



Technical Note no. 1

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The gut microbiota – the good, the bad and the ugly!

The gastrointestinal tract (GIT) is home to a rich and complex microbial community. It is (currently) estimated that the GIT hosts up to 10^{12} microbial cells per g of luminal contents and is comprised of 1000 to 5000 species (Human Microbiome Project Consortium, 2012). A further level of complexity arises from the diverse microbiota composition observed between individuals, including between farmed animals obtained from the same source, housed together in the same environment and fed the same diets (Stanley et al., 2013). However, interestingly, despite the significant taxonomic variation, it seems that the metabolic function of the microbiota is largely conserved across individuals (Oakley et al., 2014).

At the somewhat superficial phylum level, *Firmicutes* (e.g. *Clostridium*, *Lactobacillus* and *Bacillus*) and *Bacteroidetes* (e.g. *Bacteroides*) dominate GIT habitats, with lesser contributions from *Proteobacteria* (e.g. *Escherichia*) and *Actinobacteria* (e.g. *Bifidobacterium*) (Honda and Littman, 2012). In pigs, heavier individuals were reported to have higher faecal *Firmicutes* and greater *Firmicutes*:*Bacteroidetes* ratios compared to lighter weight pigs (at the same age) (Han et al., 2017). Similarly, studies in both mice and humans have shown positive relationships between (faecal) *Firmicutes* abundance and nutrient absorption, whereas an increase in *Bacteroidetes* was associated with a decrease in nutrient absorption, leading to suggestions that the *Firmicutes*:*Bacteroidetes* ratio may be important for optimum physiology and nutrient acquisition (Oakley et al., 2014; please refer to paper for various supporting references). Of course, how representative/relevant faecal samples are in different species remains a topical issue.

Again, rather superficially, a particular bacterial group or genera may typically be regarded as 'favourable' (e.g. *Lactobacillus*) or 'unfavourable' (e.g. *Clostridia*). However, some *Clostridia* are strongly correlated with good growth performance and some lactobacilli with poorer performance (Stanley et al., 2014; Torok et al., 2011). Moreover, different strains of the same bacterial species have been reported to have differing effects. For example, one strain of *Lactobacillus reuteri* (L6798) resulted in weight gain, whereas another (ATCC PTA 4659) caused weight loss in mice (Fak and Backhed, 2012). It is possible that the (negative) effects of individual lactobacilli and clostridia may be related to deconjugation of bile salts (Ranjitkara et al., 2016) and/or their specific GIT colonisation site(s) (DeLange and Wijtten, 2010).

In broiler chickens, the genus *Faecalibacterium* (*Firmicutes* phylum), and in particular *F. prausnitzii*, were repeatedly associated with good performance, as were *Bacteroides fragilis*, *Lachnospiraceae* and members of the *Ruminococcus* genus (Stanley et al., 2016). Perhaps unsurprisingly, these bacteria are also of particular interest in human gastroenterology. Reduced *F. prausnitzii* abundance is associated with a high risk of postoperative recurrence of Crohn's disease (Sokol et al., 2008) and *B. fragilis* strains, specifically their polysaccharide A (PSA) surface component, enhance T cell development and differentiation (Caballero and Pamer, 2015). In contrast, some *B. fragilis* strains that express an enterotoxin can cause diarrhoea and have been associated with intestinal cancer progression (Caballero and Pamer, 2015). These latter observations again underline the importance of appreciating bacterial differences even to strain level. Both *Lachnospiraceae* and *Ruminococcus* are members of the *Firmicutes* phylum and major short-chain fatty acid (SCFA) producers (Sagheddu et al., 2016). SCFAs are recognised as important contributors to intestinal health (Broom, 2015).

Conclusion

Initially, the scale, complexity and seemingly inherent variability of the GIT microbiota can make this a daunting research topic, particularly when attempting to draw meaningful conclusions or make recommendations. However, consistent observations in various species have indicated that greater numbers of *Firmicutes* (or ratio to *Bacteroidetes*) enhance energy/nutrient acquisition, which should be advantageous for fast growing animals (but perhaps less so for sedentary humans!). Similarly, a number of studies have identified certain bacterial families (e.g. *Lachnospiraceae*), genera (e.g. *Faecalibacterium* and *Ruminococcus*) or species (e.g. *F. prausnitzii* and *B. fragilis*) that may be of particular interest. Therefore, these parameters could be worthwhile components for specific evaluation, or as targets, in animal studies investigating the benefit of microbiota modulation and/or seeking to promote growth performance. However, differences in bacterial attributes, even to strain level, and the continual unravelling of this important research area will further challenge our existing (mis)conceptions and lead to improved understanding and more successful interventions.

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