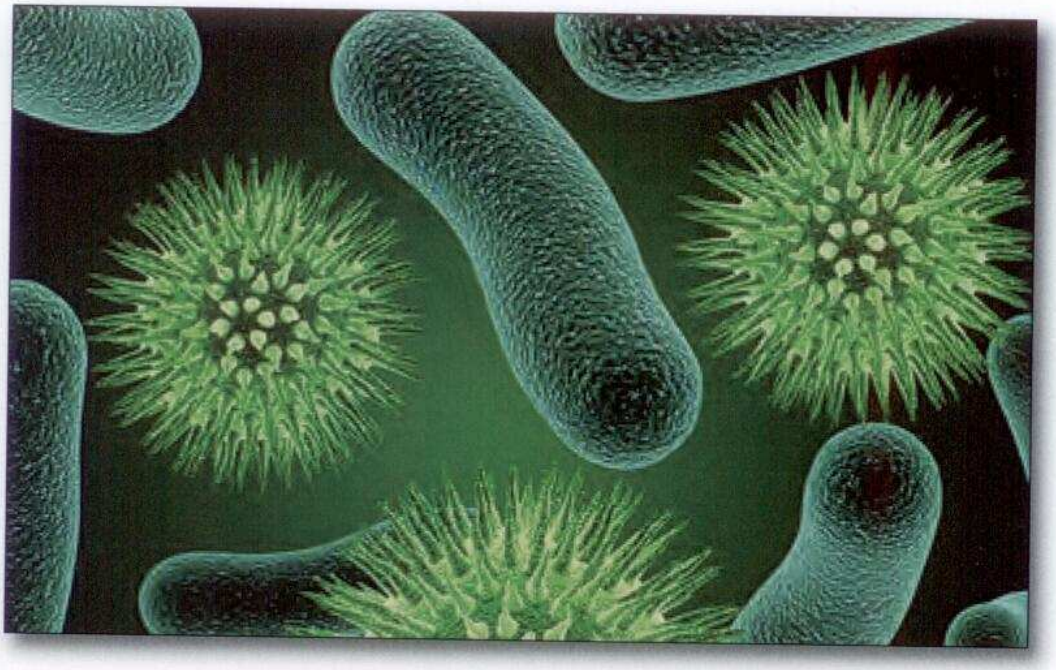
Rowett-INRA 2014
Gut Microbiology: from sequence to function

16 - 19 June 2014

Aberdeen Exhibition and
Conference Centre, Scotland, UK



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Effects of addition of *prevotella* sp. On antioxidant production in the presence of flaxseed

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Flaxseed is the richest source of the lignanas secoisolariciresinol diglucoside (SDG) and secoisolariciresinol (SECO). Both compounds are strong antioxidants, and are metabolized by rumen bacteria into enterodiol and enterolactone which have an even greater antioxidant capacity. Some species of ruminal *Prevotella* sp. has been suggested to play a role in lignan metabolism (Schogor et al., 2014; Plos One, In press). However, it is unknown if addition of *Prevotella* sp. to ruminal fluid would increase enterolignan production. To test this hypothesis *in vitro* incubations were conducted on two separate occasions and in triplicate, with the addition of 200 mg of ground flaxseed, 8 ml of Hobson's M2 broth, 1 ml of rumen fluid and 1 ml of each pure culture of Prevotella sp (*P. ruminicola*, *P. brevis*, *P. albensis*, *P. bryantii* and a proportional mix of all species). Hungate tubes were incubated for 0, 6, 24 and 48 h at 39°C. The 16S rDNA was quantified using QPCR for 0, 24 and 48 h incubations, using an iCycler iQ thermal cycler; results were analysed using the iCycler iQ detection system software (Bio-Rad UK Ltd) (Huws et al., 2013; Lett Appli. Microbiol. 56:186-196). QPCR 16S rDNA concentration data did not show differences among treatments for any of the treatments. Higher initial concentrations of the studied species of *Prevotella* added on ruminal fluid did not ensure higher conversion of lignans from flax. This data suggests that addition of *Prevotella* sp. to the ruminant diet would not increase the production of enterodiol and enterolactone.

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How to assess gastrointestinal health benefits of prebiotics: focusing on 'microbial fermentation and metabolism'

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Available evidence on the toxicological, bioactive and nutritional properties of gut microbial metabolites has been evaluated in support of a more integrated view of how prebiotics might influence host health throughout life. The literature search targeted available evidence for the physiological and nutritional effects of metabolites like short chain fatty acids (SCFA), the possible toxicity of other metabolites and determined normal concentration ranges. We assessed the biological relevance of more holistic approaches including faecal water toxicity assays, metabolomics and the limitations of fecal measurements (production v absorption rates). Existing literature indicates that protein fermentation metabolites (phenol, p-cresol, indole, ammonia), typically considered as potentially harmful, occur at concentration ranges in the colon such that no toxic effects should be produced. The various end products of saccharolytic fermentation, SCFA, may have very different effects on colonic health, host physiology, lipoprotein metabolism and appetite. Measuring SCFA concentrations in faeces however is insufficient to assess the dynamic processes of their nutrikinetics. Existing literature is limited on the usefulness of genotoxicity measures of fecal water as indicators of cancer risk. In conclusion, at present there is insufficient evidence to use changes in faecal bacterial metabolite concentrations as markers of prebiotic effectiveness. Integration of results from metabolomics and metagenomics holds promise for understanding the health implications of prebiotic microbiome modulation but currently suitable tools for data integration and interpretation are lacking. Similarly, studies measuring metabolite flux in different body compartments to provide a more accurate picture of their nutrikinetics would be useful.