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Gut Microbiology: from sequence to function

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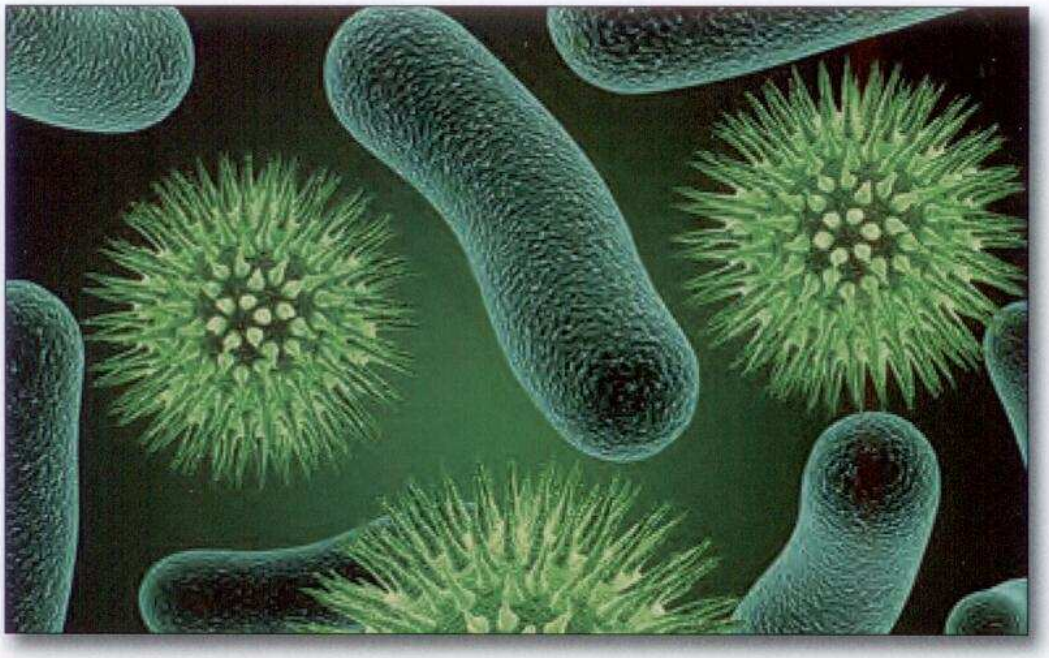

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Genome sequence of *Bacillus sp* isolated from breast tissue

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The Human Microbiome project has provided a better understanding of the bacteria that colonize the human body. However a potential microbiome in breast tissue has not been reported, even though bacteria are found in human milk, with some species originating from the gut. To explore this idea, we performed culture and 16S rRNA sequencing on breast tissue samples from 43 women undergoing different breast surgeries and discovered a diverse community in all samples, even though none of these women had any signs or symptoms of breast infection. One organism of interest was *Bacillus sp*, detected by both molecular and culture techniques and found only in women with breast cancer and not from healthy women undergoing breast reductions. To garner an understanding of the function of this organism in breast tissue we sequenced its genome using paired end reads on the Illumina platform. Gene assembly was performed using Velvet and analysis performed using RAST and JSpecies. This isolate was shown to be closely related to *B. cereus* ATCC 14579 and two clinical *B. cereus* isolates. Genome annotation showed the presence of a pathogenicity island and ability to produce multiple toxins, some of which have carcinogenic potential. A comparison with the non-clinical ATCC 14579 strain showed the presence of genes involved in antibiotic resistance and fatty acid metabolism, unique to this breast tissue isolate. Further studies will be done to examine what role this organism, as well as the others detected, may play in modulating health and disease in the mammary glands.

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Therapeutic effects of dietary iron on ulcerative colitis patient health using an *in vitro* batch culture models

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There is much interest in the relationship between diet, human health and disorders such as inflammatory bowel diseases, particularly Ulcerative Colitis (UC). Sulphate reducing bacteria (SRB) are the most prominent colonic bacteria linked with UC because of their toxic fermentation end product, hydrogen sulphide (H_2S). A possible approach to reducing the harmful impact of dietary sulphate could be trapping such gas before it is able to exert its harmful effects on the epithelium. Iron, zinc and bismuth have been indicated effectively for this purpose when used in in vitro batch culture (healthy faecal inocula). However, such experiments from UC patients have not been reported. So, triplicate 48-batch cultures were carried out (0.5 mM iron citrate; 0.5 mM sodium sulphate; 0.5 mM sodium citrate; mix of 0.5 mM iron citrate and sodium sulphate; and no additions). All cultures were sampled (0, 5, 10, 24, 36 and 48 h) for determination of bacterial densities (FISH), SCFA detection, H_2S levels and cytotoxicity effects. Results show that SRB and Clostridial growth are favoured by sulphate, whereas Bifidobacterial and Eubacterial groups were disfavoured. Sulphate shifted SCFA production away from beneficial butyrate towards acetate - inclusion of iron with the sulphate partly reversed this shift in the SCFA profile. H_2S increased by sulphate addition, but this increase was not observed when iron was also included. Culture supernatants from the sulphate-supplemented cultures displayed significant cytotoxicity against HT-29 cells reflecting the raised H_2S content. However, the supernatants from cultures containing sulphate plus iron showed no marked cytotoxic effects.