Journal of Probiotics & Health

ISSN: 2329-8901

Ricke, J Prob Health 2013, 1:2
Doi: 10.4172/jph.1000e102

Editorial

Open Access

Probiotic Gastrointestinal Microorganisms - Current and Future Prospects

Steven C Ricke*

Center for Food Safety and Food Science Department, University of Arkansas, Fayetteville, AR, 72704, USA

As a better understanding of the gastrointestinal tract (GIT) and the relationship between the indigenous microflora and the respective host emerges, the ability to modify that microflora is becoming more of a reality [1-7]. Consequently, commercial microbial products and the accompanying claims become more prominent in the marketplace. However, as more potential health and other benefits are identified or alluded to, more will be expected in terms of accountability of these products. The impact of administered probiotic cultures can be quite difficult to assess because of the sheer complexity of the GIT ecosystem and the numerous and fairly unaccounted for numbers of different microorganisms. This is in part due not just to the complexity of the dietary composition and the resulting production of highly varied substrates for microbial growth but the interaction with the host immune system [8]. The growth requirements of GIT bacteria in general are highly varied due to the richness of nutrients in the gut and in some ecosystems such as the rumen cross-feeding among indigenous microorganisms can be quite extensive. Cross feeding in the GIT can be manifested in fermentation pathways both as a function of the hydrolysis process where primary polymer degraders hydrolyze polymers generating soluble fragments that in turn can be further degraded by non-polymer degrading organisms that can only utilize shorter chain soluble carbohydrates and sugars [9-12]. In the final stages of fermentation the presence of hydrogen utilizing methanogens and acetogens can influence fermentation pathways and alter the makeup of short chain volatile fatty acids [11,13].

Fundamentally, as certain bacteria are isolated and subsequently characterized as possessing probiotic qualities based on *in vitro* experiments the ability to track and recover such cultures during and after *in vivo* applications will become critical for substantiating host responses attributable to the probiotic. Consequently, detection technologies will be needed that can confirm *in vivo* viability of such cultures. To accomplish this will require detection technologies that can specifically identify either single bacterial probiotic cultures or distinguish several strains within a mixed culture. This complexity leads to difficulty when attempting to differentiate specific microorganisms in the GIT by normal cultivation and isolation methods. Several limitations preclude routine cultivation of these bacteria. This is partially due to the strict anaerobic nature of some of these organisms particularly the methanogens which require special pre-reduced media via the addition of chemical reductants to remove all traces of oxygen [14-17].

Since growth requirements are often not known or at least not well established for many of these cultures it becomes imperative to explore non-culture based methods. Fortunately in the past few years there has been a virtual explosion of high-throughput sequence technological developments that have allowed a much more comprehensive assessment of GIT microbiomes and identification of primary microbial groups in these ecosystems [18]. This in combination with proteomics and metabolomics have opened the door for an integrated understanding of the quantitative impact of GIT microbial consortia and the corresponding proportional contributions of probiotic cultures introduced into these ecosystems [19,20]. The strategic goal of the Journal of Probiotics and Health is to provide a scientific forum that embraces all aspects of probiotics from a fundamental understanding of mechanisms to practical applications along with the various methods and experimental approaches required to reach this level of knowledge.

References

1. Fuller R (1989) Probiotics in man and animals. J Appl Bacteriol 66: 365-378.
2. Goldin BR, Gorbach SL (1992) Probiotics for humans. In Probiotics the scientific Basis ed. Fuller R pp. 355-376. London: Chapman and Hall, UK.
3. Nisbet D (2002) Defined competitive exclusion cultures in the prevention of enteropathogen colonisation in poultry and swine. Antonie Van Leeuwenhoek 81: 481-486.
4. Burr G, Gatlin III D, Ricke S (2005) Microbial ecology of the gastrointestinal tract of fish and the potential application of prebiotics and probiotics in finfish aquaculture. J World Aquaculture Soc 36: 425-436.
5. Callaway TR, Ricke SC (2012) Direct Fed Microbials/Prebiotics for Animals: Science and Mechanisms of Action, Springer Science, New York, USA.
6. Perumalla AVS, Hettiarachchy, NS, Ricke SC (2012) Current perspectives on Probiotics in poultry preharvest food safety. Direct Fed Microbials/Prebiotics for Animals 89-120.
7. Siragusa GR, Ricke SC (2012) Chapter 20. Probiotics as pathogen control agents for organic meat production. In: Ricke, SC, Van Loo, EJ, Johnson MG, O'Bryan CA (Eds.), Organic Meat Production and Processing. Wiley Scientific/IFT, New York, USA.
8. Patterson JA (2012) The commensal microbiota. In Direct Fed Microbials/Prebiotics for Animals: Science and Mechanisms of Action. T.R. Callaway and S.C. Ricke (Eds.), Springer Science, New York, 3-11.
9. Ricke SC, Martin SA, Nisbet DJ (1996) Ecology, metabolism, and genetics of ruminal selenomonads. Crit Rev Microbiol 22: 27-56.
10. Weimer PJ (1992) Cellulose degradation by ruminal microorganisms. Crit Revs Biotechnol 12: 189-223.
11. Wolin MJ, Miller TL (1983) Interactions of microbial populations in cellulose fermentation. Fed Proc 42: 109-113.
12. Flint HJ, Duncan SH, Scott KP, Louis P (2007) Interactions and competition within the microbial community of the human colon: links between diet and health. Environ Microbiol 9: 1101-1111.
13. Boccazzi P, Patterson JA (2011) Using hydrogen limited anaerobic continuous culture to isolate low hydrogen threshold ruminal acetogenic bacteria. Agric Food Anal Bacteriol 1: 33-44.
14. Balch WE, Fox GE, Magrum LJ, Woese CR, Wolfe RS (1979) Methanogens: reevaluation of a unique biological group. Microbiol Rev 43: 260-296.
15. Balch WE, Wolfe RS (1976) New approach to the cultivation of methanogenic bacteria: 2-mercaptoethanesulfonic acid (HS-CoM)-dependent growth of Methanobacterium ruminantium in a pressureized atmosphere. Appl Environ Microbiol 32: 781-791.

***Corresponding author:** Steven C Ricke, Center for Food Safety and Food Science Department, University of Arkansas, 2650 North Young Avenue, Fayetteville, AR 72704-5690, USA, Tel: (479) 575-4678; Fax: (479) 575-6936; E-mail: sricke@uark.edu

Received May 06, 2013; **Accepted** May 07, 2013; **Published** May 13, 2013

Citation: Ricke SC (2013) Probiotic Gastrointestinal Microorganisms - Current and Future Prospects. J Prob Health 1: e102. doi:10.4172/jph.1000e102

16. Bryant MP (1972) Commentary on the Hungate technique for culture of anaerobic bacteria. Am J Clin Nutr 25: 1324-1328.
17. Ricke SC, Pillai SD (1999) Conventional and molecular methods for understanding probiotic bacteria functionality in gastrointestinal tracts. Crit Rev Microbiol 25: 19-38.
18. Kwon YM, Ricke SC (2011) High-Throughput Next Generation Sequencing: Methods and Applications. Methods in Molecular Microbiology 733 - Springer Protocols, Humana Press, New York, USA.
19. De Keersmaecker SC, Thijs IM, Vanderleyden J, Marchal K (2006) Integration of omics data: how well does it work for bacteria? Mol Microbiol 62: 1239-1250.
20. Park SH, Hanning I, Perrota A, Bench BJ, Alm E, et al. (2013) Modifying the gastrointestinal ecology in alternatively raised poultry and the potential for molecular and metabolomic assessment. Poult Sci 92: 546-561.