

Special issue: The Human Intestinal Microbiota

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The human intestine is home to very large numbers of micro-organisms, with bacterial cells exceeding 10^{11} ml⁻¹ in the colon. The impact that this complex community has upon the host is increasingly recognized not only as a potential source of infection but also as a contributor to nutrient and energy supply, gut development and immune homeostasis. Recent evidence has indicated links between gut microbial activities and the aetiology of disorders such as inflammatory bowel disease and colorectal cancer, and also conditions such as heart disease, diabetes and metabolic syndrome. All this makes a special issue of *Microbiology* devoted to the human intestinal microbiota timely. This topic necessarily depends heavily on microbial ecology, a discipline that has not always been natural territory for the journal, notwithstanding some important contributions to human intestinal microbiology (e.g. Macfarlane *et al.*, 1986). Molecular methodologies have done much to accelerate recent progress by allowing the rapid analysis of this complex community, culminating in the application of in-depth metagenomics (Qin *et al.*, 2010). Nevertheless, the commonly perceived wisdom that most human intestinal bacteria are inherently unculturable may not be entirely accurate, since many of the most common intestinal bacteria found by molecular methods in faecal samples correspond to cultured species of obligate anaerobes (Walker *et al.*, 2010). The future, in which the journal can play an important role, will surely require a combination of genomics, microbial ecology and studies of single cultured organisms.

Four reviews in this special issue deal with the role of the human gut microbiota in irritable bowel syndrome (Salonen *et al.*, 2010), the metabolism of dietary phytochemicals (Kemperman *et al.*, 2010), interactions of probiotic bacteria with the gut mucosa (Sánchez *et al.*, 2010) and the impact of long-term antibiotic use on the gut microbial community (Jernberg *et al.*, 2010). The impact of a new antibiotic upon the intestinal community of *Clostridium difficile*-infected patients is reported by Tannock *et al.* (2010). The diversity of the intestinal community is explored by Roger & McCartney (2010) and by Roger *et al.* (2010) in infants, by Rajilić-Stojanović *et al.*

(2010) in an *in vitro* intestinal model system and by Contreras *et al.* (2010) in the oral cavity of Amerindians. Interactions of intestinal bacteria with the mammalian immune system are considered by Knoch *et al.* (2010) for the microbial community of the caeca of interleukin-10 gene-deficient mice, and by Donato *et al.* (2010) for a probiotic strain of *Lactobacillus rhamnosus*. Probiotic and prebiotic approaches are of course aimed at manipulating the intestinal microbial community and host responses to achieve health benefits. Penders *et al.* (2010) explore the possible relationship between lactobacilli and allergy, while O'Flaherty & Klaenhammer (2010) report on a *Lactobacillus acidophilus* surface protein, and MacKenzie *et al.* (2010) on mucin-binding proteins of *Lactobacillus reuteri*. Bifidobacteria are most commonly chosen as targets for prebiotics, and understanding of this group is advanced by a comparative genomic study by Bottacini *et al.* (2010). An informative study using an *in vitro* fermenter model (Zihler *et al.*, 2010), however, illustrates the difficulty of predicting the impact of prebiotics and probiotics on complex microbial communities. Finally, one paper focuses on an obligate anaerobe, examining the capsular polysaccharides of *Bacteroides fragilis* (Patrick *et al.*, 2010).

We would like to thank all the authors who responded to the call for manuscripts to be considered for this special issue, and to all the reviewers and editors involved in processing these papers. This has resulted in a valuable and varied set of contributions that provide a snapshot of the rapid progress taking place in this topical field. We firmly believe that *Microbiology* can make an increasingly valuable contribution to this field in the future by publishing quality papers on the ecology, physiology and genetics of micro-organisms that inhabit the human intestinal tract.

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