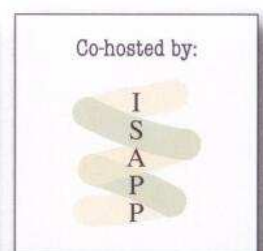
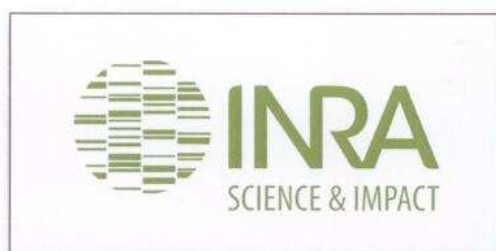
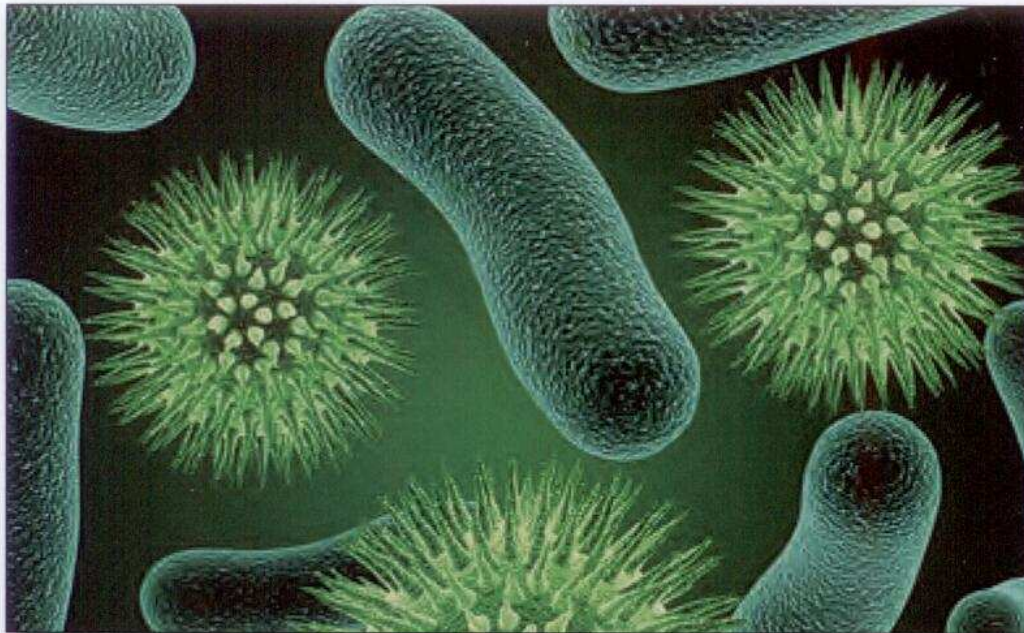


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Gut Microbiology: from sequence to function

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Probiotic potential of a BSH positive, high GABA producing strain, *Lactobacillus brevis* FEM 1874, isolated from traditional "wild" Alpine cheese.

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Probiotics appear to play a role in brain development and function through the gut:brain axis. Gamma-aminobutyric acid (GABA), a major inhibitory neurotransmitter, also works in the periphery through immuno-modulation and regulating adipocyte function. Importantly, GABA is produced in high amounts by certain lactobacilli. In *Lactobacillus brevis* ATCC 367, GABA production depends on the activity of two genes *gadA* and *gadB*, as well as the presence of an antiporter *gadC*. *gadA* and *gadC* are expressed as an operon, whereas *gadR* represents a transcriptional regulator. We isolated *Lactobacillus brevis* FEM 1874 from a traditional "wild" fermented Alpine cheese and studied its putative probiotic traits. This novel strain is bile salt hydrolase (BSH) positive, carries *gad* genes and is able to produce high levels of GABA in pure culture compared to over 100 other local cheese isolates. We studied GABA production under different conditions by modifying pH and L-glutamate concentrations, as well as assessing the strains survival and ability to produce GABA within the human gut microbiota using anaerobic, pH controlled faecal batch cultures. *L. brevis* FEM 1874 growth on different prebiotic substrates was also measured as was its ability to survive upper gut acid and bile challenge. *L. brevis* FEM 1874 appears to be a strain with promising probiotic traits and may prove an important adjuvant in production of functional dairy products. However, further investigations are needed to assess whether this strain produces GABA within the gastrointestinal tract and how this may impact on host immune system and possibly brain function.

Inulin regulates the production of protein fermentation end products in vitro using pH controlled batch cultures of human faeces

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The end products of microbial amino acid (AA) fermentation include compounds considered potentially harmful to human health. In the presence of fermentable carbohydrate however, colonic AA fermentation is switched off. We measured the profile of AA catabolites generated during human faecal fermentation of two different meat products (100% prime freshly ground beef or mechanically rendered and frozen beef, MRM, 60%) using pH (6.8) controlled batch cultures in the presence or absence of inulin. As expected bifidobacteria increased in number in batch cultures containing inulin (1% w/v). Surprisingly, bifidobacterial numbers also increased upon fermentation of prime beef, especially at the early stages of fermentation, but not in the MRM. No other significant differences were observed upon enumeration of total bacteria, *Bacteroides*, *Clostridium perfringens/histolyticum*, *Blautia coccoides/Eubacterium rectale*, lactobacilli/enterococci, *Faecalibacterium prausnitzii*, or *Desulfovibrio* spp. as determined by fluorescent *in situ* hybridization using 16S rRNA targeted oligonucleotide probes. GC-MS showed that inulin supplementation modulated both SCFA profiles and reduced the concentrations of phenol, indol and p-cresol in meat fermentations. Currently HPLC chromatography for tandem mass spectrometry is being applied to measure how metabolite profiles (targeting AA, AA derivatives, trimethylamine, gamma-amino butyric acid, tryptophan, serotonin and dopamine pathways), changed during meat fermentation in and presence and absence of inulin. These data will help us understand how prebiotics modulate production of toxic metabolites during colonic meat/protein fermentation, and also may give novel insight into the production of metabolites now recognised to play an important role in the gut:brain axis.