Results: The current study showed that vaginal *L. rhamnosus* HN001 and *L. acidophilus* La-14 levels were significantly increased. In particular, *L. acidophilus* significantly increased on days 14 and 21 while *L. rhamnosus* significantly increased on days 7 and 21.
Conclusions: The consumption of *L. acidophilus* La-14, *L. rhamnosus* HN001 in combination with bovine lactoferrin leads to vaginal detection, even 1 week after consumption was stopped. The results from the current clinical trial show for the first time the capability of orally consumed selected lactobacilli strains to reach and colonize the vagina. Our study highlight the potential use of a mixture of *L. acidophilus* La-14, *L. rhamnosus* HN001 in combination with bovine lactoferrin for the management of urogenital tract infections and contribute to vaginal health.

In Silico Approaches for the Identification of Putative Bacteriocin Gene Clusters from the Human Microbiota

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Objective: The gut is a rich source of antimicrobial-producers with the potential to alter intestinal communities in a beneficial way for human health. With this in mind, several studies have used traditional culture-dependent approaches to successfully identify bacteriocin-producers from the mammalian gut. Here we present alternative *in silico* techniques with the aim to detect potential bacteriocin-encoding gene clusters using genomic and metagenomic data from the gastrointestinal subset of the human microbiome project and compare the density of these clusters to other body sites.
Methods: *In silico* strategies to identify novel gene clusters are now also being utilised to take advantage of the vast amount of data currently being generated by next generation sequencing technologies, usually in the form of a BLAST-based approach. This poster presents alternative approaches including a Profile Hidden Markov Model pipeline and other freely-available genomic tools, such as BAGEL3, that can be applied to both genomic and metagenomic data.
Results: These techniques have resulted in the identification of numerous putative bacteriocin gene clusters from the human microbiota, including important members of the gastrointestinal tract microbiota that have not previously been associated with bacteriocin production.
Conclusions: These *in silico* techniques, and others, are a powerful tool for the identification novel biosynthetic gene clusters in a culture- independent method and have the potential to vastly improve our arsenal of microbiota-modulating probiotics.

Lactobacillus Brevis FEM1874 for the Development of GABA-enriched Cheese

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Probiotic microorganisms have recently been shown to impact on brain development and function through the gut:brain axis. *Lactobacillus brevis* FEM1874 isolated from Traditional Mountain cheese has been reported produce high concentrations of gamma-aminobutyric acid (GABA) and to possesses Bile Salt Hydrolysis activity *in vitro*. GABA is synthesized from glutamate which is the most common amino acid in cheese. The aim of this study was to test the ability of the strain to convert glutamate to GABA during cheese production. Twenty experimental micro-cheeses were produced using a commercial starter strain (10^7 CFU/mL) and FEM1874 as adjunct culture. Four different concentrations (10^2, 10^3, 10^4, 10^5 CFU/ mL) of FEM1874 were tested in quadruplicate. In order to follow the microbial evolution, samples of milk, curd and cheese after 20 days of ripening were enumerated in selective media. The control and experimental samples showed a similar trend, suggesting that both milk-resident and starter strains grew during ripening. However, the load of mesophilic lactobacilli in all experimental curd samples was higher than the control. The concentration of GABA and glutamic acid in cheese samples after 20 days of ripening was quantified by UHPLC-HQOMS. The amino acidic profiles showed that while the concentration of *Lb. brevis* FEM1874 in milk increased, the amount of both glutamic acid (from 284 ± 97 to 202 ± 44) and GABA (from 154 ± 48 to 83 ± 28) significantly decreased during cheese production. These results suggested that the experimental strain converted the glutamic acid to GABA, but that GABA may have subsequently been converted to succinate by GABA transaminases.

Gut Microbiota Meta-omics Charts Supporting CF Patients' Laboratory and Clinical Management

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Objective: Cystic fibrosis (CF), is a disorder affecting the exocrine glands of the respiratory, digestive and reproductive systems and there appear to be a link with the gut microbiota, including a possible association with its dysbiosis. High-throughput meta-omics-based approaches may actually assist in unveiling this complex network of symbiosis modifications. The aim of this work was to investigate the gut microbiota composition and modulation of CF patients by omic approach.
Methods: Thirty-one faecal samples from either CF patients and healthy children (HC) (age range 0-6 years) were collected at Bambino Gesù Children's Hospital. The metabolomic analyses were performed by GC-MS/SPME and1H-NMR, while metagenomic analysis was carried out by 454 pyrosequencing platform.
Results: About 200 volatile organic compounds, 150 shared between HC and CF children and 50 belonged only to CF patients were detected and quantified by GC-MS/SPME and about 20 molecules characterized with 1H-NMR.The inter-individual variability of molecules levels resulted high. The level of esters, alcohols and aldehydes were higher in CF patients. On the contrary, SCFA were higher in HC than CF. 1H-NMR analysis, showed lower levels of amino acids and uracil in CF patients. Metagenomic indicated *Firmicutes* as most abundant phyla in HC, while the abundance of *Bacteroidetes* and Proteobacteria varied according to the sample analyzed.
Consclusions: By this integrated approach it's possible to generate personalized "omics" charts that can be used for the monitoring of the nutritional state of the child and for the evaluation of gut absorption in CF patients, hence provide a translational medicine tool.

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