

Introduction to the special issue “Probiotic bacteria and human gut microbiota”

Marco Ventura · Giuditta Perozzi

Published online: 21 July 2011
© Springer-Verlag 2011

Humans are colonized from birth by bacteria, which form a complex and dynamic consortium of microorganisms known as microbiota. Overall, this complex microbial community outnumbers the somatic and germ cells of the host and collectively contains significantly higher genetic variability than that of the host genome (Backhed et al. 2005). Health-promoting indigenous bacteria, known as probiotic bacteria, represent a significant proportion of the human gut microbiota, whose composition is modulated by several factors including diet (Muegge et al. 2011). Probiotic bacteria are often introduced as live dietary supplements, but they are also present as live microflora in fermented foodstuffs for human consumption. The molecular mechanisms by which probiotics beneficially affect human health include strengthening of the intestinal barrier, modulation of the immune response and antagonism of pathogens through production of antimicrobial compounds or competition for mucosal binding sites (Marco et al. 2006). A significant proportion of the commercialized probiotic bacterial species was originally selected on the basis of their technological stability (e.g., resistance and viability during food processing and storage) or by a variety of easily measurable phenotypes, such as the ability to tolerate bile salts or to survive passage through the gastro-intestinal tract. These features do not necessarily associate with capabilities to provide human health

benefits. Regulatory requirements concerning probiotic products are currently undergoing a profound transformation that will require elucidation of the mechanisms by which probiotic microorganisms beneficially influence human health. In order to achieve such fine characterization, the so-called “omics” approaches involving genomics and functional analysis represent an essential tool. In particular, probiogenomics, a recently proposed genomic discipline (Ventura et al. 2009), provides insights into the diversity and the evolution of probiotic microorganisms, thus allowing to clarify the molecular basis of their health-promoting activities. Probiogenomics also includes functional genomics, as well as investigation of microbe–microbe and host–microbe interactions that represent crucial aspects to expand our understanding of the roles of probiotics.

The study of probiotic bacteria must necessarily take into account recent advances on the microbial ecology of the human gut. Elucidation of the bacterial biodiversity encompassing such a complex ecosystem is essential to highlight the presence or absence of specific groups of microorganisms (microbial biomarkers) and their association with health/disease conditions. In-depth knowledge of the composition and functionality of the human gut microbiota can also provide molecular criteria to predict individual susceptibility to specific probiotic supplements and could be utilized as a priori criteria for successful probiotic therapy. For all these reasons, we believe that a special issue of *Genes & Nutrition* devoted to probiotic bacteria and human gut microbiota is extremely appropriate.

Two reviews within this special issue deal with the genomics of lactobacilli (Alterman et al.) and bifidobacteria (Pokusaeva et al.), which are considered the golden stars among probiotic bacteria. Probiotics are subject to

M. Ventura (✉)
Laboratory of Probiogenomics, Department of Genetics,
Biology of Microorganisms, Anthropology and Evolution,
University of Parma, Parma, Italy
e-mail: marco.ventura@unipr.it

G. Perozzi
INRAN, National Research Institute on Food and Nutrition,
Via Ardeatina 546, Rome, Italy

several stressful conditions during industrial processing as well as in nature, where a fast stress-response is essential for survival (Ventura et al. 2006). Genetic characterization of the molecular players that enable probiotic bacteria to cope with such stressful stimuli are discussed by Ruiz et al. Microbial diversity within the human intestinal community is reported by Gerritsen et al., with special focus on the contribution of the gut microbiota to the health/disease balance. The impact of bacteriophages in modulating gut microbiota, as well as on bacterial survival and thus on the efficacy of probiotic treatments is described by Ventura et al. Prebiotic approaches represent new avenues for manipulating gut microbial composition and host responses to achieve health benefits. Conterno et al. explore the possible relationships between prebiotics and modulation of bifidobacterial and lactobacilli populations in the human gut, as a potential tool for obesity prevention and treatment. The effects of probiotics on human health are further discussed by Taverniti and Guglielmetti, who review the current knowledge on interactions of gut bacteria with the mammalian immune system. Safety is a crucial pre-requisite that probiotic bacteria must possess, and safety validation of probiotics includes exclusion of pathogenic potential. A key food safety issue reviewed by Devirgiliis et al. is the potential presence of horizontally transferable antibiotic resistance genes in probiotic strains naturally present in fermented foods, which can interact with the gut microbiota through the food chain.

We wish to thank all authors who provided their manuscripts for this special issue, as well as all reviewers involved in processing the submitted articles. Overall, such a collective effort has provided a clear picture of the rapid progress occurring in the field of biology of probiotic bacteria, with special focus on the health benefits resulting from their interactions with the human host.

References

- Backhed F, Ley RE, Sonnenburg JL, Peterson DA, Gordon J (2005) Host-bacterial mutualism in the human intestine. *Science* 307:1915–1920
- Marco ML, Pavan S, Klerebezem M (2006) Towards understanding molecular modes of probiotic action. *Curr Opin Biotechnol* 17:204–210
- Muegge BD, Kuczynski J, Knights D, Clemente JC, González A, Fontana L, Henrissat B, Knight R, Gordon JI (2011) Diet drives convergence in gut microbiome functions across mammalian phylogeny and within humans. *Science* 332:970–974
- Ventura M, Canchaya C, Bernini V, Fitzgerald GF, Van Sinderen D (2006) How high G + C Gram-positive bacteria and in particular bifidobacteria cope with heat stress: protein players and regulators. *FEMS Microbiol Rev* 30:734–759
- Ventura M, O’Flaherty S, Claesson MJ, Turrone F, Klaenhammer TR, van Sinderen D, O’Toole PW (2009) Genome-scale analyses of health-promoting bacteria: probiogenomics. *Nature Microbiol Rev* 7:61–71