

Gut Bacteria-Friend or Foe? Their Role in Health and in Common Chronic GI Diseases

An Essay

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By

Mohammed Fahmy Soliman

M.B., B.Ch.

Ain Shams University

Supervised by

Prof. Dr. Samir Abd Al-Hamid Ghait

*Professor of Internal Medicine, Gastroenterology and Hepatology
Faculty of Medicine- Ain Shams University*

Dr. Mohamed Abd Al-Moghny Mostafa

*Assistant Professor of Internal Medicine, Gastroenterology and Hepatology
Faculty of Medicine- Ain Shams University*

Dr. Eslam Safwat Mohamed

*Lecturer of Internal Medicine, Gastroenterology and Hepatology
Faculty of Medicine- Ain Shams University*

*Faculty of Medicine
Ain Shams University*

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List of Abbreviation

- AAD** Antibiotic associated diarrhea.
- AID** Sacquired immunodeficiency syndrome.
- ALT** Alanine amino transferase.
- AMP**..... Antimicrobial peptides.
- APRIL** ...A Proliferation inducing ligand.
- ASF** Altered schaedler flora.
- ATH** Autoimmune hepatitis.
- ATP**..... Adenosine triphosphate
- B.C** Before century.
- BO** Bacterial overgrowth.
- CD**..... Crohn's disease.
- CDC** Clostridium Difficile Colitis.
- DCs** Dendritic cells.
- EHEC** Enterohemorrhagic *E. coli*.
- ELISA** Enzyme linked immunoassay.

FMF Familial mediterranean fever.

GALT Gut-associated lymphoid tissue.

GF Germ free (animal with impaired local systemic Lymphoid organs).

GIT Gastro intestinal tract.

H. pylori . Helicobacter pylori.

HIV Human immunodeficiency virus.

HPA Hypothalamic pituitary adrenal.

IBD Inflammatory bowel disease.

IBS Irritable bowel syndrome.

IGF-I Insulin-like growth factor.

IL Interleukin.

ISIndoxyl sulphate.

IVIG..... Intravenous Immunoglobulin.

LABs Lactic acid bacterias.

LMLN Local mesenteric lymph node.

LPS Lipopolysaccharide.

MHE Minimal hepatic encephalopathy.

MMC Migrating motor complex.

NOD Nucleotide-binding oligomerization domain

NAFLD .. Non alcoholic fatty liver disease.

NASH Non alcoholic steatohepatitis.

NEC Necrotizing enterocolitis.

NKT Natural killer T.

NLRS Nod like receptors.

OEI Oligofructose enriched inulin.

ORT Oral Rehydration Therapy.

PCS P-cresyl sulphate.

PMC Pseudomembranous Colitis.

PP Peyer's patches.

PSA Polysaccharide A.

ROS Reactive oxygen species.

SCFAs Short chain fatty acids.

SIBO Small bowel bacterial overgrowth.

sIgA..... Secretory IgA.

SILT..... Small intestine lymphoid tissue.

SIRS..... Systemic inflammatory response syndrome.

SPF Specific pathogenic organ.

T¹DM Type ¹ diabetes mellitus.

Th T-helper.

TLRS Toll like receptors.

TNF..... Tumour necrosis factors.

UC Ulcerative colitis.

VRE Vancomycin-resistant *Enterococci*.

WHO World health organization.

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INTRODUCTION

The human gut is the natural habitat for a large and dynamic bacterial community, but a substantial part of these bacterial populations are still to be described. However, the relevance and effect of resident bacteria on a host's physiology and pathology has been well documented. Major functions of the gut microflora include metabolic activities that result in salvage of energy and absorbable nutrients, important trophic effects on intestinal epithelia and on immune structure and function and protection of the colonised host against invasion by alien microbes (*Guarner and Malagelada, 2003*).

Gut flora might also be an essential factor in certain pathological disorders, including multisystem organ failure, colon cancer, and inflammatory bowel diseases. Nevertheless, bacteria are also useful in promotion of human health. Probiotics and prebiotics are known to have a role in prevention or treatment of some diseases (*Guarner and Malagelada, 2003*).

Many species of bacteria have evolved and adapted to live and grow in the human intestine. The intestinal habitat of an individual contains 300–500 different species of bacteria and the number of microbial cells within the gut lumen is about 10 times larger than the number of eukaryotic cells in the

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human body. The stomach and small intestine contain only a few species of bacteria adhering to the epithelia and some other bacteria in transit. The scarcity of bacteria in the upper tract seems to be because of the composition of the luminal medium (acid, bile, pancreatic secretion), which kills most ingested microorganisms, and because of the phasic propulsive motor activity towards the ileal end, which impedes stable colonisation of bacteria in the lumen (*Hamer et al.*, 1994; *Wong et al.*, 1997).

By contrast, the large intestine contains a complex and dynamic microbial ecosystem with high densities of living bacteria, which achieve concentrations of up to 10^{11} or 10^{12} cells/g of luminal contents. These concentrations are similar to those found in colonies growing under optimum conditions over the surface of a laboratory plate (*Eckburg et al.*, 1998; *Zoetendal et al.*, 1999).

A large proportion of the faecal mass consists of bacteria (around 70% of faecal solids). Several hundred grams of bacteria living within the colonic lumen affect host homeostasis. Some of these bacteria are potential pathogens and can be a source of infection and sepsis under some circumstances—for instance when the integrity of the bowel barrier is physically or functionally breached (*Hofer and*

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Speck, 2007; Honda and Takeda, 2009; Liu et al., 2007; Penders et al., 2007).

However, the constant interaction between the host and its microbial guests can infer important health benefits to the human host. Recognition of these benefits is drawing particular attention to the functional implications of microflora in host physiology (*Macpherson and Harris, 2004; ScaleSamuel et al., 2007; Xu et al., 2007).*

AIM OF STUDY

Asses the role of gut bacteria in terms of benfits and harm to human body and its impact on public health and chronic diseases of the digestive system, role of probiotics in gut health.

Compositional Diversity of the Gut Bacteria

I. PREFACE

Hippocrates has been quoted as saying “death sits in the bowels” and “bad digestion is the root of all evil” in 400 B.C. showing that the importance of the intestines in human health has been long recognized. In the past several decades, most research on the impact of bacteria in the intestinal environment has focused on gastrointestinal pathogens and the way they cause disease. However, there has recently been a considerable increase in the study of the effect that commensal microbes exert on the mammalian gut (*Hawrelak et al.*, 2004).

In this review, we revisit the current knowledge of the role played by the gastrointestinal microbiota in human health and disease. We describe the state-of-the-art techniques used to study the gastrointestinal microbiota and also present challenging questions to be addressed in the future of microbiota research (*Hawrelak et al.*, 2004).

II. OVERVIEW OF THE MAMMALIAN GUT MICROBIOTA

A. Humans as Microbial Depots

Virtually all multicellular organisms live in close association with surrounding microbes, and humans are no exception. The human body is inhabited by a vast number of bacteria, archaea, viruses, and unicellular eukaryotes. The collection of microorganisms that live in peaceful coexistence with their hosts has been referred to as the microbiota, microflora, or normal flora (*Kunz et al.*, 2009; *Morelli*, 2008; *Neish*, 2009).

The composition and roles of the bacteria that are part of this community have been intensely studied in the past few years. It is estimated that the human microbiota contains as many as 10^{14} bacterial cells, a number that is 10 times greater than the number of human cells present in our bodies. The microbiota colonizes virtually every surface of the human body that is exposed to the external environment. Microbes flourish on our skin and in the genitourinary, gastrointestinal, and respiratory tracts (*Chiller et al.*, 2001; *Hull and Chow*, 2006; *Ley et al.*, 2006; *Neish*, 2009; *Verstraelen*, 2008).

Compositional Diversity of the Gut Bacteria

By far the most heavily colonized organ is the gastrointestinal tract (GIT); the colon alone is estimated to contain over 90% of all the microbes in the human body. The human gut has an estimated surface area of a tennis court (300 m²) and as such a large organ, represents a major surface for microbial colonization. Additionally, the GIT is rich in molecules that can be used as nutrients by microbes, making it a preferred site for colonization (*Ley et al., 2007*).

B. Who Are They?

The majority of the gut microbiota is composed of strict anaerobes, which dominate the facultative anaerobes and aerobes by two to three orders of magnitude. Although there have been over 20 bacterial phyla described to date (*Schloss and Handelsman, 2004*).

The human gut microbiota is dominated by only 2 of them: the Bacteroidetes and the Firmicutes, whereas Proteobacteria, Verrucomicrobia, Actinobacteria, Fusobacteria, and Cyanobacteria are present in minor proportions (*Eckburg et al., 2005*).

Estimates of the number of bacterial species present in the human gut vary widely between different studies, but it has been generally accepted that it contains ~200 to 1,000 species (*Xu and Gordon, 2003*).