and fungal micro-organisms of the gut microbiota is currently sparse. The low oxygen levels present within the internal environment of the GI tract favors the growth of strict anaerobic species of bacteria, which greatly outnumber facultative anaerobes (bacteria that can switch between aerobic and anaerobic metabolism depending on oxygen concentration) and the aerobic species (bacteria that require the presence of oxygen). Two major groups of bacteria dominate the GI tract with the Firmicutes (for example, Lactobacillus and Streptococcus species) comprising around 65% of the total and the Bacteroidetes (for example, Bacteroides intestinalis) around 30%. The remaining 5% are composed of primitive bacterial groups, including the proteobacteria (for example, E coli) and the actinobacteria such as Bifidobacteria species. It is estimated that all individuals have between 500 and 1,000 species of bacteria colonizing their gut. Population studies indicate much variation between individuals, with each person having a unique profile of microbial species. It is suggested up to 35,000 species form the collective human gut bacterial microbiota, with new species continually being discovered, including many previously unknown to science.

Initial colonization after birth, babies emerge from the usually sterile environment of the uterus with minimal bacterial colonization. Unsurprisingly, those born via natural vaginal delivery have an early gut microbiota that is similar to the vagina, with groups such as Lactobacillus dominating [5]. This contrasts with babies born via caesarean section, who have early gut microbiota similar to that found on the mother's skin, with groups such as Corynebacterium and Staphylococcus species present in high numbers. The diversity of bacterial species generally increases with age, as different species are acquired from environmental contact, particularly from eating different foods and through contact with other people and animals. It is thought the acquisition of a mature microbiota resembling that of an adult is attained in the first three years of life, with country of residence also affecting the microbiotic profile.

Due to vastly different conditions, particularly in terms of pH, the populations of bacteria and other micro-organisms vary markedly in the different gut regions. Unsurprisingly, the strongly acidic conditions of the stomach limit microbial colonization and so relatively few species of bacteria are able to survive there. Notable exceptions are *Lactobacillus* species and *Helicobacter* pylori, which is a key bacterium linked to the formation of gastric ulcers. Similarly, active proteases enzymes, such as trypsin, chymotrypsin and intestinal peptidases, limit

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the growth of bacteria in the small intestine, which is dominated by Lactobacillus and Streptococcal species [6].

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