Whole grain-rich diet reduces body weight and systemic low-grade inflammation without inducing major changes of the gut microbiome: a randomised cross-over trial

Objective To investigate whether a whole grain diet alters the gut microbiome and insulin sensitivity, as well as biomarkers of metabolic health and gut functionality. Design 60 Danish adults at risk of developing metabolic syndrome were included in a randomised cross-over trial with two 8-week dietary intervention periods comprising whole grain diet and refined grain diet, separated by a washout period of ≥6 weeks. The response to the interventions on the gut microbiome composition and insulin sensitivity as well on measures of glucose and lipid metabolism, gut functionality, inflammatory markers, anthropometry and urine metabolomics were assessed. Results 50 participants completed both periods with a whole grain intake of 179±50 g/day and 13±10 g/day in the whole grain and refined grain period, respectively. Compliance was confirmed by a difference in plasma alkylresorcinols (p<0.0001). Compared with refined grain, whole grain did not significantly alter glucose homeostasis and did not induce major changes in the faecal microbiome. Also, breath hydrogen levels, plasma short-chain fatty acids, intestinal integrity and intestinal transit time were not affected. The whole grain diet did, however, compared with the refined grain diet, decrease body weight (p=0.0001), serum inflammatory markers, interleukin (IL)-6 (p=0.009) and C-reactive protein (p=0.003). The reduction in body weight was consistent with a reduction in energy intake, and IL-6 reduction was associated with the amount of whole grain consumed, in particular with intake of rye. Conclusion Compared with refined grain diet, whole grain diet did not alter insulin sensitivity and gut microbiome but reduced body weight and systemic low-grade inflammation.
Aberrant intestinal microbiota in individuals with prediabetes

Aims/hypothesis: Individuals with type 2 diabetes have aberrant intestinal microbiota. However, recent studies suggest that metformin alters the composition and functional potential of gut microbiota, thereby interfering with the diabetes-related microbial signatures. We tested whether specific gut microbiota profiles are associated with prediabetes (defined as fasting plasma glucose of 6.1–7.0 mmol/l or HbA1C of 42–48 mmol/mol [6.0–6.5%]) and a range of clinical biomarkers of poor metabolic health. Methods: In the present case–control study, we analysed the gut microbiota of 134 Danish adults with prediabetes, overweight, insulin resistance, dyslipidaemia and low-grade inflammation and 134 age- and sex-matched individuals with normal glucose regulation. Results: We found that five bacterial genera and 36 operational taxonomic units (OTUs) were differentially abundant between individuals with prediabetes and those with normal glucose regulation. At the genus level, the abundance of Clostridium was decreased (mean log2 fold change −0.64 (SEM 0.23), \( p_{\text{adj}} = 0.0497 \)), whereas the abundances of Dorea, [Ruminococcus], Sutterella and Streptococcus were increased (mean log2 fold change 0.51 (SEM 0.12), \( p_{\text{adj}} = 5 \times 10^{-4} \); 0.51 (SEM 0.11), \( p_{\text{adj}} = 1 \times 10^{-4} \); 0.60 (SEM 0.21), \( p_{\text{adj}} = 0.0497 \); and 0.92 (SEM 0.21), \( p_{\text{adj}} = 4 \times 10^{-4} \), respectively). The two OTUs that differed the most were a member of the order Clostridiales (OTU 146564) and Akkermansia muciniphila, which both displayed lower abundance among individuals with prediabetes (mean log2 fold change −1.74 (SEM 0.41), \( p_{\text{adj}} = 2 \times 10^{-3} \) and −1.65 (SEM 0.34), \( p_{\text{adj}} = 4 \times 10^{-4} \), respectively). Faecal transfer from donors with prediabetes or screen-detected, drug-naive type 2 diabetes to germfree Swiss Webster or conventional C57BL/6 J mice did not induce impaired glucose regulation in recipient mice. Conclusions/interpretation: Collectively, our data show that individuals with prediabetes have aberrant intestinal microbiota characterised by a decreased abundance of the genus Clostridium and the mucin-degrading bacterium A. muciniphila. Our findings are comparable to observations in overt chronic diseases characterised by low-grade inflammation.
A low-gluten diet induces changes in the intestinal microbiome of healthy Danish adults

Adherence to a low-gluten diet has become increasingly common in parts of the general population. However, the effects of reducing gluten-rich food items including wheat, barley and rye cereals in healthy adults are unclear. Here, we undertook a randomised, controlled, cross-over trial involving 60 middle-aged Danish adults without known disorders with two 8-week interventions comparing a low-gluten diet (2 g gluten per day) and a high-gluten diet (18 g gluten per day), separated by a washout period of at least six weeks with habitual diet (12 g gluten per day). We find that, in comparison with a high-gluten diet, a low-gluten diet induces moderate changes in the intestinal microbiome, reduces fasting and postprandial hydrogen exhalation, and leads to improvements in self-reported bloating. These observations suggest that most of the effects of a low-gluten diet in non-coeliac adults may be driven by qualitative changes in dietary fibres.
Amoxicillin modulates the intestinal microbiota and impairs the development of oral tolerance to whey – a study in Brown Norway rats

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Source-ID: 159948742
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2018

Antibiotic treatment of rat dams affects bacterial colonization and causes decreased weight gain in pups

Intergenerational transmission of bacteria during birth initiates the natural successional development of the intestinal microbiota in mammals. This process can be disrupted by antibiotic exposure, potentially affecting early-life microbiota-dependent metabolic programming. In the present study, we specifically investigate the metabolic consequences of exposing neonate Wistar rats to an antibiotic-perturbed low-diversity microbiota from birth until weaning, without exposing the pups directly to antibiotics. Here, we show that pups born from both amoxicillin and vancomycin-treated dams gain less weight than controls. This was concordant with lower feed intake as well as increased colonic expression of the PYY satiety hormone gene at weaning. The weight difference persists into adulthood even though the initial differences in gut microbiota subsided. Our results demonstrate that early-life exposure to an antibiotic-perturbed low-diversity microbiota is sufficient to cause changes in body weight persisting into adulthood.

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DOIs: 10.1038/s42003-018-0140-5
Differential bacterial capture and transport preferences facilitate co-growth on dietary xylan in the human gut

Metabolism of dietary glycans is pivotal in shaping the human gut microbiota. However, the mechanisms that promote competition for glycans among gut commensals remain unclear. Roseburia intestinalis, an abundant butyrate-producing Firmicute, is a key degrader of the major dietary fibre xylan. Despite the association of this taxon to a healthy microbiota, insight is lacking into its glycan utilization machinery. Here, we investigate the apparatus that confers R. intestinalis growth on different xylans. R. intestinalis displays a large cell-attached modular xylanase that promotes multivalent and dynamic association to xylan via four xylan-binding modules. This xylanase operates in concert with an ATP-binding cassette transporter to mediate breakdown and selective internalization of xylan fragments. The transport protein of R. intestinalis prefers oligomers of 4-5 xylosyl units, whereas the counterpart from a model xylan-degrading Bacteroides commensal targets larger ligands. Although R. intestinalis and the Bacteroides competitor co-grew in a mixed culture on xylan, R. intestinalis dominated on the preferred transport substrate xylotetraose. These findings highlight the differentiation of capture and transport preferences as a possible strategy to facilitate co-growth on abundant dietary fibres and may offer a unique route to manipulate the microbiota based on glycan transport preferences in therapeutic interventions to boost distinct taxa.

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Organisations: Department of Biotechnology and Biomedicine, National Food Institute, Protein Glycoscience and Biotechnology, Regulatory Genomics, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology, Norwegian University of Science and Technology, Norwegian University of Life Sciences, Technical University of Denmark
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 7.82 SJR 7.139 SNIP 3.095
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Source: FindIt
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Faecalibacterium gut colonization is accelerated by presence of older

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Pages: 65-66
Impact of the gut microbiota on chemical risk assessment

It is well established that the multitude of microbes residing in the human intestine play a key role for health. Recently, it has become apparent that ingested chemicals affect the composition of the human gut microbiota. Additionally, the gut microbes affect the uptake and metabolism of chemicals in multiple ways. Here, we outline the current knowledge about the complex interplay between gut microbes, ingested xenobiotics and toxicological effects. We propose that the intestinal microbiota plays a key role in chemical toxicity, which is typically overlooked in existing approaches for risk assessment. This means that factors such as animal provider, batch/litter differences, and co-caging may significantly influence the outcome of toxicity evaluations based on rodent experiments. The effect of ingested chemicals may be significantly influenced by the gut microbiota of individual experimental animals. This should be considered in toxicological risk assessment.

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Contributors: Licht, T. R., Bahl, M. I.
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10.1016/j.cotox.2018.09.004
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Integrative data analysis of genotype, microbiome and metabolomics for prediction of response to diet for improved metabolic health

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Integrative_data_analysis_of_genotype_abstract.pdf
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2018
Microbial tryptophan catabolites in health and disease
Accumulating evidence implicates metabolites produced by gut microbes as crucial mediators of diet-induced host-microbial cross-talk. Here, we review emerging data suggesting that microbial tryptophan catabolites resulting from proteolysis are influencing host health. These metabolites are suggested to activate the immune system through binding to the aryl hydrocarbon receptor (AHR), enhance the intestinal epithelial barrier, stimulate gastrointestinal motility, as well as secretion of gut hormones, exert anti-inflammatory, antioxidative or toxic effects in systemic circulation, and putatively modulate gut microbial composition. Tryptophan catabolites thus affect various physiological processes and may contribute to intestinal and systemic homeostasis in health and disease.

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Contributors: Roager, H. M., Licht, T. R.
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BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 12.41 SJR 6.582 SNIP 2.912
Web of Science (2017): Impact factor 12.353
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 11.8 SJR 6.414 SNIP 2.855
Web of Science (2016): Impact factor 12.124
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 11.23 SJR 6.287 SNIP 2.86
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 10.77 SJR 6.41 SNIP 3.034
Web of Science (2014): Impact factor 11.47
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 9.85 SJR 6.206 SNIP 2.797
Web of Science (2013): Impact factor 10.742
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Scopus rating (2012): CiteScore 8.32 SJR 5.866 SNIP 2.829
Web of Science (2012): Impact factor 10.015
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Scopus rating (2011): CiteScore 4.44 SJR 3.137 SNIP 1.825
Web of Science (2011): Impact factor 7.396
ISI indexed (2011): ISI indexed no
Web of Science (2010): Impact factor
Web of Science (2010): Indexed yes
Perturbation of neonatal microbial gut community by peripartum antibiotics leads to decreased weight gain in Wistar rats

Background and purpose: Inter-generational transmission of bacteria during birth initiates the natural successional development of the child’s intestinal microbiota. This process can be disrupted by antibiotic exposure, potentially affecting early life microbiota-dependent metabolic programing. In the present study, we specifically investigated the metabolic consequences of exposing neonate Wistar rats to an antibiotic perturbed low-diversity microbiota from birth until weaning, without exposing the offspring directly to antibiotics.

Methods: Pregnant rats were administered daily with therapeutic doses of amoxicillin, vancomycin or water by oral gavage from 8 days before delivery until weaning (n=10-12/group). Weight gain in pups as well as successional development of intestinal microbiota, serum bile acids and colonic gene expression profiles related to appetite regulation was assessed at two, four and fourteen weeks of age by 16S rRNA gene sequencing, LC-MS and qPCR.

Results: Offspring from both amoxicillin and vancomycin treated dams gained less weight than controls, which persisted into adulthood even though initial differences in gut microbiota had subsided. This was concordant with lower feed intake as well as colonic up-regulation of the satiety hormone PYY gene, down-regulation of the bile acid receptor TGR5 gene and decreased levels of caecal SCFA levels in 4 weeks old offspring. Results are consistent with recent studies substantiating a microbial impact on early-life metabolic programing and provide new knowledge concerning potential risks associated with antibiotic administration during pregnancy.

Conclusion: We demonstrate that early-life exposure to an antibiotic perturbed low-diversity microbiota is sufficient to cause changes in body weight persisting into adulthood.

Administration of two probiotic strains during early childhood does not affect the endogenous gut microbiota composition despite probiotic proliferation

Probiotics are increasingly applied to prevent and treat a range of infectious, immune related and gastrointestinal diseases. Despite this, the mechanisms behind the putative effects of probiotics are poorly understood. One of the suggested modes of probiotic action is modulation of the endogenous gut microbiota, however probiotic intervention studies in adults have failed to show significant effects on gut microbiota composition. The gut microbiota of young children is known to be unstable and more responsive to external factors than that of adults. Therefore, potential effects of probiotic intervention on gut microbiota may be easier detectable in early life. We thus investigated the effects of a 6 month placebo-controlled probiotic intervention with Bifidobacterium animalis subsp. lactis (BB-12®) and Lactobacillus rhamnosus (LGG®) on gut microbiota composition and diversity in more than 200 Danish infants (N = 290 enrolled; N = 201 all samples analyzed), as assessed by 16S rRNA amplicon sequencing. Further, we evaluated probiotic presence and proliferation by use of specific quantitative polymerase chain reaction (qPCR). Probiotic administration did not significantly alter gut microbiota community structure or diversity as compared to placebo. The probiotic strains were detected in 91.3% of the fecal samples from children receiving probiotics and in 1% of the placebo treated children. Baseline gut microbiota was not found to predict the ability of probiotics to establish in the gut after the 6 month intervention. Within the probiotics group, proliferation of the strains LGG® and BB-12® in the gut was detected in 44.7% and 83.5% of the participants, respectively. A sub-analysis of the gut microbiota including only individuals with detected growth of the probiotics LGG® or BB-12® and comparing these to placebo revealed no differences in community structure or diversity. Six months of probiotic administration during early life did not change gut microbiota community structure or diversity, despite active proliferation of the administered probiotic strains. Therefore, alteration of the healthy infant gut
microbiota is not likely to be a prominent mechanism by which these specific probiotics works to exert beneficial effects on host health. NCT02180581. Registered 30 June 2014.

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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.95 SJR 1.242 SNIP 0.953
Web of Science (2017): Impact factor 2.829
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.82 SJR 1.282 SNIP 0.993
Web of Science (2016): Impact factor 2.644
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.93 SJR 1.42 SNIP 0.994
Web of Science (2015): Impact factor 2.581
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.95 SJR 1.519 SNIP 1.069
Web of Science (2014): Impact factor 2.729
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.32 SJR 1.571 SNIP 1.179
Web of Science (2013): Impact factor 2.976
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.38 SJR 1.507 SNIP 1.146
Web of Science (2012): Impact factor 3.104
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.4 SJR 1.487 SNIP 1.125
Web of Science (2011): Impact factor 3.044
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.433 SNIP 1.034
Web of Science (2010): Impact factor 2.96
Do pesticides affect the intestinal bacterial community and does this have health implications?

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Organisations: National Food Institute, Research Group for Gut Microbiology and Immunology, Research group for Analytical Food Chemistry, Aarhus University
Effects of Gliadin consumption on the Intestinal Microbiota and Metabolic Homeostasis in Mice Fed a High-fat Diet

Dietary gluten causes severe disorders like celiac disease in gluten-intolerant humans. However, currently understanding of its impact in tolerant individuals is limited. Our objective was to test whether gliadin, one of the detrimental parts of gluten, would impact the metabolic effects of an obesogenic diet. Mice were fed either a defined high-fat diet (HFD) containing 4% gliadin (n = 20), or a gliadin-free, isocaloric HFD (n = 20) for 23 weeks. Combined analysis of several parameters including insulin resistance, histology of liver and adipose tissue, intestinal microbiota in three gut compartments, gut barrier function, gene expression, urinary metabolites and immune profiles in intestinal, lymphoid, liver and adipose tissues was performed. Mice fed the gliadin-containing HFD displayed higher glycated hemoglobin and higher insulin resistance as evaluated by the homeostasis model assessment, more hepatic lipid accumulation and smaller adipocytes than mice fed the gliadin-free HFD. This was accompanied by alterations in the composition and activity of the gut microbiota, gut barrier function, urine metabolome, and immune phenotypes within liver and adipose tissue. Our results reveal that gliadin disturbs the intestinal environment and affects metabolic homeostasis in obese mice, suggesting a detrimental effect of gluten intake in gluten-tolerant subjects consuming a high-fat diet.

General information

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Organisations: National Food Institute, Department of Biotechnology and Biomedicine, Disease Systems Immunology, Research Group for Gut Microbiology and Immunology, Research group for Analytical Food Chemistry, Systems Metabolic Lipidology, Copenhagen Center for Health Technology, University of Copenhagen, Technical University of Denmark, University Hospital of Schleswig-Holstein
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Web of Science (2019): Indexed yes
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.36 SJR 1.533 SNIP 1.245
Web of Science (2017): Impact factor 4.122
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.63 SJR 1.692 SNIP 1.354
Web of Science (2016): Impact factor 4.259
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 5.3 SJR 2.034 SNIP 1.597
Web of Science (2015): Impact factor 5.228
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.75 SJR 2.163 SNIP 1.554
Web of Science (2014): Impact factor 5.578
Environmental spread of microbes impacts the development of metabolic phenotypes in mice transplanted with microbial communities from humans

Microbiota transplantation to germ-free animals is a powerful method to study involvement of gut microbes in the aetiology of metabolic syndrome. Owing to large interpersonal variability in gut microbiota, studies with broad coverage of donors are needed to elucidate the establishment of human-derived microbiotas in mice, factors affecting this process and resulting impact on metabolic health. We thus transplanted faecal microbiotas from humans (16 obese and 16 controls) separately into 64 germ-free Swiss Webster mice caged in pairs within four isolators, with two isolators assigned to each phenotype, thereby allowing us to explore the extent of microbial spread between cages in a well-controlled environment. Despite high group-wise similarity between obese and control human microbiotas, transplanted mice in the four isolators developed distinct gut bacterial composition and activity, body mass gain, and insulin resistance. Spread of microbes between cages within isolators interacted with establishment of the transplanted microbiotas in mice, and contributed to the transmission of metabolic phenotypes. Our findings highlight the impact of donor variability and reveal that inter-individual spread of microbes contributes to the development of metabolic traits. This is of major importance for design of animal studies, and indicates that environmental transfer of microbes between individuals may affect host metabolic traits.

General information
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Organisations: National Food Institute, Research Group for Gut Microbiology and Immunology, Department of Systems Biology, Research group for Analytical Food Chemistry, Holbæk University Hospital, University of Copenhagen
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BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 9.5 SJR 4.813 SNIP 2.284
Web of Science (2017): Impact factor 9.52
Web of Science (2017): Indexed yes
Faecalibacterium Gut Colonization Is Accelerated by Presence of Older Siblings

Faecalibacterium prausnitzii is a highly abundant human gut microbe in healthy individuals, but it is present at reduced levels in individuals with gastrointestinal inflammatory diseases. It has therefore been suggested to constitute a marker of a healthy gut and is associated with anti-inflammatory properties. However, factors affecting the colonization of F. prausnitzii in the human gut during early life are very poorly understood. By analysis of 16S rRNA amplicon sequencing data from three separate infant study populations, we determined the colonization dynamics of Faecalibacterium and factors affecting its establishment in the gut. We found that in particular, the presence of older siblings in the family was consistently associated with Faecalibacterium gut colonization during late infancy and conclude that acquisition of Faecalibacterium is very likely to be accelerated through transfer between siblings. IMPORTANCE Faecalibacterium prausnitzii has been suggested to constitute a key marker of a healthy gut, yet the factors shaping the colonization of this highly oxygen-sensitive, non-spore-forming species in the intestinal environment remain poorly understood. Here, we provide evidence from three separate infant study populations that F. prausnitzii colonization in the gut happens during late infancy and is affected by the number of older siblings in the family. We conclude that Faecalibacterium acquisition is highly likely to be
accelerated by contact between siblings. Bearing in mind the immunoregulatory properties of F. prausnitzii and the well-established protective effects against allergic disorders related to the presence of older siblings, early colonization of this species may have profound consequences for child health.

**General information**

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- Web of Science (2019): Indexed yes
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): SJR 2.03 SNIP 0.985
- Web of Science (2017): Impact factor 3.575
- Web of Science (2017): Indexed yes
- Scopus rating (2016): CiteScore 3 SJR 1.576 SNIP 1.043
- Web of Science (2016): Impact factor
- Web of Science (2016): Indexed yes
- Scopus rating (2015): CiteScore 3.12 SJR 1.873 SNIP 0.852
- Web of Science (2015): Impact factor 2.946
- Scopus rating (2014): CiteScore 3.13 SJR 1.784 SNIP 0.9
- Web of Science (2014): Impact factor 2.82
- Scopus rating (2013): CiteScore 3.58 SJR 2.073 SNIP 0.997
- Web of Science (2013): Impact factor 3.179
- ISI indexed (2013): ISI indexed no
- Scopus rating (2012): CiteScore 3.81 SJR 2.162 SNIP 0.998
- ISI indexed (2012): ISI indexed no
- Scopus rating (2011): CiteScore 3.71 SJR 2.049 SNIP 0.931
- Web of Science (2011): Impact factor 3.604
- ISI indexed (2011): ISI indexed no
- Scopus rating (2010): SJR 2.139 SNIP 0.943
- Web of Science (2010): Indexed yes
- Scopus rating (2009): SJR 2.29 SNIP 0.948
- Web of Science (2009): Indexed yes
- Scopus rating (2008): SJR 2.672 SNIP 0.931
- Scopus rating (2007): SJR 2.479 SNIP 0.892
- Scopus rating (2006): SJR 2.698 SNIP 0.908
- Scopus rating (2005): SJR 3.076 SNIP 1.001
- Scopus rating (2004): SJR 2.704 SNIP 1.021
- Scopus rating (2003): SJR 2.689 SNIP 0.649

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Fatty acid composition and phospholipid types used in infant formulas modifies the establishment of human gut bacteria in germ-free mice

Human milk fat contains high concentrations of medium-chained fatty acids (MCFA) and triacylglycerols emulsified by a sphingomyelin-rich phospholipid membrane (milk phospholipids, MPL). Infant formula comprises mainly long-chained fatty acids (LCFA) emulsified with dairy proteins and soy lecithin (SL) lacking sphingomyelin. Sphingomyelin content and saturation level of phospholipids affect the gut lipase activity, which alters the concentrations of lipid hydrolysis products in ileum and colon, and hereby putatively affects the competitive advantage of specific gut bacteria. Thus, differences in phospholipid and FA composition may modulate the establishment of the gut microbiota. We investigated effects of fatty acid (FA) composition and emulsification (MPL vs SL) ingested during establishment of human gut microbiota in germ-free mice, and found that cecal microbiotas from mice given MCFA-rich emulsions were characterized by high relative abundances of Bacteroidaceae and Desulfovibrionaceae, while LCFA-rich emulsions caused higher abundances of Enterobacteriaceae, Erysipelotrichaceae, Coriobacteriaceae and Enterococcaceae. Consumption of SL-emulsified lipids skewed the community towards more Enterococcaceae and Enterobacteriaceae, while MPL increased Bacteroidaceae, Desulfovibrionaceae, Rikkenellaceae and Porphyromonadaceae. Intake of SL increased cecal concentrations of iso-valeric and iso-butyric acids. This suggests that fat-type and emulsifiers applied in infant formula may have distinct effects on the establishment of the gut microbiota in formula-fed infants.
First Foods and Gut Microbes

The establishment of the human gut microbiota in early life has been associated with later health and disease. During the 1st months after birth, the microbial composition in the gut is known to be affected by the mode of delivery, use of antibiotics, geographical location and type of feeding (breast/formula). Consequently, the neonatal period and early infancy has attracted much attention. However, after this first period the gut microbial composition continues to develop until the age of 3 years, and these 1st years have been designated "a window of opportunity" for microbial modulation. The beginning and end of this window is currently debated, but it likely coincides with the complementary feeding period, marking the gradual transition from milk-based infant feeding to family diet usually occurring between 6 and 24 months. Furthermore, the 'first 1000 days,' i.e., the period from conception until age 2 years, are generally recognized to be of particular importance for the healthy development of children. While dietary changes are known to affect the adult gut microbiota, there is a gap in our knowledge on how the introduction of new dietary components into the diet of infants/young children affects the gut microbiota development. This perspective paper summarizes the currently very few studies addressing the effects of complementary diet on gut microbiota, and highlights the recent finding that transition to family foods greatly impacts the development of gut microbial diversity. Further, we discuss potential impacts on child health and the need for further studies on this important topic.

General information

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Glyphosate has limited short-term effects on commensal bacterial community composition in the gut environment due to sufficient aromatic amino acid levels

Recently, concerns have been raised that residues of glyphosate-based herbicides may interfere with the homeostasis of the intestinal bacterial community and thereby affect the health of humans or animals. The biochemical pathway for aromatic amino acid synthesis (Shikimate pathway), which is specifically inhibited by glyphosate, is shared by plants and numerous bacterial species. Several in vitro studies have shown that various groups of intestinal bacteria may be differently affected by glyphosate. Here, we present results from an animal exposure trial combining deep 16S rRNA gene sequencing of the bacterial community with liquid chromatography mass spectrometry (LC-MS) based metabolic profiling of aromatic amino acids and their downstream metabolites. We found that glyphosate as well as the commercial formulation Glyfonova®450 PLUS administered at up to fifty times the established European Acceptable Daily Intake (ADI = 0.5 mg/kg body weight) had very limited effects on bacterial community composition in Sprague Dawley rats during a two-week exposure trial. The effect of glyphosate on prototrophic bacterial growth was highly dependent on the availability of aromatic amino acids, suggesting that the observed limited effect on bacterial composition was due to the presence of sufficient amounts of aromatic amino acids in the intestinal environment. A strong correlation was observed between intestinal concentrations of glyphosate and intestinal pH, which may partly be explained by an observed reduction in acetic acid produced by the gut bacteria. We conclude that sufficient intestinal levels of aromatic amino acids provided by the diet alleviates the need for bacterial synthesis of aromatic amino acids and thus prevents an antimicrobial effect of glyphosate in vivo. It is however possible that the situation is different in cases of human malnutrition or in production animals.
High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice

Background: It is well known that the microbiota of high-fat (HF) diet-induced obese mice differs from that of lean mice, but to what extent, this difference reflects the obese state or the diet is unclear. To dissociate changes in the gut microbiota associated with high HF feeding from those associated with obesity, we took advantage of the different susceptibility of C57BL/6J BomTac (BL6) and 129S6/SvEvTac (Sv129) mice to diet-induced obesity and of their different responses to inhibition of cyclooxygenase (COX) activity, where inhibition of COX activity in BL6 mice prevents HF diet-induced obesity, but in Sv129 mice accentuates obesity.

Results: Using HiSeq-based whole genome sequencing, we identified taxonomic and functional differences in the gut microbiota of the two mouse strains fed regular low-fat or HF diets with or without supplementation with the COX-inhibitor, indomethacin. HF feeding rather than obesity development led to distinct changes in the gut microbiota. We observed a robust increase in alpha diversity, gene count, abundance of genera known to be butyrate producers, and abundance of genes involved in butyrate production in Sv129 mice compared to BL6 mice fed either a LF or a HF diet. Conversely, the abundance of genes involved in propionate metabolism, associated with increased energy harvest, was higher in BL6 mice than Sv129 mice.

Conclusions: The changes in the composition of the gut microbiota were predominantly driven by high-fat feeding rather than reflecting the obese state of the mice. Differences in the abundance of butyrate and propionate producing bacteria in the gut may at least in part contribute to the observed differences in obesity propensity in Sv129 and BL6 mice.
Microbiota composition of simultaneously colonized mice housed under either a gnotobiotic isolator or individually ventilated cage regime

Germ-free rodents colonized with microbiotas of interest are used for host-microbiota investigations and for testing microbiota-targeted therapeutic candidates. Traditionally, isolators are used for housing such gnotobiotic rodents due to optimal protection from the environment, but research groups focused on the microbiome are increasingly combining or substituting isolator housing with individually ventilated cage (IVC) systems. We compared the effect of housing systems on the gut microbiota composition of germ-free mice colonized with a complex microbiota and housed in either multiple IVC cages in an IVC facility or in multiple open-top cages in an isolator during three generations and five months. No increase in bacterial diversity as assessed by 16S rRNA gene sequencing was observed in the IVC cages, despite not applying completely aseptic cage changes. The donor bacterial community was equally represented in both housing systems. Time-dependent clustering between generations was observed in both systems, but was strongest in the IVC cages. Different relative abundance of a Rikenellaceae genus contributed to separate clustering of the isolator and IVC communities. Our data suggest that complex microbiotas are protected in IVC systems, but challenges related to temporal dynamics should be addressed.

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Påvirker pesticider tarmens bakteriesamfund - og hvad kan det betyde for sundheden?

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Publication information
Journal: Miljø og sundhed
Pre-treatment microbial Prevotella-to-Bacteroides ratio, determines body fat loss success during a 6-month randomized controlled diet intervention

Based on the abundance of specific bacterial genera, the human gut microbiota can be divided into two relatively stable groups that might play a role in personalized nutrition. We studied these simplified enterotypes as prognostic markers for successful body fat loss on two different diets. A total of 62 participants with increased waist circumference were randomly assigned to receive an ad libitum New Nordic Diet (NND) high in fiber/wholegrain or an Average Danish Diet (ADD) for 26 weeks. Participants were grouped into two discrete enterotypes by their relative abundance of Prevotella spp. divided by Bacteroides spp. (P/B ratio) obtained by quantitative PCR analysis. Modifications of dietary effects of pre-treatment P/B group were examined by linear mixed models. Among individuals with high P/B the NND resulted in a 3.15 kg (95%CI 1.55; 4.76, P<0.001) larger body fat loss compared to ADD whereas no differences was observed among individuals with low P/B (0.88 kg [95% CI −0.61; 2.37, P=0.25]). Consequently, a 2.27 kg (95%CI 0.09; 4.45, P=0.041) difference in responsiveness to the diets were found between the two groups. In summary, subjects with high P/B-ratio appeared more susceptible to lose body fat on diets high in fiber and wholegrain than subjects with a low P/B-ratio.

General information

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Peer-reviewed: Unknown
Several studies have shown associations between groups of intestinal bacterial or specific ratios between bacterial groups and various disease traits. Meanwhile, little is known about interactions and associations between eukaryotic and prokaryotic microorganisms in the human gut. In this work, we set out to investigate potential associations between common single-celled parasites such as Blastocystis spp. and Dientamoeba fragilis and intestinal bacteria. Stool DNA from patients with intestinal symptoms were selected based on being Blastocystis spp.-positive (B+)/negative (B-) and D. fragilis-positive (D+)/negative (D-), and split into four groups of 21 samples (B+ D+, B+ D-, B- D+, and B- D-). Quantitative PCR targeting the six bacterial taxa Bacteroides, Prevotella, the butyrate-producing clostridial clusters IV and XIVa, the mucin-degrading Akkermansia muciniphila, and the indigenous group of Bifidobacterium was subsequently performed, and the relative abundance of these bacteria across the four groups was compared. The relative abundance of Bacteroides in B- D- samples was significantly higher compared with B+ D- and B+ D+ samples (P...
Colonic transit time is related to bacterial metabolism and mucosal turnover in the gut

Little is known about how colonic transit time relates to human colonic metabolism, and its importance for host health, although a firm stool consistency, a proxy for a long colonic transit time, has recently been positively associated with gut microbial richness. Here, we show that colonic transit time in humans, assessed using radio-opaque markers, is associated with overall gut microbial composition, diversity and metabolism. We find that a long colonic transit time associates with high microbial richness and is accompanied by a shift in colonic metabolism from carbohydrate fermentation to protein catabolism as reflected by higher urinary levels of potentially deleterious protein-derived metabolites. Additionally, shorter colonic transit time correlates with metabolites possibly reflecting increased renewal of the colonic mucosa. Together, this suggests that a high gut microbial richness does not per se imply a healthy gut microbial ecosystem and points at colonic transit time as a highly important factor to consider in microbiome and metabolomics studies.
richness. To address the relationships between colonic transit time and the gut microbial composition and metabolism, we assessed the colonic transit time of 98 subjects using radiopaque markers, and profiled their gut microbiota by 16S rRNA gene sequencing and their urine metabolome by ultra performance liquid chromatography mass spectrometry. Based on correlation analyses, we show that colonic transit time is associated with overall gut microbial composition, diversity and metabolism. A relatively prolonged colonic transit time associates with high microbial species richness and a shift in colonic metabolism from carbohydrate fermentation to protein catabolism as reflected by higher urinary levels of potentially deleterious protein-derived metabolites. Additionally, shorter colonic transit time correlates with metabolites likely reflecting increased renewal of the colonic mucosa. Together, this suggests that a high gut microbial richness does not per se imply a healthy gut microbial ecosystem and points at colonic transit time as a highly important factor to consider in microbiome and metabolomics studies.

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Organisations: National Food Institute, Research Group for Gut Microbiology and Immunology, Department of Systems Biology, Center for Biological Sequence Analysis, Functional Human Variation, Department of Bio and Health Informatics, Research group for Analytical Food Chemistry, DTU Multi Assay Core, Metagenomics, Department of Biotechnology, Copenhagen Center for Health Technology, University of Copenhagen, Bispebjerg University Hospital
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Event: Abstract from 13th NuGOweek PHENOTYPES AND PREVENTION - THE INTERPLAY OF GENES, LIFE-STYLE FACTORS AND GUT ENVIRONMENT, Copenhagen, Denmark.

Colonic transit time relates to bacterial metabolism and mucosal turnover in the human gut
Little is known about how colonic transit time relates to human colonic metabolism, and its importance for host health, although stool consistency, a proxy for colonic transit time, has recently been negatively associated with gut microbial richness. To address the relationships between colonic transit time and the gut microbial composition and metabolism, we assessed the colonic transit time of 98 subjects using radiopaque markers, and profiled their gut microbiota by 16S rRNA gene sequencingand their urine metabolome by ultra performance liquid chromatography mass spectrometry. Based on correlation analyses, we show that colonic transit time is associated with overall gutmicrobial composition, diversity and metabolism. A relatively prolonged colonic transit time associates with high microbial species richness and a shift in colonic metabolism from carbohydrate fermentation to protein catabolism as reflected by microbial metabolites in urine. This results in a number of potentially deleterious protein-derived metabolites. Additionally, longer colonic transit time correlates with metabolites likely reflecting reduced renewal of the colonic mucosa. Together, this suggests that a high gut microbial richness does not per se imply a healthy gut microbiota, and contributes to the understanding of the pathophysiology of diseases where increased transit time is a risk factor. Finally, our findings highlight the colonic transit time as an important physiological variable, which should be considered in gut microbiota and metabolomics studies.

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Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2016
Effect of administration of antibiotics peripartum to Wistar rats on bile acid profiles in offspring

Vertical transmission of the maternal microbiota is assumed to be crucial for the offspring's development. A disrupted microbiota composition leading to an altered metabolic activity of the microbiota can affect bile acid profiles, which are known to influence host metabolism. Here, we examined whether perturbation of the maternal gut microbiota during pregnancy, induced by administration of either amoxicillin or vancomycin to pregnant rats, influenced bile acid profiles in the offspring. The dams were treated with antibiotics from 8 days before the dams gave birth and continued until weaning (4 weeks later). Blood samples were collected from offspring at ages 2, 4 and 14 weeks, and from dams at the end of treatment. From these blood samples, bile acids were extracted and 22 bile acids were quantified by targeted liquid chromatography mass spectrometry. Comparing the serum bile acid profiles of antibiotic-treated rat dams with non-treated dams, we found that the antibiotic treatments significantly changed the bile acid profiles. However, no effect was seen in the offspring of the antibiotic-treated dams at any age. The bile acid profiles of the offspring did however change significantly with age, where the largest amounts of bile acids were found in the 4-weeks old pups. Future work will involve integrating the bile acid data with physiology and microbiota data of both pups and dams.

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State: Published
Organisations: National Food Institute, Research Group for Gut Microbiology and Immunology, Research group for Analytical Food Chemistry, Copenhagen Center for Health Technology, Technical University of Denmark
Pages: 48-49
Publication date: 2016

Effect of a long-term high-protein diet on survival, obesity development, and gut microbiota in mice

Female C57BL/6J mice were fed a regular low-fat diet or high-fat diets combined with either high or low protein-to-sucrose ratios during their entire lifespan to examine the long-term effects on obesity development, gut microbiota, and survival. Intake of a high-fat diet with a low protein/sucrose ratio precipitated obesity and reduced survival relative to mice fed a low-fat diet. By contrast, intake of a high-fat diet with a high protein/sucrose ratio attenuated lifelong weight gain and adipose tissue expansion, and survival was not significantly altered relative to low-fat-fed mice. Our findings support the notion that reduced survival in response to high-fat/high-sucrose feeding is linked to obesity development. Digital gene expression analyses, further validated by qPCR, demonstrated that the protein/sucrose ratio modulated global gene expression over time in liver and adipose tissue, affecting pathways related to metabolism and inflammation. Analysis of fecal bacterial DNA using the Mouse Intestinal Tract Chip revealed significant changes in the composition of the gut microbiota in relation to host age and dietary fat content, but not the protein/sucrose ratio. Accordingly, dietary fat rather than the protein/sucrose ratio or adiposity is a major driver shaping the gut microbiota, whereas the effect of a high-fat diet on survival is dependent on the protein/sucrose ratio.

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Infant Gut Microbiota Development Is Driven by Transition to Family Foods Independent of Maternal Obesity

The first years of life are paramount in establishing our endogenous gut microbiota, which is strongly affected by diet and has repeatedly been linked with obesity. However, very few studies have addressed the influence of maternal obesity on infant gut microbiota, which may occur either through vertically transmitted microbes or through the dietary habits of the family. Additionally, very little is known about the effect of diet during the complementary feeding period, which is potentially important for gut microbiota development. Here, the gut microbiotas of two different cohorts of infants, born either of a random sample of healthy mothers (n = 114), or of obese mothers (n = 113), were profiled by 16S rRNA amplicon sequencing. Gut microbiota data were compared to breastfeeding patterns and detailed individual dietary recordings to assess effects of the complementary diet. We found that maternal obesity did not influence microbial diversity or specific taxon abundances during the complementary feeding period. Across cohorts, breastfeeding duration and composition of the complementary diet were found to be the major determinants of gut microbiota development. In both cohorts, gut microbial composition and alpha diversity were thus strongly affected by introduction of family foods with high protein and fiber contents. Specifically, intake of meats, cheeses, and Danish rye bread, rich in protein and fiber, were associated with increased alpha diversity. Our results reveal that the transition from early infant feeding to family foods is a major determinant for gut microbiota development.
Infant Gut Microbiota Development Is Driven by Transition to Family Foods Independent of Maternal Obesity

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Mechanisms behind cancer risks associated with consumption of red and processed meat

General information

State: Published
Organisations: National Food Institute, Division of Risk Assessment and Nutrition, Copenhagen Center for Health Technology, Research Group for Gut Microbiology and Immunology
Number of pages: 73
Perturbation of neonatal microbial gut community by peripartum antibiotics in wistar rats lead to decreased weight gain

Cross talk between a mammalian host and its intestinal microbiota plays a role in immune mediated diseases such as allergies, asthma, type 1 diabetes, as well as in obesity and auto immune diseases. Over the past decades, a significant increase of these diseases in young children in the developed world has been documented. In Western countries the pattern of initial colonization of the gut during the first days of life has changed dramatically. Among factors potentially modulating initial colonization, the use of antibiotics is particularly important. Antibiotics are frequently administered orally to either mothers or young children to treat or prevent bacterial infections not necessarily related to the gastrointestinal system. This has adverse effects on the commensal gut microbial community, as it disrupts the intricate balance between specific bacterial groups within this ecosystem, potentially leading to dysbiosis.

We hypothesized that modulation of community composition and function induced by peripartum antibiotics affects intestinal microbial composition and general health of the offspring.

To address this, 33 pregnant Wistar rats were dosed by oral gavage with either amoxicillin (AMX), vancomycin (VAN) or water (CON) daily from 8 days before delivery until weaning of the offspring. Significant lower weight gain of the offspring of antibiotic treated dams compared to the control were observed. The antibiotic treated dams had significantly larger caecum size and higher caecal pH as well as spleen size than control animals. Offspring were dissected at different time points and significant changes in liver, spleen and epididymal fat were measured between groups. Composition of the gut microbiota, alpha diversity, caecum short chain fatty acid levels, caloric contents of faeces, bile salt levels, acute phase protein haptoglobin in blood, social and locomotive behavior as well as gene expression of tight junction proteins are currently being analyzed.
Perturbation of Neonatal Microbial Gut Community by Peripartum Antibiotics in Wistar Rats Lead to Decreased Weight Gain

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Perturbation of Neonatal Microbial Gut Community by Peripartum Antibiotics in Wistar Rats Lead to Decreased Weight Gain

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Perturbation of Neonatal Microbial Gut Community by Peripartum Antibiotics in Wistar Rats Lead to Decreased Weight Gain

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Perturbation of Neonatal Microbial Gut Community by Peripartum Antibiotics In Wistar Rats Lead to Decreased Weight Gain

General information
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Tarmmikrobiota som følsom indikator for biologisk relevante restkoncentrationer af kemiske pesticider i fødevarer eksempliceret ved glyphosat (Roundup®)

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Electronic versions:
Poster_MST_Bekæmpelsesmiddelforskningskonference_2016.pdf

A catalog of the mouse gut metagenome
We established a catalog of the mouse gut metagenome comprising ∼2.6 million nonredundant genes by sequencing DNA from fecal samples of 184 mice. To secure high microbiome diversity, we used mouse strains of diverse genetic backgrounds, from different providers, kept in different housing laboratories and fed either a low-fat or high-fat diet. Similar to the human gut microbiome, >99% of the cataloged genes are bacterial. We identified 541 metagenomic species and defined a core set of 26 metagenomic species found in 95% of the mice. The mouse gut microbiome is functionally similar to its human counterpart, with 95.2% of its Kyoto Encyclopedia of Genes and Genomes (KEGG) orthologous groups in common. However, only 4.0% of the mouse gut microbial genes were shared (95% identity, 90% coverage) with those of the human gut microbiome. This catalog provides a useful reference for future studies.

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Organisations: National Food Institute, Department of Systems Biology, Center for Biological Sequence Analysis, University of Copenhagen, Pfizer, Chinese Academy of Sciences, Chinese University of Hong Kong, National Institute for Agronomic Research, King's College London, BGI-Shenzhen, University of Gothenburg
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Web of Science (2017): Indexed yes
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Web of Science (2016): Impact factor 41.667
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BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 11.88 SJR 18.263 SNIP 5.553
Web of Science (2015): Impact factor 43.113
Web of Science (2015): Indexed yes
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Web of Science (2014): Impact factor 41.514
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BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 10.45 SJR 13.974 SNIP 5.364
Web of Science (2013): Impact factor 39.08
ISI indexed (2013): ISI indexed yes
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Scopus rating (2012): CiteScore 8.44 SJR 10.87 SNIP 4.914
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ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 8.21 SJR 11.749 SNIP 6.196
Web of Science (2011): Impact factor 23.268
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Impact factor 31.09
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 7.942 SNIP 5.603
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 6.205 SNIP 5.026
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 5.146 SNIP 4.583
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 5.875 SNIP 4.632
Scopus rating (2005): SJR 5.333 SNIP 3.831
Scopus rating (2004): SJR 4.871 SNIP 3.832
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 4.031 SNIP 2.981
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 2.918 SNIP 3.006
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.813 SNIP 2.74
Antibiotic treatment affects intestinal permeability and gut microbial composition in Wistar rats dependent on antibiotic class

Antibiotics are frequently administered orally to treat bacterial infections not necessarily related to the gastrointestinal system. This has adverse effects on the commensal gut microbial community, by disrupting the intricate balance between specific bacterial groups within this ecosystem potentially leading to dysbiosis. We hypothesized that modulation of community composition and function induced by antibiotics affects intestinal integrity depending on the antibiotic administered. To address this a total of 60 Wistar rats (n=12 per group) were dosed by oral gavage with either amoxicillin (AMX), cefataxime (CTX), vancomycin (VAN), metronidazole (MTZ), or water (CON) daily for 10-11 days. Bacterial composition, alpha diversity and cecum short chain fatty acid levels were significantly affected by AMX, CTX and VAN, and varied among antibiotic treatments. A general decrease in diversity and increase in the relative abundance of Proteobacteria was observed for all three antibiotics. Additionally, the relative abundance of Bifidobacteriaceae was increased in the CTX group and both Lactobacillaceae and Verrucomicrobiaceae were increased in the VAN group compared to controls. No changes in microbiota composition or function were observed following MTZ treatment. Permeability to 4 kDa FITC-dextran was decreased after CTX and VAN treatment and increased following MTZ treatment. Plasma haptoglobin levels were increased by both AMX and CTX but no changes in expression of host tight junction genes were found in any treatment group. Antibiotic induced changes in microbiota could be linked to intestinal permeability, although changes in permeability did not always result from major changes in microbiota and vice versa.

General information

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Web of Science (2018): Indexed yes
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Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
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Scopus rating (2015): CiteScore 3.32 SJR 1.427 SNIP 1.136
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.54 SJR 1.559 SNIP 1.148
A single exposure to a sublethal pediocin concentration initiates a resistance-associated temporal cell envelope and general stress response in *Listeria monocytogenes*

*Listeria monocytogenes* can cause the potentially fatal food-borne disease listeriosis, and the use of bacteriocin-producing lactic acid bacteria to control *L. monocytogenes* holds great promise. However, development of bacteriocin resistance is a potential challenge and the purpose of this study was to determine if exposure to sublethal concentrations of pediocin-containing *Lactobacillus plantarum* WHE 92 supernatant could prime *L. monocytogenes* for resistance. By transcriptomic analysis, we found two, 55 and 539 genes differentially expressed after 10, 60 and 180 min of exposure to *L. plantarum* WHE 92 supernatant as compared to control exposures. We observed temporal expression changes in genes regulated by the two component system LisRK and the alternative sigma factors SigB and SigL. Additionally, several genes involved in bacteriocin resistance were induced. ΔlisR, ΔsigB and ΔsigL mutants were all more resistant than wild types to *L. plantarum* WHE 92 supernatant. LisRK, SigB and SigL regulation and genes associated with resistance are involved in the temporal adaptive response to pediocin and all three regulatory systems affect pediocin resistance. Thus, a single exposure to a sublethal pediocin concentration initiates a response pointing to resistance and indicates that further research exploring the link between adaptive responses and resistance is needed.
Effect of Antibiotics on Gut Microbiota, Gut Hormones and Glucose Metabolism

The gut microbiota has been designated as an active regulator of glucose metabolism and metabolic phenotype in a number of animal and human observational studies. We evaluated the effect of removing as many bacteria as possible by antibiotics on postprandial physiology in healthy humans. Meal tests with measurements of postprandial glucose tolerance and postprandial release of insulin and gut hormones were performed before, immediately after and 6 weeks after a 4-day, broad-spectrum, per oral antibiotic cocktail (vancomycin 500 mg, gentamycin 40 mg and meropenem 500 mg once-daily) in a group of 12 lean and glucose tolerant males. Faecal samples were collected for culture-based assessment of changes in gut microbiota composition. Acute and dramatic reductions in the abundance of a representative set of gut bacteria was seen immediately following the antibiotic course, but no changes in postprandial glucose tolerance, insulin secretion or plasma lipid concentrations were found. Apart from an acute and reversible increase in peptide YY secretion, no changes were observed in postprandial gut hormone release. As evaluated by selective cultivation of gut bacteria, a broad-spectrum 4-day antibiotics course with vancomycin, gentamycin and meropenem induced shifts in gut microbiota composition that had no clinically relevant short or long-term effects on metabolic variables in healthy glucose-tolerant males. clinicaltrials.gov NCT01633762.

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State: Published
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Number of pages: 14
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Publication information
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BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
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Web of Science (2018): Indexed yes
Gliadin affects glucose homeostasis and intestinal metagenome in C57BL6 mice fed a high-fat diet

Dietary gluten and its component gliadin are well-known environmental triggers of celiac disease and important actors in type-1 diabetes, and are reported to induce alterations in the intestinal microflora. However, research on the impact of gluten on type-2 diabetes in non-celiac subjects is more limited. The aim of this study was to investigate the effect of gliadin on glucose homeostasis and intestinal ecology in the mouse.

Forty male C57BL/6 mice were fed a high-fat diet containing either 4% gliadin or no gliadin for 22 weeks. Gliadin consumption significantly increased the HbA1c level over time, with a borderline significance of higher HOMA-IR (homeostasis model assessment of insulin resistance) after 22 weeks. Sequencing of the V3 region of the bacterial 16S rRNA genes showed that gliadin altered the abundance of 81 bacterial taxa, separating the intestinal microbial profile of...
the gliadin consuming mice from the control mice in the principal coordinate analysis (PCoA) of weighted UniFrac distance. Moreover, gliadin reduced the ileal gene expression of tight junction protein 1, occludin, cadherin 1, mucin 2 and mucin 3, indicating an impaired intestinal barrier function. No difference was found in body weight gain, feed consumption or circulating cytokines (IL-1β, IL-6, IFN-γ, TNF-α and IL-10).

Our study is the first to show that gliadin as part of a defined synthetic feed exacerbates the glycaemia and alters the intestinal microbiota composition. Comprehensive analyses of metabolites, histological sections and the profile of specific immune cells are in progress to elucidate the mechanism behind the observed effects.

**General information**

*State:* Published

*Organisations:* National Food Institute, Division of Food Microbiology, Department of Systems Biology, Center for Biological Sequence Analysis, University of Copenhagen


*Number of pages:* 1

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*Peer-reviewed:* Yes


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**Gliadin Intake alters intestinal microbiota, glucose and lipid metabolism, and adipose tissue and liver immune cells**

**General information**

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*Organisations:* Center for Biological Sequence Analysis, Department of Systems Biology, Division of Food Microbiology, National Food Institute, Research Group for Gut Microbiology and Immunology, University of Copenhagen


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*BFI (2017): BFI-level 1

*Scopus rating (2017): CiteScore 5.09 SJR 3.228 SNIP 1.619

*Web of Science (2017): Impact factor 6.023

*Web of Science (2017): Indexed yes

*BFI (2016): BFI-level 1

*Scopus rating (2016): CiteScore 5.23 SJR 3.25 SNIP 1.721

*Web of Science (2016): Impact factor 6.08

*BFI (2015): BFI-level 1

*Scopus rating (2015): CiteScore 5.57 SJR 3.61 SNIP 1.933


*Web of Science (2015): Indexed yes

*BFI (2014): BFI-level 1
Having older siblings is associated with gut microbiota development during early childhood
Evidence suggests that early life infections, presence of older siblings and furred pets in the household affect the risk of developing allergic diseases through altered microbial exposure. Recently, low gut microbial diversity during infancy has also been linked with later development of allergies. We investigated whether presence of older siblings, furred pets and early life infections affected gut microbial communities at 9 and 18 months of age and whether these differences were associated with the cumulative prevalence of atopic symptoms of eczema and asthmatic bronchitis at 3 years of age. Bacterial compositions and diversity indices were determined in fecal samples collected from 114 infants in the SKOT I cohort at age 9 and 18 months by 16S rRNA gene sequencing. These were compared to the presence of older siblings, furred pets and early life infections and the cumulative prevalence of diagnosed asthmatic bronchitis and self-reported eczema at 3 years of age. The number of older siblings correlated positively with bacterial diversity (p=0.030), diversity of the phyla Firmicutes (p=0.013) and Bacteroidetes (p=0.004) and bacterial richness (p=0.006) at 18 months. Further, having older siblings was associated with increased relative abundance of several bacterial taxa at both 9 and 18 months of age. Compared to the effect of having siblings, presence of household furred pets and early life infections had less pronounced effects on the gut microbiota. Gut microbiota characteristics were not significantly associated with cumulative occurrence of eczema and asthmatic bronchitis during the first 3 years of life. Presence of older siblings is associated with increased gut microbial diversity and richness during early childhood, which could contribute to the substantiation of the hygiene hypothesis. However, no associations were found between gut microbiota and atopic symptoms of eczema and...
asthmatic bronchitis during early childhood and thus further studies are required to elucidate whether sibling-associated
gut microbial changes influence development of allergies later in childhood.

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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.95 SJR 1.242 SNIP 0.953
Web of Science (2017): Impact factor 2.829
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.82 SJR 1.282 SNIP 0.993
Web of Science (2016): Impact factor 2.644
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.93 SJR 1.42 SNIP 0.994
Web of Science (2015): Impact factor 2.581
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.95 SJR 1.519 SNIP 1.069
Web of Science (2014): Impact factor 2.729
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.32 SJR 1.571 SNIP 1.179
Web of Science (2013): Impact factor 2.976
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.38 SJR 1.507 SNIP 1.146
Web of Science (2012): Impact factor 3.104
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.4 SJR 1.487 SNIP 1.125
Web of Science (2011): Impact factor 3.044
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.433 SNIP 1.034
Web of Science (2010): Impact factor 2.96
Lipid hydrolysis products affect the composition of infant gut microbial communities in vitro.

Some lipid hydrolysis products such as medium-chained NEFA (MC-NEFA), sphingosine and monoacylglycerols (MAG) possess antibacterial activity, while others, including oleic acid, are essential for the optimal growth of Lactobacillus species. Thus, changes in the concentrations of NEFA and MAG in the distal ileum and colon can potentially selectively modulate the composition of the gut microbiota, especially in early life when lipid absorption efficacy is reduced. As medium-chained fatty acids are enriched in mothers’ milk, such effects may be highly relevant during gut colonisation. In the present study, we examined the effect of selected NEFA, MAG and sphingosine on the composition of faecal microbial communities derived from infants aged 2–5 months during a 24 h anaerobic in vitro fermentation. We tested lipid mixtures in the concentration range of 0–200 mM, either based on MC-NEFA (10 : 0 to 14 : 0 and MAG 12 : 0) or long-chained NEFA (LC-NEFA; 16 : 0 to 18 : 1 and MAG 16 : 0) with and without sphingosine, representing lipid hydrolysis products characteristic for intestinal hydrolysis of breast milk lipids. Ion Torrent sequencing of the bacterial 16S ribosomal RNA gene revealed that the relative abundance of lactic acid-producing genera, including Lactobacillus and Bifidobacterium, was generally increased in the presence of 50mM or higher concentrations of MC-NEFA. For Bifidobacterium, the same effect was also observed in the presence of a mixture containing LC-NEFA with sphingosine. On the contrary, the relative abundance of Enterobacteriaceae was significantly decreased in the presence of both lipid mixtures. Our findings suggest that the high concentration of medium-chained fatty acids in breast milk might have functional effects on the establishment of the gut microbiota in early life.
Neonatal microbial colonization in mice promotes prolonged dominance of CD11b+Gr-1+ cells and accelerated establishment of the CD4+ T cell population in the spleen

To assess the microbial influence on postnatal hematopoiesis, we examined the role of early life microbial colonization on the composition of leukocyte subsets in the neonatal spleen. A high number of CD11b+Gr-1+ splenocytes present perinatally was sustained for a longer period in conventionally colonized (CONV) mice than in mono-colonized (MC) and germfree (GF) mice, and the CD4+ T cell population established faster in CONV mice. At the day of birth, compared to GF mice, the expression of Cxcl2 was up-regulated and Arg1 down-regulated in livers of CONV mice. This coincided with lower abundance of polylobed cells in the liver of CONV mice. An earlier peak in the expression of the genes Tjp1, Cdh1, and JamA in intestinal epithelial cells of CONV mice indicated an accelerated closure of the epithelial barrier. In conclusion, we have identified an important microbiota-dependent neonatal hematopoietic event, which we suggest impacts the subsequent development of the T cell population in the murine spleen.

Obesity-associated fecal microbiota from human modulates body mass and metabolites in mice

General information
State: Published
Organisations: National Food Institute, Research Group for Gut Microbiology and Immunology, Department of Systems Biology, Holbæk University Hospital, University of Copenhagen
Older Siblings Affect Gut Microbiota Development in Early Childhood

Background: Evidence suggests that early life infections, presence of older siblings and furred pets in the household affect the risk of developing allergic diseases through altered microbial exposure. Recently, low gut microbial diversity during infancy has also been linked with later development of allergies.

Methods: We investigated whether presence of older siblings, furred pets and early life infections affected gut microbial communities at 9 and 18 months of age and whether these differences were associated with the cumulative prevalence of atopic symptoms of eczema and asthmatic bronchitis at three years of age. Bacterial compositions and diversity indices were determined in faecal samples collected from 114 infants in the SKOT cohort at age 9 and 18 months by 16S rRNA gene sequencing. These were compared to the presence of older siblings, furred pets and early life infections and the cumulative prevalence of diagnosed asthmatic bronchitis and self-reported eczema at three years of age.

Results: The number of older siblings correlated positively with bacterial diversity ($p = 0.030$), diversity of the phyla Firmicutes ($p = 0.014$) and Bacteroidetes ($p = 0.004$) and bacterial richness ($p = 0.006$) at 18 months. Further, having older siblings was associated with increased relative abundance of several bacterial taxa at both 9 and 18 months of age. Compared to the effect of having siblings, presence of household furred pets and early life infections had less pronounced effects on the gut microbiota. Gut microbiota characteristics were not significantly associated with cumulative occurrence of eczema and asthmatic bronchitis during the first three years of life.

Conclusions: Presence of older siblings is associated with increased gut microbial diversity and richness during early childhood, which could contribute to the substantiation of the hygiene hypothesis. However, no associations were found between gut microbiota and atopic symptoms of eczema and asthmatic bronchitis during early childhood and thus further studies are required to elucidate whether sibling-associated gut microbial changes influence development of allergies later in childhood.

The work has recently (July 2015) been accepted for publication in BMC Microbiology

The effect of 2 different housing systems on germ-free mice colonized with a complex gut microbiota

Translational animal models are essential prerequisites in exploring functions and causality of the microbiome in human health and disease. Animal models targeted at microbiome research can be germ-free mice inoculated either with a monoculture or with defined (gnotobiotic) or undefined bacterial communities of varying complexity. Traditionally, gnotobiotic mice are housed in isolators, which is costly both in labor and footprint. With rigorous cage handling procedures, it is possible to maintain mice germ-free in individually ventilated cages (IVCs) for shorter periods of weeks or
a few months, but there is a lack of knowledge on the stability of complex bacterial communities in IVCs. Germ-free SW mice were inoculated with a complex murine microbiota, housed in an isolator or in IVCs and bred for two generations, corresponding to a time course of 5 months. The gut microbiota was characterized by 16S ribosomal RNA sequencing, and the community structure of the different generations was compared to the inoculum to see the effect of housing and time on the relative bacterial abundances and the appearance of contaminants and their ability to change the overall community picture. The results indicate that the stability over time is as good in IVCs as in the isolator, but that both the isolator housed mice and IVC mice differ slightly from the inoculum. The possibility of keeping a complex microbiota stable over time without using strict gnotobiotic techniques is discussed. The work was funded by Taconic Biosciences and Innovation Fund Denmark. The project is a collaboration between Taconic Biosciences, University of Copenhagen and the 3G Centre (Gut, Grain and Greens).

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BFI (2019): BFI-level 1  
Web of Science (2019): Indexed yes  
BFI (2018): BFI-level 1  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 1  
Scopus rating (2017): CiteScore 1.59 SJR 0.667 SNIP 0.899  
Web of Science (2017): Impact factor 1.218  
Web of Science (2017): Indexed yes  
BFI (2016): BFI-level 1  
Scopus rating (2016): CiteScore 1.34 SJR 0.67 SNIP 0.832  
Web of Science (2016): Impact factor 1.195  
BFI (2015): BFI-level 1  
Scopus rating (2015): CiteScore 1.1 SJR 0.583 SNIP 0.626  
Web of Science (2015): Impact factor 0.906  
Web of Science (2015): Indexed yes  
BFI (2014): BFI-level 1  
Scopus rating (2014): CiteScore 1.23 SJR 0.706 SNIP 0.837  
Web of Science (2014): Impact factor 1.118  
BFI (2013): BFI-level 1  
Scopus rating (2013): CiteScore 1.03 SJR 0.531 SNIP 0.772  
Web of Science (2013): Impact factor 0.731  
BFI (2012): BFI-level 1  
Scopus rating (2012): CiteScore 1.01 SJR 0.48 SNIP 0.734  
Web of Science (2012): Impact factor 1.145  
BFI (2011): BFI-level 1  
Scopus rating (2011): CiteScore 0.8 SJR 0.401 SNIP 0.672  
Web of Science (2011): Impact factor 0.708  
BFI (2010): BFI-level 1  
Scopus rating (2010): SJR 0.381 SNIP 0.648  
Web of Science (2010): Impact factor 0.805  
BFI (2009): BFI-level 1  
Scopus rating (2009): SJR 0.377 SNIP 0.531
The effect of gluten on the host-microbial metabolism assessed by urinary metabolomics

A gluten-free diet clearly improves the life of patients with celiac disease, but the scientific evidence supporting possible health benefits of a gluten-free diet for non-celiac adults is limited. Therefore, as urine reflects the host and gut microbial metabolism, the study aimed to assess the long-term metabolic effect of gluten on the urine metabolome of non-celiac individuals by a cross-over intervention study (gluten-poor and gluten rich, respectively) using a non-targeted metabolomics approach. Fifty-one non-celiac adult participants (30 female, 21 male) were randomized to either a gluten-rich (21.6±5.7g/day) or a gluten-poor (~1g/day) diet for 8 weeks, crossing over to the other diet after 6 weeks washout. Urine samples were standardised collected at the beginning and end of each diet intervention period and were analysed by gas chromatography mass spectrometry (GC-MS) and liquid chromatography mass spectrometry (LC-MS). Several urinary microbial metabolites were found to be significantly affected by the gluten intake, suggesting that dietary gluten affects the composition and activity of the gut microbiota, which ultimately affects the circulating metabolites. Identification of the affected metabolites as well as integration of the metabolomics data with gut microbiota metagenomics data is ongoing hereby understanding how the metabolite changes are related to the gut microbiota.

General information
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Organisations: National Food Institute, Research Group for Gut Microbiology and Immunology, Research group for Analytical Food Chemistry, University of Copenhagen, University of Auckland
Contributors: Roager, H. M., Frandsen, H. L., Gøbel, R. J., Pedersen, O., Granato Villas-Boas, S., Licht, T. R.
Number of pages: 1
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The effects of gliadin on urine metabolome in mice

Gliadin, a proline-rich protein of gluten, is thought to modulate the gut microbiota and affect the intestinal permeability and immune system. However, little is known about the long-term effects of gliadin on the host and microbial metabolism. To study this, we compared the urine metabolome of two groups of mice, which were on a high fat diet with and without gliadin, respectively, for 23 weeks. Using liquid chromatography mass-spectrometry (MS) followed by multivariate analyses we were able to show a clear separation of the two groups of mice based on their urine metabolome. Discriminating urinary metabolites were identified by tandem MS and compared to MS libraries and authentic standards. Gliadin mice had higher levels of proline-containing dipeptides most likely originating from the gliadin itself. Furthermore, higher levels of tryptophan- and tyrosine-related metabolites were observed in the gliadin mice. Also, Maillard reaction products and β-oxidized tocopherols were observed in higher levels in the urine of gliadin mice, suggesting increased oxidative stress in the gliadin mice. Indisputably, gliadin affected the urine metabolome. However, the mechanisms behind the observed metabolite changes are yet to be elucidated.

General information
State: Published
Organisations: National Food Institute, Division of Food Microbiology, Division of Food Chemistry
Contributors: Roager, H. M., Zhang, L., Frandsen, H. L., Licht, T. R.
TL1A regulates TCRγδ+ intraepithelial lymphocytes and gut microbial composition

TL1A is a proinflammatory cytokine, which is prevalent in the gut. High TL1A concentrations are present in patients with inflammatory bowel disease (IBD) and in IBD mouse models. However, the role of TL1A during steady-state conditions is relatively unknown. Here, we used TL1A knockout (KO) mice to analyse the impact of TL1A on the intestinal immune system and gut microbiota. The TL1A KO mice showed reduced amounts of small intestinal intraepithelial TCRγδ+ and CD8+ T cells, and reduced expression of the activating receptor NKG2D. Moreover, the TL1A KO mice had significantly reduced body weight and visceral adipose tissue deposits, as well as lower levels of leptin and CXCL1, compared with wild-type mice. Analysis of the gut microbial composition of TL1A KO mice revealed a reduction of caecal Clostridial cluster IV, a change in the Firmicutes/Bacteroidetes ratio in caecum and less Lactobacillus spp. in the mucosal ileum. Our results show that TL1A deficiency impacts on the gut microbial composition and the mucosal immune system, especially the intraepithelial TCRγδ+ T-cell subset, and that TL1A is involved in the establishment of adipose tissue. This research contributes to a broader understanding of TL1A inhibition, which is increasingly considered for treatment of IBD.
A combined metabolomic and phylogenetic study reveals putatively prebiotic effects of high molecular weight arabino-oligosaccharides when assessed by in vitro fermentation in bacterial communities derived from humans

Prebiotic oligosaccharides are defined by their selective stimulation of growth and/or activity of bacteria in the digestive system in ways claimed to be beneficial for health. However, apart from the short chain fatty acids, little is known about bacterial metabolites created by fermentation of prebiotics, and the significance of the size of the oligosaccharides remains largely unstudied.

By in vitro fermentations in human fecal microbial communities (derived from six different individuals), we studied the effects of high-mass (HA, >1 kDa), low-mass (LA, <1 kDa) and mixed (BA) sugar beet arabino-oligosaccharides (AOS) as carbohydrate sources. Fructo-oligosaccharides (FOS) were included as reference. The changes in bacterial communities and the metabolites produced in response to incubation with the different carbohydrates were analyzed by quantitative PCR (qPCR) and Liquid Chromatography–Mass Spectrometry (LC–MS), respectively.

All tested carbohydrate sources resulted in a significant increase of Bifidobacterium spp. between 1.79 fold (HA) and 1.64 fold (FOS) in the microbial populations after fermentation, and LC–MS analysis suggested that the bifidobacteria
contributed to decomposition of the arabino-oligosaccharide structures, most pronounced in the HA fraction, resulting in release of the essential amino acid phenylalanine. Abundance of Lactobacillus spp. correlated with the presence of a compound, most likely a flavonoid, indicating that lactobacilli contribute to release of such health-promoting substances from plant structures.

Additionally, the combination of qPCR and LC–MS revealed a number of other putative interactions between intestinal microbes and the oligosaccharides, which contributes to the understanding of the mechanisms behind prebiotic impact on human health.
Antibiotic treatment affects intestinal permeability and gut microbial composition in female Wistar rats dependent on antibiotic class

General information
State: Published
Organisations: National Food Institute, Division of Food Microbiology
Contributors: Tulstrup, M. V., Christensen, E. G., Carvalho, V., Licht, T. R., Bahl, M. I.
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Antibiotic treatment affects intestinal permeability and gut microbial composition in female Wistar rats dependent on antibiotic class

General information
State: Published
Organisations: National Food Institute, Division of Food Microbiology
Contributors: Tulstrup, M. V., Christensen, E. G., Carvalho, V., Licht, T. R., Bahl, M. I.
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Antibiotic treatment affects intestinal permeability and gut microbial composition in female Wistar rats dependent on antibiotic class

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Organisations: National Food Institute, Division of Food Microbiology
Contributors: Tulstrup, M. V., Christensen, E. G., Carvalho, V., Licht, T. R., Bahl, M. I.
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Publication date: 2014
Peer-reviewed: Yes
Dietary xylo-oligosaccharide stimulates intestinal bifidobacteria and lactobacilli but has limited effect on intestinal integrity in rats.

Background: Consumption of prebiotics may modulate gut microbiota, subsequently affecting the bacterial composition, metabolite profile, and human health. Previous studies indicate that also changes in intestinal integrity may occur. In order to explore this further we have investigated the effect of the putative prebiotic xylo-oligosaccharides (XOS) on the gut microbiota and intestinal integrity in male Wistar rats. As changes in intestinal integrity may be related to the expected bifidogenic effect of XOS, we additionally addressed effects of supplementation with a commensal Bifidobacterium pseudolongum (BIF) isolated from the same breed of laboratory rats. Results: Changes in faecal and caecal bacterial composition determined by 16S rRNA gene sequencing and quantitative PCR for selected bacterial groups revealed that the overall bacterial composition did not differ markedly between the control (CON), XOS, and BIF groups, when correcting for multiple comparisons. However as hypothesised, the relative abundance of Bifidobacterium spp. was increased in XOS-fed rats as compared to CON in faecal samples after the intervention. Also Lactobacillus spp. was
increased in both the XOS and BIF groups in caecum content compared to CON. Intestinal permeability determined in vivo by FITC-dextran permeability and in vitro using extracted caecum water in trans-epithelial resistance (TER) assay showed no effect on intestinal integrity in either the XOS or the BIF groups. However, the expression of occludin, which is part of the tight junction complex, was increased in the XOS group compared to the CON group. Conclusions: Supplementation with XOS or a commensal Bifidobacterium pseudolongum had very limited effects on intestinal integrity in rat

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Web of Science (2017): Indexed yes
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Web of Science (2016): Indexed yes
Scopus rating (2015): CiteScore 1.5 SJR 0.74 SNIP 0.757
Scopus rating (2014): CiteScore 1.43 SJR 0.669 SNIP 0.787
Web of Science (2014): Indexed yes
Scopus rating (2013): CiteScore 1.55 SJR 0.654 SNIP 0.759
ISI indexed (2013): ISI indexed no
Scopus rating (2012): CiteScore 1.55 SJR 0.616 SNIP 0.656
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
Scopus rating (2011): CiteScore 1.67 SJR 0.66 SNIP 0.652
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**Early Life Microbiota, Neonatal Immune Maturation and Hematopoiesis**

Emerging epidemiologic data supports the hypothesis that early life colonization is a key player in development of a balanced immune system. Events in early life, as birth mode and infant diet, are shown to influence development of immune related diseases, like asthma, diabetes and inflammatory bowl disease, later in life. The intestinal epithelium makes up a physical and biochemical barrier between the bacteria in the gut lumen and the immune cells in the submucosal tissue. This monolayer of intestinal epithelial cells (IEC) makes up an extremely large surface and is highly important for the synergistic coexistence between trillions of bacteria in the gastrointestinal tract and their mammalian hosts. The IEC actively communicate with the microbiota of the gut lumen and tolerance establishment in the intestine is induced as a result of a balanced and controlled communication between IEC and the commensals in the
Hematopoietic stem cells from the fetal liver seed the fetal spleen and bone marrow in perinatal phase. Granulocytosis in neonate mice and man just after birth is a natural event of early life hematopoiesis and likely contributes to elevated counts of neutrophil-like cells in the peripheral blood of newborns. Granular myeloid derived suppressor cells (MDSC) have recently been described in human cord blood. MDSC are potential immnosuppressive cells often described in cancer, inflammation and during sepsis. They evolve from immature myeloid cells during hematopoiesis. Several recent studies show a role for various myeloid derived and immune suppressive cellular subsets in the newborn.

In the present work we showed the presence of a prominent group of CD11b+Gr-1+ cells in the neonate murine spleen. The presence of these cells were dependent on the colonizing microbiota, as germfree neonate mice held notably fewer of these cells in the spleen. Microscopy of spleens and livers indicated that these cells derived from hematopoietic tissue in the liver of the neonate mouse, and that mobilization and activation of the hematopoietic tissue is promoted by the presence of colonizing microbes.

The regulation of epithelial barrier integrity was influenced by the nature of the microbiota, as expression of tight junction (TJ) protein encoding genes showed a faster and more tightly regulated rate in the murine ileum of conventionally colonized mice compared to the GF ileum. The conventional microbiota furthermore promotes the expression of genes involved in mucin secretion, TLR signaling pathways and cytokine production in the intestine, while downregulating genes encoding chemokines in the epithelial tissue.

Newly published studies indicate that the prominent CD11b+Gr-1+ cell group may have a role in early life immune regulation. This is however not proven by the data of present study.

**Establishment of Intestinal Microbiota during Early Life: a Longitudinal, Explorative Study of a Large Cohort of Danish Infants**

Fecal samples were obtained from a cohort of 330 healthy Danish infants at 9, 18, and 36 months after birth, enabling characterization of interbacterial relationships by use of quantitative PCR targeting 31 selected bacterial 16S rRNA gene targets representing different phylogenetic levels. Nutritional parameters and measures of growth and body composition were determined and investigated in relation to the observed development in microbiota composition. We found that significant changes in the gut microbiota occurred, particularly from age 9 to 18 months, when cessation of breastfeeding and introduction of a complementary feeding induce replacement of a microbiota characterized by lactobacilli, bifidobacteria, and Enterobacteriaceae with a microbiota dominated by Clostridium spp. and Bacteroides spp.

Classification of samples by a proxy enterotype based on the relative levels of Bacteroides spp. and Prevotella spp. showed that enterotype establishment occurs between 9 and 36 months. Thirty percent of the individuals shifted enterotype between 18 and 36 months. The composition of the microbiota was most pronouncedly influenced by the time of cessation of breastfeeding. From 9 to 18 months, a positive correlation was observed between the increase in body mass index and the increase of the short-chain-fatty-acid-producing clostridia, the Clostridium leptum group, and...
Eubacterium hallii. Considering previously established positive associations between rapid infant weight gain, early breastfeeding discontinuation, and later-life obesity, the corresponding microbial findings seen here warrant attention.
Gliadin affects glucose homeostasis and intestinal metagenome in C57BL/6 mice fed and high-fat diet

Dietary gluten and its component gliadin are well-known environmental triggers of celiac disease and important actors in type-1 diabetes, and are reported to induce alterations in the intestinal microbiota. However, research on the impact of gluten on type-2 diabetes in non-celiac subjects is more limited. The aim of this study was to investigate the effect of gliadin on glucose homeostasis and intestinal ecology in the mouse. Forty male C57BL/6 mice were fed a high-fat diet containing either 4% gliadin or no gliadin for 22 weeks. Gliadin consumption significantly increased the HbA1c level over time, with a borderline significance of higher HOMA-IR (homeostasis model assessment of insulin resistance) after 22 weeks. Sequencing of the V3 region of the bacterial 16S rRNA genes showed that gliadin changed the abundance of 81 bacterial taxa, separating the intestinal microbial profile of the gliadin consuming mice from the control mice in the principal coordinate analysis (PCoA) of weighted UniFrac distance. No difference was found in body weight gain, feed consumption or circulating cytokines (IL-1β, IL-6, IFN-γ, TNF-α and IL-10). Our study is the first to show that gliadin as part of a defined synthetic feed exacerbates the glycaemia and alters the intestinal microbiota composition. Comprehensive analyses of the profile of specific immune cells, metabolites and intestinal permeability are in progress to elucidate the mechanism behind the observed effects.
Lactobacillus acidophilus NCFM affects vitamin E acetate metabolism and intestinal bile acid signature in monocolonized mice

Mono-colonization of germ-free (GF) mice enables the study of specific bacterial species in vivo. Lactobacillus acidophilus is a probiotic strain, however many of the mechanisms behind its health-promoting effect remain unsolved. Here, we studied the effects of Lactobacillus acidophilus NCFM™ (NCFM) on the intestinal metabolome (jejunum, caecum, and colon) in mice by comparing NCFM mono-colonized (MC) mice with GF mice using liquid chromatography coupled to mass-spectrometry (LC-MS). The study adds to existing evidence that NCFM in vivo affects the bile acid signature of mice by deconjugation and dehydroxylation of bile acids. Furthermore, we confirmed that carbohydrate metabolism is affected by NCFM in the mouse intestine. Especially, the digestion of larger carbohydrates (penta- and tetrasaccharides) was increased in MC mice. Interestingly, we also found vitamin E (α-tocopherol acetate) in higher levels in the intestine of GF mice compared to MC mice, suggesting that NCFM either metabolizes the compound or indirectly affects the absorption by changing the metabolome in the intestine. The use of NCFM to increase the uptake of vitamin E supplements in humans and animals is a highly relevant topic for further research.

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BFI (2016): BFI-level 1
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BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.98 SJR 1.66 SNIP 0.776
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.8 SJR 1.705 SNIP 0.784
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.87 SJR 1.519 SNIP 0.724
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Scopus rating (2012): CiteScore 2.11 SJR 1.14 SNIP 0.779
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Microbial enterotypes, inferred by the prevotella-to-bacteroides ratio, remained stable during a 6-month randomized controlled diet intervention with the new nordic diet

It has been suggested that the human gut microbiota can be divided into enterotypes based on the abundance of specific bacterial groups; however, the biological significance and stability of these enterotypes remain unresolved. Here, we demonstrated that subjects (n = 62) 18 to 65 years old with central obesity and components of metabolic syndrome could be grouped into two discrete groups simply by their relative abundance of Prevotella spp. divided by Bacteroides spp. (P/B ratio) obtained by quantitative PCR analysis. Furthermore, we showed that these groups remained stable during a 6-month, controlled dietary intervention, where the effect of consuming a diet in accord with the new Nordic diet (NND) recommendations as opposed to consuming the average Danish diet (ADD) on the gut microbiota was investigated. In this study, subjects (with and without stratification according to P/B ratio) did not reveal significant changes in 35 selected bacterial taxa quantified by quantitative PCR (ADD compared to NND) resulting from the dietary interventions. However, we found higher total plasma cholesterol within the high-P/B group than in the low-P/B group after the intervention. We propose that stratification of humans based simply on their P/B ratio could allow better assessment of possible effects of interventions on the gut microbiota and physiological biomarkers.

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BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.08
Web of Science (2016): Impact factor 3.807
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Scopus rating (2015): CiteScore 4.14 SJR 1.891 SNIP 1.308
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Web of Science (2014): Impact factor 3.668
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.25 SJR 1.899 SNIP 1.414
Web of Science (2013): Impact factor 3.952
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.29 SJR 1.975 SNIP 1.429
Older siblings, pets and early life infections: impact on gut microbiota and allergy prevalence during the first three years of life

Background: Early life infections and presence of older siblings or pets in the household are factors known to affect the risk of developing allergic diseases, and this effect is suggested to be mediated by interactions between microbes and the immune system. However, very limited research has been done on the effect of these factors on the developing gut microbiota in infants. Thus, we aimed to elucidate associations between older siblings, pets and early life infections, the microbial gut communities at 9 and 18 months of age and the prevalence of allergies in three year old children.

Methods: Bacterial DNA was extracted from a total of 228 fecal samples obtained from 114 infants at both 9 and 18 months of age, belonging to the SKOT cohort. High throughput 16S rRNA gene sequencing was performed and the bacterial community composition of each sample was determined. Information on prevalence of respiratory allergy,
eczema and presence of older siblings, pets and early life infections, previously collected through interviews with parents, were compared to the obtained data on bacterial taxonomy.

Results: Early life infections were positively associated with the risk of developing respiratory allergy ($p = 0.044$), while having siblings tended to decrease the risk of developing eczema ($p = 0.105$) before the age of three years. Having siblings correlated positively with the relative abundance of several gut microbial genera at both ages. At 18 months of age, microbial alpha diversity ($p = 0.045$) and richness ($p = 0.009$) were significantly higher in individuals with siblings, whereas in children with registered early life infections, a lower alpha diversity ($p = 0.067$) and richness ($p = 0.023$) was found at 18 months of age. However, gut microbiota composition, diversity and richness in children with allergies did not differ substantially from that in children without symptoms.

Conclusions: Early life infections might precede childhood respiratory allergy and are associated with low microbial diversity/richness during late infancy. The presence of older siblings affects the gut microbiota composition, diversity and richness during late infancy and the risk of developing eczema during early childhood. However, gut microbiota in late infancy was not associated with eczema or respiratory allergy in early childhood. Further studies are warranted to assess whether the profound sibling effect on the gut microbiota has implication for development of allergies later in life.

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The effect of gluten on the urine metabolome of non-celiac adults assessed by GC-MS

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The effect of gluten on the urine metabolome of non-celiac adults assessed by GC-MS

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Transfer of gut microbiota from lean and obese mice to antibiotic-treated mice

Transferring gut microbiota from one individual to another may enable researchers to "humanize" the gut of animal models and transfer phenotypes between species. To date, most studies of gut microbiota transfer are performed in germ-free mice. In the studies presented, it was tested whether an antibiotic treatment approach could be used instead. C57BL/6 mice were treated with ampicillin prior to inoculation at weaning or eight weeks of age with gut microbiota from lean or obese donors. The gut microbiota and clinical parameters of the recipients was characterized one and six weeks after inoculation. The results demonstrate, that the donor gut microbiota was introduced, established, and changed the gut microbiota of the recipients. Six weeks after inoculation, the differences persisted, however alteration of the gut microbiota occurred with time within the groups. The clinical parameters of the donor phenotype were partly transmissible from obese to lean mice, in particularly beta cell hyperactivity in the obese recipients. Thus, a successful inoculation of gut microbiota was not age dependent in order for the microbes to colonize, and transferring different microbial compositions to conventional antibiotic-treated mice was possible at least for a time period during which the microbiota may permanently modulate important host functions.

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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.63 SJR 1.692 SNIP 1.354
Web of Science (2016): Impact factor 4.259
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 5.3 SJR 2.034 SNIP 1.597
Web of Science (2015): Impact factor 5.228
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.75 SJR 2.163 SNIP 1.554
Web of Science (2014): Impact factor 5.578
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.06 SJR 1.998 SNIP 1.57
Web of Science (2013): Impact factor 5.078
ISI indexed (2013): ISI indexed yes
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ISI indexed (2012): ISI indexed yes
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Web of Science (2011): Impact factor
Two randomized cross-over trials assessing the impact of dietary gluten or wholegrain on the gut microbiome and host metabolic health

Background: Gut microbiota composition and activity may be changed by dietary factors and possibly affect metabolic health. Dietary gluten and wholegrain are suggested to influence metabolism in a negative and positive direction, respectively.

Objective: Describe the design and rational as well as baseline characteristics of two human intervention studies, within the Gut, Grain and Greens (3G) Center, investigating the effects of a gluten-poor and wholegrain-rich diet on microbiota composition and metabolic health.

Design: The gluten and wholegrain studies had a randomized, controlled, cross-over design each comprising two eight-week dietary intervention periods, separated by a six-week wash-out period. Each trial included 60 men and women exhibiting an increased metabolic risk. In the gluten study a gluten-poor diet was compared with a gluten-rich dietary fiber-controlled diet, and in the wholegrain study a wholegrain-rich diet was compared with a refined grain diet. The control diet was identical in both studies, being concomitantly high in gluten and refined. Participants substituted all cereal products with provided intervention products which they consumed ad libitum. Before and after each intervention period, fecal samples for quantitative metagenomic analyses were collected and an examination day was conducted. The primary outcome of the gluten intervention study was changes in the gut microbiota composition, while insulin sensitivity was an additional primary outcome of the wholegrain study. Further, a number of secondary outcomes were investigated.

Results: 52 and 50 participants completed the gluten and wholegrain intervention study, respectively. Participants had slightly elevated fasting glucose levels and increased waist circumference. Biological outcomes of the two studies will be published elsewhere.

Conclusion: The studies have the potential to provide new insights into the interplay of gut microbiota and metabolic health in individuals with increased risk of developing metabolic disorders.
Bifidogenic effect of whole-grain wheat during a 12-week energy-restricted dietary intervention in postmenopausal women

Background/Objectives: Consumption of whole-grain products is known to have beneficial effects on human health. The effects of whole-grain products on the intestinal microbiota and intestinal integrity have, however, only been studied limitedly. We investigate changes of the human gut microbiota composition after consumption of whole-grain (WW) or refined wheat (RW) and further study effects on gut wall integrity.

Subjects/Methods: Quantitative PCR was used to determine changes in the gut bacterial composition in postmenopausal women following a 12-week energy-restricted dietary intervention with WW (N=38) or RW (N=34). Intestinal integrity was determined by measuring trans-epithelial resistance (TER) across a Caco-2 cell monolayer, following exposure to faecal water.

Results: No significant differences in microbiota composition were observed between the two dietary groups; however, the whole-grain intervention increased the relative abundance of Bifidobacterium compared to baseline, supporting a prebiotic effect of whole-grain wheat. Faecal water increased TER independent of dietary intervention, indicating that commensal bacteria produce metabolites that generally provide a positive effect on intestinal integrity. Combining microbiota composition data from the run-in period with its effect on TER revealed a tendency for a negative correlation between the relative abundance of Bifidobacterium and TER (P=0.09). This contradicts previous findings but supports observations of increased Salmonella infection in animal models following treatment with bifidogenic prebiotics.

Conclusions: The present study shows that whole-grain wheat consumption increases the abundance of bifidobacteria compared to baseline and may have indirect effects on the integrity of the intestinal wall. European Journal of Clinical Nutrition advance online publication, 23 October 2013; doi:10.1038/ejcn.2013.207.
Characterization of the infant gut microbiota in a cohort of 330 Danish children at 9, 18 and 36 months by quantitative PCR array (GULDA) analysis

We have developed a qPCR-based array (Gut Low Density Array, GULDA), which simultaneously determine the relative abundance of >30 different bacterial 16S rRNA gene targets in a given DNA-sample covering selected phylogenetic levels. GULDA was applied to fecal DNA from 330 healthy Danish infants (the so called SKOT-cohort), sampled at 9, 18 and 36 months after birth. The resulting data together with previously determined nutritional and anthropometrical parameters were used as input for multivariate statistics. We found significant changes in the composition of the gut microbiota between 9 and 18 months, corresponding to dietary changes during weaning; changes were far less pronounced between 18 and 36 months. Few studies have undertaken similar longitudinal and multiparametric analysis for such numerous participants. GULDA was seen to constitute a sensitive, cost-effective tool for microbial community characterization, which here provides new insights into the interactions between the gut microbiota, diet and physiology in infants.

Dietary whole-grain wheat increases intestinal levels of bifidobacteria in humans and bifidobacterial abundance is negatively correlated with the effect of fecal water on trans-epithelial resistance in vitro.

Consumption of whole grain products are considered to have beneficial effects on human health including decreased risk of cardiovascular disease. However, effects on gut microbial composition have only been studied limitedly. We used quantitative PCR to determine changes in the gut bacterial composition in post-menopausal women following a 12-week energy restricted intervention with whole-grain wheat (WW, n=37) or refined wheat (RW, n=33). The WW intervention significantly increased the relative abundance of Bifidobacterium. Caco-2 cells were exposed to fecal water to determine effects of the bacterial community metabolites on the trans-epithelial resistance (TER). Fecal water increased TER independent of diet, indicating that commensal bacteria provide metabolites facilitating an increase in intestinal integrity. TER was unexpectedly found to be negatively correlated to the relative abundance of Bifidobacterium. The present study suggests that increase of specific bacterial groups, which are considered beneficial, may in some circumstances increase the permeability of the intestinal wall.
Dietary Xylooligosaccharide Downregulates IFN-γ and the Low-Grade Inflammatory Cytokine IL-1β Systemically in Mice

Dietary carbohydrates improve growth conditions for distinct populations of bacteria that may affect mucosal and systemic immunity. In this study, we fed in a parallel experiment a 10% xylooligosaccharide (XOS)–supplemented diet or a control diet to 2 groups of male C57BL/6NTac mice for 10 wk from weaning. We found that the XOS diet significantly increased Bifidobacterium throughout the intestine compared with control-fed mice, with the highest proportions found in the ileum after XOS feeding (P <0.001). In the intestinal epithelium, most innate immune-related genes were unaffected by XOS feeding, whereas expression of interleukin 1β (Il1β) (P <0.01) and interferon γ (Ifnγ) (P <0.05) was significantly less in blood from XOS-fed mice than from control-fed mice. In vitro treatment of blood with propionate significantly decreased Il1β (P <0.01), Ifnγ (P <0.01), and interleukin 18 (Il18) (P <0.001) expression, supporting our hypothesis that increased production of short-chain fatty acids (SCFAs) in the gut, which are transported across the intestine and into the systemic compartments, results in downregulation of low-grade inflammatory cytokines. The defensin regenerating islet-derived protein 3γ (RegIIIγ) was significantly more highly expressed in the small intestine (P <0.01) in XOS-fed mice compared with control-fed mice, suggesting only minor contact between bifidobacteria and epithelial cells. In support of this, the SCFA-induced sodium/hydrogen exchanger isoform 3 expression tended to be greater in the XOS group than in the control group (P = 0.06), indicating an indirect SCFA-mediated antiinflammatory effect of XOS. In conclusion, XOS feeding decreases systemic inflammation, and this effect is most likely caused by higher SCFA concentrations as a result of an increased bifidobacterial saccharolytic fermentation in the entire gut and not only in the large intestine.
EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2013. Scientific Opinion on the maintenance of the list of QPS biological agents intentionally added to food and feed (2013 update)

EFSA is requested to assess the safety of a broad range of biological agents in the context of notifications for market authorisation as sources of food and feed additives, enzymes and plant protection products. The qualified presumption of safety (QPS) assessment was developed to provide a harmonised generic pre-assessment to support safety risk assessments performed by EFSA’s scientific Panels. The safety of unambiguously defined biological agents (at the
highest taxonomic unit appropriate for the purpose for which an application is intended), and the completeness of the body
of knowledge are assessed. Identified safety concerns for a taxonomic unit are, where possible and reasonable in number,
reflected as ‘qualifications’ in connection with a recommendation for a QPS status. The list of QPS recommended
biological agents is reviewed and updated periodically. Therefore, the only valid list is the one in the most recently
published scientific opinion. The 2013 update reviews previously assessed microorganisms including bacteria, yeasts,
filamentous fungi, oomycetes and viruses used for plant protection purposes. All taxonomic units previously recommended
for the QPS list had their status reconfirmed. The new notifications since the last QPS update were reviewed.
Gluconobacter oxydans and Alphaflexiviridae were assessed for the first time and were recommended for the QPS list.
The information of the previous opinion was updated for the taxonomic units on the QPS list. Qualifications for the
taxonomic units included in the QPS recommended list were reviewed and confirmed. Filamentous fungi and enterococci
were not recommended for the QPS list following updating and reviewing of current scientific knowledge.

Enterotypes influence temporal changes in gut microbiota
The human gut microbiota plays an important role for human health. The question is whether we can modulate the
gut microbiota by changing diet. During a 6-month, randomised, controlled dietary intervention, the effect of a moderate
diet shift from Average Danish Diet to New Nordic Diet on the gut microbiota in humans (n=62) was investigated.
Quantitative PCR analysis showed that the microbiota did not change significantly by the intervention. Nevertheless,
by stratifying subjects into two enterotypes, distinguished by the Prevotella/Bacteroides ratio (P/B), we were able to
detect significant changes in the gut microbiota composition resulting from the interventions. Subjects with a high-
P/B experienced more pronounced changes in the gut microbiota composition than subjects with a low-P/B. The study is
the first to indicate that enterotypes influence microbiota response to a dietary intervention.
(P/B), we were able to detect significant changes in the gut microbiota composition resulting from the interventions. Subjects with a high-P/B experienced more pronounced changes in the gut microbiota composition than subjects with a low-P/B. The study is the first to indicate that enterotypes influence microbiota response to a dietary intervention. The distinction of enterotypes by P/B could be a simple approach to assess the effect of diets and other treatments on the gut microbiota.

Epithelial entry rather than the ensuing systemic immune response determines the pathogenicity of two Salmonella enterica serovar Typhimurium strains in a mouse model

Most studies of Salmonella enterica serovar Typhimurium infection focus only on the pathogenicity of one strain. We investigated whether differences in pathogenicity of two wild-type S. Typhimurium strains; DT120 and SL1344, were related to gut invasion or the resulting immune response. Oral administration of a ten-fold lower number of SL1344 (106 CFU) as compared to DT120 (107 CFU) resulted in higher bacterial counts in liver and lymph nodes, and led to massive neutrophil infiltration of the spleen, while DT120 administration did not. In contrast, administration of the same dose (103 CFU) of the two strains intravenously resulted in the same levels of bacteria and neutrophils in spleen and bone marrow. Oral administration of SL1344 led to an increase in neutrophil apoptosis in both spleen and the bone marrow and four out of five mice died before Day 8, while in DT120 mice, no increase in neutrophil apoptosis was observed and all mice survived until Day 8. This study reveals that two wild-type S. Typhimurium strains, despite evoking highly comparable immune responses upon intravenous injection, exhibit diverse pathogenicity in mice and thus suggests that differences in their invasiveness and survival during gut passage determines the success of the ensuing immune response.
Gut Mucosal Regulation of Distinct Macrophage and Dendritic Cell Subsets During Early Stage Salmonella Infection

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Intake of whole apples or clear apple juice has contrasting effects on plasma lipids in healthy volunteers

PURPOSE:
Fruit consumption is associated with a decreased risk of CVD in cohort studies and is therefore endorsed by health authorities as part of the '5 or more a day' campaigns. A glass of fruit juice is generally counted as one serving. Fruit may cause protection by affecting common risk factors of CVD.

METHODS:
Apples are among the most commonly consumed fruits and were chosen for a comprehensive 5 × 4 weeks dietary crossover study to assess the effects of whole apples (550 g/day), apple pomace (22 g/day), clear and cloudy apple juices (500 ml/day), or no supplement on lipoproteins and blood pressure in a group of 23 healthy volunteers.

RESULTS:
The intervention significantly affected serum total and LDL-cholesterol. Trends towards a lower serum LDL-concentration were observed after whole apple (6.7 %), pomace (7.9 %) and cloudy juice (2.2 %) intake. On the other hand, LDL-cholesterol concentrations increased by 6.9 % with clear juice compared to whole apples and pomace. There was no effect on HDL-cholesterol, TAG, weight, waist-to-hip ratio, blood pressure, inflammation (hs-CRP), composition of the gut microbiota or markers of glucose metabolism (insulin, IGF1 and IGFBP3).

CONCLUSIONS:
Apples are rich in polyphenols and pectin, two potentially bioactive constituents; however, these constituents segregate differently during processing into juice products and clear juice is free of pectin and other cell wall components. We conclude that the fibre component is necessary for the cholesterol-lowering effect of apples in healthy humans and that clear apple juice may not be a suitable surrogate for the whole fruit in nutritional recommendations.
In vitro growth of four individual human gut bacteria on oligosaccharides produced by chemoenzymatic synthesis.

The present study aimed at examining oligosaccharides (OS) for potential stimulation of probiotic bacteria. Nineteen structurally well-defined candidate OS covering groups of β-glucosides, α-glucosides and α-galactosides with degree of polymerization 2-4 were prepared in >100 mg amounts by chemoenzymatic synthesis (i.e. reverse phosphorolysis or transglycosylation). Fourteen of the OS are not naturally occurring and five (β-d-glucosyl-fructose, β-d-glucosyl-xylitol, α-glucosyl-(1,4)-d-mannose, α-glucosyl-(1,4)-d-xylose; α-glucosyl-(1,4)-l-fucose) have recently been synthesized for the first time. These OS have not been previously tested for effects of bacterial growth and here the ability of all 19 OS to support growth of four gastrointestinal bacteria: three probiotic bacteria Bifidobacterium lactis, Bifidobacterium longum, and...
Lactobacillus acidophilus, and one commensal bacterium, Bacteroides vulgatus has been evaluated in monocultures. The disaccharides β-d-glucosyl-xylitol and β-d-glucosyl-(1,4)-xylose noticeably stimulated growth yields of L. acidophilus NCFM, and additionally, β-d-glucosyl-(1,4)-xylose stimulated B. longum Bl-05. α-Glucosyl-(1,4)-glucosamine and α-glucosyl-(1,4)-N-acetyl-glucosamine enhanced the growth rate of B. animalis subsp. lactis and B. longum Bl-05, whereas L. acidophilus NCFM and Bac. vulgatus did not grow on these OS. α-Galactosyl-(1,6)-α-galactosyl-(1,6)-glucose advanced the growth rate of B. animalis subsp. lactis and L. acidophilus NCFM. Thus several of the structurally well-defined OS supported growth of beneficial gut bacteria. This reflects a broad specificity of their sugar transporters for OS, including specificity for non-naturally occurring OS, hence showing promise for design of novel prebiotics.

**General information**

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Organisations: National Food Institute, Division of Food Microbiology, Department of Systems Biology, Enzyme and Protein Chemistry, Department of Chemical and Biochemical Engineering, Department of Chemistry, Organic Chemistry, Center for BioProcess Engineering, DuPont Nutrition and Health, Carlsberg Research Center
Pages: 784-793
Publication date: 2013
Peer-reviewed: Yes

**Publication information**

Journal: Food & Function
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Ratings:
Web of Science (2019): Indexed yes
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 3.62 SJR 1.209 SNIP 1.07
Web of Science (2017): Impact factor 3.289
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 3.38 SJR 1.131 SNIP 1.024
Web of Science (2016): Impact factor 3.247
Scopus rating (2015): CiteScore 3.15 SJR 1.013 SNIP 0.999
Web of Science (2015): Impact factor 2.686
Web of Science (2015): Indexed yes
Scopus rating (2014): CiteScore 3.04 SJR 1.022 SNIP 1.072
Web of Science (2014): Impact factor 2.791
Scopus rating (2013): CiteScore 3.29 SJR 1.128 SNIP 1.054
Web of Science (2013): Impact factor 2.907
ISI indexed (2013): ISI indexed yes
Scopus rating (2012): CiteScore 2.79 SJR 0.979 SNIP 1.103
Web of Science (2012): Impact factor 2.694
ISI indexed (2012): ISI indexed no
Scopus rating (2011): CiteScore 1.14 SJR 0.353 SNIP 0.378
Web of Science (2011): Impact factor 1.179
ISI indexed (2011): ISI indexed no
Original language: English
DOI:
10.1039/C3FO30357H
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Source-ID: n:oai:DTIC-ART:pubmed/386069823::28343
Research output: Research - peer-review : Journal article – Annual report year: 2013

**Lipid hydrolysis products affect the composition of microbiota isolated from infant fecal samples after in vitro fermentation**

Some lipid hydrolysis products such as medium-chained free fatty acids (FFA) and monoacylglycerols (MAG) have antibacterial activity, while others, including oleic acid, have been reported to be essential for optimal growth of Lactobacillus species. Thus, the FFA and MAG concentration in the distal ileum and in colon can be expected to selectively modulate the growth rate and hereby the composition of the microbiota.

In earlier studies, we have shown that this concentration is dependent on the type of emulsification of the triglycerides, which deviates between breast milk and formula milk.
Here, we have determined effects of selected combinations of FFA and MAG on microbial composition during a 24-hour anaerobic in vitro fermentation in microbiota obtained from infant fecal samples (age 2-5 months). PCR-based quantification of 11 different bacterial taxa revealed that the growth of Firmicutes, Lactobacillus and B.longum is significantly increased in the presence of a mixture of C10-C14 FFAs.

**General information**

State: Published
Organisations: Department of Systems Biology, Center for Biological Sequence Analysis, National Food Institute, Division of Food Microbiology
Publication date: 2013
Peer-reviewed: Yes
Event: Abstract from Cell Symposia, Lisbon, Portugal.

**Lipid hydrolysis products affect the composition of microbiota isolated from infant fecal samples after in vitro fermentation**

**General information**

State: Published
Organisations: Department of Systems Biology, Center for Biological Sequence Analysis, National Food Institute, Division of Food Microbiology
Publication date: 2013
Peer-reviewed: Yes
Event: Abstract from 27th Nordic Lipid Symposium, Helsinki, Finland.

**Listeria monocytogenes strains encoding premature stop codons in inlA invade mice and guinea pig fetuses in orally dosed dams**

Listeria monocytogenes is an important food-borne bacterial pathogen and listeriosis can result in abortions in pregnant women. The bacterium can colonize food-processing environments, where specific molecular subtypes can persist for years. The purpose of this study was to determine the virulence potential of a group of food-processing persistent L. monocytogenes strains encoding a premature stop codon in inlA (encoding internalin A) by using two orally dosed models, pregnant mice and pregnant guinea pigs. A food-processing persistent strain of L. monocytogenes invaded placentas (n = 58; 10 % positive) and fetuses (3 % positive) of pregnant mice (n = 9 animals per strain), similar to a genetically manipulated murinized strain, EGD-e InlAm* (n = 61; 3 and 2 %, respectively). In pregnant guinea pigs (n = 9 animals per bacterial strain), a maternofetal strain (from a human fetal clinical fatal case) was isolated from 34 % of placenta samples (n = 50), whereas both food-processing persistent strains were found in 5 % of placenta samples (n = 36 or 37). One of the food-processing persistent strains, N53-1, was found in up to 8 % of guinea pig fetal liver and brain samples, whereas the maternofetal control was found in 6 % of fetal tissue samples. As the food-processing persistent strains carry a premature stop codon in inlA but are invasive in orally dosed pregnant mice and guinea pigs, we hypothesize that listerial crossing of the placental barrier can occur by a mechanism that is independent of an interaction between E-cadherin and InlA.

**General information**

State: Published
Organisations: National Food Institute, Division of Industrial Food Research, Division of Food Microbiology, Department of Systems Biology, University of Copenhagen
Pages: 1799-1806
Publication date: 2013
Peer-reviewed: Yes

**Publication information**

Journal: Journal of Medical Microbiology
Volume: 62
Issue number: Pt 12
ISSN (Print): 0022-2615
Ratings:
Microbiotas from UC patients display altered metabolism and reduced ability of LAB to colonize mucus

We compared fecal microbial communities derived either from Ulcerative Colitis (UC) patients in remission (n = 4) or in relapse (n = 4), or from healthy subjects (n = 4). These communities were used for inoculation of a dynamic in vitro gut model, which contained integrated mucin-covered microcosms. We found that the microbiota of the 'mucus' largely differed from that of the 'lumen'. This was partly due to decreased mucus-associated populations of lactic acid producing bacterial populations (LAB), as LAB originating from UC patients had a significantly decreased capacity to colonize the mucin-covered microcosms as compared to those originating from healthy subjects. We found significant differences between the metabolomes of UC patients in relapse and remission, respectively, while the metabolome of patients in remission resembled that of healthy subjects. These novel findings constitute an important contribution to the understanding of the complex etiology of UC.
Mono-colonization with Lactobacillus acidophilus NCFM affects the intestinal metabolome as compared to germ-free mice

Every single species of the gut microbiota produce low-molecular-weight compounds that are absorbed constantly from the intestinal lumen and carried to systemic circulation where they play a direct role in health and disease. However, very few studies address the host metabolome as a function of colonizing bacteria. In this study the effect of the Lactobacillus acidophilus NCFM strain was investigated by comparing the metabolome of mono-colonized and germ-free mice in several compartments. By liquid-chromatography coupled to mass spectrometry, we were able to show that the metabolome differed between the mono-colonized and germ-free mice, not only in ileum, caecum and colon, but also in plasma and liver. These observations suggest that L. acidophilus NCFM highly influence the metabolism in multiple compartments, underlying that the gut microbiota metabolism affects the host systemic metabolism.

General information
State: Published
Organisations: National Food Institute, Division of Food Microbiology, Division of Food Chemistry, University of Auckland, University of Copenhagen
Number of pages: 1
Publication date: 2013
Peer-reviewed: Yes
Event: Abstract from Copenhagen Bioscience Conference – Genomics in metabolism, Snekkersten, Denmark.
Electronic versions:
Roager_Copenhagen_Bioscience_conference_abstract.pdf
Source: dtu
Source-ID: u::9221
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2013

Mono-colonization with Lactobacillus acidophilus NCFM affects the intestinal metabolome in mice

Mono-colonization of germ-free (GF) mice enables the study of specific bacterial species in vivo. Lactobacillus acidophilus is a probiotic strain, however many of the mechanisms behind its health-promoting effect remain unsolved. Here, we studied the effects of Lactobacillus acidophilus NCFMTM (NCFM) on the intestinal metabolome (jejunum, caecum, and colon) in mice by comparing NCFM mono-colonized (MC) mice with GF mice using liquid chromatography coupled to mass-spectrometry (LC-MS). The study adds to existing evidence that NCFM in vivo affects the bile acid signature of mice by deconjugation and dehydroxylation of bile acids. Furthermore, we confirmed that carbohydrate metabolism is affected by NCFM in the mouse intestine. Especially, the digestion of larger carbohydrates (penta- and tetrasaccharides) was increased in MC mice. Interestingly, we also found vitamin E (α-tocopherol acetate) in higher levels in the intestine of GF mice compared to MC mice, suggesting that NCFM either metabolizes the compound or indirectly affects the absorption by changing the metabolome in the intestine. The use of NCFM to increase the uptake of vitamin E supplements in humans and animals is a highly relevant topic for further research.

General information
State: Published
Organisations: National Food Institute, Division of Food Microbiology, Division of Food Chemistry, University of Auckland, University of Copenhagen
Xylo-oligosaccharides and inulin affect genotoxicity and bacterial populations differently in a human colonic simulator challenged with soy protein.

High dietary intakes of some protein sources, including soy protein, can increase colonic DNA damage in animals, whereas some carbohydrates attenuate this. We investigated whether inulin and xylo-oligosaccharides (XOS) could be protective against DNA strand breaks by adding them to a human colonic simulator consisting of a proximal vessel (PV) (pH 5.5) and a distal vessel (DV) (pH 6.8) inoculated with human faeces and media containing soy protein. Genotoxicity of the liquid phase and microbial population changes in the vessels were measured. Soy protein (3%) was fermented with 1% low amylose cornstarch for 10 day followed by soy protein with 1% XOS or 1% inulin for 10 day. Inulin did not alter genotoxicity but XOS significantly reduced PV genotoxicity and increased DV genotoxicity. Inulin and XOS significantly increased butyrate concentration in the DV but not PV. Numbers of the key butyrate-producing bacterium Faecalibacterium prausnitzii were significantly increased in the PV and DV by inulin but significantly decreased by XOS in both vessels. Other bacteria examined were also significantly impacted by the carbohydrate treatments or by the vessel (i.e., pH). There was a significant overall inverse correlation between levels of damage induced by the ferments and levels of sulphate-reducing bacteria, Bacteroides fragilis, and acetate. In conclusion, dietary XOS can potentially modulate the genotoxicity of the colonic environment and specific bacterial groups and short chain fatty acids may mediate this.
Xylo-Oligosaccharide Supplemented Diet Modulates Intestinal and Systemic Immunity

General information
State: Published
Organisations: National Food Institute, Division of Food Microbiology
Pages: 272-272
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Scandinavian Journal of Immunology
Volume: 77
Issue number: 4
ISSN (Print): 0300-9475
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.11 SJR 0.891 SNIP 0.621
Web of Science (2017): Impact factor 2.314
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.03 SJR 0.979 SNIP 0.644
Web of Science (2016): Impact factor 2.256
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.97 SJR 0.933 SNIP 0.679
Web of Science (2015): Impact factor 2.27
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.91 SJR 0.901 SNIP 0.665
A comparative analysis of the intestinal metagenomes present in guinea pigs (Cavia porcellus) and humans (Homo sapiens)

Background: Guinea pig (Cavia porcellus) is an important model for human intestinal research. We have characterized the faecal microbiota of 60 guinea pigs using Illumina shotgun metagenomics, and used this data to compile a gene catalogue of its prevalent microbiota. Subsequently, we compared the guinea pig microbiome to existing human gut metagenome data from the MetaHIT project.

Results: We found that the bacterial richness obtained for human samples was lower than for guinea pig samples. The intestinal microbiotas of both species were dominated by the two phyla Bacteroidetes and Firmicutes, but at genus level, the majority of identified genera (320 of 376) were differently abundant in the two hosts. For example, the guinea pig contained considerably more of the mucin-degrading Akkermansia, as well as of the methanogenic archaea Methanobrevibacter than found in humans. Most microbiome functional categories were less abundant in guinea pigs than in humans. Exceptions included functional categories possibly reflecting dehydration/rehydration stress in the guinea pig intestine. Finally, we showed that microbiological databases have serious anthropocentric biases, which impacts model organism research.

Conclusions: The results lay the foundation for future gastrointestinal research applying guinea pigs as models for...
A mouse fecal microbial gene catalogue established by Illumina-based sequencing

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, Division of Toxicology and Risk Assessment, BGI-Shenzhen, Pfizer, National Research Centre for the Working Environment, Sahlgrenska University Hospital, INRA Institut National de La Recherche Agronomique, University of Copenhagen
Number of pages: 1
Publication date: 2012
Peer-reviewed: Yes
Event: Poster session presented at International Human Microbiome Congress organized by MetaHIT, Paris, France.

Establishment of tolerance to commensal bacteria requires a complex microbiota and is accompanied by decreased intestinal chemokine expression

Intricate regulation of tolerance to the intestinal commensal microbiota acquired at birth is critical. We hypothesized that epithelial cell tolerance toward early gram-positive and gram-negative colonizing bacteria is established immediately after birth, as has previously been shown for endotoxin. Gene expression in the intestine of mouse pups born to dams that were either colonized with a conventional microbiota or monocolonized (Lactobacillus acidophilus or Eschericia coli) or germ free was examined on day 1 and day 6 after birth. Intestinal epithelial cells from all groups of pups were stimulated ex vivo with L. acidophilus and E. coli to assess tolerance establishment. Intestine from pups exposed to a conventional microbiota displayed lower expression of Ccl2, Ccl3, Cxcl1, Cxcl2, and Tslp than germ-free mice, whereas genes encoding proteins in Toll-like receptor signaling pathways and cytokines were upregulated. When comparing pups on day
1 and day 6 after birth, a specific change in gene expression pattern was evident in all groups of mice. Tolerance to ex vivo stimulation with E. coli was only established in conventional animals. Colonization of the intestine was reflected in the spleen displaying downregulation of Cxcl2 compared with germ-free animals on day 1 after birth. Colonization reduced the expression of genes involved in antigen presentation in the intestine-draining mesenteric lymph nodes, but not in the popliteal lymph nodes, as evidenced by gene expression on day 23 after birth. We propose that microbial detection systems in the intestine are upregulated by colonization with a diverse microbiota, whereas expression of proinflammatory chemokines is reduced to avoid excess recruitment of immune cells to the maturing intestine.
Freezing fecal samples prior to DNA extraction affects the Firmicutes to Bacteroidetes ratio determined by downstream quantitative PCR analysis

Freezing stool samples prior to DNA extraction and downstream analysis is widely used in metagenomic studies of the human microbiota but may affect the inferred community composition. In this study, DNA was extracted either directly or following freeze storage of three homogenized human fecal samples using three different extraction methods. No consistent differences were observed in DNA yields between extractions on fresh and frozen samples; however, differences were observed between extraction methods. Quantitative PCR analysis was subsequently performed on all DNA samples using six different primer pairs targeting 16S rRNA genes of significant bacterial groups, and the community composition was evaluated by comparing specific ratios of the calculated abundances. In seven of nine cases, the Firmicutes to Bacteroidetes 16S rRNA gene ratio was significantly higher in fecal samples that had been frozen compared to identical samples that had not. This effect was further supported by qPCR analysis of bacterial groups within these two phyla. The results demonstrate that storage conditions of fecal samples may adversely affect the determined Firmicutes to Bacteroidetes ratio, which is a frequently used biomarker in gut microbiology.

General information

State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Bahl, M. I., Bergström, A., Licht, T. R.
Pages: 193-197
Publication date: 2012
Peer-reviewed: Yes

Publication information

Journal: F E M S Microbiology Letters
Volume: 329
Issue number: 2
ISSN (Print): 0378-1097
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.8 SJR 0.79 SNIP 0.58
Web of Science (2017): Impact factor 11.392
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.76 SJR 0.842 SNIP 0.615
Web of Science (2016): Impact factor 12.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.08 SJR 1.156 SNIP 0.756
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.17 SJR 1.136 SNIP 0.767
Web of Science (2014): Impact factor 13.244
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.25 SJR 1.053 SNIP 0.719
Web of Science (2013): Impact factor 13.806
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.25 SJR 1.073 SNIP 0.804
Web of Science (2012): Impact factor 13.231
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.26 SJR 1.105 SNIP 0.764
Web of Science (2011): Impact factor 10.96
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.081 SNIP 0.754
Web of Science (2010): Impact factor 11.796
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.13 SNIP 0.834
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.084 SNIP 0.834
Scopus rating (2007): SJR 1.103 SNIP 0.864
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.105 SNIP 0.86
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1 SNIP 0.8
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.005 SNIP 0.725
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.018 SNIP 0.866
Scopus rating (2002): SJR 0.902 SNIP 0.791
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.944 SNIP 0.752
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.936 SNIP 0.739
Freezing fecal samples prior to DNA extraction affects the Firmicutes to Bacteroidetes ratio determined by downstream quantitative PCR analysis

Freezing stool samples prior to DNA extraction and downstream analysis is widely used in metagenomic studies of the human microbiota but may affect the inferred community composition. In this study DNA was extracted either directly or following freeze storage of three homogenized human fecal samples using three different extraction methods. No consistent differences were observed in DNA yields between extractions on fresh and frozen samples, however differences were observed between extraction methods. Quantitative PCR analysis was subsequently performed on all DNA samples using six different primer pairs targeting 16S rRNA genes of significant bacterial groups and the community composition was evaluated by comparing specific ratios of the calculated abundances. In seven out of nine cases the Firmicutes to Bacteroidetes 16S rRNA gene ratio was significantly higher in fecal samples that had been frozen compared to identical samples that had not. This effect was further supported by qPCR analysis of bacterial groups within these two phyla. The results demonstrate that storage conditions of fecal samples may adversely affect the determined Firmicutes to Bacteroidetes ratio, which is a frequently used biomarker in gut microbiology.

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Bahl, M. I., Bergström, A., Licht, T. R.
Number of pages: 1
Publication date: 2012
Peer-reviewed: No
Event: Abstract from 10th Symposium on Food Microbiology, Helsingør, Denmark.
Electronic versions:
Abstract_LMC_2012_MBAH.pdf
Source: dtu
Source-ID: u::3795
Research output: Research › Conference abstract for conference – Annual report year: 2012

Freezing fecal samples prior to DNA extraction affects the Firmicutes to Bacteroidetes ratio determined by downstream quantitative PCR analysis

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Bahl, M. I., Bergström, A., Licht, T. R.
Number of pages: 1
Publication date: 2012
Peer-reviewed: No
Event: Abstract from 7th Danish Conference on Biotechnology and Molecular Biology, Vejle, Denmark.
Electronic versions:
1.pdf

Bibliographical note
Conference Poster
Research output: Research › Conference abstract for conference – Annual report year: 2012

Gram-negative bacteria account for main differences between faecal microbiota from patients with ulcerative colitis and healthy controls

General information
State: Published
Organisations: National Food Institute, Division of Food Microbiology, Copenhagen University Hospital
Pages: 287-297
Introducing GUt Low-Density Array (GULDA) - a validated approach for qPCR-based intestinal microbial community analysis

Alterations in the human gut microbiota caused, for example, by diet, functional foods, antibiotics, or occurring as a function of age are now known to be of relevance for host health. Therefore, there is a strong need for methods to detect such alterations in a rapid and comprehensive manner. In the present study, we developed and validated a high-throughput real-time quantitative PCR-based analysis platform, termed ‘GUt Low-Density Array’ (GULDA). The platform was designed for simultaneous analysis of the change in the abundance of 31 different microbial 16S rRNA gene targets in fecal samples obtained from individuals at various points in time. The target genes represent important phyla, genera, species, or other taxonomic groups within the five predominant bacterial phyla of the gut, Firmicutes, Bacteroidetes, Actinobacteria, Proteobacteria, and Verrucomicrobia and also Euryarchaeota. To demonstrate the applicability of GULDA, analysis of fecal samples obtained from six healthy infants at both 9 and 18 months of age was performed and showed a significant increase over time of the relative abundance of bacteria belonging to Clostridial cluster IV (Clostridia leptum group) and Bifidobacterium bifidum and concurrent decrease in the abundance of Clostridium butyricum and a tendency for decrease in Enterobacteriaceae over the 9-month period.

General information
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Organisations: National Food Institute, Division of Food Microbiology, Division of Microbiology and Risk Assessment
Pages: 38-47
Publication date: 2012
Peer-reviewed: Yes
Volume: 337
Issue number: 1
ISSN (Print): 0378-1097
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.8 SJR 0.79 SNIP 0.58
Web of Science (2017): Impact factor 11.392
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.76 SJR 0.842 SNIP 0.615
Web of Science (2016): Impact factor 12.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.08 SJR 1.156 SNIP 0.756
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.17 SJR 1.136 SNIP 0.767
Web of Science (2014): Impact factor 13.244
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.25 SJR 1.053 SNIP 0.719
Web of Science (2013): Impact factor 13.806
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.25 SJR 1.073 SNIP 0.804
Web of Science (2012): Impact factor 13.231
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.26 SJR 1.105 SNIP 0.764
Web of Science (2011): Impact factor 10.96
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.081 SNIP 0.754
Web of Science (2010): Impact factor 11.796
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.13 SNIP 0.834
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.084 SNIP 0.834
Scopus rating (2007): SJR 1.103 SNIP 0.864
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.105 SNIP 0.86
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1 SNIP 0.8
Web of Science (2005): Indexed yes
In vitro fermentation of sugar beet arabino-oligosaccharides by fecal microbiota obtained from patients with ulcerative colitis to selectively stimulate the growth of Bifidobacterium spp. and Lactobacillus spp.

The commensal bacteria found in the human gut are important for host health, and an unfavorable composition of the gut microbiota can affect the synergistic interaction that exists between microbes and their host. An altered microbial composition is suggested to play a pivotal role in the pathogenesis of ulcerative colitis (UC), an inflammatory bowel disease, and compositional changes have been observed in the colonic microbiota by us as well as by other research groups 1-3. Since bifidobacteria and lactobacilli may exert anti-inflammatory effects, a reduced level of these commensal bacteria may compromise the colon health and favor intestinal inflammation.

In this study, selective stimulation of fecal bifidobacteria and lactobacilli from healthy subjects and UC patients in remission or with active disease were investigated using arabino-oligosaccharides (AOS; DP2-10) derived from sugar beet pulp. The fermentative-induced changes were compared to those for fructo-oligosaccharides (FOS), which are known to have a prebiotic effect. The fermentation studies were carried out using a validated small-scale static batch system, and changes in the fecal microbial communities and metabolites were monitored after 24 h by quantitative real-time PCR and short-chain fatty acid analysis. With a few minor exceptions, AOS affected the communities similarly to what was seen for FOS. Quantitative real-time PCR revealed that Bifidobacterium spp. and Lactobacillus spp. were selectively increased after fermentation of AOS or FOS by fecal microbiota derived from UC patients. The stimulation of growth of Lactobacillus spp. and Bifidobacterium spp. was accompanied by a high production of acetate and hence a decrease of pH. The fermentation of AOS may thus help improve the inflammatory conditions in UC patients through stimulation of bacteria eliciting anti-inflammatory responses and through production of acetate.

General information

State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, Department of Chemical and Biochemical Engineering, Center for BioProcess Engineering
Number of pages: 1
Publication date: 2012
Peer-reviewed: Yes
Event: Abstract from 10th Symposium on Food Microbiology, Helsingør, Denmark.
Electronic versions:
In vitro fermentation of sugar beet arabino-oligosaccharides - Abstract.pdf
Source: dtu
Source-ID: u::3668
Research output: Research - peer-review » Conference abstract for conference – Annual report year: 2012
pulp. The fermentative-induced changes were compared to those for fructo-oligosaccharides (FOS), which are known to have a prebiotic effect. The fermentation studies were carried out using a validated small-scale static batch system, and changes in the fecal microbial communities and metabolites were monitored after 24 h by quantitative real-time PCR and short-chain fatty acid analysis. With a few minor exceptions, AOS affected the communities similarly to what was seen for FOS. Quantitative real-time PCR revealed that Bifidobacterium spp. and Lactobacillus spp. were selectively increased after fermentation of AOS or FOS by fecal microbiota derived from UC patients. The stimulation of growth of Lactobacillus spp. and Bifidobacterium spp. was accompanied by a high production of acetate and hence a decrease of pH. The fermentation of AOS may thus help improve the inflammatory conditions in UC patients through stimulation of bacteria eliciting anti-inflammatory responses and through production of acetate.

**General information**

**State:** Published

**Organisations:** National Food Institute, Division of Microbiology and Risk Assessment, Department of Chemical and Biochemical Engineering, Center for BioProcess Engineering

**Contributors:** Vigsnæs, L. K., Holck, J., Meyer, A. S., Licht, T. R.

**Publication date:** 2012

**Peer-reviewed:** Yes

**Event:** Abstract from 7th Danish Conference on Biotechnology and Molecular Biology, Vejle, Denmark.

**Electronic versions:**

In vitro fermentation of sugar beet arabin--oligosaccharides - Abstract.pdf

**Source:** dtu

**Source-ID:** u::3669

**Research output:** Research - peer-review › Conference abstract for conference – Annual report year: 2012

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**Metabolic footprint of Lactobacillus acidophilus NCFM at different pH**

Lactobacillus acidophilus NCFM is a well known microorganism from the genomic and probiotic point of view. In order to analyze the potential interactions of NCFM with the surrounding environment, in vitro tests with the metabolic footprinting approach were performed. It was found that NCFM increased the concentration of lactic acid, succinic acid, adenine and arginine in the medium. The metabolism of NCFM did not change significantly between pH 5 and 7, suggesting that other environmental factors than pH might have bigger impact on its colonization throughout the gastrointestinal tract.

**General information**

**State:** Published

**Organisations:** Division of Microbiology and Risk Assessment, National Food Institute, Division of Food Chemistry

**Contributors:** Sulek, K., Frandsen, H. L., Smedsgaard, J., Skov, T. H., Wilcks, A., Licht, T. R.

**Pages:** 244-252

**Publication date:** 2012

**Peer-reviewed:** Yes

**Publication Information**

**Journal:** Metabolomics

**Volume:** 8

**Issue number:** 2

**ISSN (Print):** 1573-3882

**Ratings:**

BFI (2019): BFI-level 2

Web of Science (2019): Indexed yes

BFI (2018): BFI-level 2

Web of Science (2018): Indexed yes

BFI (2017): BFI-level 2

Scopus rating (2017): CiteScore 3.19 SJR 1.122 SNIP 0.841

Web of Science (2017): Impact factor 3.511

Web of Science (2017): Indexed yes

BFI (2016): BFI-level 2

Scopus rating (2016): CiteScore 3.66 SJR 1.186 SNIP 1.054

Web of Science (2016): Impact factor 3.692

Web of Science (2016): Indexed yes

BFI (2015): BFI-level 2

Scopus rating (2015): CiteScore 3.49 SJR 1.318 SNIP 1.113

Web of Science (2015): Impact factor 3.661

Web of Science (2015): Indexed yes
Metabolic footprint of Lactobacillus acidophilus NCFM at different pH

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, Division of Food Chemistry
Number of pages: 1
Publication date: 2012
Peer-reviewed: Yes
Event: Abstract from 7th International Conference of the Metabolomics Society, Cairns, Australia.
Source: dtu
Source-ID: u::3886
Research output: Research - peer-review \ Conference abstract for conference – Annual report year: 2012

Metabolomics of UC bacterial ecosystem compared to the healthy donors

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, Division of Food Chemistry, Ghent University, Copenhagen University Hospital, University of Copenhagen
Metabolomics of UC bacterial ecosystem compared to the healthy donors

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, Division of Food Chemistry, Ghent University, Copenhagen University Hospital
Number of pages: 1
Publication date: 2012
Peer-reviewed: No
Event: Abstract from 7th Danish Conference on Biotechnology and Molecular Biology, Vejle, Denmark.
Electronic versions:
Metabolomics abstract Vejle.pdf
Source: dtu
Source-ID: u::3887
Research output: Research › Conference abstract for conference – Annual report year: 2012

Nature of bacterial colonization influences transcription of mucin genes in mice during the first week of life

In summary, our data show that development of the expression of genes encoding secreted (Muc2/Tff3) and membrane-bound (Muc1/Muc3/Muc4) mucus regulatory proteins, respectively, is distinct and that the onset of this development may be accelerated by specific groups of bacteria present or absent at the mucosal site.

General information
State: Published
Organisations: National Food Institute, Division of Food Microbiology, Center for Biological Sequence Analysis, University of Copenhagen
Number of pages: 7
Pages: 402
Publication date: 2012
Peer-reviewed: Yes

Publication information
Journal: BMC Research Notes
Volume: 5
Issue number: 1
ISSN (Print): 1756-0500
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.54 SJR 0.691 SNIP 0.801
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 1.29 SJR 0.662 SNIP 0.7
Web of Science (2016): Indexed yes
Scopus rating (2015): CiteScore 1.5 SJR 0.74 SNIP 0.757
Prebiotics for Prevention of Gut Infections

It is our postulate that the field of prebiotic research has until now been characterized by a one-view-fits-all approach, implicating that if a putatively prebiotic compound is good for something, it is good for everything. One area where this implication has been proved insufficient regards the putative preventive effect of prebiotics against intestinal pathogenic bacteria. Although indeed most evidence on effects of prebiotics against infections is positive, some studies indicate that prebiotic carbohydrates cause increased susceptibility to specific gastrointestinal infections. Here, we review existing knowledge about the impact of prebiotics on infective agents in vitro and in vivo.
Qualified Presumption of Safety (QPS): an EFSA Tool for Microbial Safety Assessment

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, European Food Safety Authority
Contributors: Leuschner, R., Licht, T. R., Hugas, M.
Number of pages: 1
Publication date: 2012
Peer-reviewed: Yes
Event: Abstract from USP–IFT Workshop on Identity and Characterization of a Probiotic Microorganism used as a Food Ingredient, Rockville, MD, United States.
Electronic versions:
prod11334928942499.USP_Abstract_form_26_03_2012_RENATA.pdf
Source: dtu
Source-ID: u::3672
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2012

The effect of whole-grain compared to refined wheat on the gut microbial composition and integrity in a colonic epithelial cell model following a 12-week energy-restricted dietary intervention in postmenopausal women

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, University of Copenhagen
Contributors: Christensen, E. G., Licht, T. R., Kristensen, M., Bahl, M. I.
Number of pages: 1
Publication date: 2012
Peer-reviewed: No
Event: Abstract from 7th Danish Conference on Biotechnology and Molecular Biology, Vejle, Denmark.
Electronic versions:
prod11340801348884.Abstract_vejle_2012_Ellen_Christensen.pdf

Bibliographical note
Conference Poster
Source: dtu
Source-ID: u::4234
Research output: Research › Conference abstract for conference – Annual report year: 2012

The effect of whole-grain compared to refined wheat on the gut microbial composition and integrity in a colonic epithelial cell model following a 12-week energy-restricted dietary intervention in postmenopausal women
Intake of whole-grain products are considered to decrease the risk of cardiovascular disease (CVD). This effect could potentially be linked to a prebiotic effect, hence positive modulation of the gut microbial composition or activity. Kristensen and coworkers recently conducted a study in postmenopausal women who were randomized to either whole-grain wheat (WW) (n=38) or refined wheat (RW) (n=34) consumption as part of an energy-restricted diet for 12-weeks following a 2-week run-in period with RW. Percentage fat mass as well as serum total and LDL cholesterol were found to differ between the two groups (Kristensen, et al, 2012). We used fecal samples from the same study to examine effects of WW and RW on the bacterial composition by quantitative PCR targeting the phylums Bacteroidetes and Firmicutes, and the genera Bifidobacteria, Lactobacillus, Bacteroides, and Prevotella, as well as the Enterobacteriaceae family. Potential bifidogenic effects were examined in depth by determining the levels of B. bifidum, B. adolescentis, B. catenulatum, and B. longum. The ratios of both Bifidobacteria and Lactobacillus increased following the WW intervention.

The composition of the gut microbiota may affect the intestinal integrity, which in this study was evaluated in vitro by determining transepithelial resistance (TER) across a Caco-2 cell monolayer. Fecal water collected after the run-in period and following the intervention period for 26 participants (WW; 15 participants, RW; 11 participants) were used to determine effects of WW, RW, and microbiota composition on TER. Preliminary results indicate that fecal water from WW and RW both before and after intervention in general had a positive effect on TER, however, there was no difference in TER between WW and RW. Correlations between microbial composition and effect on intestinal integrity indicated a negative correlation between Bifidobacteria and TER as well as a positive correlation between the Firmicutes/Bacteroidetes ratio and TER.

Validation of GUT Low Density Array (GULDA), a novel qPCR approach to the study of the intestinal microbial ecosystem
Causal relationships between the vast numbers of bacterial species present in the human intestines contain a lot of potential information on the regulation of the gut in the healthy as well as in diseased states. Based on the hypothesis that the human gut microbiota constitutes a dynamic ecosystem, interesting correlations between the presences of the given species should exist at any time. In order to analyze this, we have developed GULDA, a cheap, flexible, reliable and high throughput qPCR-based gut low-density array (GULDA), which simultaneously gives the quantities of approximately 40 different selected bacterial 16S rRNA targets on all relevant phylogenetic levels in a given sample of DNA. In comparison to other strategies e.g. metagenomic sequencing and microarrays, GULDA focuses on selected targets only and requires only little complex bioinformatical post-processing.

Given the setup, where one standard qPCR program is used for ~40 primer sets, validation is important. We present here strategies involved in verification of GULDA as a valid tool for analysis of the human gut microbiota.
different selected bacterial 16S rRNA targets on all relevant phylogenetic levels in a given sample of DNA. In comparison to other strategies e.g. metagenomic sequencing and microarrays, GULDA focuses on selected targets only and requires only little complex bioinformatical post-processing.

Given the setup, where one standard qPCR program is used for ~40 primer sets, validation is important. We present here strategies involved in verification of GULDA as a valid tool for analysis of the human gut microbiota.

**General information**
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Number of pages: 1
Publication date: 2012
Peer-reviewed: Yes
Event: Poster session presented at 10th Symposium on Food Microbiology, Helsingør, Denmark.
Electronic versions:
GULDA_validationposter_LMC_2012.pdf
Source: dtu
Source-ID: u::3852
Research output: Research - peer-review › Poster – Annual report year: 2012

**Xylo-oligosaccharides inhibit pathogen adhesion to enterocytes in vitro**

We previously reported that the non-digestible carbohydrates inulin and apple pectin promoted Listeria monocytogenes infection in guinea pigs, whereas xylo- and galacto-oligosaccharides (XOS and GOS), prevented infection by this pathogen. In the present study, mechanisms that could explain the previous in vivo observations were explored. Mixing bacterial cultures with XOS significantly (P < 0.05) decreased the ability of two out of three strains of L. monocytogenes to adhere to Caco-2 cells. Additionally, 2 h incubation with XOS followed by washing of the bacteria significantly (P < 0.05) decreased the ability of all three strains to adhere to Caco-2 cells. Consistently, expression of the adhesion-relevant genes inlA and lap was reduced by the presence of XOS. The observation that XOS inhibit the adhesion of Listeria to the intestinal epithelium in vitro may explain the reported preventive effect of XOS on Listeria infection in guinea pigs in vivo, while the preventive effect of GOS was not explicable by the assays chosen here.

**General information**
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, University of Nebraska
Pages: 22-27
Publication date: 2012
Peer-reviewed: Yes

**Publication Information**
Journal: Research in Microbiology
Volume: 163
Issue number: 1
ISSN (Print): 0923-2508
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.11 SJR 0.82 SNIP 0.848
Web of Science (2017): Impact factor 2.372
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.27 SJR 1.01 SNIP 0.855
Web of Science (2016): Impact factor 2.549
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.08 SJR 1.089 SNIP 0.747
Web of Science (2015): Impact factor 2.154
BFI (2014): BFI-level 1
Daily intake of apples decrease total cholesterol

**General information**

State: Published

Organisations: Division of Toxicology and Risk Assessment, National Food Institute, Division of Microbiology and Risk Assessment, Research Institute of Pomology and Floriculture, Technical University of Denmark, University of Copenhagen


Pages: 272-272

Publication date: 2011

Peer-reviewed: Yes
Effect of the vitamin B12-binding protein haptocorrin present in human milk on a panel of commensal and pathogenic bacteria

Background: Haptocorrin is a vitamin B12-binding protein present in high amounts in different body fluids including human milk. Haptocorrin has previously been shown to inhibit the growth of specific E. coli strains, and the aim of the present study was to elucidate whether the antibacterial properties of this protein may exert a general defense against pathogens and/or affect the composition of the developing microbiota in the gastrointestinal tracts of breastfed infants. Findings: The present work was the first systematic study of the effect of haptocorrin on bacterial growth, and included 34 commensal and pathogenic bacteria to which infants are likely to be exposed. Well-diffusion assays addressing antibacterial effects were performed with human milk, haptocorrin-free human milk, porcine holo-haptocorrin (saturated with B-12) and human apo-haptocorrin (unsaturated). Human milk inhibited the growth of S. thermophilus and the pathogenic strains L. monocytogenes LO28, L. monocytogenes 4446 and L. monocytogenes 7291, but the inhibition could not be ascribed to haptocorrin. Human apo-haptocorrin inhibited the growth of only a single bacterial strain (Bifidobacterium breve), while porcine holo-haptocorrin did not show any inhibitory effect. Conclusions: Our results suggest that haptocorrin does not have a general antibacterial activity, and thereby contradict the existing hypothesis implicating such an effect. The study contributes to the knowledge on the potential impact of breastfeeding on the establishment of a healthy microbiota in infants.
Feruloylated and Nonferuloylated Arabino-oligosaccharides from Sugar Beet Pectin Selectively Stimulate the Growth of Bifidobacterium spp. in Human Fecal in Vitro Fermentations

The side chains of the rhamnogalacturonan I fraction in sugar beet pectin are particularly rich in arabinan moieties, which may be substituted with feruloyl groups. In this work the arabinan-rich fraction resulting from sugar beet pulp based pectin production was separated by Amberlite XAD hydrophobic interaction and membrane separation into four fractions based on feruloyl substitution and arabinono-oligosaccharide chain length: short-chain (DP 2–10) and long-chain (DP 7–14) feruloylated and nonferuloylated arabinono-oligosaccharides, respectively. HPAEC, SEC, and MALDI-TOF/TOF analyses of the fractions confirmed the presence of singly and doubly substituted feruloylated arabinono-oligosaccharides in the feruloyl-substituted fractions. In vitro microbial fermentation by human fecal samples (n = 6 healthy human volunteers) showed a selective stimulation of bifidobacteria by both the feruloylated and the nonferuloylated long-chain arabinono-oligosaccharides to the same extent as the prebiotic fructo-oligosaccharides control. None of the fractions stimulated the growth of the potential pathogen Clostridium difficile in monocultures. This work provides a first report on the separation of potentially bioactive feruloylated arabinono-oligosaccharides from sugar beet pulp and an initial indication of the potentially larger bifidogenic effect of relatively long-chain arabinono-oligosaccharides as opposed to short-chain arabinono-oligosaccharides.

General information
State: Published
Gut Low Density Array (GULDA), a novel qPCR approach to the study of the intestinal microbial ecosystem

Causal relationships between the vast numbers of bacterial species present in the human intestines contain a lot of potential information on the regulation of the gut in the healthy as well as in diseased states. Based on the hypothesis that the human gut microbiota constitutes a dynamic ecosystem, interesting correlations between the presences of the given species should exist at any time. However, due to technical restrictions, it has not previously been possible to analyze such intrinsic bacterial patterns and correlations rapidly for a sufficiently large number of samples. To this purpose, we developed GULDA; a qPCR low-density array with particular focus on bacteria of relevance to the human gut microbiota. The output is given as arbitrary bacterial quantities, which for large sample numbers allow for further characterization of the gut microbiota by uni- and multivariate statistical methods.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Bergström, A., Andersen, J. B., Licht, T. R.
Publication date: 2011
Peer-reviewed: Yes
Event: Abstract from Keystone symposium on Microbial Communities as Drivers of Ecosystem Complexity, Colorado, Denver, USA.
Source: orbit
Source-ID: 277049
Research output: Research - peer-review › Journal article – Annual report year: 2011

Gut Low Density Array (GULDA), a novel qPCR approach to the study of the intestinal microbial ecosystem

Causal relationships between the vast numbers of bacterial species present in the human intestines contain a lot of potential information on the regulation of the gut in the healthy as well as in diseased states. Based on the hypothesis that the human gut microbiota constitutes a dynamic ecosystem, interesting correlations between the presences of the given species should exist at any time. However, due to technical restrictions, it has not previously been possible to analyze such intrinsic bacterial patterns and correlations rapidly for a sufficiently large number of samples. To this purpose, we developed GULDA; a qPCR low-density array with particular focus on bacteria of relevance to the human gut microbiota. The output is given as arbitrary bacterial quantities, which for large sample numbers allow for further characterization of the gut microbiota by uni- and multivariate statistical methods.
In Vitro Fermentation of Sugar Beet Arabino-Oligosaccharides by Fecal Microbiota Obtained from Patients with Ulcerative Colitis To Selectively Stimulate the Growth of Bifidobacterium spp. and Lactobacillus spp.

The potential prebiotic properties of arabino-oligosaccharides (AOS) derived from sugar beet pulp was studied using mixed cultures of human fecal bacteria from patients with ulcerative colitis (UC), in remission or with active disease, and in healthy controls. These results were compared to those for fructo-oligosaccharides (FOS), which are known to have a prebiotic effect. Fermentation studies were carried out using a small-scale static batch system, and changes in the fecal microbial communities and metabolites were monitored after 24 h by quantitative real-time PCR and short-chain fatty acid analysis. With a few minor exceptions, AOS affected the communities similarly to what was seen for FOS. Quantitative real-time PCR revealed that Bifidobacterium spp. and Lactobacillus spp. were selectively increased after fermentation of AOS or FOS by fecal microbiota derived from UC patients. The stimulation of growth of Lactobacillus spp. and Bifidobacterium spp. was accompanied by a high production of acetate and hence a decrease of pH. The fermentation of AOS may help improve the inflammatory conditions in UC patients through stimulation of bacteria eliciting anti-inflammatory responses and through production of acetate. AOS may therefore represent a new prebiotic candidate for reduction of the risk of flare-ups in UC patients. However, human trials are needed to confirm a health-promoting effect.
Listeria monocytogenes strains encoding inlA with premature stop codons are able to infect pregnant mice
Maximal release of highly bifidogenic soluble dietary fibers from industrial potato pulp by minimal enzymatic treatment

Potato pulp is a poorly utilized, high-volume co-processing product resulting from industrial potato starch manufacturing. Potato pulp mainly consists of the tuber plant cell wall material and is particularly rich in pectin, notably galactan branched rhamnogalacturonan I type pectin which has previously been shown to exhibit promising properties as dietary fiber. The objective of this study was to solubilize dietary fibers from potato pulp by a one-step minimal treatment procedure and evaluate the prebiotic potential of the fibers.Statistically designed experiments were conducted to investigate the influence of enzyme type, dosage, substrate level, incubation time, and temperature on the enzyme catalyzed solubilization to define the optimal minimal enzyme treatment for maximal fiber solubilization. The result was a method that within 1 min released 75% [weight/weight (w/w)] dry matter from 1% (w/w) potato pulp treated with 1.0% (w/w) [enzyme/substrate (E/S)] pectin lyase from Aspergillus nidulans and 1.0% (w/w) E/S polygalacturonase from Aspergillus aculeatus at pH 6.0 and 60 °C. Molecular size fractionation of the solubilized fibers revealed two major fractions: one fraction rich in galacturonic acid of 10–100 kDa indicating mainly homogalacturonan, and a fraction >100 kDa rich in galactose, presumably mainly made up of β-1,4-galactan chains of rhamnogalacturonan I. When fermented in vitro by microbial communities derived from fecal samples from three healthy human volunteers, both of the solubilized fiber fractions were more bifidogenic than fructo-oligosaccharides (FOS). Notably the fibers having molecular masses of >100 kDa selectively increased the densities of Bifidobacterium spp. and Lactobacillus spp. 2–3 times more than FOS.
Metagenomic sequencing of the faecal microbiota of guinea pigs fed with prebiotics
Qualified presumption of safety (QPS): a generic risk assessment approach for biological agents notified to the European Food Safety Authority (EFSA) (vol 21, pg 425, 2010)

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Center for Microbial Biotechnology, Department of Systems Biology
Pages: 51-52
Publication date: 2011
Peer-reviewed: Yes

Publication information
Journal: Trends in Food Science & Technology
Volume: 22
Issue number: 1
ISSN (Print): 0924-2244
Ratings:
BFI (2019): BFI-level 2
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 6.67 SJR 2.344 SNIP 2.444
Web of Science (2017): Impact factor 6.609
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 6 SJR 2.357 SNIP 2.775
Web of Science (2016): Impact factor 5.191
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 5.51 SJR 2.232 SNIP 2.626
Web of Science (2015): Impact factor 5.15
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 5.17 SJR 2.173 SNIP 2.767
Web of Science (2014): Impact factor 4.651
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.83 SJR 2.216 SNIP 2.653
Web of Science (2013): Impact factor 4.651
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.91 SJR 2.048 SNIP 2.417
Web of Science (2012): Impact factor 4.135
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Role of Intestinal Microbiota in Ulcerative Colitis – Effects of Novel Carbohydrate Preparations

The microbiota of the human intestinal tract is complex with variable populations of bacteria who are either permanent gut residents (commensal bacteria) or transient inhabitants introduced from the environment. The commensal bacteria are believed to be important for human health due to actions such as protection against pathogens, induction of immune regulatory functions and nutrient processing. Hence, the composition of commensal bacteria is important to preserve colonic health.

Ulcerative colitis (UC) is an inflammatory bowel disease and dysbiosis in the composition of commensals has been reported, which could affect colonic health. In the experimental part of this thesis, the fecal microbiota derived from UC patients in either remission or with active disease and healthy subjects was quantified using quantitative Real-Time PCR (qPCR) to examine the microbiota composition. The results demonstrated that the microbiota composition was different in UC patients in relapse compared to healthy subjects and the difference could be ascribed Gramnegative bacteria, hence indicating that an altered microbiota composition is associated with colonic inflammation. Additionally, results revealed that the microbiota composition in remission either resembled the composition in healthy or in relapse, demonstrating that the microbiota in remission is unstable.

The mucus layer lining the epithelium of the intestinal tract is important for the protection of the epithelium in humans. The commensal bacteria that colonize the colonic mucus are suggested to play an important role in stimulating regulatory immune responses compared to luminal bacteria, since they reside closer to the intestinal epithelial cells. The ability of fecal microbiota derived from healthy subjects and UC patients to colonize mucus was examined in a study of this thesis to elucidate, if the adhesion capacity is different depending on disease state. For this purpose, an in vitro dynamic gut model was used. Several bacterial taxa from both lumen and mucus were
quantified using qPCR. The results revealed that the bacterial community of the mucus differed from that of the lumen and that lactobacilli and bifidobacteria derived from UC patients had a significant decreased capacity to colonize mucus than observed for similar bacterial groups originating from healthy subjects. This suggests that the inflammatory state in UC may influence the adhesion capacity of commensal bacteria such as beneficial Gram-positive bacteria lactobacilli and bifidobacteria.

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Vigsnæs, L. K., Licht, T. R.
Number of pages: 195
Publication date: 2011

Publication information
Original language: English
Electronic versions:
Ph.D. Thesis
Resume af Ph.D. afhandling
Research output: Research › Ph.D. thesis – Annual report year: 2012

Tailored enzymatic production of oligosaccharides from sugar beet pectin and evidence of differential effects of a single DP chain length difference on human faecal microbiota composition after in vitro fermentation
Sugar beet pectin was degraded enzymatically and separated by ion exchange chromatography into series of highly purified homogalacturonides and rhamnogalacturonides. MALDI-TOF/TOF mass-spectrometry was used to determine sizes and structural features. The methodology was based on the sequential use of monocomponent enzymes that were selected to target specific substructures in the sugar beet pectin. Notably pectin lyase and rhamnogalacturonan I lyase were used, which allowed detection of the resulting cleavage products by UV spectroscopy. Seven different homogalacturonides (HG) with degrees of polymerization (DP) from 2 to 8 and six different rhamnogalacturonide (RGI) structures, ranging from DP4 to 6 with defined galactose substitutions were purified. Total recoveries of 200 mg homogalacturonides and 67 mg rhamnogalacturonides per gram sugar beet pectin were obtained. This integrated biorefining method provides an option for advanced upgrading of sugar beet pectin into HG and RGI oligosaccharides of defined size and structure. In vitro microbial fermentation by human faecal samples (n = 9) showed a different response to the DP4 and DP5 HG structures on the ratio between Bacteroidetes and Firmicutes. This indicates that pectic oligosaccharides with only slightly different structures have significantly different biological effects. This is the first report of pectic oligosaccharide activity on gut bacterial populations related to the metabolic syndrome associated with obesity.

General information
State: Published
Organisations: Center for BioProcess Engineering, Department of Chemical and Biochemical Engineering, Division of Microbiology and Risk Assessment, National Food Institute, BioChemical Engineering, University of Southern Denmark
Pages: 1039-1049
Publication date: 2011
Peer-reviewed: Yes

Publication information
Journal: Process Biochemistry
Volume: 46
Issue number: 5
ISSN (Print): 1359-5113
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SJR 0.761 SNIP 1.012
Web of Science (2017): Impact factor 2.616
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.87 SJR 0.825 SNIP 1.087
Original language: English
Keywords: Human faeces, Rhamnogalacturonan oligomers, Ion exchange chromatography, Homogalacturonan oligomers, Sugar beet pectin, In vitro fermentation
DOIs: 10.1016/j.procbio.2011.01.013
The complexity of the murine microbiota influences the important recruitment of immune cells in early life

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Systems Biology
Contributors: Kristensen, M. B., Frøkiær, H., Bergström, A., Licht, T. R.
Publication date: 2011
Peer-reviewed: Yes
Event: Abstract from 9th Symposium on Food Microbiology, Helsingør, Denmark.
Source: orbit
Source-ID: 275712
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2011

The effect of specific fibers and foods on the composition and functionality of the gut microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R.
Publication date: 2011
Peer-reviewed: Yes
Event: Abstract from LMC congress: May, Odense, Denmark.
Source: orbit
Source-ID: 276371
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2011

The pathogenicity of S. Typhimurium SL1344 is coupled to invasiveness and not the ensuing immune response

General information
State: Published
Organisations: Department of Systems Biology, Center for Biological Sequence Analysis, Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Brandt, R., Petersen, A., Pedersen, S. B., Licht, T. R., Frøkiær, H.
Publication date: 2011
Peer-reviewed: Yes
Event: Abstract from 15th International Congress of Mucosal Immunology, Paris, France.
Source: orbit
Source-ID: 276372
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2011

The pathogenicity of S. Typhimurium SL1344 is coupled to invasiveness and not the ensuing immune response

General information
State: Published
Organisations: Department of Systems Biology, Center for Biological Sequence Analysis, Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Brandt, R., Petersen, A., Pedersen, S. B., Licht, T. R., Frøkiær, H.
Publication date: 2011
Peer-reviewed: Yes
Event: Poster session presented at 15th International Congress of Mucosal Immunology, Paris, France.
Source: orbit
Source-ID: 276373
Research output: Research - peer-review › Poster – Annual report year: 2011

The qualified presumption of safety (QPS) concept in support of EFSA risk assessments of notified microorganisms and viruses

General information
Analysis of the intestinal microbiota of oligo-saccharide fed mice exhibiting reduced resistance to Salmonella infection

Certain indigestible carbohydrates, known as prebiotics, are claimed to be beneficial for gut health through a selective stimulation of certain gut microbes including bifidobacteria. However, stimulation of such microbes does not necessarily imply a preventive effect against pathogen infection. We recently demonstrated a reduced resistance to Salmonella infection in mice fed diets containing fructo-oligosaccharides (FOS) or xylo-oligosaccharides (XOS). In the present study, faecal and caecal samples from the same mice were analysed in order to study microbial changes potentially explaining the observed effects on the pathogenesis of Salmonella. Denaturing gradient gel electrophoresis revealed that the microbiota in faecal samples from mice fed FOS or XOS were different from faecal samples collected before the feeding trial as well as from faecal profiles generated from control animals. This difference was not seen for caecal profiles.

Further analysis of faecal samples by real-time PCR demonstrated a significant increase in the Bacteroidetes phylum, the Bacteroides fragilis group and in Bifidobacterium spp. in mice fed FOS or XOS. The observed bifidogenic effect was more pronounced for XOS than for FOS. The Firmicutes phylum and the Clostridium coccoides group were reduced by both FOS and XOS. Surprisingly, no significant differences were detected between faecal samples collected before and after pathogen challenge in any of the groups. Furthermore, no effect of diets on caecal concentrations of short-chain fatty acids was recorded. In conclusion, diets supplemented with FOS or XOS induced a number of microbial changes in the faecal microbiota of mice. The observed effects of XOS were qualitatively similar to those of FOS, but the most prominent bifidogenic effect was seen for XOS. An increased level of bifidobacteria is thus not in itself preventive against Salmonella infection, since the same XOS or FOS-fed mice were previously reported to be more severely affected by Salmonella than control animals.

General information

State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, Division of Toxicology and Risk Assessment
Pages: 271-282
Publication date: 2010
Peer-reviewed: Yes

**Publication information**

Journal: Beneficial Microbes
Volume: 3
Issue number: 1
ISSN (Print): 1876-2883
Ratings:

- Web of Science (2019): Indexed yes
- Web of Science (2018): Indexed yes
- Scopus rating (2017): CiteScore 2.63 SJR 0.962 SNIP 0.79
- Web of Science (2017): Impact factor 2.31
- Web of Science (2016): Indexed yes
- Scopus rating (2016): CiteScore 2.72 SJR 0.95 SNIP 0.787
- Web of Science (2016): Impact factor 2.923
- Scopus rating (2015): CiteScore 2.94 SJR 1.028 SNIP 0.867
- Web of Science (2015): Impact factor 3.301
- Scopus rating (2014): CiteScore 2.05 SJR 0.837 SNIP 0.574
- Web of Science (2014): Impact factor 2.614
- Scopus rating (2013): CiteScore 1.71 SJR 0.763 SNIP 0.66
- Web of Science (2013): Impact factor 1.5
- ISI indexed (2013): ISI indexed yes
- Scopus rating (2012): CiteScore 1 SJR 0.602 SNIP 0.523
Bacterial Impact on the Gut Metabolome

During the last decade, it has become evident that the complex ecosystem of micro-organisms inhabiting the human gut plays an important role for human health. An increasing number of publications have shown that the composition and activity of our intestinal microbiota affects a number of different so-called lifestyle diseases including allergy, obesity, and colorectal cancer, as well as our susceptibility to intestinal infections and inflammation. Additionally, it has become evident that the intestinal microbiota can be modulated by intake of pre- and probiotics. A large number of studies have addressed the effects of dietary interventions on the presence of specific bacterial metabolites, which are anticipated to play a role for gut health. However, such data evidently provide only small parts of the complex puzzle constituting the interactions between diet, microbiota, and mammalian host. This project’s objective is to elucidate the mechanism behind the beneficial effects of pre- and probiotics. This will lead to development of new pre- and probiotics targeting specific lifestyle related disorders. The innovative design of pre- and probiotics will lead to increased value for Danish companies. The major hypotheses to be addressed in the project are as follows: Specific probiotic bacteria growing in an intestinal environment produce metabolites, which are qualitatively and quantitatively different from those produced by the same bacteria in vitro. The production of metabolites by specific probiotic bacteria can be affected by prebiotic substances. The presence of specific prebiotics and/or probiotic bacteria in the intestine induces production of specific metabolites from the host epithelium. These effects will be altered by the presence of other specific bacteria in the gnotobiotic gut. The effects will be different in different gut compartments (e.g. ileum versus colon and mucosa versus lumen). Also metabolites in blood will be affected by probiotic colonization and/or prebiotic administration. To map metabolites, gnotobiotic animal models and in vitro fermentation tests in an anaerobic chamber are used, which allow studies of a simple well-defined intestinal microbiota – in this case Lactobacillus acidophilus NCFM. Usage of Mass Spectrometry makes it possible to measure metabolites in intestinal and other mammalian samples as well as in vitro samples. Newly developed advanced (‘omics-’) methodologies are used for analysis of biological interactions.

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Source: orbit
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Bibliographic review on the potential of microorganisms, microbial products and enzymes to induce respiratory sensitization

The immune system has evolved to protect individuals from microbial pathogens as well as larger parasites. However, the immune system can sometimes react inappropriately to innocuous antigens, triggering allergic reactions. The potential of microorganisms, microbial products and enzymes to induce respiratory sensitization when used as food and feed additives was investigated in this report. A short review of the state-of-the-art methods to predict allergenicity was also conducted. Our results indicate that there is currently no established model to predict the allergenicity of a molecule. Although in-silico models can be useful to predict cross-reactivity between allergens, they do not take into account phenomena like the context of presentation of the antigen to the immune system. There is no realiable, predictive in-vitro or in-vivo model of allergenicity. Cases of occupational allergy to both fungi and bacteria have been documented, but allergic reactions to microorganisms purposely introduced in the work environment seem to concern only a limited number of fungi. Enzymes were more a matter of concern, with 17 out of 71 enzymes investigated in this report being linked to respiratory allergies. Because these risks are well known, enzyme exposures are strictly controlled both by regulatory authorities and companies. The patterns of prevalence of allergic reactions to enzyme indicate that they are more common at the level of enzyme manufacturers and large-scale users than in the general population.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Center for Microbial Biotechnology, Department of Systems Biology, National Research Centre for the Working Environment, Center for Clinical and...
Certain dietary carbohydrates promote *Listeria* infection in a guinea pig model, while others prevent it

It has been proposed that dietary non-digestible carbohydrates can improve host resistance to intestinal infections by stimulating health-promoting bacteria in the gut. However, evidence from in vivo infection studies is scarce, particularly for gram-positive infections. We studied the effect of five non-digestible carbohydrates on the resistance of guinea pigs to *Listeria monocytogenes* infections. Animals were fed a diet supplemented with 10% xylooligosaccharides (XOS), galactooligosaccharides (GOS), inulin, apple pectin or polydextrose for three weeks before oral infection with a mixture of three different fluorescently labeled *L. monocytogenes* strains. Colonisation of *L. monocytogenes* in the intestine was determined by quantification of *L. monocytogenes* in faecal, ileal and caecal samples while translocation was determined by quantification of *L. monocytogenes* in mesenteric lymph nodes, spleen and liver. XOS and GOS significantly (P
Effects of apples and specific apple components on the cecal environment of conventional rats: Role of apple pectin

Background: Our study was part of the large European project ISAFRUIT aiming to reveal the biological explanations for the epidemiologically well-established health effects of fruits. The objective was to identify effects of apple and apple product consumption on the composition of the cecal microbial community in rats, as well as on a number of cecal parameters, which may be influenced by a changed microbiota. Results: Principal Component Analysis (PCA) of cecal microbiota profiles obtained by PCR-DGGE targeting bacterial 16S rRNA genes showed an effect of whole apples in a
long-term feeding study (14 weeks), while no effects of apple juice, puree or pomace on microbial composition in cecum were observed. Administration of either 0.33 or 3.3% apple pectin in the diet resulted in considerable changes in the DGGE profiles. A 2-fold increase in the activity of beta-glucuronidase was observed in animals fed with pectin (7% in the diet) for four weeks, as compared to control animals (P <0.01). Additionally, the level of butyrate measured in these pectin-fed animal was more than double of the corresponding level in control animals (P <0.01). Sequencing revealed that DGGE bands, which were suppressed in pectin-fed rats, represented Gram-negative anaerobic rods belonging to the phylum Bacteroidetes, whereas bands that became more prominent represented mainly Gram-positive anaerobic rods belonging to the phylum Firmicutes, and specific species belonging to the Clostridium Cluster XIVa. Quantitative real-time PCR confirmed a lower amount of given Bacteroidetes species in the pectin-fed rats as well as in the apple-fed rats in the four-week study (P <0.05). Additionally, a more than four-fold increase in the amount of Clostridium cocoides (belonging to Cluster XIVa), as well as of genes encoding butyryl-coenzyme A CoA transferase, which is involved in butyrate production, was detected by quantitative PCR in fecal samples from the pectin-fed animals. Conclusions: Our findings show that consumption of apple pectin (7% in the diet) increases the population of butyrate- and beta-glucuronidase producing Clostridiales, and decreases the population of specific species within the Bacteroidetes group in the rat gut. Similar changes were not caused by consumption of whole apples, apple juice, puree or pomace.
Effects of specific carbohydrates on the intestinal microbiota

The current screening study aimed at testing a set of well-characterized carbohydrates derived from pectic oligosaccharides (POS) from sugar beet for their specific effect on intestinal microbiotas derived from healthy people and from patients suffering from the inflammatory bowel disease designated Ulcerative Colitis (UC). Two such oligosaccharides having different degrees of polymerization, in the following designated S1 and S2, respectively, were tested. Small scale anaerobic fermentation studies were performed to test the effect of S1 and S2 on the composition of the intestinal microbiotas. Changes in the microbial composition were addressed by Denaturing Gradient Gel Electrophoresis, DGGE, using Fructo-Oligosaccharides (FOS, a goldenstandard prebiotic) and glucose as reference substrates. Comparison between the DGGE profiles obtained by fermentations of S1, S2 and FOS showed that S2 produced a DGGE profile different from fermentations of S1 and the control substrate FOS in a Pearson correlation cluster analysis, indicating that the degree of polymerization (DP) was decisive for which bacteria were stimulated by the oligosaccharides. Additionally, DGGE results of this screening study showed that there were no significant differences between the numbers of bands in the fermentations of all four substrates, indicating that S1, S2 and FOS had similar degrees of selectivity.

General information
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Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Center for BioProcess Engineering, Department of Chemical and Biochemical Engineering
Faecal Bacterial Communities in Healthy Controls and Ulcerative Colitis Patients

Ulcerative colitis (UC) is an idiopathic inflammatory bowel disease (IBD) that is characterized by chronic inflammation of the colonic mucosa. The aetiology of IBD is not well understood, however the commensal intestinal microbiota is thought to play an important pathogenetic role. Hence, a detailed knowledge about the composition of the intestinal microbiota may be critical to unravel the pathogenesis of IBD. The aim of this study was to examine if the faecal microbiota of patients with UC differs from that of healthy subjects. Faecal samples were collected from healthy subjects and from UC patients with either clinically inactive or active disease. To analyse the composition of the faecal microbiota, we performed quantitative PCR (qPCR) using species and group-specific primers targeting Bifidobacterium spp., Lactobacillus spp., Firmicutes, Bacteroidetes and Faecalibacterium prausnitzii. Denaturing Gradient Gel Electrophoresis (DGGE) analysis using a universal primer targeting bacterial 16S rRNA genes were carried out in order to identify differences in species composition. The results obtained from the qPCR showed that the UC patients, irrespective of the stage of disease activity had a significantly lower amount of Bacteroidetes compared to the healthy controls (p

Influence of the gut microbiota on transcriptional regulation of genes involved in early life development of the intestinal mucus layer

The interplay between the gut microbiota and the intestinal mucus layer is important both in the maintenance of the epithelial barrier as part of the innate immune defense, and in the conservation of gut homeostasis. Little is known about how the microbiota regulates mucin proteins, which protect the mucosal surfaces of all epithelial linings by physical hindrance or specific binding of pathogenic agents including virus and bacteria. It has been shown that the presence and composition of the microbiota is directly involved in the regulation of gene transcription in the intestinal epithelium. The intestinal mucus layer of germ free mice has been shown to display a distinctly different composition and structure compared to mucus from conventionally bred animals in vitro and in vivo. This points towards an important role of the microbiota in the regulation of mucin production. To which extent expression of all mucin genes are dependent on the presence of microorganisms and whether specific bacteria are capable of regulating mucus production in early life remains, however, to be established. The very first period after birth is believed to be vulnerable for establishment of the gut microbiota and consequently for the health and integrity of the epithelium throughout life. In this period, a development regulated by endogenous factors such as hormones, in parallel with gene regulation caused by the microorganisms present in the gut, takes place. Although the microflora undoubtedly plays a regulatory role in the regulation of production of mucin, the importance of endogenous regulation as opposed to gut microbiota has not been investigated. Four groups of mouse pups (n=8 in each group) from differently colonized dams were analyzed with respect to expression of genes involved in mucin production (muc1-4, tff3) in ileal segments isolated on Day 1 and Day 6 after birth. Additionally, the presence of Lactobacillus and E. coli in the ileal samples was assessed by 16S rRNA gene quantification. The pups in the groups were born from dams that were either: 1) germ free (GF), 2) conventional specific pathogen free (SPF), 3) monocolonized with Lactobacillus acidophilus NCFM (Lb NCFM), or 4) monocolonized with E. coli Nissle (E. coli). All data was found by quantitative real-time PCR (qPCR) on Applied Biosystems platforms. Results from these studies showed interesting differences between the four tested animal groups and the two different days tested, which will be presented at the meeting. This is the first study to examine effects of different colonizing bacteria on mucins related gene expression levels in new born mice. These results may thus improve our understanding of the complex interplay between the gut microbiota and epithelial development in the very early life phases.
Influence of the gut microbiota on transcriptional regulation of genes involved in early life development of the intestinal mucus layer

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Bibliographical note
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Influence of the intrinsic gut microbiota on transcriptional regulation of genes involved in early life development of intestinal epithelial integrity

The interplay between the gut microbiota and the integrity of the intestinal mucus layer is important both in the maintenance of the epithelial barrier as part of the innate immune defense, and in the conservation of gut homeostasis. Interesting parameters are the mucins, which protect the mucosal surfaces of all epithelial linings by physical or specific hindrance of pathogenic species e.g. virus and bacteria. Moreover, the proteins constituting the tight junctions in the apical membrane of the epithelial cells are important as they take part in controlling, which substances can penetrate the barrier from the gut lumen to the blood circulation. Previously, it has been shown that the early life mucus layer in germ-free mice has a distinctly different composition than in conventionally colonized animals. In this study, four groups of differently
Influence of the intrinsic gut microbiota on transcriptional regulation of genes involved in the early life development of intestinal epithelial integrity

The interplay between the gut microbiota and the integrity of the intestinal mucus layer is important both in the maintenance of the epithelial barrier as part of the innate immune defense, and in the conservation of gut homeostasis. Interesting parameters are the mucins, which protect the mucosal surfaces of all epithelial linings by physical or specific hindrance of pathogenic species e.g. virus and bacteria. Moreover, the proteins constituting the tight junctions in the apical membrane of the epithelial cells are important as they take part in controlling, which substances can penetrate the barrier from the gut lumen to the blood circulation. Previously, it has been shown that the early life mucus layer in germ-free mice has a distinctly different composition than in conventionally colonized animals. In this study, four groups of differently colonized mice were used to analyze mRNA expression by real-time quantitative PCR of relevant mucin (Muc1-4) and tight junction genes (JAM-A, E-Cad, Tjp-1) on RNA purified from isolated ileum samples (n=8 in each group). The groups were: 1) Germ Free (GF), 2) Specific Pathogen Free (SPF) i.e. – “conventional microbiota”, 3) NCFM (GF monocolonized with Lactobacillus NCFM), 4) E.coli (GF monocolonized with E.coli). Ileal samples were taken on day 1 and day 6 after birth in order to analyze early life developmental parameters. On the day 6 samples, mucin-related mRNA’s showed significantly higher expression levels in the GF animals compared to the SPF animals, possibly as part of protective mechanism. Monocolonization with Lactobacillus NCFM and E.coli seemed to decrease levels towards levels observed in the SPF animals (except for Muc-3 in E.coli). Two of the tight junction genes (JAM-A, E-Cad) showed similar tendencies, whereas Tjp-1 showed high levels in both GF and SPF. Cornelli EM et al (2008) have shown very similar results on the mucin genes, when colonizing with human adult or baby “full” microbiota. This is the first study with monocolonization however. Finally, we observed inverse correlation between Muc-1 and Lactobacillus 16S rRNA expression. The analysis of the day 1 samples is ongoing and results will be presented at the meeting.

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Contributors: Bergström, A., Kristensen, M. B., Frøkjær, H., Licht, T. R.
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Lactobacillus acidophilus induces a slow but more sustained chemokine and cytokine response in naïve foetal enterocytes compared to commensal Escherichia coli

The first exposure to microorganisms at mucosal surfaces is critical for immune maturation and gut health. Facultative anaerobic bacteria are the first to colonise the infant gut, and the impact of these bacteria on intestinal epithelial cells (IEC) may be determinant for how the immune system subsequently tolerates gut bacteria. RESULTS: To mirror the influence of the very first bacterial stimuli on infant IEC, we isolated IEC from mouse foetuses at gestational day 19 and from germfree neonates. IEC were stimulated with gut-derived bacteria, Gram-negative Escherichia coli Nissle and Gram-positive...
Lactobacillus acidophilus NCFM, and expression of genes important for immune regulation was measured together with cytokine production. E. coli Nissle and L. acidophilus NCFM strongly induced chemokines and cytokines, but with different kinetics, and only E. coli Nissle induced down-regulation of Toll-like receptor 4 and up-regulation of Toll-like receptor 2. The sensitivity to stimulation was similar before and after birth in germ-free IEC, although Toll-like receptor 2 expression was higher before birth than immediately after. CONCLUSIONS: In conclusion, IEC isolated before gut colonisation occurs at birth, are highly responsive to stimulation with gut commensals, with L. acidophilus NCFM inducing a slower, but more sustained response than E. coli Nissle. E. coli may induce intestinal tolerance through very rapid up-regulation of chemokine and cytokine genes and down-regulation of Toll-like receptor 4, while regulating also responsiveness to Gram-positive bacteria.
New Insights on the Apple and Health

Regular consumption of fruits and vegetables is associated with reduced risks of certain cancers, cardiovascular diseases, stroke, Alzheimer disease etc. In this project, we focused on apples as a model fruit for some of this research due to its high contents of soluble and insoluble fibers, flavonoids and phenolic acids and because of the high intakes of apples in northern parts of Europe. A series of 4-16 w rat feeding studies with fresh whole apples, dried apple, apple puree, clear and cloudy apple juices, apple pomace, and apple pectins have been conducted. A human cross-over dietary intervention study in 24 healthy volunteers with apple and apple products has also been performed. They supplemented a polyphenol and pectin restricted diet with whole apples, apple pomace, cloudy or clear apple juices or nothing for 4 weeks. Feeding rats with 10g apple/d reduced plasma total, HDL cholesterol, and VLDL cholesterol at 4w and 16w without significantly affecting cholesterol ratios, plasma triacylglycerols, or gastrointestinal transit times. Screening the genes coding for 16s RNA in the intestinal flora and applying multivariate statistics revealed significant changes in the flora related to feeding with apple or apple pectin. This was also reflected in changed gut flora enzymatic activities, whereas caecum short chain fatty acid concentrations were unaffected by feeding with all apple products, except high doses of apple pectin. In the human study the whole apple had the strongest hypocholesterolemic effect, followed by apple pomace and cloudy apple juice. The clear apple juice, which is free of cell wall components showed adverse effect on serum cholesterol concentration and the effect differed markedly compared to the other apple products. There was no effect on HDL-cholesterol, triacylglycerol, bile acid excretion, weight, waist-to-hip circumference or blood pressure. We conclude that the cholesterol-lowering effect of apples is most likely due to the content of soluble fibre in combination with other cell wall components.

Oxygen restriction increases the infection potential of Listeria monocytogenes - a transcriptional analysis.

Listeria monocytogenes has been implicated in several food borne outbreaks as well as sporadic cases of disease during the last two decades. Increased understanding of the biology of this organism is important in the prevention of food borne listeriosis. This is highly relevant for safety assessment of this organism in food. We have previously shown (Andersen et al., BMC Microbiology; 2007, 7:55) that the environmental conditions to which L. monocytogenes is exposed prior to
ingestion are decisive for its in vivo infective potential in the gastrointestinal tract after passage of the gastric barrier. Infection of Caco-2 cells revealed that Listeria cultivated under oxygen-restricted conditions were approximately 100 fold more invasive than similar cultures grown without oxygen restriction. This means that not only the number of Listeria present in a given food item, but that also the physiological condition of these bacteria is important for food safety. The in vitro and in vivo data suggest that an oxygen-restricted L. monocytogenes cell represents a significantly higher risk than a cell grown without oxygen restriction. In order to identify transcriptional differences contributing to different invasiveness, microarray gene chip technology was applied to cDNA created from RNA isolated from oxygen restricted and non-restricted cultures. The analysis confirmed several relevant genes to be differentially transcribed in the two environmental conditions e.g. genes related to virulence potential of Listeria monocytogenes.

Qualified Presumption of Safety (QPS) is a generic risk assessment approach applied by the European Food Safety Authority (EFSA)

Qualified Presumption of Safety (QPS) is a generic risk assessment approach applied by the European Food Safety Authority (EFSA) to notified biological agents aiming at simplifying risk assessments across different scientific Panels and Units. The aim of this review is to outline the implementation and value of the QPS assessment for EFSA and to explain its principles such as the unambiguous identity of a taxonomic unit, the body of knowledge including potential safety concerns and how these considerations lead to a list of biological agents recommended for QPS which EFSA keeps updated through an annual scientific review and assessment.

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Web of Science (2015): Impact factor 5.15
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Contributors: EFSA Publication
The effect of different in vitro conditions on the metabolic footprint of Lactobacillus acidophilus NCFM

Background and objective: The present project is part of the large ISAFRUIT project, where one of the objectives is to identify effects of apple and apple product on parameters related to gut health. In a previous rat study we observed changes in the intestinal microbiota of rats fed whole apples, pomace or apple pectin ([1], and we were interested in finding out if the same effect can be observed in humans. Method: The study was conducted as a randomized, controlled 5 x 28 days cross-over study with 24 healthy persons of both genders. The persons were following a pectin- and polyphenol free restriction diet during the control period, and in the four other periods it was supplied with four different apple based supplements. Between the diets there was a 2-week wash-out period still on the restriction diet. The four apple based supplements were: 1) whole apples, 2) clear apple juice (pectin-free), 3) cloudy juice (apple juice with pulp), and 4) pomace (press cake from the cloudy juice production process). Fecal samples were taken before and after each diet period. After DNA extraction, Denaturing Gradient Gel Electrophoresis (DGGE) with universal primers and specific primers for bifidobacteria and Clostridium cluster XIVa was performed. Bands differing between the periods were sequenced, and qPCR was performed to verify the changes observed by DGGE. Results: Changes in the microbiota was observed by DGGE in persons consuming whole apples and pomace. In contrast, the two juice supplements did not show any effect on the microbiota by DGGE. Conclusion: Consumption of whole apples or pomace is able to modify the intestinal microbiota of humans.
The Influence of Different Apple Based Supplements on the Intestinal Microbiota of Humans.

Background and objective: The present project is part of the large ISAFRUIT project, where one of the objectives is to identify effects of apple and apple product on parameters related to gut health. In a previous rat study we observed changes in the intestinal microbiota of rats fed whole apples, pomace or apple pectin ([1], and we were interested in finding out if the same effect can be observed in humans. Method: The study was conducted as a randomized, controlled 5 x 28 days cross-over study with 24 healthy persons of both genders. The persons were following a pectin- and polyphenol free restriction diet during the control period, and in the four other periods it was supplied with four different apple based supplements. Between the diets there was a 2-week wash-out period still on the restriction diet. The four apple based supplements were: 1) whole apples, 2) clear apple juice (pectin-free), 3) cloudy juice (apple juice with pulp), and 4) pomace (press cake from the cloudy juice production process). Fecal samples were taken before and after each diet period. After DNA extraction, Denaturing Gradient Gel Electrophoresis (DGGE) with universal primers and specific primers for bifidobacteria and Clostridium cluster XIVa was performed. Bands differing between the periods were sequenced, and qPCR was performed to verify the changes observed by DGGE. Results: Changes in the microbiota was observed by DGGE in persons consuming whole apples and pomace. In contrast, the two juice supplements did not show any effect on the microbiota by DGGE. Conclusion: Consumption of whole apples or pomace is able to modify the intestinal microbiota of humans.

Xylooligosaccharides reduce protein-induced faecal water genotoxicity and alter bacterial populations in a two-stage continuous fermenter

Comparison of three Listeria monocytogenes strains in a guinea-pig model simulating food-borne exposure

Three different Listeria monocytogenes strains, LO28 (a laboratory strain with truncated InlA), 4446 (a clinical isolate) and 7291 (a food isolate), were compared in a guinea-pig model designed to mimic food-borne exposure. The objectives were (1) to verify the applicability of the animal model for distinguishing between Listeria with different virulence properties and (2) to explore whether it was possible to reduce the required number of animals by dosing with mixed cultures instead of monocultures. Consistent with in vitro observations of infectivity in Caco-2 cells, faecal densities and presence in selected organs were considerably lower for LO28 than for the other two strains. Additionally, the animal study revealed a
difference in prevalence in faeces as well as in internal organs between the clinical isolate and the food isolate, which was not reproduced in vitro. Dosage with monocultures of Listeria strains gave similar results as dosage with a mixture of the three strains; thus, the mixed infection approach was a feasible way to reduce the number of animals needed for determination of listerial virulence.
Does an onion-enriched diet beneficially affect the microbiotal composition in healthy human subjects?

Regular onion consumption may have many beneficial effects on human health due mainly to well documented probiotic and antioxidant effects. Health effects comprise e.g. anti-inflammatory, anti-tumorigenic, cardiovascular, and gastrointestinal properties. However little is known of the specific mechanisms involved. Onions are rich in fructooligosaccharides (FOS), which are well acknowledged prebiotic substances. FOS consumption have previously been associated with an increased level of fermenting bacterial genera e.g. Lactobacillus and Bifidobacterium. Generally, these groups of bacteria are considered to have beneficial effects on the intestinal environment. The aim of the present study was to analyze the effects of onion consumption on the gut microbiotal profile. In this project, five male and five female subjects were randomized to two 14 days intervention periods including one onion enriched diet and one non-enriched supplemented diet in a double-blinded crossover design with a 25 days wash-out period in between. Six of the subjects delivered fecal samples on the last two days before starting on the diet and on the two last days of the 14 day diet. Total DNA was isolated from these samples using the Qiagen Stool Kit and subsequently quantitative PCR was performed with primers representing the Genera: Lactobacillus, Bifidobacterium, Bacteroidetes, and Clostridium to analyze effects of onion consumption on the gut microbial composition. Moreover, principal component analysis of profiles of the faecal microbiota obtained by denaturing gradient gel electrophoresis of PCR amplified universal bacterial 16S rRNA genes was done to analyze for differences in the phylogenetic profiles as a consequence of the onion consumption. Results from these experiments will be presented at the LMC symposium.
Effect of apple pectin on gut microbiota - qPCR in applied microbiology
This study was part of the large European project ISAFRUIT aiming to reveal the biological explanations for the epidemiologically well-established health effects of fruits. The objective was to identify effects of apple and apple product consumption on the composition of the cecal microbial community in rats, as well as on a number of cecal parameters, which could be influenced by a changed microbiota. Principal Component Analysis (PCA) of cecal microbiota profiles obtained by PCR-DGGE targeting bacterial 16S rRNA genes showed an effect of whole apples in a long-term feeding study (14 weeks), while no effects of apple juice, purée or pomace on microbial composition in cecum were observed. Administration of pectin derived from apples resulted in considerable changes of these DGGE profiles. A 2-fold increase in the activity of beta-glucuronidase was observed in animals fed with pectin (7% in the diet) for four weeks, as compared to control animals (P

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Research output: Research › Conference abstract for conference – Annual report year: 2009

Effect of onion consumption on the composition of the gut microbiota
This study was part of the large European project ISAFRUIT aiming to reveal the biological explanations for the epidemiologically well-established health effects of fruits. The objective was to identify effects of apple and apple product consumption on the composition of the cecal microbial community in rats, as well as on a number of cecal parameters, which could be influenced by a changed microbiota. Principal Component Analysis (PCA) of cecal microbiota profiles obtained by PCR-DGGE targeting bacterial 16S rRNA genes showed an effect of whole apples in a long-term feeding study (14 weeks), while no effects of apple juice, purée or pomace on microbial composition in cecum were observed. Administration of pectin derived from apples resulted in considerable changes of these DGGE profiles. A 2-fold increase in the activity of beta-glucuronidase was observed in animals fed with pectin (7% in the diet) for four weeks, as compared to control animals (P

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Effect of onion consumption on the composition of the gut microbiota

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Research output: Research - peer-review › Report – Annual report year: 2009

Handling and describing metabolomics data more rationally

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Publication date: 2009
Peer-reviewed: No
Event: Abstract from NuGO and SYSDIET Metabolomics workshop, Copenhagen, Denmark.
Source: orbit
Source-ID: 245616
Research output: Research › Conference abstract for conference – Annual report year: 2009

Molecular fingerprinting of the interaction of carbohydrates and gut microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Publication date: 2009
Peer-reviewed: No
Source: orbit
Source-ID: 250041
Research output: Research › Conference abstract for conference – Annual report year: 2009
Oxygen restriction and virulence of *Listeria monocytogenes*: A transcriptome analysis

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Andersen, J. B., Licht, T. R.
Publication date: 2009

**Event information**
Event: 7th Symposium of Food Microbiology
Location: Helsingør, Denmark
Keywords:
Source: orbit
Source-ID: 245316
Research output: Research › Sound/Visual production (digital) – Annual report year: 2009

**Oxygen restriction and virulence of *Listeria monocytogenes*: A transcriptome analysis**

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Microbial Ecology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Andersen, J. B., Bergström, A., Hansen, T. B., Roldgaard, B., Christensen, B. B., Boye, M., Licht, T. R.
Number of pages: 44
Publication date: 2009

**Host publication information**
Title of host publication: 7th Symposium on Food Microbiology: Abstracts
Place of publication: Copenhagen
Publisher: LMC
Source: orbit
Source-ID: 245315
Research output: Research › Conference abstract in proceedings – Annual report year: 2009

**Oxygen restriction increases the infection potential of Listeria monocytogenes – verification of microarray chip data by quantitative real-time PCR**

*Listeria monocytogenes* has been implicated in several food borne outbreaks as well as sporadic cases of disease during the last two decades. Increased understanding of the biology of this organism is important in the prevention of food borne listeriosis. This is highly relevant for safety assessment of this organism in food. We have previously shown (Andersen et al., BMC Microbiology; 2007, 7:55) that the environmental conditions to which *L. monocytogenes* is exposed prior to ingestion are decisive for its in vivo infective potential in the gastrointestinal tract after passage of the gastric barrier. Infection of Caco-2 cells revealed that *Listeria* cultivated under oxygen-restricted conditions were approximately 100 fold more invasive than similar cultures grown without oxygen restriction. This means that not only the number of *Listeria* present in a given food item, but that also the physiological condition of these bacteria is important for food safety. The in vitro and in vivo data suggest that an oxygen-restricted *L. monocytogenes* cell represents a significantly higher risk than a cell grown without oxygen restriction. In order to identify transcriptional differences contributing to different invasiveness, microarray gene chip technology was applied to cDNA created from RNA isolated from oxygen restricted and non-restricted cultures. The analysis confirmed several relevant genes to be differentially transcribed in the two environmental conditions e.g. genes related to virulence potential of *Listeria monocytogenes*. Quantitative PCR was used to verify the quantitative differences identified with the microarray chip for a selection of relevant and differentially transcribed genes.

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Bergström, A., Andersen, J. B., Christensen, B. B., Licht, T. R.
Publication date: 2009
Peer-reviewed: No
Event: Poster session presented at 4th International qPCR Symposium & Industrial Exhibition & Application Workshop, Freising, Germany.
Electronic versions:
jens poster 040309 vester kopi.ppt
Source: orbit
Source-ID: 246140
Oxygen restriction increases the infection potential of Listeria monocytogenes – verification of microarray chip data by quantitative real-time PCR

Listeria monocytogenes has been implicated in several food borne outbreaks as well as sporadic cases of disease during the last two decades. Increased understanding of the biology of this organism is important in the prevention of food borne listeriosis. This is highly relevant for safety assessment of this organism in food. We have previously shown (Andersen et al., BMC Microbiology; 2007, 7:55) that the environmental conditions to which L. monocytogenes is exposed prior to ingestion are decisive for its in vivo infective potential in the gastrointestinal tract after passage of the gastric barrier. Infection of Caco-2 cells revealed that Listeria cultivated under oxygen-restricted conditions were approximately 100 fold more invasive than similar cultures grown without oxygen restriction. This means that not only the number of Listeria present in a given food item, but that also the physiological condition of these bacteria is important for food safety. The in vitro and in vivo data suggest that an oxygen-restricted L. monocytogenes cell represents a significantly higher risk than a cell grown without oxygen restriction. In order to identify transcriptional differences contributing to different invasiveness, microarray gene chip technology was applied to cDNA created from RNA isolated from oxygen restricted and non-restricted cultures. The analysis confirmed several relevant genes to be differentially transcribed in the two environmental conditions e.g. genes related to virulence potential of Listeria monocytogenes. Quantitative PCR was used to verify the quantitative differences identified with the microarray chip for a selection of relevant and differentially transcribed genes.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Bergström, A., Andersen, J. B., Christensen, B. B., Licht, T. R.
Publication date: 2009
Peer-reviewed: No
Event: Abstract from 4th International qPCR Symposium & Industrial Exhibition & Application Workshop, Freising, Germany.
Source: orbit
Source-ID: 246144
Research output: Research › Conference abstract for conference – Annual report year: 2009

Pediocin PA-1 and a pediocin producing Lactobacillus plantarum strain do not change the HMA rat microbiota

The bacteriocin pediocin PA-1 has potential use as a food biopreservative, and understanding its effect on the commensal gut microbiota is important for assessment of consumer risks associated with the use of biopreservative cultures. Effects of ingested (i) pediocin PA-1 producing Lactobacillus plantarum DDEN 11007, (ii) the plasmid cured pediocin negative L. plantarum DDEN 12305, or (iii) supernatants of either of these two strains on the composition of the intestinal microbiota of Human Microbiota Associated (HMA) rats were examined by selective cultivation and molecular methods. The culturable microbiota was in all treatments dominated by lactic acid bacteria and coliforms and no changes in the rat commensal microbiota were detected after ingestion of either of the two L plantarum strains as determined by both culturable methods and molecular methods (DGGE). Both strains were detected in the faeces after ingestion. Pediocin PA-1 did not mediate changes of the rat microbiota, and a biological assay indicated that the bacteriocin was degraded or inactivated during passage through the intestine.

General information
State: Published
Organisations: Section for Aquatic Microbiology and Seafood Hygiene, National Institute of Aquatic Resources, National Food Institute, Division of Microbiology and Risk Assessment
Pages: 251-257
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: International Journal of Food Microbiology
Volume: 130
Issue number: 3
ISSN (Print): 0168-1605
Ratings:
BFI (2019): BFI-level 2
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 3.76 SJR 1.366 SNIP 1.436
Web of Science (2017): Impact factor 3.451
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.97 SJR 1.481 SNIP 1.553
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.02 SJR 1.614 SNIP 1.683
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.62 SJR 1.493 SNIP 1.695
Web of Science (2014): Impact factor 3.082
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3.8 SJR 1.612 SNIP 1.841
Web of Science (2013): Impact factor 3.155
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.7 SJR 1.603 SNIP 1.705
Web of Science (2012): Impact factor 3.425
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63 SJR 1.607 SNIP 1.713
Web of Science (2011): Impact factor 3.327
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.61 SNIP 1.666
Web of Science (2010): Impact factor 3.143
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.475 SNIP 1.539
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.442 SNIP 1.509
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.349 SNIP 1.692
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.541 SNIP 1.788
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.511 SNIP 1.834
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.502 SNIP 1.638
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.233 SNIP 1.612
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.226 SNIP 1.289
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.031 SNIP 1.506
Some putative prebiotics increase the severity of Salmonella enterica serovar Typhimurium infection in mice

Prebiotics are non-digestible food ingredients believed to beneficially affect host health by selectively stimulating the growth of the beneficial bacteria residing in the gut. Such beneficial bacteria have been reported to protect against pathogenic infections. However, conflicting results on prevention of Salmonella infections with prebiotics have been published. The aim of the present study was to examine whether S. Typhimurium SL1344 infection in mice could be prevented by administration of dietary carbohydrates with different structures and digestibility profiles. BALB/c mice were fed a diet containing 10% of either of the following carbohydrates: inulin, fructo-oligosaccharide, xylo-oligosaccharide, galacto-oligosaccharide, apple pectin, polydextrose or beta-glucan for three weeks prior to oral Salmonella challenge (10^7 CFU) and compared to mice fed a cornstarch-based control diet. RESULTS: The mice fed with diets containing fructo-oligosaccharide (FOS) or xylo-oligosaccharide (XOS) had significantly higher (P <0.01 and P <0.05) numbers of S. Typhimurium SL1344 in liver, spleen and mesenteric lymph nodes when compared to the mice fed with the cornstarch-based control diet. Significantly increased amounts (P <0.01) of Salmonella were detected in ileal and fecal contents of mice fed with diets supplemented with apple pectin, however these mice did not show significantly higher numbers of S. Typhimurium in liver, spleen and lymph nodes than animals from the control group (P <0.20). The acute-phase protein haptoglobin was a good marker for translocation of S. Typhimurium in mice. In accordance with the increased counts of Salmonella in the organs, serum concentrations of haptoglobin were significantly increased in the mice fed with FOS or XOS (P <0.001). Caecum weight was increased in the mice fed with FOS (P <0.01), XOS (P <0.01), or polydextrose (P <0.001), and caecal pH was reduced in the mice fed with polydextrose (P <0.001). In vitro fermentation in monocultures revealed that S. Typhimurium SL1344 is capable of fermenting FOS, beta-glucan and GOS with a corresponding decline in pH. CONCLUSION: Supplementing a cornstarch-based rodent diet with 10% FOS or XOS was found to increase the translocation of S. Typhimurium SL1344 to internal organs in mice, while 10% apple pectin was found to increase the numbers of S. Typhimurium in intestinal content and feces.

General information

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Innate Immunology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Department of Systems Biology, Division of Toxicology and Risk Assessment
Number of pages: 11
Pages: 245
Publication date: 2009
Peer-reviewed: Yes

Publication information

Journal: B M C Microbiology
Volume: 9
ISSN (Print): 1471-2180
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.95 SJR 1.242 SNIP 0.953
Web of Science (2017): Impact factor 2.829
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.82 SJR 1.282 SNIP 0.993
Research output: Research - peer-review › Journal article – Annual report year: 2009
Effect of apple pectin consumption on the rat caecal microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment, University of Copenhagen
Publication date: 2008

Event information
Event: LMC 6th Symposium on Food Microbiology
Location: Helsingør, Denmark
Source: orbit
Source-ID: 250181
Research output: Research › Sound/Visual production (digital) – Annual report year: 2008

Effects of apple pectin consumption on the rat caecal microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Publication date: 2008
Peer-reviewed: No
Event: Abstract from 6th Joint INRA-RRI Symposium on Gut Microbiome, Functionality, Interaction with the host and Impact on the environment, Clermont-Ferrand, France.
Source: orbit
Source-ID: 234073
Research output: Research › Conference abstract for conference – Annual report year: 2008

Effects of apple pectin consumption on the rat caecal microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Publication date: 2008
Peer-reviewed: No
Effects of apple pectin consumption on the rat caecal microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Publication date: 2008
Peer-reviewed: No
Event: Abstract from 3rd Danish Conference on Biotechnology and Molecular Biology, Vejle, Denmark.
Source: orbit
Source-ID: 234063
Research output: Research › Conference abstract for conference – Annual report year: 2008

Effects of apple pectin consumption on the rat caecal microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Publication date: 2008
Peer-reviewed: No
Event: Abstract from 3rd Danish Conference on Biotechnology and Molecular Biology, Vejle, Denmark.
Source: orbit
Source-ID: 234067
Research output: Research › Poster – Annual report year: 2008

Germination and conjugation of Bacillus thuringiensis subsp. israelensis in the intestine of gnotobiotic rats

Aims: To study the ability of Bacillus thuringiensis subsp. israelensis spores to germinate and subsequently transfer a conjugative plasmid in the intestinal tract of gnotobiotic rats. Methods and Results: Germination was studied by feeding germ-free rats with spores of a B. thuringiensis strain harbouring a plasmid encoding green fluorescent protein (GFP), which enabled quantification of germinated bacteria by flow cytometry. To study in vivo conjugation, germ-free rats were first associated with a B. thuringiensis recipient strain and after 1 week an isogenic donor strain harbouring the conjugative plasmid pXO16 was introduced. Both strains were given as spores and transfer of pXO16 was observed from the donor to the recipient strain. Conclusions: Bacillus thuringiensis is able to have a full life cycle in the intestine of gnotobiotic rats including germination of spores, several cycles of growth and sporulation of vegetative cells. For the first time conjugative plasmid transfer in a mammalian intestinal tract was shown between two B. thuringiensis strains. Significance and Impact of the Study: Strains of B. thuringiensis are used worldwide to combat insect pests, and this study brings new insights into the nature of B. thuringiensis showing the potential of the bacteria to germinate and transfer DNA in the mammalian intestinal tract.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Microbiology
Pages: 1252-1259
Publication date: 2008
Peer-reviewed: Yes

Publication information
Journal: Journal of Applied Microbiology
Volume: 104
Issue number: 5
ISSN (Print): 1364-5072
Ratings:
BFI (2019): BFI-level 1
Impact of first bacterial colonizers on immune system development

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Contributors: Kristensen, M. B., Fink, L. N., Metzdorff, S. B., Frøkiær, H., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Abstract from 3rd Danish Conference on Biotechnology and Molecular Biology, Vejle, Denmark.
Source: orbit
Source-ID: 234052
Research output: Research › Conference abstract for conference – Annual report year: 2008

Impact of first bacterial colonizers on immune system development

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Contributors: Kristensen, M. B., Fink, L. N., Metzdorff, S. B., Frøkiær, H., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at 3rd Danish Conference on Biotechnology and Molecular Biology, Vejle, Denmark.
Source: orbit
Source-ID: 234055
Research output: Research › Poster – Annual report year: 2008

Impact of first bacterial colonizers on immune system development

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Center for Biological Sequence Analysis, Department of Systems Biology, Division of Toxicology and Risk Assessment
Contributors: Kristensen, M. B., Fink, L. N., Zeuthen, L., Metzdorff, S. B., Frøkiær, H., Licht, T. R.
Publication date: 2008
Event information
Event: Workshop i Nutritional Immunology
Location: Helsingør, Denmark
Source: orbit
Source-ID: 235672
Research output: Research › Sound/Visual production (digital) – Annual report year: 2008

Impact of first bacterial colonizers on immune system development and homeostasis

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Center for Biological Sequence Analysis, Department of Systems Biology
Contributors: Kristensen, M. B., Fink, L. N., Metzdorff, S. B., Frøkiær, H., Licht, T. R.
Publication date: 2008
Event information
Event: 6th Joint INRA-RRI Symposium on Gut Microbiome, Functionality, Interaction with the host and Impact on the environment
Location: Clermont-Ferrand, France
Source: orbit
Source-ID: 235669
Research output: Research › Sound/Visual production (digital) – Annual report year: 2008
Prebiotics for prevention of Listeria infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Contributors: Ebersbach, T., Poulsen, M., Lahtinen, S., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at Symposium for Biotech Research, Lyngby, Denmark.
Source: orbit
Source-ID: 233896
Research output: Research › Poster – Annual report year: 2008

Prebiotics for prevention of Listeria infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Contributors: Ebersbach, T., Poulsen, M., Lahtinen, S., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Abstract from 6th Joint INRA-RRI Symposium on Gut Microbiome, Functionality, Interaction with the host and Impact on the environment, Clermont-Ferrand, France.
Source: orbit
Source-ID: 233884
Research output: Research › Conference abstract for conference – Annual report year: 2008

Prebiotics for prevention of Listeria infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Contributors: Ebersbach, T., Poulsen, M., Lahtinen, S., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at 6th Joint INRA-RRI Symposium on Gut Microbiome, Functionality, Interaction with the host and Impact on the environment, Clermont-Ferrand, France.
Source: orbit
Source-ID: 233885
Research output: Research › Poster – Annual report year: 2008

Prebiotics for prevention of Listeria infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Ebersbach, T., Poulsen, M., Lahtinen, S., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at 2nd ASM Conference on Beneficial Microbes, San Diego, CA, United States.
Source: orbit
Source-ID: 233893
Research output: Research › Poster – Annual report year: 2008

Prebiotics for prevention of Listeria infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Ebersbach, T., Poulsen, M., Lahtinen, S., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at 2nd ASM Conference on Beneficial Microbes, San Diego, CA, United States.
Source: orbit
Source-ID: 233894
Prebiotics for prevention of Listeria infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Ebersbach, T., Poulsen, M., Ouwehand, A., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Abstract from Symposium for Biotech Research, Lyngby, Denmark.
Source: orbit
Source-ID: 233895

Prebiotics for Prevention of Listeria infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Jørgensen, J. B., Ebersbach, T., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Abstract from 3rd Danish Conference on Biotechnology and Molecular Biology, Vejle, Denmark.
Source: orbit
Source-ID: 233953

Prebiotics for Prevention of Listeria infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Jørgensen, J. B., Ebersbach, T., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at 3rd Danish Conference on Biotechnology and Molecular Biology, Vejle, Denmark.
Source: orbit
Source-ID: 233955

Prebiotics for prevention of Salmonella infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Contributors: Petersen, A., Wilcks, A., Poulsen, M., Licht, T. R.
Publication date: 2008
Peer-reviewed: Yes
Event: Abstract from 6th Joint INRA-RRI Symposium on Gut Microbiome, Functionality, Interaction with the host and Impact on the environment, Clermont-Ferrand, France.
Source: orbit
Source-ID: 234133

Prebiotics for prevention of Salmonella infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Prebiotics for Prevention of Salmonella Infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Contributors: Petersen, A., Lahtinen, S., Poulsen, M., Wilcks, A., Licht, T. R.
Publication date: 2008
Peer-reviewed: Yes
Event: Abstract from 2nd ASM Conference on Beneficial Microbes, San Diego, CA, United States.
Source: orbit
Source-ID: 234125
Research output: Research - peer-review » Conference abstract for conference – Annual report year: 2008

Prebiotics for Prevention of Salmonella Infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Contributors: Petersen, A., Lahtinen, S., Poulsen, M., Wilcks, A., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at Symposium for Biotech Research, Lyngby, Denmark.
Source: orbit
Source-ID: 234131
Research output: Research » Poster – Annual report year: 2008

Prebiotics for Prevention of Salmonella Infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Petersen, A., Lahtinen, S., Poulsen, M., Wilcks, A., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at Symposium for Biotech Research, Lyngby, Denmark.
Source: orbit
Source-ID: 234132
Research output: Research » Poster – Annual report year: 2008

Prebiotics for Prevention of Salmonella Infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Petersen, A., Lahtinen, S., Poulsen, M., Wilcks, A., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at 2nd ASM Conference on Beneficial Microbes, San Diego, CA, United States.
Source: orbit
Source-ID: 234126
Research output: Research » Poster – Annual report year: 2008
Prebiotics for Prevention of Salmonella typhimurium

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Pedersen, A. L., Petersen, A., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Abstract from 3rd Danish Conference on Biotechnology and Molecular Biology, Vejle, Denmark.
Source: orbit
Source-ID: 234078
Research output: Research › Conference abstract for conference – Annual report year: 2008

Prebiotics for Prevention of Salmonella typhimurium

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Pedersen, A. L., Petersen, A., Licht, T. R.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at 3rd Danish Conference on Biotechnology and Molecular Biology, Vejle, Denmark.
Source: orbit
Source-ID: 234080
Research output: Research › Poster – Annual report year: 2008

Scientific opinion of the panel on biological hazards on a request from EFSA on the maintenance of the QPS list of microorganisms intentionally added to food or feed: Question No EFSA q-2008-006

General information
State: Published
Organisations: National Food Institute
Contributors: EFSA Publication
Publication date: 2008

Publication information
Publisher: European Food Safety Authority
Original language: English
(The EFSA Journal; No. 1226).
Source: orbit
Source-ID: 250097
Research output: Research - peer-review › Report – Annual report year: 2008

Selective pressure affects transfer and establishment of a Lactobacillus plantarum resistance plasmid in the gastrointestinal environment

Objectives and methods: A Lactobacillus plantarum strain recently isolated from French raw-milk cheese was tested for its ability to transfer a small plasmid pLFE1 harbouring the erythromycin resistance gene erm(B) to Enterococcus faecalis. Mating was studied in vitro and in different gastrointestinal environments using gnotobiotic rats as a simple in vivo model and streptomycin-treated mice as a more complex model. Transfer and establishment of transconjugants in the intestine were investigated with and without selective pressure. Results: Compared with the relatively low transfer frequency of similar to 5.7 x 10(-8) transconjugants/recipient obtained in vitro by filter mating, a surprisingly high number of transconjugants (10(-4) transconjugants/recipient) was observed in gnotobiotic rats even without antibiotic treatment. When erythromycin was administered, a transfer rate of similar to 100% was observed, i.e. the recipient population turned completely into transconjugants (3 x 10(9) cfu/g faeces). Additionally, the time to reach a stable transconjugant population level was much faster in the erythromycin-treated gnotobiotic rats (1 day) than in the untreated animals (4-5 days). Transconjugants persisted in the gut in relatively stable numbers at least 12 days after termination of antibiotic treatment. In the streptomycin-treated mice, no transfer was observed either with or without erythromycin treatment. Conclusions: The overall results imply that the gastrointestinal tract may comprise a more favourable environment for antibiotic resistance transfer than conditions provided in vitro. However, the indigenous gut microbiota severely restricts transfer, thus minimizing the number of detectable transfer events. Treatment with erythromycin strongly favoured transfer and establishment of pLFE1.
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.076 SNIP 1.506
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.744 SNIP 1.509
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.771 SNIP 1.437
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.768 SNIP 1.5
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.435 SNIP 1.465
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.367 SNIP 1.338
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.4 SNIP 1.284
Scopus rating (2001): SJR 1.388 SNIP 1.232
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.113 SNIP 1.248
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.111 SNIP 1.388
Original language: English
Keywords: gastrointestinal tract, L. plantarum, antibiotic resistance, horizontal gene transfer
DOIs: 10.1093/jac/dkn033
Source: orbit
Source-ID: 221378
Research output: Research - peer-review › Journal article – Annual report year: 2008

Apples and apple pectin change the rat caecal microbiota. Second ISAFRUIT General Assembly

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 2007
Peer-reviewed: No
Event: Poster session presented at 5th Symposium on Food Microbiology, Helsingør, Denmark.
Source: orbit
Source-ID: 237716
Research output: Research › Poster – Annual report year: 2007

Apples and pectin change the rat caecal microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Publication date: 2007
Peer-reviewed: No
Event: Poster session presented at XXX International Congress on Microbial Ecology and Disease Joint with the 4th Probiotics, Prebiotics and New Foods, Rome, Italy.
URLs:
http://www.somed.nu
Source: orbit
Source-ID: 245270
Research output: Research › Poster – Annual report year: 2007

Apples and pectin change the rat caecal microbiota
Apples and pectin change the rat caecal microbiota

Conjugative transfer facilitates stable maintenance of IncP-1 plasmid pKJK5 in Escherichia coli cells colonizing the gastrointestinal tract of the germfree rat

Quantitative determination of IncP-1 plasmid loss from Escherichia coli cells colonizing the gastrointestinal tracts of germfree rats was achieved by flow cytometry. Results show that the plasmid's ability to conjugate counteracts plasmid loss and is thus an important mechanism for the stable maintenance of 1RcP-1 plasmids within the gastrointestinal environment.
Consumption of apples and apple pectin changes the rat caecal microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 76-76
Publication date: 2007
Peer-reviewed: No

Publication information
Journal: Cibus
Volume: 3
ISSN (Print): 1126-6929
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: English
Source: orbit
Source-ID: 279613
Research output: Research - peer-review › Journal article – Annual report year: 2007

Effects of food components on the intestinal microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R.
Publication date: 2007
Peer-reviewed: No
Event: Abstract from Food and Feed – Nutrition, Safety and improved use of raw materials, Hyderabad, India.
Source: orbit
ISAFRUIT health research: Integrating experimental and observational studies on fruit and health with nutrigenomics

General information
State: Published
Organisations: Division of Toxicology and Risk Assessment, National Food Institute, Division of Microbiology and Risk Assessment, Technical University of Denmark
Publication date: 2007
Peer-reviewed: No
Event: Abstract from The International meeting in FAV, Houston, Texas.
Source: orbit
Source-ID: 245276
Research output: Research › Conference abstract for conference – Annual report year: 2007

Opinion of the Scientific Committee on a request from EFSA on the introduction of a Qualified Presumption of Safety (QPS) approach for assessment of selected microorganisms referred to EFSA: Question No EFSA-Q-2005-293

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: EFSA Publication
Publication date: 2007

Publication information
Publisher: European Food Safety Authority
Original language: English
(The EFSA Journal; No. 587).
Source: orbit
Source-ID: 245240
Research output: Research › Conference abstract for conference – Annual report year: 2007

Oxygen restriction increases the infective potential of Listeria monocytogenes in vitro in Caco-2 cells and in vivo in guinea pigs

Background: Listeria monocytogenes has been implicated in several food borne outbreaks as well as sporadic cases of disease. Increased understanding of the biology of this organism is important in the prevention of food borne listeriosis. The infectivity of Listeria monocytogenes ScottA, cultivated with and without oxygen restriction, was compared in vitro and in vivo. Fluorescent protein labels were applied to allow certain identification of Listeria cells from untagged bacteria in in vivo samples, and to distinguish between cells grown under different conditions in mixed infection experiments. Results: Infection of Caco-2 cells revealed that Listeria cultivated under oxygen-restricted conditions were approximately 100 fold more invasive than similar cultures grown without oxygen restriction. This was observed for exponentially growing bacteria, as well as for stationary-phase cultures. Oral dosage of guinea pigs with Listeria resulted in a significantly higher prevalence (p <0.05) of these bacteria in jejunum, liver and spleen four and seven days after challenge, when the bacterial cultures had been grown under oxygen-restricted conditions prior to dosage. Additionally, a 10-100 fold higher concentration of Listeria in fecal samples was observed after dosage with oxygen-restricted bacteria. These differences were seen after challenge with single Listeria cultures, as well as with a mixture of two cultures grown with and without oxygen restriction. Conclusion: Our results show for the first time that the environmental conditions to which L. monocytogenes is exposed prior to ingestion are decisive for its in vivo infective potential in the gastrointestinal tract after passage of the gastric barrier. This is highly relevant for safety assessment of this organism in food.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Andersen, J. B., Roldgaard, B., Christensen, B. B., Licht, T. R.
Pages: 55
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: BMC Microbiology
Volume: 7
ISSN (Print): 1471-2180
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.95 SJR 1.242 SNIP 0.953
Web of Science (2017): Impact factor 2.829
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.82 SJR 1.282 SNIP 0.993
Web of Science (2016): Impact factor 2.644
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.93 SJR 1.42 SNIP 0.994
Web of Science (2015): Impact factor 2.581
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.95 SJR 1.519 SNIP 1.069
Web of Science (2014): Impact factor 2.729
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.32 SJR 1.571 SNIP 1.179
Web of Science (2013): Impact factor 2.976
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.38 SJR 1.507 SNIP 1.146
Web of Science (2012): Impact factor 3.104
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.4 SJR 1.487 SNIP 1.125
Web of Science (2011): Impact factor 3.044
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.433 SNIP 1.034
Web of Science (2010): Impact factor 2.96
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.474 SNIP 0.964
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.398 SNIP 0.979
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.388 SNIP 0.949
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.304 SNIP 0.834
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.931 SNIP 0.803
Web of Science (2005): Indexed yes
Prebiotics for prevention of salmonella infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Contributors: Petersen, A., Wilcks, A., Poulsen, M., Licht, T. R.
Pages: 75-75
Publication date: 2007
Peer-reviewed: No

Publication information
Journal: Cibus
Volume: 3
ISSN (Print): 1126-6929
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: English
Source: orbit
Source-ID: 245229
Research output: Research › Conference article – Annual report year: 2007

Prebiotics for prevention of Salmonella infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Contributors: Petersen, A., Wilcks, A., Poulsen, M., Licht, T. R.
Publication date: 2007
Peer-reviewed: No
Event: Poster session presented at The 4th meeting on Probiotics, Prebiotics and New Foods jointly with the XXX International Congress on Microbial Ecology and Disease, Rome, Italy.
Source: orbit
Source-ID: 245273
Research output: Research › Poster – Annual report year: 2007

Prebiotics for Prevention of Salmonella Infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Division of Toxicology and Risk Assessment
Contributors: Petersen, A., Wilcks, A., Poulsen, M., Licht, T. R.
Publication date: 2007
Peer-reviewed: Yes
Event: Abstract from The 4th meeting on Probiotics, Prebiotics and New Foods jointly with the XXX International Congress on Microbial Ecology and Disease, Rome, Italy.
Source: orbit
Source-ID: 234788
Research output: Research › peer-review › Conference abstract for conference – Annual report year: 2007

PreGI - Prebiotics for Prevention of Gastrointestinal Infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R.
Publication date: 2007
Peer-reviewed: No
Event: Abstract from Nutrigenomics in Denmark, Slagelse, Denmark.
Source: orbit
PreGI - Prebiotics for Prevention of Gastrointestinal Infections

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R.
Publication date: 2007
Peer-reviewed: No
Event: Poster session presented at Nutrigenomics in Denmark, Slagelse, Denmark.
Source: orbit
Source-ID: 247764
Research output: Research › Poster – Annual report year: 2007

Selection of bacteria originating from a human intestinal microbiota in the gut of previously germ-free rats

Denaturing gradient gel electrophoresis (DGGE) was applied to separate PCR-amplified 16S rRNA genes originating from human microbiota associated (HMA) rat faeces as well as from the human faecal sample used for inoculation of the animals. Subsequently, a total of 15 dominant bands were excised from the DGGE gels, cloned and sequenced. Comparison of the obtained sequences with the Ribosomal Database revealed that species of Bacteroides/Prevotella and Faecalibacterium gave rise to the majority of the dominant bands in the human sample and in the HMA rats. In the HMA rats, two dominant bands, which were not present in the human DGGE profile, originated from species of Ruminococcus. With the exception of the Ruminococcus sequences, sequences originating from both rats and human samples were represented in all major branches of a maximum parsimony tree, indicating that the rat feed and gut environment allows colonization of the dominant taxonomic units from the human microbiota, but additionally selects for Ruminococci. Bands representing Prevotella and Faecalibacterium, which were found in identical positions of the DGGE gels originating from human and HMA rat faecal samples, originated from completely identical sequences, indicating that the same strains of these species were dominating in the human and rat samples.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R., Madsen, B., Wilcks, A.
Pages: 205-209
Publication date: 2007
Peer-reviewed: Yes

Publication information
Journal: Fems Microbiology Letters
Volume: 277
Issue number: 2
ISSN (Print): 0378-1097
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.8 SJR 0.79 SNIP 0.58
Web of Science (2017): Impact factor 11.392
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.76 SJR 0.842 SNIP 0.615
Web of Science (2016): Impact factor 12.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.08 SJR 1.156 SNIP 0.756
Web of Science (2015): Indexed yes
The Human Biota Associated Rat as a Model for the Human Intestinal Microbiota
The Human Biota Associated Rat as a Model for the Human Intestinal Microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R., Wilcks, A.
Publication date: 2007
Peer-reviewed: No
Event: Poster session presented at 5th Symposium on Food Microbiology, Helsingør, Denmark.
Source: orbit
Source-ID: 247767
Research output: Research › Poster – Annual report year: 2007

The Human Biota Associated Rat as a Model for the Human Intestinal Microbiota. 4th Probiotics, Prebiotics and New Foods

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R., Wilcks, A.
Publication date: 2007
Peer-reviewed: No
Event: Poster session presented at XXX Somed Meeting, Rome, Italy.
Source: orbit
Source-ID: 237718
Research output: Research › Poster – Annual report year: 2007

Bakterier anvendt til biologisk insektbekæmpelse – Kan de give diarré?

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 2006
Peer-reviewed: Unknown
Comparison of methods and animal models commonly used for investigation of fecal microbiota: Effects of time, host and gender

Denaturing gradient gel electrophoresis (DGGE), terminal restriction fragment length polymorphism (T-RFLP) and plating on selective agars were used to study variation in the fecal microbiota of rats over time as well as variation between individuals. Investigated rats were either conventional and specific pathogen free (SPF), or human flora associated (HFA). A higher variation (p <0.05) in fecal microbiota over time was observed for HFA than for SPF animals. Analysis of DGGE and T-RFLP profiles of fecal microbiota from SPF and HFA rats revealed that variation over time was less significant than variation between individuals, and that phylogenetic profiles clustered according to gender. These observations should be taken into account when designing future research addressing changes in fecal microbiota.
Conjugative gene transfer in the gastrointestinal environment

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R., Wilcks, A.
Publication date: 2006

Host publication information
Title of host publication: Advances in Applied Microbiology
Volume: 58
Place of publication: San Diego
Publisher: Elsevier Academic Press Inc
ISBN (Print): 0-12-002660-0
(Advances in Applied Microbiology; No. 58).
Construction of a multiple fluorescence labeling system for use in co-invasion studies of Listeria monocytogenes

Background Existing virulence models are often difficult to apply for quantitative comparison of invasion potentials of Listeria monocytogenes. Well-to-well variation between cell-line based in vitro assays is practically unavoidable, and variation between individual animals is the cause of large deviations in the observed capacity for infection when animal models are used. One way to circumvent this problem is to carry out virulence studies as competition assays between 2 or more strains. This, however, requires invasion-neutral markers that enable easy discrimination between the different strains.

Results A fluorescent marker system, allowing visualization and identification of single L. monocytogenes cells as well as colonies in a non-destructive manner, was developed. Five different fluorescent labels are available, and allowed simultaneous visual discrimination between three differently labelled strains at the single cell level by use of fluorescence microscopy. More than 90% of the L. monocytogenes host cells maintained the fluorescence tags for 40 generations. The fluorescence tags did not alter the invasive capacity of the L. monocytogenes cells in a traditional Caco-2 cell invasion assay, and visual discrimination between invaded bacteria carrying different fluorescent labels inside the cells was possible. Conclusion The constructed fluorescent marker system is stable, easy to use, does not affect the virulence of L. monocytogenes in Caco-2 cell assays, and allows discrimination between differently labelled bacteria after internalization in these cells.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Andersen, J. B., Roldgaard, B., Lindner, A. B., Christensen, B. B., Licht, T. R.
Pages: 86
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: BMC Microbiology
Volume: 6
ISSN (Print): 1471-2180
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.95 SJR 1.242 SNIP 0.953
Web of Science (2017): Impact factor 2.829
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.82 SJR 1.282 SNIP 0.993
Web of Science (2016): Impact factor 2.644
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.93 SJR 1.42 SNIP 0.994
Web of Science (2015): Impact factor 2.581
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.95 SJR 1.519 SNIP 1.069
Web of Science (2014): Impact factor 2.729
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.32 SJR 1.571 SNIP 1.179
Web of Science (2013): Impact factor 2.976
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Dietary carbohydrate source determines molecular fingerprints of the rat fecal microbiota

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Technical University of Denmark
Pages: S102-S102
Publication date: 2006
Peer-reviewed: Yes

**Publication information**
Journal: Reproduction Nutrition Development
Volume: 46
ISSN (Print): 0926-5287
Ratings:
Scopus rating (2009): SJR 0.776 SNIP 2.395
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.778 SNIP 1.497
Scopus rating (2007): SJR 0.572 SNIP 1.293
Scopus rating (2006): SJR 0.587 SNIP 0.862
Dietary carbohydrate source determines molecular fingerprints of the rat fecal microbiota

Background: A study was designed to elucidate effects of selected carbohydrates on composition and activity of the intestinal microbiota. Five groups of eight rats were fed a western type diet containing cornstarch (reference group), sucrose, potato starch, inulin (a long-chained fructan) or oligofructose (a short-chained fructan). Fructans are, opposite sucrose and starches, not digestible by mammalian gut enzymes, but are known to be fermentable by specific bacteria in the large intestine. Results: Animals fed with diets containing potato starch, or either of the fructans had a significantly (p <0.05) higher caecal weight and lower caecal pH when compared to the reference group, indicating increased fermentation. Selective cultivation from faeces revealed a higher amount of lactic acid bacteria cultivable on Rogosa agar in these animals. Additionally, the fructan groups had a lower amount of coliform bacteria in faeces. In the inulin and oligofructose groups, higher levels of butyrate and propionate, respectively, were measured. Principal Component Analysis of profiles of the faecal microbiota obtained by Denaturing Gradient Gel Electrophoresis (DGGE) of PCR amplified bacterial 16S rRNA genes as well of Reverse Transcriptase-PCR amplified bacterial 16S rRNA resulted in different phylogenetic profiles for each of the five animal groups as revealed by Principal Component Analysis (PCA) of band patterns. Conclusion: Even though sucrose and cornstarch are both easily digestible and are not expected to reach the large intestine, the DGGE band patterns obtained indicated that these carbohydrates indeed affected the composition of bacteria in the large gut. Also the two fructans resulted in completely different molecular fingerprints of the faecal microbiota, indicating that even though they are chemically similar, different intestinal bacteria ferment them. Comparison of DNA-based and RNA-based profiles suggested that two species within the phylum Bacteroidetes were not abundant in numbers but had a particularly high ribosome content in the animals fed with inulin.
Dietary carbohydrate sources affects intestinal microbiota and short-chain fatty acid composition in rats

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Technical University of Denmark
Number of pages: 1
Pages: 28
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: Food & Nutrition Research
Volume: 50
Issue number: Suppl. 1
ISSN (Print): 1654-6628
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.28 SJR 0.823 SNIP 0.779
Web of Science (2017): Impact factor 2.086
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.24 SJR 0.906 SNIP 0.768
Web of Science (2016): Impact factor 2.039
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.19 SJR 1.024 SNIP 0.911
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.37 SJR 1.03 SNIP 0.918
Web of Science (2014): Impact factor 2.162
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Effects of Lactococcus lactis on composition of intestinal microbiota: Role of nisin
This study examined the ability of (i) pure nisin, (ii) nisin-producing Lactococcus lactis strain CHCC5826, and (iii) the non-nisin-producing L. lactis strain CHCH2862 to affect the composition of the intestinal microbiota of human flora-associated rats. The presence of both the nisin-producing and the non-nisin-producing L. lactis strains significantly increased the number of Bifidobacterium cells in fecal samples during the first 8 days but decreased the number of enterococci/streptococci in duodenum, ileum, cecum, and colon samples as detected by selective cultivation. No significant changes in the rat fecal microbiota were observed after dosage with nisin. Pearson cluster analysis of denaturing gradient gel electrophoresis profiles of the 16S rRNA genes present in the fecal microbial population revealed that the microbiota of animals dosed with either of the two L. lactis strains were different from that of control animals dosed with saline. However, profiles of the microbiota from animals dosed with nisin did not differ from the controls. The concentrations of nisin estimated by competitive enzyme-linked immunosorbent assay (ELISA) were approximately 10-fold higher in the small intestine and 200-fold higher in feces than the corresponding concentrations estimated by a biological assay. This indicates that nisin was degraded or inactivated in the gastrointestinal tract, since fragments of this bacteriocin are detected by ELISA while an intact molecule is needed to retain biological activity.

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Pages: 239-244
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: Applied and Environmental Microbiology
Volume: 72
Issue number: 1
ISSN (Print): 0099-2240
Ratings:
BFI (2019): BFI-level 2
Fate and effect of ingested Bacillus cereus spores and vegetative cells in the intestinal tract of human-flora-associated rats

The fate and effect of Bacillus cereus F4433/73R in the intestine of human-flora-associated rats was studied using bacteriological culturing techniques and PCR-denaturing gradient gel electrophoresis in combination with cell assays and immunoadsays for detection of enterotoxins. In faecal samples from animals receiving vegetative cells, only few B. cereus cells were detected. Spores survived the gastric barrier well, and were in some cases detected up to 2 weeks after ingestion. Selective growing revealed no major changes in the intestinal flora during passage of B. cereus. However, denaturing gradient gel electrophoresis analysis with universal 16S rRNA gene primers revealed significant changes in the intestinal microbiota of animals dosed with spores. Vero cell assays and a commercial kit (BCET-R PLA) did not reveal any enterotoxin production from B. cereus F4433/73R in the intestinal tract.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 70-77
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: Fems Immunology and Medical Microbiology
Volume: 46
Issue number: 1
ISSN (Print): 0928-8244
Ratings:
Web of Science (2019): Indexed yes
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 2.52
Web of Science (2017): Impact factor 2.337
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 2.23
Web of Science (2016): Impact factor 2.335
Scopus rating (2015): CiteScore 2.12 SJR 1.306 SNIP 0.739
Web of Science (2015): Impact factor 2.483
Scopus rating (2014): CiteScore 2.32 SJR 1.284 SNIP 0.903
Web of Science (2014): Impact factor 2.403
Web of Science (2014): Indexed yes
Scopus rating (2013): SJR 1.222 SNIP 0.784
Web of Science (2013): Impact factor
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.042 SNIP 0.828
Web of Science (2012): Impact factor 2.684
ISI indexed (2012): ISI indexed yes
Germination and conjugation of Bacillus thuringiensis in the gut of gnotobiotic rats

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Microbiology
Pages: 121-121
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: Reproduction Nutrition Development
Volume: 46
ISSN (Print): 0926-5287
Ratings:
Scopus rating (2009): SJR 0.776 SNIP 2.395
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.778 SNIP 1.497
Scopus rating (2007): SJR 0.572 SNIP 1.293
Scopus rating (2006): SJR 0.587 SNIP 0.862
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.428 SNIP 0.823
Germination and conjugation of Bacillus thuringiensis in the gut of gnotobiotic rats

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 2006
Peer-reviewed: No
Event: Abstract from Ecology of Bacteria used for Insect Control. The COST action 862 Workshop, Goniadz, Poland.
Source: orbit
Source-ID: 245430
Research output: Research › Conference abstract for conference – Annual report year: 2006

Germination and conjugation of Bacillus thuringiensis in the gut of gnotobiotic rats

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 2006
Peer-reviewed: No
Event: Poster session presented at The 5th joint RRI INRA Symposium "Gut Microbiology: research to improve health, immune response and nutrition", Aberdeen, United Kingdom.
Source: orbit
Source-ID: 247924
Research output: Research › Poster – Annual report year: 2006

Germination and conjugation of Bacillus thuringiensis in the gut of gnotobiotic rats

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 2006
Peer-reviewed: No
Event: Abstract from The 5th joint RRI INRA Symposium "Gut Microbiology: research to improve health, immune response and nutrition", Aberdeen, United Kingdom.
Source: orbit
Source-ID: 247925
Research output: Research › Conference abstract for conference – Annual report year: 2006

Human Flora Associated rodent as models for the human gut microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R.
Human Flora Associated rodents as models for the human gut microbiota

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R.
Publication date: 2006
Peer-reviewed: No
Event: Abstract from Scandinavian Laboratory Animal Society Meeting, Helsingør, Denmark.
Source: orbit
Source-ID: 247968
Research output: Research › Conference abstract for conference – Annual report year: 2006

Internalin A (inlA) plays a key role in the persistence of Listeria monocytogenes in the jejunum of Guinea pigs

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Roldgaard, B., Andersen, J. B., Licht, T. R., Christensen, B. B.
Publication date: 2006
Peer-reviewed: No
Event: Poster session presented at 4th Symposium on Food Microbiology, Helsingør, Denmark.
Source: orbit
Source-ID: 247959
Research output: Research › Poster – Annual report year: 2006

Internalin A (inlA) plays a key role in the persistence of Listeria monocytogenes in the jejunum of Guinea pigs

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment
Contributors: Roldgaard, B., Andersen, J. B., Licht, T. R., Christensen, B. B.
Publication date: 2006
Peer-reviewed: No
Event: Abstract from 4th Symposium on Food Microbiology, Helsingør, Denmark.
Source: orbit
Source-ID: 247958
Research output: Research › Conference abstract for conference – Annual report year: 2006

Lactobacillus plantarum inhibits growth of Listeria monocytogenes in an in vitro continuous flow gut model, but promotes invasion of L. monocytogenes in the gut of gnotobiotic rats

The ability of the pediocin AcH producing Lactobacillus plantarum DDEN 11007 and its non-producing plasmid-cured isogenic variant, DDEN 12305 to prevent the persistence and growth of Listeria monocytogenes EP2 in two gastrointestinal (GI) tract models was examined. In vitro studies conducted in a two-stage continuous flow system showed that L. plantarum DDEN 11007 inhibited L. monocytogenes EP2 under these conditions, while less effect was seen of the non-bacteriocin producing variant. The inhibitory effect was more pronounced at pH 5 than at pH 7. No effect on persistence of L. monocytogenes in the GI tract was seen in gnotobiotic rats colonized with either the pediocin AcH producing or the non-bacteriocin producing variant of L. plantarum when compared to rats inoculated with L. monocytogenes EP2 alone. Surprisingly, inoculation of the gnotobiotic animals with either of the L. plantarum strains prior to inoculation with L. monocytogenes EP2 resulted in increased occurrence of L. monocytogenes in liver and spleen when compared to the animals inoculated with L. monocytogenes EP2 alone. Our results indicate that the presence of L. plantarum in the gut of gnotobiotics facilitates L. monocytogenes invasion by an unknown mechanism. This observation is however not necessarily specifically related to L. plantarum, and should not be interpreted as the expected effect in animals carrying a conventional intestinal microflora.

General information
Mikrobiologiske plantebeskyttelsesmidlers skæbne i mave-tarm kanalen - Studier af Bacillus thuringiensis

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 2006

Publication information
Publisher: Miljøstyrelsen
Original language: Danish
Source: orbit
Source-ID: 247855
Research output: Research › Report – Annual report year: 2006

Persistence of Bacillus thuringiensis bioinsecticides in the gut of human-flora-associated rats
The capability of two bioinsecticide strains of Bacillus thuringiensis (ssp. israelensis and ssp. kurstaki) to germinate and persist in vivo in the gastrointestinal tract of human-flora-associated rats was studied. Rats were dosed either with vegetative cells or spores of the bacteria for 4 consecutive days. In animals fed spores, B. thuringiensis cells were detected in faecal and intestinal samples of all animals, whereas vegetative cells only poorly survived the gastric passage. Heat-treatment of intestinal samples, which kills vegetative cells, revealed that B. thuringiensis spores were capable of germination in the gastrointestinal tract. In one animal fed spores of B. thuringiensis ssp. kurstaki, these bacteria were detected at high density ($10^{3}$-$10^{4}$ CFU g$^{-1}$ faecal and intestinal samples) even 2 weeks after the last dosage. In the same animal, passage of B. thuringiensis ssp. kurstaki to the spleen was observed; however, no other adverse effects were observed. Denaturing gradient gel electrophoresis of PCR-amplified bacterial 16S RNA genes in faecal samples revealed no major effect of B. thuringiensis on the composition of the indigenous gut bacteria. Additionally, no cytotoxic effect was detectable in gut samples by Vero cell assay.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 410-418
The Human Biota Associated Rat as a Model for the Human Intestinal Microbiota

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R., Madsen, B., Wilcks, A.
Pages: 39-39
Publication date: 2006
Peer-reviewed: No

**Publication information**
Journal: Cibus
Volume: 3
ISSN (Print): 1126-6929

The impact of conjugal transfer on the stability of the IncP-1 plasmid pKJK5 in bacterial populations

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 2006
Peer-reviewed: No
Event: Abstract from 11th International Symposium on Microbial Ecology, Vienna, Austria.
Source: orbit
Source-ID: 245428
Research output: Research › Conference abstract for conference – Annual report year: 2007

Characterization of transferable tetracycline resistance genes in Enterococcus faecalis isolated from raw food

The prevalence of tetracycline resistance, and of specific genetic determinants for this resistance was investigated in 1003 strains of Enterococcus faecalis isolated from various raw food products originating from five categories including chicken meat, other poultry meat, beef, pork, and ‘other’. For the 238 resistant isolates identified, the ability to transfer the resistant phenotype to a given recipient in vitro was investigated. New and interesting observations were that the tet(L) resistance determinant was more readily transferred than tet(M), and that the presence of Trn916-like elements known to encode tet(M) did not correlate with increased transferability of the resistant phenotype.

**General information**
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 15-19
Publication date: 2005
Peer-reviewed: Yes

**Publication information**
Journal: Fems Microbiology Letters
Volume: 243
Issue number: 1
ISSN (Print): 0378-1097
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.8 SJR 0.79 SNIP 0.58
Web of Science (2017): Impact factor 11.392
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.76 SJR 0.842 SNIP 0.615
Web of Science (2016): Impact factor 12.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.08 SJR 1.156 SNIP 0.756
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.17 SJR 1.136 SNIP 0.767
Web of Science (2014): Impact factor 13.244
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.25 SJR 1.053 SNIP 0.719
Web of Science (2013): Impact factor 13.806
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.25 SJR 1.073 SNIP 0.804
Web of Science (2012): Impact factor 13.231
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.26 SJR 1.105 SNIP 0.764
Web of Science (2011): Impact factor 10.96
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.081 SNIP 0.754
Web of Science (2010): Impact factor 11.796
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.13 SNIP 0.834
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.084 SNIP 0.834
Scopus rating (2007): SJR 1.103 SNIP 0.864
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.105 SNIP 0.86
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1 SNIP 0.8
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.005 SNIP 0.725
Web of Science (2004): Indexed yes
Conjugative gene transfer in the gastro-intestinal environment

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R., Wilcks, A.
Pages: 77-95
Publication date: 2005
Peer-reviewed: Yes

Publication information
Journal: Advances in Applied Microbiology
Volume: 58
ISSN (Print): 0065-2164
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 5.39 SJR 2.089 SNIP 1.622
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 5.54 SJR 2.203 SNIP 1.765
Web of Science (2016): Impact factor 5.59
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.55 SJR 1.323 SNIP 1.02
Web of Science (2015): Impact factor 4.128
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.96 SJR 1.116 SNIP 0.962
Web of Science (2014): Impact factor 2.737
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.15 SJR 1.621 SNIP 1.027
Web of Science (2013): Impact factor 2.243
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 5.57 SJR 2.138 SNIP 2.101
Web of Science (2012): Impact factor 4.974
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.41 SJR 1.971 SNIP 1.377
Microorganisms in Food and Feed. Qualified Presumption of Safety – QPS

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: EFSA Publication
Publication date: 2005

Publication information
Publisher: European Food Safety Authority
ISBN (Print): 92-9199-012-4
Original language: English
(Summary Report EFSA Scientific Colloquium; No. 2).
Source: orbit
Source-ID: 245238
Research output: Research - peer-review › Report – Annual report year: 2005

Opinion of the Scientific Committee on a request from EFSA related to A generic approach to the safety assessment by EFSA of microorganisms used in food/feed and the production of food/feed additives: Request No EFSA-Q-2004-021

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: EFSA Publication
Publication date: 2005

Publication information
Publisher: European Food Safety Authority
Original language: English
(The EFSA Journal; No. 226).
Source: orbit
Source-ID: 247821
Research output: Research - peer-review › Report – Annual report year: 2005
**Qualified Presumption of Safety of Micro-organisms in Food and Feed**

**General information**
State: Published  
Organisations: Division of Microbiology and Risk Assessment, National Food Institute  
Contributors: EFSA Publication  
Publication date: 2005

**Publication information**
Publisher: European Food Safety Authority  
ISBN (Print): 92-91-99012-4  
Original language: English  
Source: orbit  
Source-ID: 247820  
Research output: Research - peer-review  
Annual report year: 2005

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**Biological Control - Assessment of Health Risks**

**General information**
State: Published  
Organisations: Division of Microbiology and Risk Assessment, National Food Institute  
Contributors: Licht, T. R.  
Publication date: 2004  
Peer-reviewed: No  
Event: Abstract from Workshop Health Environmental Risks by the use of Organisms for Biological Control of Pests and Diseases in Agriculture, LO-skolen, Denmark.  
Source: orbit  
Source-ID: 247798  
Research output: Conference abstract for conference  
Annual report year: 2004

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**Effect of tetracycline on transfer and establishment of the tetracycline-inducible conjugative transposon Tn916 in the guts of gnotobiotic rats**

We have investigated the transfer of Tn916 among strains of Enterococcus faecalis OG1 colonizing in the intestines of gnotobiotic rats. This animal model allows a low limit of detection and efficient colonization of the chosen bacteria. The animals continuously received tetracycline in drinking water. A tetracycline-sensitive recipient strain was allowed to colonize the animals before the resistant donor was introduced. The numbers of donors, recipients, and transconjugants in fecal samples and intestinal segments were estimated. The bioavailable amounts of tetracycline in fecal samples and intestinal segments were monitored by using bacterial biosensors carrying a transcriptional fusion of a tetracycline-regulated promoter and a lacZ reporter gene. Chromosomal locations of Tn916 in transconjugants isolated either from the same animal or from different animals were compared by Southern blot analysis. Our results indicated that selection for the resistant phenotype was the major factor causing higher numbers of transconjugants in the presence of tetracycline. Tetracycline-sensitive E. faecalis cells colonized the intestine even when the concentrations of tetracycline in feces and intestinal luminal contents exceeded growth-inhibitory concentrations. This suggests the existence of tetracycline-depleted microhabitats in the intestinal environment.

**General information**
State: Published  
Organisations: Division of Microbiology and Risk Assessment, National Food Institute  
Contributors: Bahl, M. I., Sørensen, S. J., Hansen, L. H., Licht, T. R.  
Pages: 758-764  
Publication date: 2004  
Peer-reviewed: Yes

**Publication information**
Journal: Applied and Environmental Microbiology  
Volume: 70  
Issue number: 2  
ISSN (Print): 0099-2240  
Ratings:  
BFI (2019): BFI-level 2  
Web of Science (2019): Indexed yes  
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 3.99
Web of Science (2017): Impact factor 3.633
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.08
Web of Science (2016): Impact factor 3.807
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.14 SJR 1.891 SNIP 1.308
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.02 SJR 1.857 SNIP 1.384
Web of Science (2014): Impact factor 3.668
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.25 SJR 1.899 SNIP 1.414
Web of Science (2013): Impact factor 3.952
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.29 SJR 1.975 SNIP 1.429
Web of Science (2012): Impact factor 3.678
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 4.12 SJR 1.914 SNIP 1.455
Web of Science (2011): Impact factor 3.829
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.887 SNIP 1.436
Web of Science (2010): Impact factor 3.778
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.972 SNIP 1.528
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 2.156 SNIP 1.572
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.043 SNIP 1.647
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.054 SNIP 1.602
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.074 SNIP 1.653
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.108 SNIP 1.648
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.097 SNIP 1.821
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 2.046 SNIP 1.754
Effects of bacteria used for biopreservation of food on the composition of intestinal bacteria

General information
State: Published
Organisations: Section for Aquatic Microbiology and Seafood Hygiene, National Institute of Aquatic Resources, Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Bernbom, N., Saadbye, P., Licht, T. R., Nørrung, B.
Number of pages: 107
Publication date: 2004

Host publication information
Title of host publication: Reproduction Nutrition Development
Volume: 44 Suppl.
Publisher: EDP Sciences
Electronic versions: Proceedings.pdf
Source: orbit
Source-ID: 229674
Research output: Research - peer-review › Journal article – Annual report year: 2004

Fate and effect of B. thuringiensis in rats

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Wilcks, A., Licht, T. R.
Publication date: 2004
Peer-reviewed: No
Event: Abstract from International Workshop on Health and Environmental Risks by the Use of Organisms for Biological Control of Pests and Diseases in Agriculture, .
Source: orbit
Source-ID: 245444
Research output: Research › Conference abstract for conference – Annual report year: 2004

Fate and effect of B. thuringiensis in rats

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Wilcks, A., Licht, T. R.
Publication date: 2004
Peer-reviewed: No
Event: Poster session presented at International Workshop on Health and Environmental Risks by the Use of Organisms for Biological Control of Pests and Diseases in Agriculture, .
Source: orbit
Source-ID: 245445
Research output: Research › Poster – Annual report year: 2004
In vivo detection and quantification of tetracycline by use of a whole-cell biosensor in the rat intestine

An Escherichia coli biosensor strain, harboring the plasmid pTGFP2, was introduced into the gastrointestinal tract of gnotobiotic rats that continuously received drinking water containing tetracycline. Plasmid pTGFP2 contains a transcriptional fusion between a green fluorescent protein (GFP) gene and a tetracycline-regulated promoter and was shown to produce a proportional GFP signal in response to exposure to various tetracycline concentrations when harbored by an E. coli strain. The plasmid was highly unstable in the host bacteria colonizing the intestinal system of the animals, and rapid plasmid loss was observed. Reintroduction of the E. coli MC4100/pTGFP2 strain into animals already colonized by the plasmid-free E. coli strain the day before euthanasia made it possible to extract and analyze the biosensors from intestinal samples. The induction of GFP in the biosensor cells extracted from the animals was estimated on a single-cell basis by use of flow cytometry, and the mean induction of GFP in the samples was compared to a standard curve prepared from known tetracycline concentrations. The results showed that the bioavailable tetracycline concentration within the bacterial growth habitat of the intestine was proportional to the concentration of tetracycline in drinking water but represented only approximately 0.4% of the intake concentration. This is a significant finding which will help to clarify antimicrobial therapy in the intestinal environment.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Pages: 1112-1117
Publication date: 2004
Peer-reviewed: Yes

Publication information
Journal: Antimicrobial Agents and Chemotherapy
Volume: 48
Issue number: 4
ISSN (Print): 0066-4804
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.15 SJR 2.291 SNIP 1.263
Web of Science (2017): Impact factor 4.255
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.275 SNIP 1.328
Web of Science (2016): Impact factor 4.302
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.28 SJR 2.343 SNIP 1.361
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.45 SJR 2.361 SNIP 1.428
Web of Science (2014): Impact factor 4.476
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.67 SJR 2.423 SNIP 1.411
Web of Science (2013): Impact factor 4.451
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.88 SJR 2.363 SNIP 1.5
Web of Science (2012): Impact factor 4.565
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Mikrobiologiske plantebeskyttelsesmidlers skæbne i mave-tarmkanalen

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R.
Publication date: 2004
Peer-reviewed: No
Event: Abstract from Miljøstyrelsens Pesticidforskningsseminar, Kolding, Danmark, .
Source: orbit
Source-ID: 245450
Research output: Research › Conference abstract for conference – Annual report year: 2004

Effect of tetracycline on transfer of the conjugative transposon Tn916 between Enterococcus faecalis cells in the animal intestine

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Effect of tetracycline on transfer of the conjugative transposon Tn916 between Enterococcus faecalis cells in the animal intestine

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Bahl, M. I., Sørensen, S. J., Hansen, L. H., Licht, T. R.
Publication date: 2003
Peer-reviewed: No
Event: Abstract from 1st FEMS Congress of European Microbiologists, Ljubljana, Slovenia.
Source: orbit
Source-ID: 245455
Research output: Research › Conference abstract for conference – Annual report year: 2003

Enterococci in food products constitute a reservoir for transferable tetracycline resistance genes

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Andersen, S. R., Wilcks, A., Licht, T. R.
Publication date: 2003
Peer-reviewed: No
Event: Poster session presented at 1st FEMS Congress of European Microbiologists, Ljubljana, Slovenia.
Source: orbit
Source-ID: 245456
Research output: Research › Poster – Annual report year: 2003

Enterococci in food products constitute a reservoir for transferable tetracycline resistance genes

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Andersen, S. R., Wilcks, A., Licht, T. R.
Publication date: 2003
Peer-reviewed: No
Event: Poster session presented at 1st FEMS Congress of European Microbiologists, Ljubljana, Slovenia.
Source: orbit
Source-ID: 245460
Research output: Research › Poster – Annual report year: 2003

Evidence of increased spread and establishment of plasmid RP4 in the intestine under sub-inhibitory tetracycline concentrations

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Center for Biomedical Microbiology, Department of Systems Biology, Statens Serum Institut
Pages: 217-223
Publication date: 2003
Peer-reviewed: Yes

Publication information
Journal: Fems Microbiology Ecology
Volume: 44
Scopus rating (2004): SJR 1.731 SNIP 1.044
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.597 SNIP 1.248
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.352 SNIP 1.013
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.564 SNIP 1.17
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.41 SNIP 1.254
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.507 SNIP 1.108
Original language: English
DOIs:
10.1016/S0168-6496(03)00016-3
Source: orbit
Source-ID: 46199
Research output: Research - peer-review › Journal article – Annual report year: 2003

Genoverførsel fra jord til bord

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R.
Pages: 16-17
Publication date: 2003
Peer-reviewed: Unknown

Publication information
Journal: Dansk Veterinærtidsskrift
Volume: 10
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 245253
Research output: Communication › Journal article – Annual report year: 2003

In situ visualization of plasmid transfer from Pseudomonas putida to the indigenous bacterial population of Alfalfa sprouts

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 2003
Peer-reviewed: No
Event: Abstract from 1st FEMS Congress of European Microbiologists, Ljubljana, Slovenia.
Source: orbit
Source-ID: 245462
Research output: Research › Conference abstract for conference – Annual report year: 2003

Plasmid transfer from Pseudomonas putida to the indigenous bacteria on alfalfa sprouts: Characterization, direct quantification, and in situ location of transconjugant cells

General information
State: Published
Organisations: Microbial Ecology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Department of Systems Biology
Sub-inhibitory tetracycline concentrations are optimal for spread and establishment of plasmid RP4 in an intestinal ecosystem

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Publication date: 2003
Peer-reviewed: No
Event: Poster session presented at Workshop on Biological pest control arranged by the National Institute of Occupational Health, Copenhagen, Denmark, .
Source: orbit
Source-ID: 245453
Research output: Research › Poster – Annual report year: 2003
Transfer of the pheromone-inducible plasmid pCF10 among Enterococcus faecalis microorganisms colonizing the intestine of mini-pigs

A new animal model, the streptomycin-treated mini-pig, was developed in order to allow colonization of defined strains of Enterococcus faecalis in numbers sufficient to study plasmid transfer. Transfer of the pheromone-inducible pCF10 plasmid between streptomycin-resistant strains of E. faecalis OG1 was investigated in the model. The plasmid encodes resistance to tetracycline. Numbers of recipient, donor, and transconjugant bacteria were monitored by selective plating of fecal samples, and transconjugants were subsequently verified by PCR. After being ingested by the mini-pigs, the recipient strain persisted in the intestine at levels between 10^6 and 10^7 CFU per g of feces throughout the experiment. The donor strain, which carried different resistance markers but was otherwise chromosomally isogenic to the recipient strain, was given to the pigs 3 weeks after the recipient strain. The donor cells were initially present in high numbers (10^6 CFU per g) in feces, but they did not persist in the intestine at detectable levels. Immediately after introduction of the donor bacteria, transconjugant cells appeared and persisted in fecal samples at levels between 10^6 and 10^7 CFU per g until the end of the experiment. These observations showed that even in the absence of selective tetracycline pressure, plasmid pCF10 was transferred from ingested E. faecalis cells to other E. faecalis organisms already present in the intestinal environment and that the plasmid subsequently persisted in the intestine.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Technical University of Denmark
Contributors: Licht, T. R., Laugesen, D., Jensen, L. B., Jacobsen, B. L.
Pages: 187-193
Publication date: 2002
Peer-reviewed: Yes

Publication information
Journal: Applied and Environmental Microbiology
Volume: 68
Issue number: 1
ISSN (Print): 0099-2240
Ratings:
BFI (2019): BFI-level 2
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 3.99
Web of Science (2017): Impact factor 3.633
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.08
Web of Science (2016): Impact factor 3.807
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.14 SJR 1.891 SNIP 1.308
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.02 SJR 1.857 SNIP 1.384
Web of Science (2014): Impact factor 3.668
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.25 SJR 1.899 SNIP 1.414
Web of Science (2013): Impact factor 3.952
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.29 SJR 1.975 SNIP 1.429
Web of Science (2012): Impact factor 3.678
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 4.12 SJR 1.914 SNIP 1.455
Web of Science (2011): Impact factor 3.829
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.887 SNIP 1.436
Web of Science (2010): Impact factor 3.778
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.972 SNIP 1.528
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 2.156 SNIP 1.572
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.043 SNIP 1.647
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.054 SNIP 1.602
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.074 SNIP 1.653
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.108 SNIP 1.648
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.097 SNIP 1.821
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 2.046 SNIP 1.754
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.989 SNIP 1.736
Web of Science (2001): Indexed yes
Effect of pheromone induction on transfer of the Enterococcus faecalis plasmid pCF10 in intestinal mucus ex vivo

The effect of synthetic sex pheromone on pheromone-inducible conjugation between the isogenic Enterococcus faecalis strains OG1RF and OG1SS was investigated in (i) Todd-Hewitt broth medium and (ii) intestinal mucus isolated from germ-free rats. In broth, the presence of synthetic pheromone cCF10 had no detectable effect on the transfer kinetics observed for the tetracycline resistance encoding plasmid pCF10. In MUCUS, presence of the same pheromone significantly increased the transfer efficiency observed during the first 2 h of conjugation, while the effect was less pronounced later in the experiment. We suggest that due to differences in diffusion rates and medium-binding of the pheromones, the effect of the synthetic cCF10 was immediately dominated by the effect of pheromones produced by the recipient E. faecalis strain in broth, while this happened later in mucus.
Monitoring bacterial growth activity in biofilms from laboratory flow chambers, plant rhizosphere, and animal intestine

General Information
State: Published
Organisations: Center for Biomedical Microbiology, Department of Microbiology, Division of Microbiology and Risk Assessment, National Food Institute, Center for Systems Microbiology, Department of Systems Biology
Pages: 21-42
Publication date: 2001
Peer-reviewed: Yes

ORIGINAL LANGUAGE: English

Keywords: intestinal mucus, Enterococcus faecalis, pCF10, plasmid transfer rate, pheromone

DOI: 10.1016/S0378-1097(01)00408-6
Source: orbit
Source-ID: 230637
Research output: Research - peer-review ; Journal article ; Annual report year: 2001
A functional cra gene is required for Salmonella enterica serovar typhimurium virulence in BALB/c mice

A minitransposon mutant of Salmonella enterica serovar Typhimurium SR-11, SR-11 Fad(-), is unable to utilize gluconeogenic substrates as carbon sources and is avirulent and immunogenic when administered perorally to BALB/c mice (M. J. Utley et al., FEMS Microbiol. Lett., 163:129-134, 1998). Here, evidence is presented that the mutation in SR-11 Fad(-) that renders the strain avirulent is in the cra gene, which encodes the Cra protein, a regulator of central carbon metabolism.

General information
State: Published
Organisations: Department of Microbiology
Pages: 3772-3775
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Infection and Immunity
Volume: 68
Issue number: 6
ISSN (Print): 0019-9567
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.43 SJR 1.954 SNIP 0.953
Web of Science (2017): Impact factor 3.256
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.34 SJR 2.04 SNIP 0.915
Web of Science (2016): Impact factor 3.593
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.72 SJR 2.361 SNIP 1.053
Web of Science (2015): Impact factor 3.603
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.74 SJR 2.344 SNIP 1.08
Web of Science (2014): Impact factor 3.731
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.25 SJR 2.433 SNIP 1.168
Web of Science (2013): Impact factor 4.156
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.32 SJR 2.386 SNIP 1.167
Web of Science (2012): Impact factor 4.074
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Bakteriers overførsel af resistensgener fra Jord til Bord: Foreningen af Levnedsmiddelingeniører og –kandidater

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute
Contributors: Licht, T. R.
Pages: 7-9
Publication date: 2000
Peer-reviewed: Unknown

Publication Information
Journal: Alimenta
Volume: 10
ISSN (Print): 0002-5402
Ratings:
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
Molecular Ecology of Biofilms

General information
State: Published
Organisations: Center for Biomedical Microbiology, Department of Systems Biology, Division of Microbiology and Risk Assessment, National Food Institute, Department of Microbiology
Pages: 89-120
Publication date: 2000

Host publication information
Title of host publication: Biofilms
Publisher: John Wiley & Sons Ltd
Editor: Bryers, J.
Edition: 2.
Source: orbit
Source-ID: 189325
Research output: Research › Book chapter – Annual report year: 2000

Monitoring of cellular activities in multispecies bacterial surface communities

General information
State: Published
Organisations: Center for Systems Microbiology, Department of Systems Biology, Division of Microbiology and Risk Assessment, National Food Institute, Department of Microbiology
Pages: 497-502
Publication date: 2000

Host publication information
Title of host publication: Atlantic Canada Society for Microbial Ecology
Place of publication: Halifax, Canada
Publisher: Atlantic Canada Society for Microbial Ecology
Editors: Bell, C. R., Brylinsky, M., Johnson-Green, P.
ISBN (Print): 09-88-67630-8
Source: orbit
Source-ID: 247352
Research output: Research › Article in proceedings – Annual report year: 2000

Estimation of growth rates of Escherichia coli BJ4 in streptomycin-treated and previously germ-free mice by in situ rRNA hybridization

General information
State: Published
Organisations: Department of Microbiology, University of Gothenburg, Karolinska Institutet, University of New South Wales, University of Maryland, Statens Serum Institut
Pages: 434-436
Publication date: 1999
Peer-reviewed: Yes

Publication information
Volume: 6
Issue number: 3
Inhibition of Escherichia coli precursor-16S rRNA processing by mouse intestinal contents

The correlation between ribosome content and growth rate found in many bacterial species has proved useful for estimating the growth activity of individual cells by quantitative in situ rRNA hybridization. However, in dynamic environments, the stability of mature ribosomal RNA causes problems in using cellular rRNA contents for direct monitoring of bacterial growth activity in situ. In a recent paper, Cangelosi and Brabant suggested monitoring the content of precursors in rRNA synthesis (pre-rRNAs) as an alternative approach. These are rapidly broken down after the cessation of bacterial growth. We have applied fluorescence in situ hybridization of pre-16S rRNA to Escherichia coli cells growing in vitro in extracts from two different compartments of the mouse intestine: the caecal mucus layer, where E. coli grew rapidly, and the contents of the caecum, which supported much slower bacterial growth. The amounts of 23S rRNA and pre-16S rRNA measured for E. coli growing in intestinal mucus corresponded to that expected for bacteria with the observed growth rate. In contrast, the slow-growing E. coli cells present in intestinal contents turned out to have an approximately ninefold higher content of pre-16S rRNA than cultures of the same strain growing rapidly in rich media. We present results suggesting that the mouse intestinal contents contain an agent that inhibits the growth of E. coli by disturbing its ability to process pre-16S rRNA.
Kinetics of plasmid transfer in different flow systems including chemostats, biofilms and the mouse intestine

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Center for Systems Microbiology, Department of Systems Biology
Pages: 2615-2622
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: Microbiology
Volume: 145
ISSN (Print): 1350-0872
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.78 SJR 0.924 SNIP 0.6
Web of Science (2017): Impact factor 1.866
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.56 SJR 1.035 SNIP 0.663
Web of Science (2016): Impact factor 2.151
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.05 SJR 1.352 SNIP 0.859
Web of Science (2015): Impact factor 2.268
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.69 SJR 1.461 SNIP 0.97
Web of Science (2014): Impact factor 2.557
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3.34 SJR 1.674 SNIP 1.028
Web of Science (2013): Impact factor 2.835
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.12 SJR 1.6 SJNIP 0.969
Web of Science (2012): Impact factor 2.852
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.18 SJR 1.659 SNIP 1.036
Web of Science (2011): Impact factor 3.061
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.804 SNIP 0.988
Web of Science (2010): Impact factor 2.957
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.71 SNIP 0.995
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.743 SNIP 1.011
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.739 SNIP 1.062
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.794 SNIP 1.063
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.76 SNIP 1.024
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.705 SNIP 1.065
Web of Science (2004): Indexed yes
Klebsiella pneumoniae capsule expression is necessary for colonization of large intestines of streptomycin-treated mice

The role of the Klebsiella pneumoniae capsular polysaccharide (K antigen) during colonization of the mouse large intestine was assessed with mild-type K. pneumoniae LM21 and its isogenic capsule-defective mutant. When bacterial strains were fed alone to mice, the capsulated bacteria persisted in the intestinal tract at levels of $10^8$ CFU/g of feces while the capsule-defective strain colonized at low levels, $10^4$ CFU/g of feces. In mixed-infection experiments, the mutant was rapidly outcompeted by the wild type. In situ hybridization on colonic sections revealed that bacterial cells of both strains were evenly distributed in the mucus layer at day 1 after infection, while at day 20 the wild type remained dispersed and the capsule-defective strain was seen in clusters in the mucus layer. These results suggest that capsular polysaccharide plays an important role in the gut colonization ability of K. pneumoniae.

General information
State: Published
Organisations: Department of Microbiology
Pages: 6152-6156
Publication date: 1999
Peer-reviewed: Yes

Publication information
Journal: Infection and Immunity
Volume: 67
Issue number: 11
ISSN (Print): 0019-9567
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.43 SJR 1.954 SNIP 0.953
Web of Science (2017): Impact factor 3.256
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.34 SJR 2.04 SNIP 0.915
Web of Science (2016): Impact factor 3.593
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.72 SJR 2.361 SNIP 1.053
Web of Science (2015): Impact factor 3.603
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.74 SJR 2.344 SNIP 1.08
Web of Science (2014): Impact factor 3.731
Web of Science (2014): Indexed yes
Plasmid transfer in the animal intestine and other dynamic bacterial populations: the role of community structure and environment

General information
State: Published
Organisations: Department of Microbiology, Danish Veterinary and Food Administration, Statens Serum Institut
Pages: 2615-2622
Publication date: 1999
Peer-reviewed: Yes
Plasmid transfer kinetics in dynamic bacterial populations, and in the animal gut: The significance of donor-recipient mixing

General information
State: Published
Organisations: Department of Microbiology, Division of Microbiology and Risk Assessment, Department of Systems Biology, Center for Systems Microbiology
Contributors: Licht, T. R., Christensen, B. B., Krogfelt, K., Molin, S.
Publication date: 1999

Host publication information
Title of host publication: Plasmid biology 98 : international symposium on plasmid biology.
Inhibition of Escherichia coli precursor-16S rRNA processing by mouse intestinal contents

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Systems Biology, Department of Microbiology, Center for Systems Microbiology
Contributors: Licht, T. R., Tolker-Nielsen, T., Holmstrøm, K., Krogfelt, K., Molin, S.
Publication date: 1998
Peer-reviewed: No
Event: Poster session presented at 8th International Symposium on Microbial Ecology, Halifax, Canada.
Source: orbit
Research output: Research › Poster – Annual report year: 1998

Inhibition of Escherichia coli precursor-16S rRNA processing by mouse intestinal contents

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Systems Biology, Department of Microbiology, Center for Systems Microbiology
Contributors: Licht, T. R., Tolker-Nielsen, T., Holmstrøm, K., Krogfelt, K., Molin, S.
Publication date: 1998
Peer-reviewed: No
Event: Abstract from 8th International Symposium on Microbial Ecology, Halifax, Canada.
Source: orbit
Research output: Research › Conference abstract for conference – Annual report year: 1998

Kinetics of plasmid transfer in different flow systems including chemostats, biofilms, and the mouse intestine

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Systems Biology, Center for Systems Microbiology
Contributors: Licht, T. R., Christensen, B. B., Krogfelt, K., Molin, S.
Publication date: 1998
Peer-reviewed: No
Source: orbit
Research output: Research › Conference abstract for conference – Annual report year: 1998

Kinetics of plasmid transfer in different flow systems including chemostats, biofilms, and the mouse intestine

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Systems Biology, Center for Systems Microbiology
Contributors: Licht, T. R., Christensen, B. B., Krogfelt, K., Molin, S.
Publication date: 1998
Peer-reviewed: No
Source: orbit
Research output: Research › Poster – Annual report year: 1998
Applications of ribosomal in situ hybridization for the study of bacterial cells in the mouse intestine

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, Department of Systems Biology, Center for Systems Microbiology, Novo Nordisk AS, Statens Serum Institut
Contributors: Licht, T. R., Poulsen, L. K., Molin, S., Krogfelt, K. A.
Pages: 81-90
Publication date: 1997
Host publication information
Title of host publication: Ecology of pathogenic bacteria ; Molecular and evolutionary aspects
Place of publication: Amsterdam
Publisher: Royal Netherlands Academy of Arts and Sciences
Source-ID: 169062
Research output: Research - peer-review › Article in proceedings – Annual report year: 1997

Lipopolysaccharide's role in the association of Salmonella cells to the mouse intestine studied by ribosomal in situ hybridization

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, Department of Systems Biology, Center for Systems Microbiology, Statens Serum Institut
Contributors: Krogfelt, K., Licht, T. R., Molin, S.
Pages: 123-128
Publication date: 1996
Host publication information
Title of host publication: Toward anti-adhesion therapy for microbial diseases
Place of publication: New York
Publisher: Plenum Publishing Corporation
Source-ID: 165436
Research output: Research - peer-review › Article in proceedings – Annual report year: 1996

Lipopolysaccharide's role in the association of Salmonella cells to the mouse intestine studied by ribosomal in situ hybridization
Role of Lipopolysaccharide in colonization of the mouse intestine by Salmonella typhimurium

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Department of Systems Biology, Center for Systems Microbiology
Contributors: Licht, T. R., Krogfelt, K., Molin, S.
Publication date: 1996
Peer-reviewed: No
Source: orbit
Source-ID: 245187
Research output: Research - peer-review › Journal article – Annual report year: 1996

Role of Lipopolysaccharide in colonization of the mouse intestine by Salmonella typhimurium studied by in situ hybridization

General information
State: Published
Organisations: National Food Institute, Division of Microbiology and Risk Assessment, Department of Systems Biology, Center for Systems Microbiology, Statens Serum Institut, University of Rhode Island, Novo Nordisk AS, Michigan State University
Pages: 3811-3817
Publication date: 1996
Peer-reviewed: Yes

Publication information
Journal: Infection and Immunity
Volume: 64
Issue number: 9
ISSN (Print): 0019-9567
Ratings:
BFI (2019): BFI-level 1
Web of Science (2019): Indexed yes
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.43 SJR 1.954 SNIP 0.953
Web of Science (2017): Impact factor 3.256
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.34 SJR 2.04 SNIP 0.915
Web of Science (2016): Impact factor 3.593
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.72 SJR 2.361 SNIP 1.053
Web of Science (2015): Impact factor 3.603
Physiological state of Escherichia coli BJ4 growing in the large intestines of streptomycin-treated mice

General information
State: Published
Organisations: Department of Systems Biology, Division of Microbiology and Risk Assessment, Department of Microbiology, Center for Systems Microbiology
Contributors: Poulsen, L. K., Licht, T. R., Rang, C., Krogfelt, K., Molin, S.
Ribosomal in situ hybridization of bacterial cells in the mouse intestine

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Center for Microbial Biotechnology, Department of Systems Biology, Center for Systems Microbiology
Contributors: Licht, T. R., Poulsen, L. K., Krogfelt, K., Molin, S.
Publication date: 1995
Peer-reviewed: No
Event: Abstract from Academy Colloquium of the Koninklijke Akademie van Wetenschappen: "Ecology of pathogenic bacteria: molecular and evolutionary aspects", Amsterdam, Netherlands.
Source: orbit
Source-ID: 245260
Research output: Research - Conference abstract for conference – Annual report year: 1995

Colonization of bacteria in the mouse intestine - Visualized by in situ hybridization of rRNA

General information
State: Published
Organisations: Department of Microbiology, Center for Systems Microbiology, Department of Systems Biology
Publication date: 1994
Peer-reviewed: No
Event: Poster session presented at Academy Colloquium of the Koninklijke Akademie van Wetenschappen: "Ecology of pathogenic bacteria: molecular and evolutionary aspects", Amsterdam, Netherlands.
Source: orbit
Source-ID: 245261
Research output: Research - Poster – Annual report year: 1995
Colonization of bacteria in the mouse intestine - Visualized by in situ hybridization of rRNA

General information
State: Published
Organisations: Department of Microbiology, Center for Systems Microbiology, Department of Systems Biology
Publication date: 1994
Peer-reviewed: No
Source: orbit

Projects:

Effect of Probiotic Supplementation on Infant Gut Microbiome and Immune System Development
Colberg, O., PhD Student, National Food Institute
Licht, T. R., Main Supervisor, National Food Institute
Laursen, M. F., Supervisor, National Food Institute
Wichmann, A. E., Supervisor
01/12/2018 → 30/11/2021
Project: PhD

Characterization of anti-obesity drug effects on gut microbiome function
Madsen, M. S. A., PhD Student, Novo Nordisk Foundation Center for Biosustainability
Sommer, M. O. A., Main Supervisor, Novo Nordisk Foundation Center for Biosustainability
Licht, T. R., Supervisor, National Food Institute
Björk Hansen, H., Supervisor
Mikkelsen, M., Supervisor
01/11/2018 → 31/10/2021
Project: PhD

Strategies to control colonization of advanced microbiome therapeutics in the intestine
Holst, A., PhD Student, National Food Institute
Bahl, M. I., Main Supervisor, National Food Institute
Licht, T. R., Supervisor, National Food Institute
01/11/2018 → 31/10/2021
Project: PhD

Application of advanced microbial therapeutics to enhance production of beneficial bacterial metabolites in the intestine
Dimopoulou, C., PhD Student, National Food Institute
Bahl, M. I., Main Supervisor, National Food Institute
Licht, T. R., Supervisor, National Food Institute
01/11/2018 → 31/10/2021
Project: PhD

Application of advanced delivery systems for live bacteria to the gut environment
Meyer Torp, A., PhD Student, National Food Institute
Licht, T. R., Main Supervisor, National Food Institute
Bahl, M. I., Supervisor, National Food Institute
Samfinansieret - Andet
01/05/2018 → 30/04/2021
Award relations: Application of advanced delivery systems for live bacteria to the gut environment
Project: PhD
Alleviation of ulcerative colitis by application of new oral delivery systems for bacteria
Bondevaard, P. W., PhD Student, National Food Institute
Licht, T. R., Main Supervisor, National Food Institute
Bahl, M. I., Supervisor, National Food Institute
Samfinansieret - Andet
01/05/2018 → 30/04/2021
Award relations: Alleviation of ulcerative colitis by application of new oral delivery systems for bacteria
Project: PhD

Microbiota and cow's milk tolerance
Graversen, K. B., PhD Student, National Food Institute
Bøgh, K. L., Main Supervisor, National Food Institute
Bahl, M. I., Supervisor, National Food Institute
Licht, T. R., Supervisor, National Food Institute
Samfinansieret - Andet
15/12/2015 → 09/09/2019
Award relations: Microbiota and cow's milk tolerance
Project: PhD

Interactions Between the Microbiome and Host Immune System
Masche, A. C., PhD Student, National Food Institute
Pamp, S. J., Main Supervisor, National Food Institute
Aarestrup, F. M., Supervisor, National Food Institute
Lund, O., Supervisor, National Food Institute
Müller, K. G., Supervisor
Licht, T. R., Examiner, National Food Institute
Andersen, P. S., Examiner
Van Den Brink, M. R. M., Examiner
Samfinansieret - Andet
01/10/2015 → 31/12/2018
Award relations: Interactions Between the Microbiome and Host Immune System
Project: PhD

Infektion og kolonisering af salmonella i tarmen
Licht, T. R., PhD Student, National Food Institute
Molin, S., Main Supervisor, Novo Nordisk Foundation Center for Biosustainability
Anden Forskningsrådsfinans.-SU
01/02/1994 → 26/05/1997
Award relations: Infektion og kolonisering af salmonella i tarmen
Project: PhD

Bacterial Impact on the Gut Metabolome
Sulek, K., PhD Student, National Food Institute
Licht, T. R., Main Supervisor, National Food Institute
Skov, T. H., Supervisor, National Food Institute
Smedsgaard, J., Supervisor, National Food Institute
Bahl, M. I., Examiner, National Food Institute
Dragsted, L. O., Examiner
Institut stipendie (DTU) Samf.
01/08/2009 → 06/02/2013
Award relations: Bacterial Impact on the Gut Metabolome
Project: PhD

Metagenomic systems biology of the human oral microbiome
Bonde, I., PhD Student
Sicheritz-Pontén, T., Main Supervisor
Nielsen, H. B., Supervisor, Department of Systems Biology
Licht, T. R., Examiner
Hansen, L. H., Examiner
Kleerebezem, M., Examiner
Ekstern finansieret virksomhed
01/02/2011 → 29/09/2014
Award relations: Metagenomic systems biology of the human oral microbiome
Project: PhD

**Effects of emulgating dietary fat with dairy phospholipids on establishment of the gut microbiota**
Bennike, R. M. G., PhD Student, Department of Systems Biology
Hellgren, L., Main Supervisor
Licht, T. R., Supervisor
Jacobsen, C., Examiner
Ahrne, S., Examiner
Lauridsen, C., Examiner
Institut stipendie (DTU) Samf.
01/12/2011 → 02/09/2015
Award relations: Effects of emulgating dietary fat with dairy phospholipids on establishment of the gut microbiota
Project: PhD

**Microbiota and Metabolic Diseases - Dietary intervention studies in animal models**
Zhang, L., PhD Student, Division of Food Microbiology
Licht, T. R., Main Supervisor, National Food Institute
Bahl, M. I., Supervisor, National Food Institute
Hansen, A. K., Supervisor
Pamp, S. J., Examiner, National Food Institute
Ahrne, S., Examiner
Wichmann, A. E., Examiner
Wichmann, A. E., Examiner
Institut stipendie (DTU) Samf.
01/11/2012 → 02/06/2016
Award relations: Microbiota and Metabolic Diseases - Dietary intervention studies in animal models
Project: PhD

**The Microbiome and Functional foods for cloned lean/obese pigs**
Pedersen, R., PhD Student, National Veterinary Institute
Boye, M., Main Supervisor, National Veterinary Institute
Stagsted, J., Supervisor
Licht, T. R., Examiner
Ahrne, S., Examiner
Thymann, T., Examiner
Institut stipendie (DTU) Samf.
01/12/2008 → 06/02/2013
Award relations: The Microbiome and Functional foods for cloned lean/obese pigs
Project: PhD

**Impact of Colonization on Immune System Development**
Kristensen, M. B., PhD Student, National Food Institute
Licht, T. R., Main Supervisor, National Food Institute
Frokiaer, H., Supervisor
Hellgren, L., Examiner
Pedersen, A. E., Examiner
Sanz, Y., Examiner
Globaliseringsmidler
01/11/2007 → 02/07/2014
Award relations: Impact of Colonization on Immune System Development
Project: PhD

**A symbiotic feed for piglets**
Manurung, S., PhD Student, National Veterinary Institute
Boye, M., Main Supervisor, National Veterinary Institute
Jensen, B. B., Supervisor
Malbak, L., Supervisor, National Veterinary Institute
Licht, T. R., Examiner
Smidt, H., Examiner
Thymann, T., Examiner
Institut stipendie (DTU) Samf.
01/12/2009 → 06/02/2013
Award relations: A symbiotic feed for piglets
Project: PhD

Prebiotics for Prevention of Listeria Infections
Ebersbach, T., PhD Student, National Food Institute
Licht, T. R., Main Supervisor, National Food Institute
Poulsen, M., Supervisor, National Food Institute
Gram, L., Examiner, National Food Institute
Ingmer, H., Examiner
Rastall, R., Examiner
Programbevilling
01/04/2007 → 22/09/2010
Award relations: Prebiotics for Prevention of Listeria Infections
Project: PhD

Prebiotics for Prevention of Salmonella Infections
Petersen, A., PhD Student, Others
Licht, T. R., Main Supervisor, National Food Institute
Poulsen, M., Supervisor, National Food Institute
Aabo, S., Examiner, National Food Institute
Kleerebezem, M., Examiner
Forskningsrådsfinansiering
01/04/2007 → 25/08/2010
Award relations: Prebiotics for Prevention of Salmonella Infections
Project: PhD

Risk-Benefit assessment of function foods - Focus on intestinal integrity
Christensen, E. G., PhD Student, National Food Institute
Bahl, M. I., Main Supervisor, National Food Institute
Licht, T. R., Supervisor, National Food Institute
Boye, M., Examiner
Van den Abbeelee, P., Examiner
Hejberg, O., Examiner
Forskningsrådsfinansiering
01/03/2011 → 04/06/2014
Award relations: Risk-Benefit assessment of function foods - Focus on intestinal integrity
Project: PhD

Control of Foodborne Pathogenic Bacteria by Cleaning and Disinfection
Kastbjerg, V. G., PhD Student, National Institute of Aquatic Resources
Gram, L., Main Supervisor, National Institute of Aquatic Resources
Vogel, B. F., Supervisor, National Institute of Aquatic Resources
Licht, T. R., Examiner
Knøchel, S., Examiner
Webber, M., Examiner
Anden EU-finansiering
01/04/2006 → 23/09/2009
Award relations: Control of Foodborne Pathogenic Bacteria by Cleaning and Disinfection
Project: PhD

In Vitro Investigation of New Prebiotic Compounds
Vigsnæs, L. K., PhD Student, National Food Institute
Licht, T. R., Main Supervisor, National Food Institute
Mølbak, L., Examiner
Ahrne, S., Examiner
Krogfelt, K. A., Examiner
DTU, Samfinansiering
01/12/2007 → 29/02/2012
Award relations: In Vitro Investigation of New Prebiotic Compounds
Project: PhD
Development of the Human Gut Microbiota during Early Life
Laursen, M. F., PhD Student, National Food Institute
Licht, T. R., Main Supervisor, National Food Institute
Bahl, M. I., Supervisor, National Food Institute
Jelsbak, L., Examiner, Department of Biotechnology and Biomedicine
Kristiansen, K., Examiner
O'Toole, P. W., Examiner
O'Toole, P. W., Examiner
Forskningsrådssfinsiering
01/09/2013 → 31/01/2018
Award relations: Development of the Human Gut Microbiota during Early Life
Project: PhD

Deciphering complex regulatory traits relating to host metabolism and immunity
Moll, J. M., PhD Student, Department of Biotechnology and Biomedicine
Pedersen, S. B., Main Supervisor, Department of Biotechnology and Biomedicine
Hellgren, L., Supervisor, Department of Biotechnology and Biomedicine
Workman, C., Supervisor, Department of Biotechnology and Biomedicine
Licht, T. R., Examiner, National Food Institute
Clavel, T., Examiner
Paludan, S. R., Examiner
Paludan, S. R., Examiner
Institut stipendie (DTU)
15/12/2012 → 15/02/2017
Award relations: Deciphering complex regulatory traits relating to host metabolism and immunity
Project: PhD

Intestinal Microbial Metabolomics
Roager, H. M., PhD Student, National Food Institute
Licht, T. R., Main Supervisor, National Food Institute
Skov, T. H., Supervisor, National Food Institute
Smedsgaard, J., Supervisor, National Food Institute
Søndergaard, M., Examiner
Dragsted, L. O., Examiner
Kleerebezem, M., Examiner
Institut stipendie (DTU)
15/12/2012 → 21/04/2016
Award relations: Intestinal Microbial Metabolomics
Project: PhD

Prebiotika til hindring af tarmygdomme hos svin
Strube, M. L., PhD Student, National Veterinary Institute
Boye, M., Main Supervisor, National Veterinary Institute
Meyer, A. S., Supervisor, Department of Biotechnology and Biomedicine
Licht, T. R., Examiner, National Food Institute
Hotchkiss, Jr., A. T., Examiner
Thyman, T., Examiner
Hotchkiss, Jr., A. T., Examiner
Thyman, T., Examiner
Institut stipendie (DTU)
01/07/2012 → 25/11/2015
Award relations: Prebiotika til hindring af tarmygdomme hos svin
Project: PhD

Microbiota and cow's milk tolerance
Cow's milk allergy is a health problem of growing concern for which reason efficient strategies for the prevention is urgently needed. In recent years it has been demonstrated that the gut microbiota composition influences the development of allergy. However, our knowledge about how the microbiota composition influences the sensitising or tolerance inducing capacities of the food is only scarcely described. The objectives of this project are: (1) to increase our knowledge about the interplay between food proteins and the gut microbiota, and how this interplay impact on induction of cow’s milk allergy versus tolerance, and (2) in a broader perspective to gain knowledge about mechanisms influenced by microbiota, which
drives the immune system towards allergy or tolerance. Intact whey, which is one fraction of cow’s milk often used for infant formula, and enzymatic hydrolysed products hereof, used for hypoallergic infant formulas, will used as model protein ingredients. The interplay between whey-based ingredients and the gut microbiota will be investigated in vitro fermentation studies based on faecal samples from food allergic and healthy infants, as well as in animal studies in which the gut microbiota is manipulated by antibiotics treatment. Microbial composition will be analysed by 16S rRNA gene sequencing in combination with quantitative real-time PCR. The allergy or tolerance inducing capacity of the different whey-based ingredients and the influence of the gut microbiota composition will be analysed by evaluating different serological and cell based end-points. Appropriate functional in vitro, in vivo and ex vivo assays will be applied to investigate the mechanism by which the gut microbiota and metabolites hereof impact on directing the immune system towards allergy or tolerance.

Bøgh, K. L., Project Manager, National Food Institute, Research Group for Gut Microbiology and Immunology
Graversen, K. B., Project Participant, National Food Institute, Research Group for Gut Microbiology and Immunology
Licht, T. R., Project Participant, National Food Institute, Research Group for Gut Microbiology and Immunology
Bahl, M. I., Project Participant, National Food Institute, Research Group for Gut Microbiology and Immunology

**Novo_Gut Symposium: Symposium on Gut Microbiota and Host Metabolic Health**

The idea with the symposium is to invite four esteemed foreign speakers within the field of Gut Microbiota and Metabolic Health, who can thereby inspire and interact with Danish senior researchers as well as young Danish scientists. Additionally, the symposium will be used as a platform to disseminate the new results from the 3G Center and related research. This will contribute to the continuous development of Danish research as a major international player within this field of science.

Licht, T. R., Project Coordinator, National Food Institute, Research Group for Gut Microbiology and Immunology
Skiby, J. E., Project Manager, National Food Institute, Research group for Genomic Epidemiology
Bang-Berthelsen, I., Project Manager, National Food Institute
Novo Nordisk Fonden: DKK130.00
01/07/2015 → 30/06/2017

**Keywords:** gut, microbiota, diabetes

**Collaborators:** Spanish National Research Council, Wageningen IMARES, Cornell University, Louvain Drug Research Institute

**Award relations:** Symposium on Gut Microbiota and Host Metabolic Health

**Project: Research**

**PestiGUT: The gut microbiota as a sensitive indicator for biologically relevant residues of chemical pesticides in food produce exemplified by glyphosate (Roundup®)**

Det er i løbet af det sidste årti blevet klart, at den naturlige bakterieflora i tarmen (kaldet tarmens mikrobiota) har meget stor betydning for menneskers generelle sundhedstilstand. Således er tarmmikrobiotaens sammensætning og aktivitet blevet koblet til en række vestlige livstilssygdomme som fx metabolisk syndrom. Valg af kost er naturligvis vigtigt i forhold til påvirke mikrobiota’en, men også eventuelle restkoncentrationer af pesticider i fødevarer kan spille en rolle da flere pesticider, heriblandt glyphosat, er kendteget ved også at besidde antimikrobielle egenskaber. I forbindelse med risikovurdering af pesticider og faststæggelse af grænseværdier for indtag er mikrobielle påvirkninger med eventuelt negative langsigtede konsekvenser stort set ikke belyst. Formålet med dette projekt er at undersøge påvirkninger af minimums effekt koncentrationen (MEC) af pesticidet glyphosat, samt de hjælpestoffer (adjuvanter) som er til stede i det komмерcielle produkt Roundup® på tarmmikrobiotaens sammensætning og funktion. I projektet udvikles en in vitro fermenteringsmodel, som vil blive valideret in vivo i en dyremodel. De bestemte MEC værdier vil blive holdt op imod gældende grænseværdier (MRL) i fødevarer samt det fastsatte maksimale daglige indtag på 0,3 mg/kg legemsvægt, for derved at vurdere om arbejds- eller forbruger relateret ekspøning for glyphosat kan have effekt på tarmens bakteriesammensætning og dermed kan udgøre en sundhedsmæssig risiko. Inducerede ændringer i tarmmikrobiotaen vil i den udviklede model fungere som en fælsm indicator, der kan bruges til at bestemme restkoncentrationer af andre kemiske pesticider, der er biologisk relevante i forhold til tarmens bakteriesammensætning. Påvirkninger af værtsorganismens tarmintegritet (permeabilitet) samt ændringer i kortkædet fedtsyres produktion forårsages af en ændret tarmmikrobiota eller glyphosat i sig selv vil indgå som en parameter.

Bahl, M. I., Project Participant, National Food Institute, Research Group for Gut Microbiology and Immunology
Licht, T. R., Project Participant, National Food Institute, Research Group for Gut Microbiology and Immunology
01/10/2015 → 30/09/2017

Collaborators: Arla Foods

**Project: Research**

**The intestinal microbial ecosystem: A novel approach to the study of the intestinal microbial ecosystem and its putative role in obesity development**

Causal relationships between the large number of bacterial species present in the human gut contains potentially important information on the regulation of intestinal function. Although the broad taxonomic groups of bacteria and their
physiological functions are common to all people, there is tremendous individual variation in the bacterial composition, also known as the microbiota. As the composition of the microbiota is formed in the early years of life, it is highly relevant to analyze correlations of microbiota, diet and trends of overweight in infants, in particular, since there is a strong correlation between overweight/obesity in infants/children and associated correlated serious Western lifestyle diseases in adults. Relevant examples are Type 2 Diabetes and cardiovascular disease. Due to technical restrictions, it has not previously been possible to effectively analyze internal bacterial patterns and relationships for a large number of samples. To this purpose, we have developed a fast, cheap and reliable "gut-low-density array" (GULDA), which utilize quantitative PCR (qPCR) to simultaneously quantify approximately 50 different selected bacterial species in a given sample of fecal DNA. The aim of this project is to use GULDA to analyze a large number of stool samples collected at a recent cohort study at KU-LIFE of very young (0-3 years) Danish children (SKOT cohort = Småbærns KOst og Trivsel). Hopefully, this should elucidate important internal causal relationships in the microbiota and correlations between microbiota, diet and biomarkers for risk of obesity development in infants. Project financing: The project is fully financed by a personal post.doc grant to Anders Bergström from The Danish Agency for Science, Technology and Innovation/Technology and Production. The grant awarded was 2.181.600 DKR.

Licht, T. R., Project Manager, National Food Institute, Division of Food Microbiology

Prebiotic potential of novel carbohydrate preparations : Evaluation of Prebiotic potential of novel carbohydrate preparations

This project constitutes workpackage 2 in the 'Prebiotic Center, headed by Anne Meyer at DTU Chemical Engeneering. The task of the Gut Ecology group at the Nationel Food Institutes, Technical University of Denmark in the Center approach is to test for effects of novel carbohydrate preparations on the intestinal microbiota which may be relevant for human health. Specifically, we focus on the possibilities to prevent outbreaks of Ulcerative Colitis (UC). We perform small-scale batch fermentations in pure cultures as well as in intestinal communities derived from healthy subjects and from subjects suffering from UC. We analyse microbiota composition and metabolites produced by host and bacteria. Project financing: Danish Strategic Research Council Øresund Food network

Licht, T. R., Project Manager, National Food Institute, Division of Food Microbiology

Vigsnæs, L. K., Project Participant, National Food Institute, Division of Food Microbiology

Sulek, K., PhD Student

Holck, J., Project Participant, Department of Chemical and Biochemical Engineering, Center for BioProcess Engineering

Brynskov, J., Project Participant, University Hospital Herlev

Steinholdt, C., Project Participant, University Hospital Herlev

Project: Research

Effects of bacterial colonization on immune maturation

The Gut Ecology group at the National Food Institute, Technical University of Denmark investigates effects of bacterial colonization on the maturation of the immune system in early life. We do this by use of germ-free and monocolonized mouse models. The project is closely related to other projects in the Gut Ecology research group, where we analyze the intestinal microbiota in infants. Project financing: Globalization funds (through FoodDTU)

Licht, T. R., Project Manager, National Food Institute, Division of Food Microbiology

Kristensen, M. B., PhD Student

Bergström, A., Project Participant

Nellemann, C., Project Participant, National Food Institute, Communications and Management Secretariat

Frekær, H., Project Participant

Metzdorff, S. B., Project Participant

Fink, L. N., Project Participant

Project: Research

Can the use of dairy phospholipids as emulgators protect against a pro-obesogenic intestinal microbiota?

The results from a pilot-study in our labs, indicates that it possible to modulate the composition of the intestinal microbiota by emulsifying fat in milk phospholipids (MPL), instead of using soy-lecithin that is normally used f ex. in infant formulas. In the study, we mimicked the intestinal colonization occurring at birth, by transferring germ-free mice out of the sterile environment and into cages containing faeces from a normal mouse, while they were given the emulsions for three week. The results show that the numbers of bacteria from the phylum Firmicutes decreased in the colon lumen in mice that were given the MPL-based emulsions (fig. 1 below) while Bacteriodetes was not affected. Since obesity-development have been linked to increased ratio between Firmicutes and Bacteriodetes in the colon, the result indicates that it could be possible to reduce the risk of developing obesity later in life by exchanging soy-lecithin with MPL in infant formulas. To
elucidate this possibility, we want to perform three studies in which we will validate the results from the pilot-study in a bigger study, determine the mechanism that is explaining the effect on microbial composition and determine whether this effect is persistent also after intake of the emulsion have stopped and whether it actually reduce the risk of developing obesity and metabolic diseases later in life.

Licht, T. R., Project Participant, National Food Institute, Division of Food Microbiology
Hellgren, L., Project Manager, Department of Systems Biology, Center for Biological Sequence Analysis
Bennike, R. M. G., Project Participant, Department of Systems Biology, Center for Biological Sequence Analysis, National Food Institute, Division of Food Microbiology
Mejeribruggets ForskningsFond: DKK360,000.00
02/01/2012 → 31/12/2015
Award relations: Can the use of dairy phospholipids as emulgators protect against a pro-obesogenic intestinal microbiota?
Project: Research

3G Center: 3G Center: Center for Gut Microbiota, Metabolic disorders, and Grain/Fibre-based Diets (Guts, Grains and Greens)
We hypothesize that the interplay between human host genome expression and gut microbiota (GM) affects the development of chronic metabolic disorders, and that interventions targeting the microbiome and mucosa can therefore reduce the risk of developing metabolic dysfunctions such as obesity, Type 2 Diabetes (T2D), and cardiovascular diseases (CVD). Our intention is to develop an internationally competitive research platform to address this hypothesis. The platform builds on integration of data from human studies, animal models and in vitro studies with state-of-the art methods for high-throughput sequencing and analysis of biomarkers of metabolic disorders. The hypothesis will be tested by intervention studies undertaken in this integrated setup. Grain/vegetable-based interventions, which are known to affect the host gut microbiota and metabolism either positively (dietary fibers/whole grain), or negatively (gluten-rich diet), will be applied. We will actively discuss and develop our research in dialogue with companies that produce foods or food ingredients that influence the GM, industries involved in prevention and/or treatment of metabolic and inflammatory diseases, as well as to public health authorities. This will form the basis for development of new functional foods, new innovative products and improved dietary advice, which in a short-term perspective will add to the value of these companies, and in the long-term perspective reduce the occurrence of lifestyle related metabolic diseases. Once developed, the research platform will be available for further intervention studies, and will provide the possibility to study other endpoints and biomarkers than the ones included in the present proposal. The success of the project will place Danish research at the absolute forefront within GM manipulation and host response.
Licht, T. R., Project Coordinator, National Food Institute, Division of Food Microbiology
Vigsnæs, L. K., Project Participant, National Food Institute, Division of Food Microbiology
Laursen, M. F., Project Participant, National Food Institute, Division of Food Microbiology
Bahl, M. I., Project Participant, National Food Institute, Division of Food Microbiology
Skiby, J. E., Project Participant, National Food Institute, Division of Food Microbiology
Roager, H. M., Project Participant, National Food Institute, Division of Food Microbiology
Madsen, B., Project Participant, National Food Institute, Division of Food Microbiology
Zhang, L., Project Participant, National Food Institute, Division of Food Microbiology
Danish Council for Strategic Research: DKK34,749,243.00
01/04/2012 → 31/03/2017
Collaborators: University of Copenhagen, Taconic Europe A/S, Technical University of Denmark, DuPont Nutrition and Health
Award relations: 3G Center: Center for Gut Microbiota, Metabolic disorders, and Grain/Fibre-based Diets (Guts, Grains and Greens)
Project: Research

PrimeGerm: PrimeGerm : Effects and consequences of neonatal gut community perturbation by antibiotics
The extreme success of antibiotics for treatment of infectious diseases has caused increased attention towards non-infectious so called life-style diseases including type 2 diabetes, obesity and inflammatory bowel diseases. Although the etiology of these diseases is not fully understood, they are inevitably linked to host-microbe interactions driven by the dynamics of the naturally occurring microbial gut community. Modulation of this microbiota by exposure to specific antibiotics, especially during early life, is known to disrupt the natural balance of the fine-tuned microbial ecosystem, which may lead to adverse physiological effects later in life including increased risk of obesity. We will investigate specific effects of different classes of commonly used antibiotics on the developing gut microbiota of neonate mice and further determine effects on gut permeability and host metabolic parameters. This will provide valuable new insight for risk assessment of antibiotics.
Tulstrup, M. V., Project Participant, National Food Institute, Division of Food Microbiology
Bahl, M. I., Project Manager, National Food Institute, Division of Food Microbiology
Licht, T. R., Project Participant, National Food Institute, Division of Food Microbiology
Skiby, J. E., Other, National Food Institute, Division of Food Microbiology
Danish Council for Independent Research, Technology and Production Sciences
01/09/2013 → 31/08/2016
Award relations: PrimeGerm : Effects and consequences of neonatal gut community perturbation by antibiotics
Project: Research
ProbiComp: Probiotics in childhood

Young children suffer from many infections especially after they start day care resulting in approximately 700,000 days of parental leave in Denmark per year. There is evidence that probiotics can reduce the incidence and severity of acute diarrhoea, atopic eczema and possibly respiratory tract infections most likely through acceleration of the immune system development. In ProbiComp, we will test the effect of treatment with a probiotic strain (vs a placebo) in children attending day care. The primary outcome in the study will be the number of days of absence from day care due to infections, but also a number of secondary outcomes will be measured. The role of DTU Food in ProbiComp is to test the effect of the probiotic treatment on the intestinal microbiota, since this is believed to be connected e.g. to risk of allergies and infections.

Michaelsen, K. F., Project Manager
Licht, T. R., Project Participant, National Food Institute, Division of Food Microbiology
Laursen, M. F., Project Participant, National Food Institute, Division of Food Microbiology
Bahl, M. I., Project Participant, National Food Institute, Division of Food Microbiology
01/09/2013 → 31/12/2016
Collaborators: University of Bergen, Chr. Hansen AS, Odense University Hospital, Copenhagen University Hospital, Institute of Food and Resource Economics
Project: Research

MICROBESE: MICROBESE – A novel approach to the study of the intestinal microbial ecosystem and its putative role in obesity development

Det er formålet med dette projekt at udnytte GULDA til at analysere et stort antal fæcesprøver indsamlet ved en nyligt afsluttet kohorteundersøgelse ved KU-Life af helt små (0-3 år) danske børn (SKOT-kohorte=Småbørns KØst og Trivsel). Derved vil interne kausale sammenhænge i mikrobiotaven, samt korrelationer mellem mikrobiota, kost og biomarkerer for risiko for fedmeudvikling i helt små børn, forhåbentlig kunne aflækket ses. Bergstrøm, A., Project Manager, National Food Institute, Division of Food Microbiology
Licht, T. R., Project Participant, National Food Institute, Division of Food Microbiology
Bro, R., Project Participant, Department of Systems Biology
Skov, T. H., Project Participant, National Food Institute
Michaelisen, K. F., Project Participant
Det Fri Forskningsråd/Teknologi og Produktion: DKK2,181,600.00
01/01/2011 → 20/09/2013
Keywords: Gut microbiota low density array, Early life obesity biomarkers, qPCR, Multivariate statistics, Gut community analysis
Award relations: MICROBESE – A novel approach to the study of the intestinal microbial ecosystem and its putative role in obesity development
Project: Research

Mikrobiologiske plantebeskyttelsesmidlers skæbne i mave-tarmkanalen

Licht, T. R., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Wilcks, A., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Forskningsprojekter - Miljø- og Energiministeriet: DKK2,018,524.00
01/12/2003 → 01/01/2006
Award relations: Mikrobiologiske plantebeskyttelsesmidlers skæbne i mave-tarmkanalen
Project: Research
Assessment and Critical Evaluation of Antibiotic Resistance Transferability in the Food Chain

ACE-ART is a EU STREP project under the 6th framework programme. The main aim of the project is to generate knowledge on the source of food-related antibiotic resistant bacteria, their genetic composition and potential for resistance transfer. The bacteria of interest include Lactobacillus, Bifidobacterium, Lactococcus and Streptococcus thermophilus. The National Food Institute (Andrea Wilcks) is coordinator for WP2: Transfer of antibiotic resistance genes in non-pathogenic bacteria associated with the food chain.

Wilcks, A., Project Manager, National Food Institute
Licht, T. R., Project Participant, National Food Institute
Morelli, L., Project Participant, Catholic University of the Sacred Heart
Wind, A., Project Participant, Chr. Hansen AS
Krogfelt, K., Project Participant, Statens Serum Institut
Bardowski, J., Project Participant, Polish Academy of Sciences
Bolton, D., Project Participant, TEAGASC
Aarts, H., Project Participant, Institute of Food Safety
Huys, G., Project Participant, Ghent University
01/01/2003 → 30/06/2007
Collaborators: Institute of Food Safety, Catholic University of the Sacred Heart, Chr. Hansen AS, Statens Serum Institut, TEAGASC, Polish Academy of Sciences, Ghent University
Project: Research

Fate of Bacillus thuringiensis bacteria, applied for biological pest control, in the gastro-intestinal tract.

Bacillus thuringiensis (Bt), which forms specific insecticidal toxins during sporulation, constitutes the active organism in many products used for biological control of insects. Bt is therefore often present on treated fruits and vegetables sold for consumption. The aim of the project is to assess specific putative risks associated with ingestion of Bt spores. The project seeks to answer the following questions: (i) Do Bt spores germinate in the intestinal tract, (ii) does heat treatment prior to ingestion induce the germination, (iii) do they influence the composition of the intestinal microflora, (iv) do they produce enterotoxins in the gut, and (v) are they capable of exchanging genetic material with the indigenous gut microorganisms?

Licht, T. R., Project Manager, National Food Institute
Wilcks, A., Project Participant, National Food Institute
01/12/2003 → 01/12/2006
Collaborators: Aarhus University, National Research Centre for the Working Environment
Project: Research

PreGI: Prebiotics for Prevention of Gastrointestinal Infections


Licht, T. R., Project Manager, National Food Institute
Wilcks, A., Project Participant, National Food Institute
Bergström, A., Project Participant, National Food Institute
Andersen, J. B., Project Participant, National Food Institute
Poulsen, M., Project Participant, National Food Institute
Frøkiær, H., Project Manager, Department of Systems Biology
Pedersen, S. B., Project Manager, Department of Systems Biology
Forskningsrådene - Andre: DKK8,500,000.00
01/01/2007 → 01/09/2011
Award relations: Prebiotics for Prevention of Gastrointestinal Infections
Project: Research

Direct monitoring of gene transfer in the animal gut flora

Bacteria like E. coli and S. typhimurium colonize the gut of mammals by establishing in the mucus of the large intestine. The model system used is the streptomycin treated mouse in which streptomycin resistant strains of the two bacteria may be introduced stably. Plasmid transfer in situ is studied after introducing donor strains carrying either narrow-host-range or
broad-host-range conjugative plasmids. The major goal is to understand how genetic information is transferred in the bacterial ecosystem of the mammal gut, and to what extent selection pressure, properties of the donor, recipient and plasmid affect the transfer efficiency.

Molin, S., Project Manager, Department of Systems Biology
Licht, T. R., Project Participant, Department of Systems Biology
Krogfelt, K. A., Project Participant, Statens Serum Institut
Cohen, P., Project Participant, University of Rhode Island
Ukendt: DKK740,000.00
01/01/1996 → 31/12/1998
Collaborators: Statens Serum Institut, University of Rhode Island
Award relations: Direct monitoring of gene transfer in the animal gut flora

WP2 in Prebiotic Center: Gut microbiota and Immune Response Effects
The Role of WP2 in Prebiotic center is to reveal effects of putatively prebiotic carbohydrates on gut microbiota and immune fuction. We collaborate with Danisco and Herlev Hospital within this WP.

Wilcks, A., Project Participant, National Food Institute
Licht, T. R., Project Manager, National Food Institute
Meyer, A. S., Project Manager, National Food Institute
Forskningsrådene - Andre: DKK3,436,000.00
01/01/2007 → 31/12/2011
Award relations: WP2 in Prebiotic Center: Gut microbiota and Immune Response Effects
Project: Research

Virulence of Listeria monocytogenes: Influence of genetic sub-type, persistence capacity and environmental factors on risk from the human foodborne pathogen Listeria monocytogenes
The purpose of this project is to determine if the particular molecular sub-types of Listeria monocytogenes that persists in food processing are more or less virulent that other sub-types. We work with their invasion and spread in mammalian cell lines. Also, the sequence and function of virulence genes is determined. In collaboration with USDA we are sequencing the genomes of two strains of persistent L. monocytogenes.

Holch, A., Project Manager, National Food Institute, Division of Seafood Research
Gram, L., Project Participant, National Food Institute, Division of Seafood Research
Licht, T. R., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
01/01/2009 → 07/07/2011
Project: Research

Workpackage 2 in Prebiotic Center: Gut microbiota and Immune Response Effects
The Prebiotic Center is a large research effort aiming to develop, synthesize and characterize new carbohydrates with beneficial effects on human health (e.g. prebiotics). This offers new possibilities for use of biological waste products. The Role of WP2 in Prebiotic Center is to reveal effects of putatively prebiotic carbohydrates on gut microbiota and immune fuction. We collaborate with Danisco and Herlev Hospital within this WP.

Licht, T. R., Project Manager, National Food Institute
Wilcks, A., Project Participant, National Food Institute
Hemningsen, L., Project Participant, National Food Institute
Vigsnaes, L. K., Project Participant, National Food Institute
Sulek, K., Project Participant, National Food Institute
Byrnskov, J., Project Participant, University Hospital Herlev
Steenholdt, C., Project Participant, University Hospital Herlev
Lahtinen, S., Project Participant, Danisco AS
01/01/2007 → 31/12/2011
Collaborators: Danisco AS, University of Copenhagen, University Hospital Herlev
Project: Research

Influence of food environment on the infective potential of Listeria monocytogenes
The main hypothesis behind this project is that not only the number of pathogenic bacteria in a given food product, but also their physiological condition, is decisive for whether or not the contaminated food will cause disease after ingestion. The influence of a number of food-related environmental conditions on the infectivity of Listeria in vitro and in vivo is investigated. The observations of infectivity are coupled to the expression patterns of Listeria monocytogenes as monitored by use of micro arrays. The obtained results will be highly relevant for risk assessment of Listeria in various types of food.

Licht, T. R., Project Manager, National Food Institute
Andersen, J. B., Project Participant, National Food Institute
Boye, M., Project Participant, National Food Institute
Assessment and Critical Evaluation of Antibiotic Resistance Transferability in the Food Chain

ACE-ART is a EU STREP project under the 6th framework programme. The main aim of the project is to generate knowledge on the source of food-related antibiotic resistant bacteria, their genetic composition and potential for resistance transfer. The bacteria of interest include Lactobacillus, Bifidobacterium, Lactococcus and Streptococcus thermophilus. The National Food Institute (Andrea Wilcks) is coordinator for WP2: Transfer of antibiotic resistance genes in non-pathogenic bacteria associated with the food chain.

Morelli, L., Project Participant, Catholic University of the Sacred Heart
Wind, A., Project Participant, Chr. Hansen AS
Krogfelt, K., Project Participant, Statens Serum Institut
Bardowski, J., Project Participant, Polish Academy of Sciences
Bolton, D., Project Participant, TEAGASC
Aarts, H., Project Participant, Institute of Food Safety
Huys, G., Project Participant, Ghent University
Wilcks, A., Project Manager, National Food Institute
Licht, T. R., Project Participant, National Food Institute
01/01/2003 → 30/06/2007

Collaborators: Institute of Food Safety, Catholic University of the Sacred Heart, Chr. Hansen AS, Statens Serum Institut, TEAGASC, Polish Academy of Sciences, Ghent University

Project: Research

Nutritional Immunology

This project runs under the FoodDTU umbrella, and one of its purposes is to create new collaborations between different DTU institutes with ongoing research related to food science. The participating institutes are DTU-Food, DTU-Biosys and DTU-Aqua. The purpose is to elucidate the impact of specific dietary components including e.g. fish oil on the intestinal microbiota and thereby on the development of the immune system in early life. The results are expected to create a basis for better nutritional advice for pregnant women.

Kristensen, M. B., Project Participant, National Food Institute
Wilcks, A., Project Participant, National Food Institute
Bergström, A., Project Participant, National Food Institute
Nellemann, C., Project Participant, National Food Institute
Kalln, C., Project Participant, National Food Institute
Licht, T. R., Project Manager, National Food Institute
Jacobson, C., Project Participant, National Food Institute
Nielsen, N. S., Project Participant, National Food Institute
Horn, A. F., Project Participant, National Food Institute
Mathiassen, J. H., Project Participant, Department of Systems Biology
Hellgren, L., Project Participant, Department of Systems Biology
Fink, L. N., Project Participant, Department of Systems Biology
Frequjær, H., Project Participant, University of Copenhagen
Metzdorff, S. B., Project Participant, University of Copenhagen
07/08/2007 → 30/11/2011

Collaborators: University of Copenhagen

Project: Research

PreGI - Prebiotics for Prevention of Gut Infections

There is increasing evidence that (i) intestinal beneficial bacteria are selectively stimulated by ingestion of specific (prebiotic) carbohydrates, and that (ii) beneficial bacteria ingested as probiotics are capable of suppression of bacterial pathogens in the gut. The idea of this project is to utilize existing animal models to identify dietary (prebiotic) carbohydrates that inhibit infection with selected pathogenic bacterial challengers. Carbohydrates with the best potential for pathogen inhibition will then be further studied with respect to effects on beneficial gut bacteria, production of short-chain fatty acids (SCFAs), and immune modulation in the host animals. Visualization of pathogenic challengers as well as of prebiotic-stimulated beneficial species in the intestinal environment will reveal whether an observed inhibition of a given pathogen results e.g. from competition for adhesion sites. The results obtained will be analyzed in a multivariate approach, in order to determine which of the above-mentioned factors have important impact on the anti-pathogen effect of prebiotics.

Poulsen, M., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Wilcks, A., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Bergström, A., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Petersen, A., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Ebersbach, T., Project Participant, National Food Institute, Division of Microbiology and Risk Assessment
Bacterial Impact on Gut Metabolomics

The complex ecosystem of microbes inhabiting the human gut plays an important role for human health. An increasing number of publications show that the composition and activity of our intestinal microbiota affects a number of so-called lifestyle diseases including allergy, obesity, colorectal cancer, and susceptibility to intestinal infections. Additionally, it has become evident that the intestinal microbiota can be modulated by intake of probiotic bacteria or prebiotic carbohydrates. Recently developed approaches allow simultaneous mapping of multiple bacterial metabolites present in gut contents. Our intention is to use these stage-of-the-art approaches to elucidate the impact of selected bacteria and carbohydrates, which will be supplied by dietary interventions, on the intestinal metabolome. For this purpose, we will use gnotobiotic animal models, which allow establishment of a simple, well-defined intestinal microbiota.

Workpackage 2 in Prebiotic Center: Gut microbiota and Immune Response Effects

The Prebiotic Center is a large research effort aiming to develop, synthesize and characterize new carbohydrates with beneficial effects on human health (e.g. prebiotics). This offers new possibilities for use of biological waste products. The Role of WP2 in Prebiotic Center is to reveal effects of putatively prebiotic carbohydrates on gut microbiota and immune function. We collaborate with Danisco and Herlev Hospital within this WP.

Nutritional Immunology

This project runs under the FoodDTU umbrella, and one of its purposes is to create new collaborations between different DTU institutes with ongoing research related to food science. The participating institutes are DTU-Food, DTU-Biosys and DTU-Aqua. The purpose is to elucidate the impact of specific dietary components including e.g. fish oil on the intestinal microbiota and thereby on the development of the immune system in early life. The results are expected to create a basis for better nutritional advice for pregnant women.
**Bacterial Impact on Gut Metabolomics**

The complex ecosystem of microbes inhabiting the human gut plays an important role for human health. An increasing number of publications show that the composition and activity of our intestinal microbiota affects a number of so-called lifestyle diseases including allergy, obesity, colorectal cancer, and susceptibility to intestinal infections. Additionally, it has become evident that the intestinal microbiota can be modulated by intake of probiotic bacteria or prebiotic carbohydrates. Recently developed approaches allow simultaneous mapping of multiple bacterial metabolites present in gut contents. Our intention is to use these stage-of-the-art approaches to elucidate the impact of selected bacteria and carbohydrates, which will be supplied by dietary interventions, on the intestinal metabolome. For this purpose, we will use gnotobiotic animal models, which allow establishment of a simple, well-defined intestinal microbiota.

Wilcks, A., Project Manager, National Food Institute  
Sulek, K., Project Participant, National Food Institute  
Licht, T. R., Project Participant, National Food Institute  
Smedsgaard, J., Project Participant, National Food Institute  
01/08/2009 → 31/07/2011

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**Nutritional Immunology**

Ernæringsimmunologi etablerer og udbygger synergier mellem BioCentrum, Fødevareinstituttet og Danmarks Fiskeri Undersøgelser. Samarbejdet omfatter udvikling og anvendelse af gnotobiotiske (kimfrifri) dyremodeller til kortlægning af effekter af specifikke tarmbakterier og n-3 fedtsyrer på immunsystemet hos værtsdyret. Transkriptomanalyse, cytokinmåling og traditionelle immunologiske metoder skal anvendes i kombination med in vitro og in vivo modeller for modning af immunsystemet. Arbejdet bygges op omkring to delprojekter, der hver tilknyttes en PhD studerende:

Licht, T. R., Project Manager, National Food Institute  
Wilcks, A., Project Participant, National Food Institute  
Bergstrøm, A., Project Participant, National Food Institute  
Andersen, J. B., Project Participant, National Food Institute  
Metzdorff, S. B., Project Participant, National Food Institute  
Frøkjær, H., Project Manager, Department of Systems Biology  
Fink, L. N., Project Participant, Department of Systems Biology  
Hellgren, L., Project Manager, Department of Systems Biology  
Jacobsen, C., Project Manager, National Institute of Aquatic Resources  
Nielsen, N. S., Project Participant, National Institute of Aquatic Resources  

[Ordinær drift UK 10]: DKK3,250,000.00  
04/01/2007 → 31/12/2011

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**Influence of Food Environment on the infective potential of Listeria**

Licht, T. R., Project Manager, National Food Institute  
Andersen, J. B., Project Participant, National Food Institute  
Christensen, B. B., Project Participant, National Food Institute  
Boye, M., Project Participant, National Veterinary Institute, Division of Veterinary Diagnostics and Research  

Forskningsrådene - Andre: DKK2,100,000.00  
01/01/2004 → 31/12/2006

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**Activities:**

**Oxygen restriction and virulence of Listeria monocytogenes: A transcriptome analysis**  
Period: 13 May 2009  
Tine Rask Licht (Speaker)  
National Food Institute  
Division of Microbiology and Risk Assessment  

Description  
Place: LO skolen, Helsingør
**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

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**Effects of food components on the intestinal microbiota**
Period: 1 Jan 2007 → …
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

**Description**
Place: Food and Feed – Nutrition, Safety and improved use of raw materials. Hyderabad, India

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**PreGI - Prebiotics for Prevention of Gastrointestinal Infections**
Period: 1 Jan 2007 → …
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

**Description**
Place: Nutrigenomics in Denmark, Slagelse

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**Germination and conjugation of Bacillus thuringiensis in the gut of gnotobiotic rats**
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

**Description**
Place: The COST action 862 Workshop, Goniads, Poland

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**Germination and conjugation of Bacillus thuringiensis in the gut of gnotobiotic rats**
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

**Description**
Place: The 4th Symposium on Food Microbiology, Gl. Avernæs, Ebberup, Fyn, Denmark
Dietary carbohydrate source determines molecular fingerprints of the rat fecal microbiota
Period: 1 Jan 2006 → …
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment
Description
Place: LMC Fourth Symposium on Food Microbiology

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Dietary carbohydrate sources affects intestinal microbiota and short-chain fatty acid composition in rats
Period: 1 Jan 2006 → …
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment
Description
Place: LMC International Food Congress

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Human Flora Associated rodent as models for the human gut microbiota
Period: 1 Jan 2006 → …
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment
Description
Place: Scandinavian Laboratory Animal Society meeting, Helsingør, Denmark

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Human Flora Associated rodents as models for the human gut microbiota
Period: 1 Jan 2006 → …
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment
Description
Place: Scandinavian Laboratory Animal Society meeting, Helsingør, Denmark

Related external organisation
Unknown external organisation
Bacillus thuringiensis: fate and effect in human flora associated rats: Workshop: Health and Environmental Risks by the use of Organisms for Biological Control of Pests and Diseases in Agriculture
Period: 16 Nov 2004 → 17 Nov 2004
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: LO-skolen, Helsingør, Denmark

Related external organisation
Unknown external organisation

Activity: Talks and presentations › Conference presentations
Biological control – assessment of health risks
Period: 1 Jan 2004 → …
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: International Workshop arranged by the National Environmental Research Institute: ‘Health and Environmental Risks by the use of organisms for biological control of pests and diseases in agriculture’

Related external organisation
Unknown external organisation

Activity: Talks and presentations › Conference presentations
Mikrobiologiske plantebeskyttelsesmidlers skæbne i mave-tarmkanalen
Period: 1 Jan 2004 → …
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: Miljøstyrelsesens Pesticidforskningsseminar, Kolding, Danmark

Related external organisation
Unknown external organisation

Activity: Talks and presentations › Conference presentations
In situ visualization of plasmid transfer from Pseudomonas putida to the indigenous bacterial population of Alfalfa sprouts
Period: 1 Jan 2003 → …
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: FEMS Congress of European Microbiologists. Ljubljana, Slovenia

Related external organisation
Horizontal transfer of antibiotic resistance genes among Enterococci in the intestinal enviorinment
Period: 1 Jan 2002 → …
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: International Committee on Food Microbiology and Hygiene: 18th international ICFMH symposion, Food Micro 2002, Lillehammer, Norge

Related external organisation

Role of Lipopolysaccharide in colonization of the mouse intestine by Salmonella typhimurium
Period: 1 Jan 1996 → …
Tine Rask Licht (Speaker)
National Food Institute
Division of Microbiology and Risk Assessment

Description
Place: Society for Microbial Ecology and Disease: "21rst International Congress on Microbial Ecology and Disease". Institut Pasteur, Paris, France

Related external organisation

Press clippings:

Nyt studie viser ikke, at gluten er skidt for maven
Tine Rask Licht
16/11/2018
National Food Institute, Copenhagen Center for Health Technology

Media coverage (1)

Nyt studie viser ikke, at gluten er skidt for maven
16/11/2018
Mandag Morgen (National), Denmark, Web
Andreas Oved Askjaer Rasmussen
https://www.mm.dk/tjekdet/artikel/15311-gluten
Tine Rask Licht
Copenhagen Center for Health Technology, National Food Institute
Press/Media: Press / Media

Nyt studie af gluteinreduceret kost
Tine Rask Licht
15/11/2018
National Food Institute, Copenhagen Center for Health Technology

Media coverage (1)

Nyt studie af gluteinreduceret kost
15/11/2018
Nyt studie af glutenreduceret kost
Tine Rask Licht
14/11/2018
National Food Institute, Copenhagen Center for Health Technology

Media coverage (1)

Sammenhæng mellem indtag af grønt og bakteriediversitet i tarmen
Tine Rask Licht
15/05/2018
National Food Institute, Copenhagen Center for Health Technology

Media contribution (1)

Hvad betyder kosten for tarmbakterier og helbred
Tine Rask Licht
30/01/2018
National Food Institute, Copenhagen Center for Health Technology

Media coverage (1)

Hvad er mavefornemmelse?
Tine Rask Licht
30/01/2018
National Food Institute, Copenhagen Center for Health Technology

Media coverage (1)
Mavefornemmelse
Tine Rask Licht
19/01/2018
National Food Institute, Copenhagen Center for Health Technology, Research group for Gut, Microbes and Health

Media coverage (1)

Mavefornemmelse
19/01/2018
Videnskab.dk (National), Denmark, Web
Maria Barse
https://videnskab.dk/krop-sundhed/hvad-er-mavefornemmelsen
Tine Rask Licht
Research group for Gut, Microbes and Health, Copenhagen Center for Health Technology, National Food Institute
Press/Media: Press / Media

Sandt og falsk om tarmens mikrobiota
Tine Rask Licht
12/01/2018
National Food Institute, Copenhagen Center for Health Technology

Media contribution (1)

Sandt og falsk om tarmens mikrobiota
12/01/2018
DYNAMO, Denmark, Print
Lotte Krull
Tine Rask Licht
National Food Institute, Copenhagen Center for Health Technology
Press/Media: Press / Media

Effekterne af en fuldkornskost på sundhed og tarmbakterier
Tine Rask Licht
08/11/2017
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

Media coverage (1)

Effekterne af en fuldkornskost på sundhed og tarmbakterier
08/11/2017
HealthDay (International), Denmark, Web
Serena Gordon
Tine Rask Licht
Copenhagen Center for Health Technology, National Food Institute, Research Group for Gut Microbiology and Immunology
Press/Media: Press / Media

Effekterne af en fuldkornskost på sundhed og tarmbakterier
Tine Rask Licht
03/11/2017
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

Media coverage (1)

Effekterne af en fuldkornskost på sundhed og tarmbakterier
03/11/2017
Effekterne af en fuldkornskost på sundhed og tarmbakterier
Tine Rask Licht
01/11/2017
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

Media coverage (1)

Tarmbakterier og væggtab
Tine Rask Licht
12/09/2017
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

Media coverage (1)

Tarmbakterier
Tine Rask Licht
06/09/2017
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

Media coverage (1)

Tarmbakterier og hjertesundhed
Tine Rask Licht
15/08/2017
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology
Media coverage (1)

**Tarmbakterier og hjertesundhed**
15/08/2017
Videnskab.dk, Denmark, Other
Sussi Boberg Bæch
Tine Rask Licht
Copenhagen Center for Health Technology, National Food Institute, Research Group for Gut Microbiology and Immunology
Press/Media: Press / Media

**DTU Fødevareinstituttets studie af tarmbakterier og fedme**
Tine Rask Licht
16/01/2017
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology
Press/Media: Press / Media

**Tarmbakterier og kostomsætning**
Tine Rask Licht
11/01/2017
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology
Press/Media: Press / Media

**Kommenteret irsk studie om stress og bifidobakterier**
Tine Rask Licht
11/01/2017
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology
Press/Media: Press / Media
Tarmbakteriers påvirkning af forbrændingen
Tine Rask Licht
28/11/2016
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

Media contribution (1)

Tarmbakterier
Tine Rask Licht
12/09/2016

Subject
Tarmbakterier
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

Media contribution (1)

24 spørgsmål til professoren
Tine Rask Licht
02/09/2016

Subject
24 spørgsmål til professoren
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

Media contribution (1)
**Transittidsstudiet**
Tine Rask Licht
24/08/2016

**Subject**
Interview (ca. 1 time, klippes ned) i forbindelse med vores studie af sammenhængen mellem tarmens transittid, mikrobiota, og bakterielle metabolitter (Nature Microbiology, Juni 2016)
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

**Media contribution (1)**

**Transittidsstudiet**
24/08/2016
DR P1, Radio
Kristoffer Frøkjær
Tine Rask Licht
Copenhagen Center for Health Technology, National Food Institute, Research Group for Gut Microbiology and Immunology
Press/Media: Press / Media

**kogebog med ’god mad til tarmens bakterier’**
Tine Rask Licht
18/08/2016

**Subject**
Der skal udkomme en ny kogebog med ’god mad til tarmens bakterier’ eller noget i den retning.
Den vil de skrive om, og kombinere det med lidt viden om området
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

**Media contribution (1)**

**mælkesyrebakterier**
Tine Rask Licht
04/08/2016

**Subject**
mælkesyrebakterier
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

**Media contribution (1)**

**Transittid**
Tine Rask Licht
28/06/2016

Subject
Transittid
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

Media contribution (1)

Transittid
28/06/2016
NutraIngredients | FoodNavigator, Web
Will Chu, Science editor
Tine Rask Licht
Copenhagen Center for Health Technology, National Food Institute, Research Group for Gut Microbiology and Immunology

Press/Media: Press / Media

Transittid
Tine Rask Licht
27/06/2016

Subject
Transittid
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

Media contribution (1)

Transittid
27/06/2016
videnskab.dk, Web
Malene Sommer Christiansen
Tine Rask Licht
Copenhagen Center for Health Technology, National Food Institute, Research Group for Gut Microbiology and Immunology

Press/Media: Press / Media

Transittid
Tine Rask Licht
27/06/2016

Subject
Transittid
National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology

Media contribution (1)

Transittid
27/06/2016
Ritzau, Web
Jan Bjerre Lauridsen
Tine Rask Licht
Copenhagen Center for Health Technology, National Food Institute, Research Group for Gut Microbiology and Immunology

Press/Media: Press / Media

Transittid
Tine Rask Licht
27/06/2016

Subject
Transittid
Det korte svar er nej. Har elaboreret omkring bakteriesamfund, resistensspredning, konkurrence mellem bakterier i forskellige miljøer.
Telefoninterview. Forinden havde journalisten sendt mig en kommende artikel fra Science Translational Medicine (embargo til 30. sept), som han bad om mine kommentarer til.
Tine Rask Licht
29/09/2015
Subject
Telefoninterview. Forinden havde journalisten sendt mig en kommende artikel fra Science Translational Medicine (embargo til 30. sept), som han bad om mine kommentarer til.
National Food Institute, Research Group for Gut Microbiology and Immunology

Media contribution (1)

Telefoninterview. Forinden havde journalisten sendt mig en kommende artikel fra Science Translational Medicine (embargo til 30. sept), som han bad om mine kommentarer til.
29/09/2015
Weekendavisen (Tillægget 'Idéer'), Print
Henrik Prætorius
Tine Rask Licht
National Food Institute, Research Group for Gut Microbiology and Immunology
Press/Media: Press / Media

Skriftigt 'interview 'om tarmbakterier og kostens betydning
Tine Rask Licht
24/09/2015

Subject
Skriftigt 'interview 'om tarmbakterier og kostens betydning
National Food Institute, Research Group for Gut Microbiology and Immunology

Media contribution (1)

Skriftigt 'interview 'om tarmbakterier og kostens betydning
24/09/2015
Kost & Ernæringsforbundets fagblad., Print
Tina Juul Rasmussen
Tine Rask Licht
National Food Institute, Research Group for Gut Microbiology and Immunology
Press/Media: Press / Media

Interview om tarmbakterier og kostens betydning til brug for en eller flere populærvidenskabelige artikler
Tine Rask Licht
08/09/2015

Subject
Interview om tarmbakterier og kostens betydning til brug for en eller flere populærvidenskabelige artikler
National Food Institute, Research Group for Gut Microbiology and Immunology

Media contribution (1)

Interview om tarmbakterier og kostens betydning til brug for en eller flere populærvidenskabelige artikler
08/09/2015
TV2 digital, Web
CHRISTIAN SEJER RASMUSSEN
Tine Rask Licht
National Food Institute, Research Group for Gut Microbiology and Immunology
Press/Media: Press / Media

Tarmbakterier – især i relation til psyke/humør
Tine Rask Licht
27/08/2015

Subject
Tarmbakterier – især i relation til psyke/humør
National Food Institute, Research Group for Gut Microbiology and Immunology

Media contribution (1)

Tarmbakterier – især i relation til psyke/humør
27/08/2015
Samvirke, Print
Emma Libner
Tine Rask Licht
National Food Institute, Research Group for Gut Microbiology and Immunology
Press/Media: Press / Media

Tarmbakterier – især i relation til psyke/humør
Tine Rask Licht
27/08/2015

Subject
Tarmbakterier – især i relation til psyke/humør
National Food Institute, Research Group for Gut Microbiology and Immunology

Media contribution (1)

Tarmbakterier – især i relation til psyke/humør
27/08/2015
Samvirke, Print
Emma Libner
Tine Rask Licht
National Food Institute, Research Group for Gut Microbiology and Immunology
Press/Media: Press / Media

En times interview – populærvidenskabelig formidling om tarmbakterier
Tine Rask Licht
16/04/2015

Subject
En times interview – populærvidenskabelig formidling om tarmbakterier
National Food Institute, Division of Food Microbiology

Media contribution (1)

En times interview – populærvidenskabelig formidling om tarmbakterier
16/04/2015
Politiken, Print
Line Felholt
Tine Rask Licht
National Food Institute, Division of Food Microbiology
Press/Media: Press / Media

Bidrag med ‘facts’ til artikel om aldring
Tine Rask Licht
27/02/2015

Subject
Bidrag med ‘facts’ til artikel om aldring.
National Food Institute, Division of Food Microbiology

Media contribution (1)

Bidrag med ‘facts’ til artikel om aldring
27/02/2015
Technologist Magazine, Print
Line Fedders
Tine Rask Licht
National Food Institute, Division of Food Microbiology
Press/Media: Press / Media

Selvdiagnosticering
Tine Rask Licht
07/01/2015

Subject
Vil gerne have min medvirken som interviewperson i et program, der skal handle om 'selvdagnosticering' – hvad får man egentlig ud af at få sit genom eller sine tarmbakterier kortlagt. (Min rolle er ift det sidste).

National Food Institute, Division of Food Microbiology

Media contribution (1)

Selvdagnosticering
07/01/2015
DR3, Television
Sofie Maria Vangsbjerg Mogensen
Tine Rask Licht
National Food Institute, Division of Food Microbiology

De 'gode' bakterier i tarmen
Tine Rask Licht
18/11/2014

Subject
De 'gode' bakterier i tarmen
National Food Institute, Division of Food Microbiology

Media contribution (1)

De 'gode' bakterier i tarmen
18/11/2014
videnskab.dk, Web
Charlotte Price Persson
Tine Rask Licht
National Food Institute, Division of Food Microbiology

Bidrag til populærvidenskabelig artikel i 'JP Newton' søndagstillægget.
Tine Rask Licht
05/11/2014

Subject
Bidrag til populærvidenskabelig artikel i 'JP Newton' søndagstillægget.
National Food Institute, Division of Food Microbiology

Media contribution (1)

Bidrag til populærvidenskabelig artikel i 'JP Newton' søndagstillægget.
05/11/2014
Jyllandsposten, Print
Kristian Sjøgren
Tine Rask Licht
National Food Institute, Division of Food Microbiology

Press/Media: Press / Media

Sødemidler
Tine Rask Licht
19/09/2014

Subject
Et nyt paper i Nature som viser at kunstige sødemidler skader glucosetolerancen, og at dette skyldes en ændring i tarmens bakteriesammensætning.
National Food Institute, Division of Food Microbiology

Media contribution (1)

Sødemidler
19/09/2014
Web
Tine Rask Licht
Bakterier fra babylort i spegepølser
Tine Rask Licht
27/03/2014
National Food Institute, Division of Food Microbiology

Media contribution (1)

Bakterier fra babylort i spegepølser
27/03/2014
Videnskab.dk, Web
Thomas Hoffman
http://videnskab.dk/krop-sundhed/bakterier-fra-babylort-gor-spegepolsen-sundere
Tine Rask Licht
National Food Institute, Division of Food Microbiology

Etablering af tarmfloraen
Tine Rask Licht
01/03/2014
National Food Institute, Division of Food Microbiology

Media contribution (1)

Etablering af tarmfloraen
01/03/2014
Superhuman Radio, Radio
Tine Rask Licht
National Food Institute, Division of Food Microbiology

Gavnlige effekter af probiotiske bakterier i yoghurt
Tine Rask Licht
09/12/2013
National Food Institute, Division of Food Microbiology

Media contribution (1)

Gavnlige effekter af probiotiske bakterier i yoghurt
09/12/2013
Bitz & Frisk, Television
Amalie Kaldan
Tine Rask Licht
National Food Institute, Division of Food Microbiology

Sådan kan man forbedre sin tarmflora
Tine Rask Licht
08/10/2013
National Food Institute, Division of Food Microbiology

Media contribution (1)

Sådan kan man forbedre sin tarmflora
08/10/2013
DR P1, Radio
Anne Sofie Lytken
Tine Rask Licht
National Food Institute, Division of Food Microbiology
Probiotika, prebiotika, tarmbakterier og betydningen for immunsystemet
Tine Rask Licht
02/10/2013
National Food Institute, Division of Food Microbiology

Media contribution (1)

Probiotika, prebiotika, tarmbakterier og betydningen for immunsystemet
02/10/2013
Sundhed, Print
Karin Svennevign
Tine Rask Licht
National Food Institute, Division of Food Microbiology
Press/Media: Press / Media

Sund kost giver dig ikke automatisk et bedre helbred
Tine Rask Licht
12/09/2013
National Food Institute, Division of Food Microbiology

Media contribution (1)

Sund kost giver dig ikke automatisk et bedre helbred
12/09/2013
Videnskab.dk, Web
Tine Rask Licht
National Food Institute, Division of Food Microbiology
Press/Media: Press / Media

Uden grundforskning ingen innovation
Tine Rask Licht
12/09/2013
National Food Institute, Division of Food Microbiology

Media contribution (1)

Uden grundforskning ingen innovation
12/09/2013
Jyllands-Posten, Print
Tine Rask Licht
National Food Institute, Division of Food Microbiology
Press/Media: Press / Media

Giv plads til opfindsomhed
Tine Rask Licht
27/08/2013
National Food Institute, Division of Food Microbiology

Media contribution (1)

Giv plads til opfindsomhed
27/08/2013
Jyllands-Posten, Print
Tine Rask Licht
National Food Institute, Division of Food Microbiology
Press/Media: Press / Media

Vigtigheden i at bevare støtte til fri forskning
Tine Rask Licht
24/04/2013
National Food Institute, Division of Food Microbiology
Vigtigheden i at bevare støtte til fri forskning
24/04/2013
Politiken, Print
Tine Rask Licht
National Food Institute, Division of Food Microbiology
Press/Media: Press / Media

Gavnlig effekter ved mælkesyrebakterier
Tine Rask Licht
24/04/2013
National Food Institute, Division of Food Microbiology

Pro- og præbiotika
Tine Rask Licht
06/12/2012
National Food Institute, Division of Food Microbiology

Indhold og perspektiver i Gut, Grain and Greens
Tine Rask Licht
12/01/2012
National Food Institute, Division of Food Microbiology

Ikke alle bakterier er skadelige
Tine Rask Licht
10/01/2012
National Food Institute, Division of Food Microbiology

Ikke alle bakterier er skadelige
10/01/2012
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Fedme og tarmens mikroflora
Tine Rask Licht
04/01/2012
National Food Institute, Division of Food Microbiology

Media contribution (1)

Fedme og tarmens mikroflora
04/01/2012
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Media contribution (1)

Fibre og sundhed
Tine Rask Licht
01/07/2010
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Fibre og sundhed
01/07/2010
Print
Tine Rask Licht
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Mælkezyrebakterier
Tine Rask Licht
01/01/2010
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Mælkezyrebakterier
01/01/2010
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Tine Rask Licht
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Tine Rask Licht som modtager af Danisco Prisen 2010
Tine Rask Licht
01/01/2010
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Tine Rask Licht som modtager af Danisco Prisen 2010
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Tine Rask Licht
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)
Mave-tarmkanalen og dens bakterier, probiotika og prebiotika
Tine Rask Licht
01/01/2009
National Food Institute, Division of Microbiology and Risk Assessment

Media contribution (1)

Mave-tarmkanalen og dens bakterier, probiotika og prebiotika
01/01/2009
Radio
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National Food Institute, Division of Microbiology and Risk Assessment

Tarmbakteriers betydning for sundheden
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Media contribution (1)

Tarmbakteriers betydning for sundheden
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Radio24Syv - Fitness M/K, Radio
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Press/Media: Press / Media