



ELSEVIER

Contents lists available at SciVerse ScienceDirect

## Best Practice & Research Clinical Gastroenterology



12

# Influence of fermented milk products, prebiotics and probiotics on microbiota composition and health



Corina Ceapa, MSc, PhD student, Scientist – Gut & Microbiology Platform<sup>a,b,1,2</sup>, Harm Wopereis, BSc, Scientist – Gut & Microbiology Platform<sup>a,b,3</sup>, Lahcene Rezaïki, PhD, R&D Milk Science Manager<sup>a,4</sup>, Michiel Kleerebezem, PhD, Professor Personal Chair<sup>b,c,d,e,5,6</sup>, Jan Knol, Professor Special Chair, Director Gut Biology & Microbiology<sup>a,b,7,8</sup>, Raish Oozeer, PhD, Gut Microbiota Team Leader – Gut & Microbiology Platform<sup>a,\*</sup>

<sup>a</sup> Danone Research – Centre for Specialized Nutrition, Bosrandweg 20, 6704 PH Wageningen, The Netherlands

<sup>b</sup> Laboratory of Microbiology, Wageningen University, Wageningen, The Netherlands

<sup>c</sup> TI Food and Nutrition, Wageningen, The Netherlands

<sup>d</sup> NIZO Food Research, Ede, The Netherlands

<sup>e</sup> Host-Microbe Interactomics, Wageningen University and Research Centre, Wageningen, The Netherlands

### A B S T R A C T

#### Keywords:

Fermented milk  
Probiotic  
Prebiotic

The gut microbiota is a highly diverse and relative stable ecosystem increasingly recognized for its impact on human health.

\* Corresponding author. Tel.: +31 317 467 861.

E-mail addresses: [corina.ceapa@wur.nl](mailto:corina.ceapa@wur.nl), [corina.ceapa@danone.com](mailto:corina.ceapa@danone.com) (C. Ceapa), [harm.wopereis@danone.com](mailto:harm.wopereis@danone.com) (H. Wopereis), [lahcene.rezaïki@danone.com](mailto:lahcene.rezaïki@danone.com) (L. Rezaïki), [michiel.kleerebezem@wur.nl](mailto:michiel.kleerebezem@wur.nl) (M. Kleerebezem), [jan.knol@wur.nl](mailto:jan.knol@wur.nl), [jan.knol@danone.com](mailto:jan.knol@danone.com) (J. Knol), [raish.oozeer@danone.com](mailto:raish.oozeer@danone.com) (R. Oozeer).

<sup>1</sup> WU Agrotechnology & Food Sciences, Laboratory of Microbiology, Dreijenplein 10, 6703HB Wageningen, The Netherlands.

<sup>2</sup> Tel.: +31 317 467 800 (direct line 871).

<sup>3</sup> Tel.: +31 317 467 800 (direct line 837).

<sup>4</sup> New address: Laboratoire Gallia, 383, rue Philippe Héron, 69654 Villefranche-sur-Saône Cedex, France. Tel.: +33 474 627 846.

<sup>5</sup> WU Animal Sciences, Host Microbe Interactomics, PO Box 338, 6700AH Wageningen, The Netherlands.

<sup>6</sup> Visitors' address: Building/Room: 122/E1206, De Elst 1, 6708WD Wageningen, The Netherlands. Tel.: +31 (0)317 483822; Secretary: +31 0317 483952; Messenger Number: 97.

<sup>7</sup> Building/Room 316/0.029, WU Agrotechnology & Food Sciences, Laboratory of Microbiology, Dreijenplein 10, 6703HB Wageningen, The Netherlands. Tel.: +31 317483107. Courier 33.

<sup>8</sup> Tel.: +31 317 467 898.

Microbiota  
Mechanisms of action  
Clinical evidence

The homeostasis of microbes and the host is also referred to as eubiosis. In contrast, deviation from the normal composition, defined as dysbiosis, is often associated with localized diseases such as inflammatory bowel disease or colonic cancer, but also with systemic diseases like metabolic syndrome and allergic diseases. Modulating a gut microbiota dysbiosis with nutritional concepts may contribute to improving health status, reducing diseases or disease symptoms or supporting already established treatments. The gut microbiota can be modulated by different nutritional concepts, varying from specific food ingredients to complex diets or by the ingestion of particular live microorganisms. To underpin the importance of bacteria in the gut, we describe molecular mechanisms involved in the crosstalk between gut bacteria and the human host, and review the impact of different nutritional concepts such as pre-, pro- and synbiotics on the gastrointestinal ecosystem and their potential health benefits. The aim of this review is to provide examples of potential nutritional concepts that target the gut microbiota to support human physiology and potentially health outcomes.

© 2013 Elsevier Ltd. All rights reserved.

---

## Introduction

### *Gut microbiota changes in health and disease*

The human body hosts roughly ten times more microorganisms than eukaryotic human cells. These organisms are part of a complex ecosystem comprising more than 3.3 million genes and corresponding to a large spectrum of enzymatic activities leading to molecular signals and metabolites that may directly influence our health and well-being. It is clear that our diet can have a significant impact on the composition and functionality of the gut microbiota and in this way can influence our health status [1–3]. As long as recorded human history goes, a strong relation was recognized between diet and our state of health [4,5].

During the last decade the human intestinal microbiota has gained increased interest for its postulated impact on human health. Its potential implication in diseases within the gastrointestinal tract and beyond has been widely reported [6–10]. Among these, especially the immune related diseases such as allergy, inflammatory bowel disease, but also metabolic and degenerative diseases, typically increasing in industrialized societies, have been associated with altered patterns in the gut microbiota [11,12].

Even though it is difficult to demonstrate causative relationships for specific commensal bacterial species in health and disease, there is emerging evidence for certain gut microbial species being involved in disease aetiology [13–17]. In addition, in many cases, reduced microbiota diversity can be correlated to compromised health, implicating this more generic microbiota-related parameter in health and disease [18–20]. The diversity, defined as the observed number of types of species and or genes in the gut ecosystem, is generally reduced in obese individuals and IBD patients when compared to healthy controls, for example [21].

Interestingly, several microbiota transplantation studies in animals have shown that the transmission of a dysbiosed gut microbiota to their healthy counterparts is sufficient to induce the disease outcome, indicating indeed a causative relationship [22]. More recently, transplantation of a human microbiota from a lean donor to obese subjects induced an improvement of insulin-resistance confirming that microbial imbalance is not solely a secondary consequence, but can contribute to the aetiology of certain diseases [23].

In-depth genetic characterization of the microbiota has recently demonstrated that human beings can be divided in three different clusters based on their microbiota composition [24]. If distinct microbiota patterns, also referred to as enterotypes, can be recognized, one can hypothesize that based on the microbiota composition different concepts can be developed to target health benefits

Download English Version:

<https://daneshyari.com/en/article/6086374>

Download Persian Version:

<https://daneshyari.com/article/6086374>

[Daneshyari.com](https://daneshyari.com)