Probiotic Gastrointestinal Microorganisms - Current and Future Prospects

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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 particularly 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

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