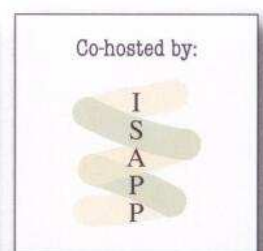
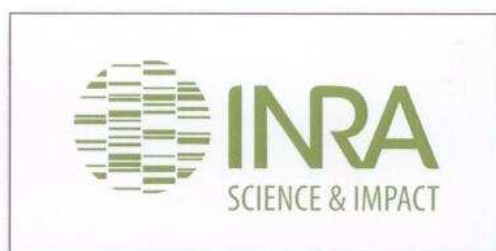
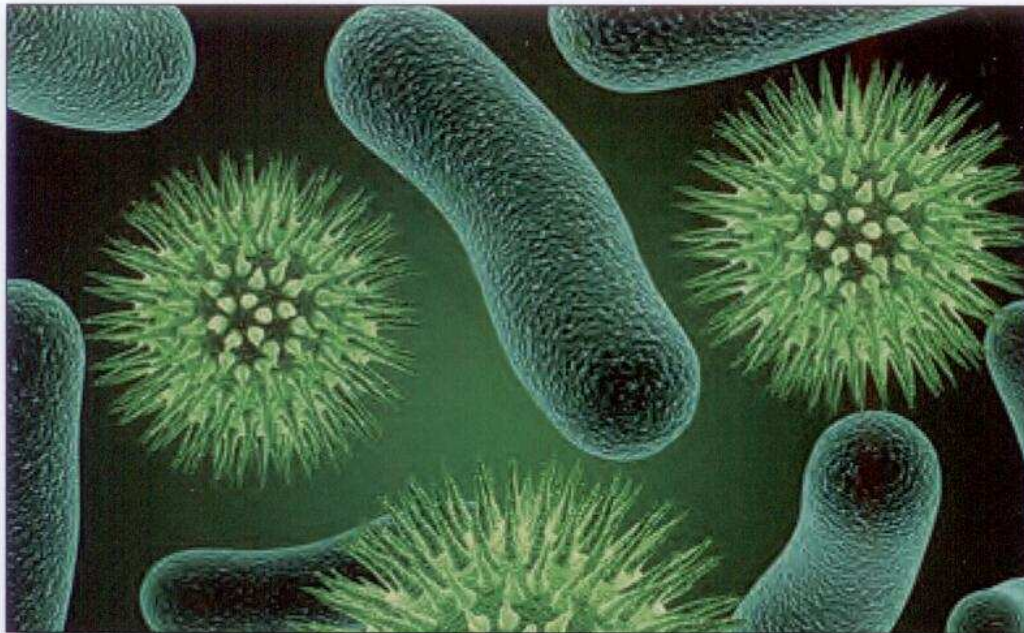


Rowett-INRA 2014

Gut Microbiology: from sequence to function

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The bees knees – and guts, and microbiota, and pollen: functional foods based on apiculture for bees and humans.

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Honey-bees are essential pollinators in agriculture and the fact that they are under threat in Europe from colony collapse disorder may have considerable economic import. Recently, lactobacilli and bifidobacteria isolated from the bee honey-crop suggest a possible role for probiotics/prebiotics in honey-bee health, and moreover, that strains of these bacteria isolated from honey may also be considered part of the traditional human diet. We enumerated putative lactic acid bacteria at 7×10^4 CFU per g honey and 5×10^5 from bee-pollen and isolated 45 lactic acid bacteria for assessment of probiotic potential both for human and/or honey-bee use. Using quantitative PCR we enumerated bifidobacteria within the gut microbiota of bees from 4 hives mean 4.5×10^7 copies/g and examined the honey-bee gut microbiota using the fingerprinting technique, ARISA and are currently characterising the composition of the bee gut microbiota through 454-pyrosequencing. Further, we assessed the prebiotic potential of honeybee-collected pollen, an apiculture product with an ancient history of use as a traditional medicine throughout the world, rich in polyphenols and complex carbohydrates. The main beneficial effects are associated with its purported antioxidant and antimicrobial potential but little scientific data exists on its mode of action. We tested the impact of honey-bee collected pollen on the human gut microbiota using simulated digestion followed by pH-controlled anaerobic faecal batch cultures. Our initial results confirm that the non-digestible fraction of honeybee-collected pollen leads to a significant increase in faecal bifidobacteria and suggest pollen may modulate the human gut microbiota in a positive manner.

Are reds better than blonds? Impact of raspberries high and low in anthocyanins on the composition and metabolic output of the human gut microbiota in vitro

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Red fruit are associated with health and red in fruit is usually produced by anthocyanins. Fruit polyphenols have been linked to various health effects and the majority of these compounds require microbial transformation in the gut for bioavailability and often bioactivity. Raspberries can be red fruit (with anthocyanins) or yellow fruit (without anthocyanins) and offer the possibility to study how the presence of anthocyanins within a given whole plant food matrix impacts on the gut microbiome, and conversely, how the gut microbiota metabolises anthocyanins in a form commonly encountered in the human diet. We monitored the fermentation of 5 varieties of raspberry *Rubus ideaus* (red and yellow) using a pH controlled faecal batch cultures (5 replicates) following simulated gastric and small intestinal digestion. FISH and qPCR showed that raspberries in general, regardless of anthocyanin content, gave a significant increase in bifidobacteria but had little effect on total bacteria, *Bacteroides*, *Blautia coccoides*/*Eubacterium rectale* group, *Faecalibacterium prausnitzii*, lactobacilli/enterococci, *Clostridium perfringens*/*histolyticum* group or enterobacteria. Targeted metabolomics for polyphenols using UPLC-MS and SCFA measured by GC-MS showed that in all raspberry fermentations SCFA concentrations increased significantly, and allowed us to follow the microbial metabolism of anthocyanins and other polyphenols, particularly the ellagitannins, over the course of the fermentation. These studies shed new light on the metabolic fate of raspberry polyphenols in the presence of the human gut microbiota, and on their capability to mediate a prebiotic type modulation of the human gut microbiota regardless of their colour.