Coexistence of two distinct Sulfurospirillum populations respiring tetrachloroethene - genomic and kinetic considerations

Two anaerobic bacterial consortia, each harboring a distinct Sulfurospirillum population, were derived from a ten year old consortium, SL2, previously characterized for the stepwise dechlorination of tetrachloroethene (PCE) to cis-dichloroethene (cis-DCE) via accumulation of trichloroethene (TCE). Population SL2-1 dechlorinated PCE to TCE exclusively, while SL2-2 produced cis-DCE from PCE without substantial TCE accumulation. The reasons explaining the long-term coexistence of the populations were investigated. Genome sequencing revealed a novel Sulfurospirillum species, designated 'Candidatus Sulfurospirillum diekertiae', whose genome differed significantly from other Sulfurospirillum spp. (78-83% ANI). Genomewise, SL2-1 and SL2-2 populations are almost identical, but differences in their tetrachloroethene reductive dehalogenase sequences explain the distinct dechlorination patterns. An extended series of batch cultures were performed at PCE concentrations of 2-200 μM. A model was developed to determine their dechlorination kinetic parameters. The affinity constant and maximal growth rate differ between the populations: the affinity is 6- to 8-fold higher and the growth rate 5-fold lower for SL2-2 than SL2-1. Mixed cultivation of the enriched populations at 6 and 30 μM PCE showed that a low PCE concentration could be the driving force for both functional diversity of reductive dehalogenases and niche specialization of organohalide-respiring bacteria with overlapping substrate ranges.
Evolution of exploitative interactions during diversification in Bacillus subtilis biofilms

Microbial biofilms are tightly packed, heterogeneous structures that serve as arenas for social interactions. Studies on Gram negative models reveal that during evolution in structured environments like biofilms, isogenic populations commonly diversify into phenotypically and genetically distinct variants. These variants can settle in alternative biofilm niches and develop new types of interactions that greatly influence population productivity. Here, we explore the evolutionary diversification of pellicle biofilms of the Gram positive, spore-forming bacterium Bacillus subtilis. We discover that similarly to other species-B. subtilis diversifies into distinct colony variants. These variants dramatically differ in biofilm formation abilities and expression of biofilm-related genes. In addition, using a quantitative approach, we reveal striking differences in surface complexity and hydrophobicity of the evolved colony types. Interestingly, one of the morphotypes completely lost the ability of independent biofilm formation and evolved to hitchhike with other morphotypes with improved biofilm forming abilities. Genome comparison suggests that major phenotypic transformations between the morphotypes can be triggered by subtle genetic differences. Our work demonstrates how positive complementarity effects and exploitative interactions intertwine during evolutionary diversification in biofilms.

General information

State: Published
Organisations: Department of Biotechnology and Biomedicine, Friedrich-Schiller-Universitat Jena, Seqomics Biotechnology Ltd, Hungarian Academy of Sciences, Technical University of Munich, Technical University of Denmark Authors: Dragoş, A. (Ekstern), Lakshmanan, N. (Ekstern), Martin, M. (Ekstern), Horváth, B. (Ekstern), Maróti, G. (Ekstern), García, C. F. (Ekstern), Lieleg, O. (Ekstern), Kovács, Á. T. (Intern)
Number of pages: 32
Publication date: 2018
Main Research Area: Technical/natural sciences
Publication information
Journal: Fems Microbiology Ecology
Volume: 94
Issue number: 1
Article number: fix155
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Prebiotic potential of pectin and pectic oligosaccharides to promote anti-inflammatory commensal bacteria in the human colon

Dietary plant cell wall carbohydrates are important in modulating the composition and metabolism of the complex gut microbiota, which can impact on health. Pectin is a major component of plant cell walls. Based on studies in model systems and available bacterial isolates and genomes, the capacity to utilize pectins for growth is widespread among colonic Bacteroidetes but relatively uncommon among Firmicutes. One Firmicutes species promoted by pectin is Eubacterium eligens. E. eligens DSM3376 utilizes apple pectin and encodes a broad repertoire of pectinolytic enzymes, including a highly abundant pectate lyase of around 200 kDa that is expressed constitutively. We confirmed that certain Faecalibacterium prausnitzii strains possess some ability to utilize apple pectin and report here that F. prausnitzii strains in common with E. eligens, can utilize the galacturonide oligosaccharides DP4 and DP5 derived from sugar beet pectin. F. prausnitzii strains have been shown previously to exert anti-inflammatory effects on host cells, but we show here for the first time that E. eligens strongly promotes the production of the anti-inflammatory cytokine IL-10 in in vitro cell-based assays. These findings suggest the potential to explore further the prebiotic potential of pectin and its derivatives to re-balance the microbiota towards an anti-inflammatory profile.

General information
State: Published
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Bacteroides thetaiotaomicron, Eubacterium eligens, Faecalibacterium prausnitzii, Firmicutes, Glycosyl hydrolase, Pectate lyase

DOIs:
10.1093/femsec/fix127
Short-term effect of oral amoxicillin treatment on the gut microbial community composition in farm mink (Neovison vison)

It is well documented that antibiotics have pronounced modulatory effects on the intestinal bacterial community of both humans and animals, with potential health consequences. The gut microbiota of mink has however attracted little attention due to low bacterial load and fast gastrointestinal transit time, questioning its relevance. In this study, we hypothesise that oral amoxicillin treatment affects the gut microbiota in mink. This was investigated in a controlled trial including 24 animals of which 12 were treated with amoxicillin for 7 days. By applying 16S rRNA gene sequencing, we found that the faecal microbiota was markedly altered already after 2 days of treatment, with a surprising increase in diversity to resemble the feed. The diversity within the mucosa at termination was however reduced, which indicates this compartment as an important colonisation site in mink. No impact on blood biochemistry, lipid metabolism, serum amyloid A, vitamins A and E and histomorphology of the gut and liver was found; however, a slight decrease in fat digestibility was observed. We suggest that early-life use of amoxicillin in mink production may be counteractive as dysbiosis of the microbiota during infancy is increasingly being recognised as a risk factor for future health.

General information
State: Published
Organisations: National Food Institute, Research Group for Gut Microbiology and Immunology, University of Copenhagen, Danish Fur Breeders Research Centre, Aarhus University
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Number of pages: 10
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Fems Microbiology Ecology
Volume: 93
Issue number: 7
Article number: fix092
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
Cultivation and isolation of N$_2$-fixing bacteria from suboxic waters in the Baltic Sea

Nitrogenase genes (nifH) from heterotrophic dinitrogen (N$_2$)-fixing bacteria appear ubiquitous in marine bacterioplankton, but the significance of these bacteria for N cycling is unknown. Quantitative data on the N$_2$-fixation potential of marine and estuarine heterotrophs are scarce, and the shortage of cultivated specimens currently precludes ecophysiological characterization of these bacteria. Through the cultivation of diazotrophs from suboxic (1.79 μmol O$_2$ L$^{-1}$) Baltic Sea water in an artificial seawater medium devoid of combined N, we report the cultivability of a considerable fraction of the diazotrophic community in the Gotland Deep. Two nifH clades were present both in situ and in enrichment cultures showing gene abundances of up to $4.6 \times 10^5$ and $5.8 \times 10^5$ nifH gene copies L$^{-1}$ within two vertical profiles in the Baltic Sea. The distributions of the two clades suggested a relationship with the O$_2$ concentrations in the water column as abundances increased in the suboxic and anoxic waters. It was possible to cultivate and isolate representatives from one of these prevalent clades, and preliminary analysis of their ecophysiology demonstrated growth optima at 0.5-15 μmol O$_2$ L$^{-1}$ and 186-194 μmol O$_2$ L$^{-1}$ in the absence of combined N.
Exploring the immediate and long-term impact on bacterial communities in soil amended with animal and urban organic waste fertilizers using pyrosequencing and screening for horizontal transfer of antibiotic resistance

We investigated immediate and long-term effects on bacterial populations of soil amended with cattle manure, sewage sludge or municipal solid waste compost in an ongoing agricultural field trial. Soils were sampled in weeks 0, 3, 9 and 29 after fertilizer application. Pseudomonas isolates were enumerated, and the impact on soil bacterial community structure was investigated using 16S rRNA amplicon pyrosequencing. Bacterial community structure at phylum level remained mostly unaffected. Actinobacteria, Proteobacteria and Chloroflexi were the most prevalent phyla significantly responding to sampling time. Seasonal changes seemed to prevail with decreasing bacterial richness in week 9 followed by a significant increase in week 29 (springtime). The Pseudomonas population richness seemed temporarily affected by fertilizer treatments, especially in sludge- and compost-amended soils. To explain these changes, prevalence of antibiotic- and mercury-resistant pseudomonads was investigated. Fertilizer amendment had a transient impact on the resistance profile of the soil community; abundance of resistant isolates decreased with time after fertilizer application, but persistent strains appeared multiresistant, also in unfertilized soil. Finally, the ability of a P.putida strain to take up resistance genes from indigenous soil bacteria by horizontal gene transfer was present only in week 0, indicating a temporary increase in prevalence of transferable antibiotic resistance genes.

General information
State: Published
Organisations: National Food Institute, Division of Epidemiology and Microbial Genomics, Aarhus University, University of Copenhagen
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Synbiotic Lactobacillus acidophilus NCFM and cellobiose does not affect human gut bacterial diversity but increases abundance of lactobacilli, bifidobacteria and branched-chain fatty acids: a randomized, double-blinded cross-over trial

Probiotics, prebiotics, and combinations thereof, that is synbiotics, have been reported to modulate gut microbiota of humans. In this study, effects of a novel synbiotic on the composition and metabolic activity of human gut microbiota were investigated. Healthy volunteers (n=18) were enrolled in a double-blinded, randomized, and placebo-controlled cross-over study and received synbiotic [Lactobacillus acidophilus NCFM (10^9)CFU and cellobiose (5g)] or placebo daily for 3 weeks. Fecal samples were collected and lactobacilli numbers were quantified by qPCR. Furthermore, 454 tag-encoded amplicon pyrosequencing was used to monitor the effect of synbiotic on the composition of the microbiota. The synbiotic increased levels of Lactobacillus spp. and relative abundances of the genera Bifidobacterium, Collinsella, and Eubacterium while the genus Dialister was decreased (P<0.05).

General information
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Pages: 225-236
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: FEMS Microbiology Ecology
Volume: 90
Issue number: 1
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
Centimetre-scale vertical variability of phenoxy acid herbicide mineralization potential in aquifer sediment relates to the abundance of tfdA genes

Centimetre-scale vertical distribution of mineralization potential was determined for 2,4-dichlorophenoxyacetic acid (2,4-D), 4-chloro-2-methylphenoxyacetic acid (MCPA) and 2-(4-chloro-2-methylphenoxy)propanoic acid (MCPP) by 96-well microplate radiorepirometric analysis in aquifer sediment sampled just below the groundwater table. Mineralization of 2,4-D and MCPA was fastest in sediment samples taken close to the groundwater table, whereas only minor mineralization of MCPP was seen. Considerable variability was exhibited at increasing aquifer depth, more so with 2,4-D than with MCPA. This suggests that the abundance of MCPA degraders was greater than that of 2,4-D degraders, possibly due to the fact that the overlying agricultural soil had long been treated with MCPA. Mineralization of 2,4-D and MCPA was followed by increased abundance of tfdA class I and class III catabolic genes, which are known to be involved in the metabolism of phenoxy acid herbicides. tfdA class III gene copy number was approximately 100-fold greater in samples able to mineralize MCPA than in samples able to mineralize 2,4-D, suggesting that tfdA class III gene plays a greater role in the metabolism of MCPA than of 2,4-D. Degradation rate was found to correlate positively with tfdA gene copy number, as well as with the total organic carbon content of the sediment.

General information
State: Published
Organisations: Department of Environmental Engineering, Urban Water Engineering, Geological Survey of Denmark and Greenland
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Pages: 331-341
Publication date: 2012
Main Research Area: Technical/natural sciences

Publication information
Journal: FEMS Microbiology Ecology
Volume: 80
Issue number: 2
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Decreased colonization of fecal *Clostridium coccoides/Eubacterium rectale* species from ulcerative colitis patients in an in vitro dynamic gut model with mucin environment

The mucous layer in the colon, acting as a barrier to prevent invasion of pathogens, is thinner and discontinuous in patients with ulcerative colitis (UC). A recently developed in vitro dynamic gut model, the M-SHIME, was used to compare long-term colonization of the mucin layer by the microbiota from six healthy volunteers (HV) and six UC patients and thus distinguish the mucin adhered from the luminal microbiota. Although under the same nutritional conditions, short-chain fatty acid production by the luminal communities from UC patients showed a tendency toward a lower butyrate production. A more in-depth community analysis of those microbial groups known to produce butyrate revealed that the diversity of the *Clostridium coccoides/Eubacterium rectale* and *Clostridium leptum* group, and counts of *Faecalibacterium prausnitzii* were lower in the luminal fractions of the UC samples. Counts of *Roseburia* spp. were lower in the mucosal fractions of the UC samples. qPCR analysis for butyryl-CoA:acetate CoA transferase, responsible for butyrate production, displayed a lower abundance in both the luminal and mucosal fractions of the UC samples. The M-SHIME model revealed depletion in butyrate producing microbial communities not restricted to the luminal but also in the mucosal samples from UC patients compared to HV.

**General information**

State: Published
Organisations: National Food Institute, Division of Food Microbiology, Ghent University
Pages: 685-696
Publication date: 2012

DOI: 10.1111/j.1574-6941.2012.01300.x
Source: orbit
Source-ID: 318451
Publication: Research - peer-review › Journal article – Annual report year: 2012
An individual-based approach to explain plasmid invasion in bacterial populations

We present an individual-based experimental framework to identify and estimate the main parameters governing bacterial conjugation at the individual cell scale. From this analysis, we have established that transient periods of unregulated...
plasmid transfer within newly formed transconjugant cells, together with contact mechanics arising from cellular growth and division, are the two main processes determining the emergent inability of the pWW0 TOL plasmid to fully invade spatially structured Pseudomonas putida populations. We have also shown that pWW0 conjugation occurs mainly at advanced stages of the growth cycle and that nongrowing cells, even when exposed to high nutrient concentrations, do not display conjugal activity. These results do not support previous hypotheses relating conjugation decay in the deeper cell layers of bacterial biofilms to nutrient depletion and low physiological activity. We observe, however, that transient periods of elevated plasmid transfer in newly formed transconjugant cells are offset by unfavorable cell-to-cell contact mechanics, which ultimately precludes the pWW0 TOL plasmid from fully invading tightly packed multicellular P. putida populations such as microcolonies and biofilms.
Hypersaline waters - a potential source of foodborne toxigenic aspergilli and penicillia

Previous studies of hypersaline environments have revealed the dominant presence of melanized yeast-like fungi and related Cladosporium spp. In this study, we focused on the genera Aspergillus and Penicillium and their teleomorphic forms. From oligotrophic and eutrophic hypersaline waters around the world, 60 different species were identified, according to their morphological characteristics and extrolite profiles. For the confirmation of five new species, additionally, sequence analysis of the internal transcribed spacer region, the partial large subunit-rDNA and the partial beta-tubulin gene was performed. The species Aspergillus niger, Eurotium amstelodami and Penicillium chrysogenum were detected with the highest frequencies at all of the sampled sites; thus, they represent the pan-global stable mycobiota in hypersaline environments. Possible candidates were also Aspergillus sydowi and Eurotium herbariorum, as they were quite evenly distributed among the sampled sites, and Aspergillus candidus, which was abundant, but more locally distributed. These species and their byproducts can accumulate downstream following evaporation of brine, and they can become entrapped in the salt crystals. Consequently, marine salt used for consumption can be a potential source of foodborne fungi and their byproducts. For example, ochratoxin-A-producing species Penicillium nordicum was recovered from brine, salt and salted meat products.
Structure and activity of lacustrine sediment bacteria involved in nutrient and iron cycles.

Knowledge of the bacterial community structure in sediments is essential to better design restoration strategies for eutrophied lakes. In this regard, the aim of this study was to quantify the abundance and activity of bacteria involved in nutrient and iron cycling in sediments from four Azorean lakes with distinct trophic states (Verde, Azul, Furnas and Fogo). Inferred from quantitative PCR, bacteria performing anaerobic ammonia oxidation were the most abundant in the eutrophic lakes Verde, Azul and Furnas (4.5-16.6%), followed by nitrifying bacteria (0.8-13.0%), denitrifying bacteria (DNB) (0.5-6.8%), iron-reducing bacteria (0.2-1.4%) and phosphorus-accumulating organisms (PACs).
High abundance and diversity of Bacillus anthracis plasmid pXO1-like replicons in municipal wastewater

Water from the influent of a municipal wastewater treatment plant as well as soil samples collected from the shoreline of 10 lakes were screened for the presence of the Bacillus anthracis pXO1-like plasmid replicon repX using a PCR assay. Specific PCR products were retrieved from all samples, indicating a widespread presence of pXO1-like plasmid replicons in various environmental settings. Initial screening by restriction enzyme analysis revealed at least two forms of the repX gene in the wastewater sample, which was consequently subjected to further investigation. Nine of 51 Bacillus cereus group strains isolated from the wastewater sample were shown to contain a repX-specific gene sequence. Two of these strains also contained replicon-specific sequences with high homology to those of pXO2-like plasmids, but did not contain the pXO1-associated cya and lef virulence genes. Collectively, the sequence information from the isolated strains and PCR products obtained using total genomic DNA as a template suggests the existence of three subgroups of pXO1-like plasmid replicons in the wastewater sample.

Keyword: Bacillus cereus sensu lato, phylogeny, pXO1, repX

General information
State: Published
Presence, distribution, and diversity of iron-oxidizing bacteria at a landfill leachate-impacted groundwater surface water interface

We examined the presence of iron-oxidizing bacteria (IOB) at a groundwater surface water interface (GSI) impacted by reduced groundwater originating as leachate from an upgradient landfill. IOB enrichments and quantifications were obtained, at high vertical resolution, by an iron/oxygen opposing gradient cultivation method. The depth-resolved soil distribution profiles of water content, Fe2+, and total Fe indicated sharp gradients within the top 10 cm sediments of the GSI, where the IOB density was the highest. In addition, the vertical distribution of iron-reducing bacteria at the same sampling site mirrored the IOB distribution. Clone libraries from two separate IOB enrichments indicated a stratified IOB community with clear differences at short vertical distances. Alpha- and Betaproteobacteria were the dominant phylotypes. Clones from the near-surface sediment (1-2 cm below ground surface) were dominated by members of the Bradyrhizobiaceae and Comamonadaceae; clones from the deeper sediments were phylogenetically more diverse, dominated by members of the Rhodocyclaceae. The iron deposition profiles indicated that active iron oxidation occurred only within the near-to-surface GSI sediments. The match between the iron deposition profiles and the IOB abundance profiles strongly hints at the contribution of the IOB community to Fe oxidation in this Fe-rich GSI ecosystem.

General information
State: Published
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Pages: 260-271
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: F E M S Microbiology Ecology
Volume: 71
Issue number: 2
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
Vibrio vulnificus produces quorum sensing signals of the AHL-class

Vibrio vulnificus is an aquatic pathogenic bacterium that can cause vibriosis in humans and fish. The species is subdivided into three biotypes with the fish-virulent strains belonging to biotype 2. The quorum sensing (QS) phenomenon mediated by furanosyl borate diester or autoinducer 2 (AI-2) has been described in human strains of biotype 1, and here we show that the luxS gene which encodes AI-2 is present in all strains of V. vulnificus regardless of origin, biotype or serovar. In this study, we also demonstrate that V. vulnificus produces QS signals of the acylated homoserine lactone (AHL) class (AI-1). AHLs were detected in strains of biotype 1 and 2 from water, fish and human wound infections but not in strains isolated from human septicemic cases. The AHL compound was identified as N-butanoyl-homoserine lactone (C4-HL) by both reporter strains and by HPLC-high-resolution MS. C4-HL was detected when AHL-positive strains were grown in low-nutrient medium [modified sea water yeast extract (MSWYE)] but not in rich media (tryptic soy broth or brain-heart infusion) and its production was enhanced when blood factors were added to MSWYE. C4-HL was detected in vivo, in eels infected with AHL-positive biotype 2 strains. No known AHL-related gene was detected by PCR or Southern blot suggesting that AHL-related genes in V. vulnificus are different from those found in other Gram-negative bacteria.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Center for Microbial Biotechnology, Department of Systems Biology, Section for Aquatic Microbiology and Seafood Hygiene
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Pages: 16-26
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: FEMS Microbiology Ecology
Volume: 69
Issue number: 1
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
We studied the acclimation to mercury of bacterial communities of different depths from contaminated and noncontaminated floodplain soils. The level of mercury tolerance of the bacterial communities from the contaminated site was higher than those of the reference site. Furthermore, the level of mercury tolerance and functional versatility of bacterial communities in contaminated soils initially were higher for surface soil, compared with the deeper soils. However, following new mercury exposure, no differences between bacterial communities were observed, which indicates a high adaptive potential of the subsurface communities, possibly due to differences in the availability of mercury. IncP-1 trfA genes were detected in extracted community DNA from all soil depths of the contaminated site, and this finding was correlated to the isolation of four different mercury-resistance plasmids, all belonging to the IncP-1 beta group. The abundance of merA and IncP-1 plasmid carrying populations increased, after new mercury exposure, which could be the result of selection as well as horizontal gene exchange. The data in this study suggest a role for IncP-1 plasmids in the acclimation to mercury of surface as well as subsurface soil microbial communities.

**Keyword:** subsurface soil, microbial diversity, plasmids, Oak Ridge

**General information**

**State:** Published

**Organisations:** Aarhus University, University of Copenhagen

**Authors:** de Lipthay, J. R. (Ekstern), Rasmussen, L. D. (Intern), Øregaard, G. (Ekstern), Simonsen, K. (Ekstern), Bahl, M. I. (Intern), Kroer, N. (Ekstern), Sørensen, S. J. (Ekstern)

**Pages:** 145-155

**Publication date:** 2008

**Main Research Area:** Technical/natural sciences
Architecture and spatial organization in a triple-species bacterial biofilm synergistically degrading the phenylurea herbicide linuron

Members of a triple-species 3-(3,4-dichlorophenyl)-1-methoxy-1-methyl urea (linuron)-mineralizing consortium, i.e. the linuron- and 3,4-dichloroaniline-degrading Variovorax sp. WDL1, the 3,4-dichloroaniline-degrading Comamonas testosteroni WDL7 and the N,O-dimethylhydroxylamine-degrading Hyphomicrobium sulfonivorans WDL6, were cultivated as mono- or multi-species biofilms in flow cells irrigated with selective or nonselective media, and examined with confocal
laser scanning microscopy. In contrast to mono-species biofilms of Variovorax sp. WDL1, the triple-species consortium biofilm degraded linuron completely through apparent synergistic interactions. The triple-species linuron-fed consortium biofilm displayed a heterogeneous structure with an irregular surface topography that most resembled the topography of linuron-fed mono-species WDL1 biofilms, indicating that WDL1 had a dominating influence on the triple-species biofilm architecture. This architecture was dependent on the carbon source supplied, as the biofilm architecture of WDL1 growing on alternative carbon sources was different from that observed under linuron-fed conditions. Linuron-fed triple-species consortium biofilms consisted of mounds composed of closely associated WDL1, WDL7 and WDL6 cells, while this association was lost when the consortium was grown on a nonselective carbon source. In addition, under linuron-fed conditions, microcolonies displaying associated growth developed rapidly after inoculation. These observations indicate that the spatial organization in the linuron-fed consortium biofilm reflected the metabolic interactions within the consortium.

**General information**
State: Published
Organisations: Center for Biomedical Microbiology, Department of Systems Biology, Catholic University of Leuven, Flemish Institute for Technological Research
Authors: Breugelmans, P. (Ekstern), Barken, K. B. (Intern), Tolker-Nielsen, T. (Intern), Hofkens, J. (Ekstern), Dejonghe, W. (Ekstern), Springael, D. (Ekstern)
Pages: 271-282
Publication date: 2008
Main Research Area: Technical/natural sciences

**Publication information**
Journal: FEMS Microbiology Ecology
Volume: 64
Issue number: 2
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Web of Science (2008): Indexed yes
Limited diffusive fluxes of substrate facilitate coexistence of two competing bacterial strains

Soils are known to support a great bacterial diversity down to the millimeter scale, but the mechanisms by which such a large diversity is sustained are largely unknown. A feature of unsaturated soils is that water usually forms thin, poorly-connected films, which limit solute diffusive fluxes. It has been proposed, but never unambiguously experimentally tested, that a low substrate diffusive flux would impact bacterial diversity, by promoting the coexistence between slow-growing bacteria and their potentially faster-growing competitors. We used a simple experimental system, based on a Petri dish and a perforated Teflon® membrane to control diffusive fluxes of substrate (benzoate) whilst permitting direct observation of bacterial colonies. The system was inoculated with prescribed strains of Pseudomonas, whose growth was quantified by microscopic monitoring of the fluorescent proteins they produced. We observed that substrate diffusion limitation reduced the growth rate of the otherwise fast-growing Pseudomonas putida KT2440 strain. This strain out-competed Pseudomonas fluorescens F113 in liquid culture, but its competitive advantage was less marked on solid media, and even disappeared under conditions of low substrate diffusion. Low diffusive fluxes of substrate, characteristic of many unsaturated media (e.g. soils, food products), can thus promote bacterial coexistence in a competitive situation between two strains. This mechanism might therefore contribute to maintaining the noncompetitive diversity pattern observed in unsaturated soils.

General information
State: Published
Organisations: Environmental Chemistry, Department of Environmental Engineering
Authors: Dechesne, A. (Intern), Or, D. (Ekstern), Smets, B. F. (Intern)
Pages: 1-8
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: FEMS Microbiology Ecology
Volume: 64
Issue number: 1
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
Microbial dynamics in anaerobic enrichment cultures degrading di-n-butyl phthalic acid ester

Although anaerobic biodegradation of di-n-butyl phthalic acid ester (DBP) has been studied over the past decade, only little is known about the microorganisms involved in the biological anaerobic degradation pathways. The aim of this work is to characterize the microbial community dynamics in enrichment cultures degrading phthalic acid esters under methanogenic conditions. A selection pressure was applied by adding DBP at 10 and 200 mg L\(^{-1}\) in semi-continuous anaerobic reactors. The microbial dynamics were monitored using single strand conformation polymorphism (SSCP). While only limited abiotic losses were observed in the sterile controls (20-22%), substantial DBP biodegradation was found in the enrichment cultures (90-99%). In addition, significant population changes were observed. The dominant bacterial species in the DBP-degrading cultures was affiliated to Soehngenia saccharolytica, a microorganism described previously as an anaerobic benzaldehyde degrader. Within the archaeal community, there was a shift between two different species of the genus Methanosaeta sp., indicating a highly specific impact of DBP or degradation products on archaeal species. RNA-directed probes were designed from SSCP sequences, and FISH observations confirmed the dominance of S. saccharolytica, and indicated floccular microstructures, likely providing favourable conditions for DBP degradation.

General information
State: Published
Organisations: Department of Environmental Engineering
Authors: Trably, E. (Intern), Batstone, D. J. (Intern), Christensen, N. (Intern), Patureau, D. (Intern), Schmidt, J. E. (Intern)
Pages: 472-483
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: FEMS Microbiology Ecology
Volume: 66
Issue number: 2
ISSN (Print): 0168-6496
Ratings:
Archaeal diversity in Icelandic hot springs

Whole-cell density gradient extractions from three solfataras (pH 2.5) ranging in temperature from 81 to 90 degrees C and one neutral hot spring (81 degrees C, pH 7) from the thermal active area of Hveragerethi (Iceland) were analysed for genetic diversity and local geographical variation of Archaea by analysis of amplified 16S rRNA genes. In addition to the three solfataras and the neutral hot spring, 10 soil samples in transects of the soil adjacent to the solfataras were analysed using terminal restriction fragment length polymorphism (t-RFLP). The sequence data from the clone libraries in combination with 14 t-RFLP profiles revealed a high abundance of clones clustering together with sequences from the nonthermophilic I.1b group of Crenarchaeota. The archaeal diversity in one solfatara was high; 26 different RFLP patterns were found using double digestion of the PCR products with restriction enzymes AluI and BsuRI. The sequenced clones from this solfatara belonged to Sulfolobales, Thermoproteales or were most closest related to sequences from uncultured Archaea. Sequences related to group I.1b were not found in the neutral hot spring or the hyperthermophilic solfata (90 degrees C).
Different bacterial communities associated with the roots and bulk sediment of the seagrass Zostera marina

The bacterial community of Zostera marina-inhabited bulk sediment vs. root-associated bacteria was investigated by terminal restriction fragment length polymorphism and sequencing, and the spatial extension of the oxygen loss from roots was determined by oxygen microsensors. Extensive oxygen loss was found in the tip region of the youngest roots, and most of the rhizoplane of Z. marina roots was thus anoxic. A significant difference between the bacterial communities associated with the roots and bulk sediment was found. No significant differences were found between differently aged root-bundles. Terminal restriction fragments (TRFs) assigned to sulfate-reducing Deltaproteobacteria showed a relative mean distribution of 12% and 23% of the PCR-amplified bacterial community in the bulk-sediment at the two sites, but only contributed <2% to the root-associated communities. TRFs assigned to Epsilonproteobacteria showed a relative mean distribution of between 5% and 11% in the root-associated communities of the youngest root bundle, in contrast to the bulk-sediment where this TRF only contributed <1.3%. TRFs assigned to Actinobacteria and Gammaproteobacteria also seemed important first root-colonizers, whereas TRFs assigned to Deltaproteobacteria became increasingly important in the root-associated community of the older root bundles. The presence of the roots thus apparently selects for a distinct bacterial community, stimulating the growth of potential symbiotic Epsilon- and Gammaproteobacteria and/or inhibiting the growth of sulfate-reducing Deltaproteobacteria.
Horizontal transfer of tet(M) and erm(B) resistance plasmids from food strains of Lactobacillus plantarum to Enterococcus faecalis JH2-2 in the gastrointestinal tract of gnotobiotic rats

Two wild-type strains of Lactobacillus plantarum previously isolated from fermented dry sausages were analysed for their ability to transfer antibiotic resistance plasmids in the gastrointestinal tract. For this purpose, we used gnotobiotic rats as an in vivo model. Rats were initially inoculated with the recipient Enterococcus faecalis JH2-2 at a concentration of 10(10) CFU mL(-1). After a week, either of the two donors L. plantarum DG 522 (harbouring a tet(M)-containing plasmid of c. 40 kb) or L. plantarum DG 507 [harbouring a tet(M)-containing plasmid of c. 10 kb and an erm(B)-containing plasmid of c. 8.5 kb] was introduced at concentrations in the range of 10(8)-10(10) CFU mL(-1). Two days after donor introduction, the first transconjugants (TCs) were detected in faecal samples. The detected numbers of tet(M)-TCs were comparable for the two donors. In both cases, this number increased to c. 5 x 10(2) CFU g(-1) faeces towards the end of the experiment. For erm(B)-TCs, the number was significantly higher and increased to c. 10(3) CFU g(-1) faeces. To our knowledge, this is the first study showing in vivo transfer of wild-type antibiotic resistance plasmids from L. plantarum to E. faecalis.
Root growth and exudate production define the frequency of horizontal plasmid transfer in the Rhizosphere

General information
State: Published
Organisations: Microbial Ecology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Center for Systems Microbiology, Department of Systems Biology
Authors: Mølbak, L. (Intern), Molin, S. (Intern), Kroer, N. (Ekstern)
Pages: 167-76
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: FEMS Microbiology Ecology
Volume: 59
Issue number: 1
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
A soil-based microbial biofilm exposed to 2,4-D: bacterial community development and establishment of conjugative plasmid pJP4

A soil suspension was used as a source to initiate the development of microbial communities in flow cells irrigated with 2,4-dichlorophenoxyacetic acid (2,4-D) (25 μg ml⁻¹). Culturable bacterial members of the community were identified by 16S rRNA gene sequencing and found to be members of the genera Pseudomonas, Burkholderia, Collimonas and Rhodococcus. A 2,4-D degrading donor strain, Pseudomonas putida SM 1443 (pJP4::gfp), was inoculated into flow cell chambers containing 2-day old biofilm communities. Transfer of pJP4::gfp from the donor to the bacterial community was detectable as GFP fluorescing cells and images were captured using confocal scanning laser microscopy (GFP fluorescence was repressed in the donor due to the presence of a chromosomally located lac(q) repressor gene). Approximately 5-10 transconjugant microcolonies, 20-40 μm in diameter, could be seen to develop in each chamber. A 2,4-D degrading transconjugant strain was isolated from the flow cell system belonging to the genus Burkholderia.

General information
State: Published
Organisations: Department of Systems Biology
Authors: Aspray, T. (Ekstern), Hansen, S. K. (Intern), Burns, R. (Ekstern)
Pages: 317-327
Comparison of secondary metabolite production by Penicillium crustosum strains, isolated from Arctic and other various ecological niches
Genus Eurotium – members of indigenous fungal community in hypersaline waters of salterns

General information
State: Published
Organisations: Department of Systems Biology
Authors: Butinar, L. (Ekstern), Zalar, P. (Ekstern), Frisvad, J. C. (Intern), Gunde-Cimerman, N. (Ekstern)
Pages: 155-166
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: F E M S Microbiology Ecology
Volume: 51
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes
Original language: English
Source: orbit
Source-ID: 183916
Publication: Research - peer-review › Journal article – Annual report year: 2005
Bacterial diversity and community structure of a sub-surface aquifer exposed to realistic low herbicide concentrations

General information
State: Published
Organisations: Department of Environmental Engineering
Authors: De Lipthay, J. (Ekstern), Johnsen, K. (Ekstern), Albrechtsen, H. (Intern), Rosenberg, P. (Ekstern), Aamand, J. (Ekstern)
Pages: 59-69
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: F EM S Microbiology Ecology
Volume: 49
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes
Original language: English
Combined use of different Gfp reporters for monitoring single-cell activities of a genetically modified PCB degrader in the rhizosphere of alfalfa

Single-cell localization and activity of Pseudomonas fluorescens F113, colonizing alfalfa roots, were monitored using fusions of the Escherichia coli rnbP1 ribosomal promoter and gfp genes encoding green fluorescent protein (Gfp) of different stability. The monitoring systems permitted non-destructive in situ detection of F113rifpcb cells on the entire root system grown in both the presence and absence of 3-chlorobiphenyl (PCB-2). The root tip and sites of lateral root emergence were found to be hotspots for fast-growing cells. In addition, a reporter strain of P. fluorescens F113rifpcb for degradation of chlorinated biphenyl was constructed, using another gfp fusion with the meta-pathway Pin promoter from Pseudomonas putida (TOL plasmid). Expression of this promoter, which is strongly induced by the PCB-2 degradation product, 3-chlorobenzoate, was tested in vitro and subsequently monitored in vivo on alfalfa roots using the P. fluorescens F113rifpcb reporter. A small but distinct fraction of the introduced bacteria activated the Pm promoter and thus appeared to sense a PCB-2 degradation product in the alfalfa rhizosphere. The degrading cells, which by design were identical to the sensing cells, were located in distinct microcolonies on the root surface or in intercellular crevices between the root epidermal cells. However, PCB-degrading cells were not observed in the root areas containing fast-growing cells, indicating that PCB degradation was not linked to high cellular activity.

General information
State: Published
Organisations: Center for Biomedical Microbiology, Department of Systems Biology
Authors: Boldt, T. (Ekstern), Sørensen, J. (Ekstern), Karlsson, U. (Ekstern), Molin, S. (Intern), Ramos, C. (Ekstern)
Pages: 139-148
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: F E M S Microbiology Ecology
Volume: 48
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Microbial community response to petroleum hydrocarbon contamination in the unsaturated zone at the experimental field site Værløse, Denmark

General information
State: Published
Organisations: Department of Environmental Engineering
Authors: Kaufman, K. (Ekstern), Christophersen, M. (Intern), Buttler, A. (Ekstern), Harms, H. (Ekstern), Höhener, P. (Ekstern)
Pages: 387-399
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: F E M S Microbiology Ecology
Volume: 48
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
Subsurface microbiology - from exploration to working tools. Editorial

General information
State: Published
Organisations: Department of Environmental Engineering
Authors: Albrechtsen, H. (Intern), Aamand, J. (Ekstern)
Pages: 1-2
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication Information
Journal: F E M S Microbiology Ecology
Volume: 49
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Effects of copper amendment on the bacterial community in agricultural soil analyzed by the T-RFLP technique

The impact of copper amendment on the bacterial community in agricultural soil was investigated by a 2-year field experiment complemented by short-term microcosm studies. In the field, the amendments led to total copper contents that were close to the safety limits laid down by European authorities. In parallel, bioavailable copper was determined with a copper-specific bioluminescent Pseudomonas reporter strain. The amounts of total Cu as well as of bioavailable Cu in the field declined throughout the experiment. Bacterial community structure was examined by terminal restriction fragment length polymorphism (T-RFLP) analysis of community DNA amplified with primers specific for 16S rDNA from the Bacteria domain, the Rhizobium-Agrobacterium group and the Cytophaga group. Similarity analysis of T-RFLP profiles from field samples demonstrated an impact of copper at the domain level and within the Rhizobium-Agrobacterium group. Comparable Cu effects were observed for microcosms, but in addition an impact on community structure within the Cytophaga group was observed.
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
Authors: Licht, T. R. (Intern), Struve, C. (Ekstern), Christensen, B. B. (Intern), Poulsen, R. L. (Ekstern), Molin, S. (Intern), Krogfelt, K. (Ekstern)
Pages: 217-223
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Fems Microbiology Ecology
Volume: 44
Issue number: 2
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
In situ detection of horizontal transfer of mobile genetic elements

Plasmid transfer was investigated in microbial populations associated with different types of surfaces. The general strategy behind these investigations was to label the transferable plasmid with a gene encoding a fluorescent protein in order to make it a transfer reporter. This was achieved by fusing the reporter gene with a lac promoter expression cassette and combining this with a donor cell-associated lacI repressor cassette. After construction of a range of strains and plasmids with combinations of genes expressing fluorescent proteins from constitutive (cell tagging) or regulated promoters (transfer reporters) it was thus possible to detect transfer events in situ and correlate these with either the location of donor and recipient cells or with the growth activity of the cells. In some cases, expression of unstable Gfp from a growth-controlled promoter, rrnB from Escherichia coli, was used to monitor bacterial growth activity in situ. Differential tagging of mobilizing and mobilizable plasmids with different genes encoding fluorescent proteins with varying emission wavelengths allowed in situ detection of plasmid mobilization and detection of retro-transfer on agar surfaces. The obtained data show that the several different types of fluorescent reporters, which are now available, allow more informative in situ investigations of horizontal gene transfer to be carried out, and by combining these genes with various expression systems it is possible to simultaneously monitor donor/recipient positioning, cellular activity and appearance of...
transconjugants.

**General information**

State: Published
Organisations: Center for Biomedical Microbiology, Department of Systems Biology
Pages: 261-268
Publication date: 2002
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Fems Microbiology Ecology
Volume: 42
Issue number: 2
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes
Original language: English
Source: orbit
Source-ID: 45969
Population structure and pathogenicity of members of the Fusarium oxysporum complex isolated from soil and root necrosis of pea (Pisum sativum L.)

Forty-nine strains of the Fusarium oxysporum complex were isolated from five different sample locations within two neighboring pea fields. Of these, 39 strains were isolated from soil and 10 from pea plants showing symptoms of root rot. Twenty-eight of the isolates were tested for pathogenicity towards pea. Based on percentage discoloration of the roots and stem base, the isolates were divided into three groups: seven strains were pathogenic, 14 strains were weakly pathogenic, and seven strains were non-pathogenic towards pea. To assess the genetic relatedness of all 49 strains, gene genealogies were constructed from aligned DNA sequences from part of the translation elongation factor, nitrate reductase, beta tubulin, and mitochondrial small subunit rDNA. Maximum parsimony analysis of the combined data set yielded a single most-parsimonious tree containing three strongly supported clades which may represent cryptic species. No correlation was observed between the multigene phylogeny and pathogenicity toward pea, strain geographic origin and substrate (soil or plant) from which the strains were isolated. Strains that were non-pathogenic, weakly pathogenic or pathogenic sometimes shared the same multilocus genotype. These results suggest that strains pathogenic and putatively non-pathogenic to pea are very closely related genetically. (C) 2002 Federation of European Microbiological Societies. Published by Elsevier Science B.V. All rights reserved.
Recombinogenic engineering of conjugative plasmids with fluorescent marker cassettes

An efficient approach for the insertion of fluorescent marker genes with sequence specificity into conjugative plasmids in Escherichia coli is described. For this purpose, homologous recombination of linear double-stranded targeting DNA was mediated by the bacteriophage lambda recombination functions using very short regions of homology. Initial manipulation of the IncFII target plasmids R1 and R1drd19 indicated that the linear targeting DNA should be devoid of all extraneous homologies to the target molecule for optimal insertion specificity. Indeed, a simple recombination assay proved that in the presence of additional homologous regions in the targeting DNA, strand exchanges occurred exclusively within the longest regions of homology. A versatile panel of vectors was created to facilitate convenient PCR amplification of targeting DNAs containing various combinations of different antibiotic resistance genes and fluorescent markers. The choice of 5' non-homologous extensions in primer pairs used for amplifying the marker cassettes determines the site specificity of the targeting DNA. This methodology is applicable to the modification of all plasmids that replicate in E.coli and is not restricted by plasmid size.
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, Center for Systems Microbiology, Department of Systems Biology
Authors: Licht, T. R. (Intern), Struwe, C. (Ekstern), Christensen, B. B. (Intern), Poulsen, R. L. (Ekstern), Molin, S. (Intern), Krogfelt, K. A. (Ekstern)
Pages: 217-222
Publication date: 2002
Main Research Area: Technical/natural sciences

**Publication information**
Journal: FEMS Microbiology Ecology
Volume: 44
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
Effects of mercury contamination on the culturable heterotrophic, functional and genetic diversity of the bacterial community in soil

This study investigates the effect of mercury contamination on the culturable heterotrophic, functional and genetic diversity of the bacterial community in soil. The changes in diversity were monitored in soil microcosms, enriched with 25 µg Hg(II) g(-1) soil, over a period of 3 months. The culturable heterotrophic diversity was investigated by colony morphology and colony appearance on solid LB medium. Functional diversity was analysed as sole carbon utilisation patterns in ECOplates. Genetic diversity was measured as bands on denaturing gradient gel electrophoresis (DGGE) gels obtained by purification of total soil DNA and amplification of bacterial 16S rDNA fragments by polymerase chain reaction. Concentrations of bioavailable and total mercury were measured throughout the experiment. The effect on the culturable heterotrophic and genetic diversity was very similar, showing an immediate decrease after mercury addition but then slowly increasing throughout the entire experimental period. Pre-exposure levels were not reached within the time span of this investigation. The DGGE band pattern indicated that a shift in the community structure was responsible for recovered diversity. When analysed by Shannon-Weaver indices, functional diversity was found to increase almost immediately after mercury addition and to remain at a level higher than the control soil for the rest of the experiment. The fraction of culturable heterotrophic bacteria increased from 1% to 10% of the total bacterial number as a result of mercury addition, and the mercury-resistant population increased to represent the entire heterotrophic population. (C) 2001 Federation of European Microbiological Societies. Published by Elsevier Science B.V.. All rights reserved.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, L. D. (Intern), Sørensen, S. J. (Ekstern)
Pages: 1-9
Publication date: Jun 2001
Main Research Area: Technical/natural sciences
Identification of copper-induced genes in Pseudomonas fluorescens and use of a reporter strain to monitor bioavailable copper in soil

Copper (Cu) is an essential trace metal required by living organisms but it is potentially toxic at higher concentrations. Cu salts are used as bactericides in agriculture and as growth promoters in pig production. They are consequently introduced to the environment, e.g. through manure, and might negatively affect the bacterial soil community. In this study, our goal
was to develop a specific and stable Cu reporter construction harboured by an indigenous soil bacterium to measure bioavailability of Cu in soil. Following mutagenesis of Pseudomonas fluorescens strain DF57 with a Tn5::luxAB promoter probe transposon, we identified four mutants with elevated luxAB expression in response to Cu. Two of the mutated loci encoded proteins homologous to Cop proteins conferring Cu resistance to Pseudomonas syringae, while a third displayed homology to metal-transporting ATPases. In the fourth mutant, DF57-Cu15, the gene interrupted by the transposon encoded a protein carrying a Cu-binding domain but with low homology to known proteins. DF57-Cu15 was the most suitable Cu reporter due to its high specific response and tolerance to Cu in pure culture. DF57-Cu15 responded to soil solutions from Cu-amended soil microcosms in a concentration-dependent manner. The chelator EDTA reduced the availability of Cu to P. fluorescens in soil. This showed that complex-bound Cu is not necessarily available to bacteria. We compared chemical analysis of soluble Cu and the reporter assay on soil solutions from Cu-containing soil microcosms supplemented with either manure or straw. Organic matter increased the amount of soluble Cu but not the amount of bioavailable Cu. Probably, Cu binds with high affinity to organic constituents in pig manure or barley straw. Hence, determination of soluble Cu by chemical analysis cannot always predict the bioavailability of Cu to a specific bacterium.

General information
State: Published
Organisations: National Veterinary Institute, Technical University of Denmark
Authors: Tom-Petersen, A. (Ekstern), Hosbond, C. (Ekstern), Nybroe, O. (Ekstern)
Pages: 59-67
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: Fems Microbiology Ecology
Volume: 38
Issue number: 1
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Web of Science (2008): Indexed yes
A bioluminescent derivative of Pseudomonas putida KT2440 for deliberate release into the environment

General information
State: Published
Organisations: Department of Microbiology, Microbial Ecology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Rodriguez, C. J. R. (Intern), Mølbak, L. (Intern), Ramos, J. L. (Ekstern), Molin, S. (Intern)
Pages: 91-102
Publication date: 2000
Main Research Area: Technical/natural sciences

Publication information
Journal: FEMS Microbiology Ecology
Volume: 34
Issue number: 2
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
Growth kinetics of thermophilic Methanosarcina spp. isolated from full-scale biogas plants treating animal manures

General information
State: Published
Organisations: Department of Biotechnology
Authors: Mladenovska, Z. (Intern), Ahring, B. K. (Intern)
Pages: 225-229
Publication date: 2000
Main Research Area: Technical/natural sciences

Publication information
Journal: F E M S Microbiology Ecology
Volume: 31
Issue number: 3
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Unravelling the genetic diversity of ruminal bacteria belonging to the CFB phylum

Molecular biology approaches were employed to examine the genetic diversity of bacteria from the Cytophaga/Flexibacter/Bacteroides (CFB) phylum in the rumen of cattle. By this means we were able to identify cultured strains that represent some of the larger CFB clusters previously identified only by PCR amplification and sequencing. Complete 16S rDNA sequences were obtained for 16 previously isolated rumen strains, including the type strains of Prevotella ruminicola, P. bryantii, P. brevis and P. albensis to represent a wide range of diversity. Phylogenetic analysis of cultured strains revealed the existence of three clusters of ruminal CFB: (i) a cluster of Prevotella strains, which have been found only in the rumen, including the two type strains, P. brevis GA33(T) and P. ruminicola 23(T), (ii) Prevotella spp. that cluster with prevotellas from other ecological niches such as the oral cavity and which include the type strains, P. bryantii B(1)4(T) and P. albensis M384(T); (iii) two Bacteroides spp. strains clustering with B. forsythus of oral origin. In order to establish whether the cultivated isolates cover the whole range of ruminal CFB genetic diversity, 16S rRNA gene sequences were amplified and cloned from DNA extracted from the same rumen samples (one cow in Slovenia, one in Scotland and three in Japan). Sequencing and phylogenetic analysis of 16S rRNA genes confirmed the existence of two superclusters of ruminal Prevotella, one exclusively ruminal and the other including non-ruminal species. In the case of ruminal Bacteroides spp., however, phylogenetic analysis revealed the existence of three new superclusters, one of which has as yet no cultivable counterpart. Interestingly, these Bacteroides clusters were represented almost exclusively by clone libraries from the Japanese cattle and only three sequences were from the European cattle. This study agrees with previous analyses in showing that rumen Prevotella/Bacteroides strains exhibit a remarkable degree of genetic diversity and suggests that different strain groupings may differ greatly in their recovery by cultural methods. The most important conclusion, however, is that cultured strains can be identified that represent some of the larger clusters previously identified only by PCR amplification and sequencing. (C) 2000 Federation of European Microbiological Societies. Published by Elsevier Science B.V. All rights reserved.
ribosome DNA, bacterium, genetic variation, phylogeny, rumen, article, Bacteroides, biodiversity, cattle, DNA library, Flexibacteraceae, nonhuman, nucleotide sequence, Prevotella, priority journal, rumen microorganism, sequence analysis, Bacteria (microorganisms), Bacteroides phylum, Bacteroides sp., Bacteroidetes, Bos taurus, Cytophaga, Flexibacter, Prevotella albensis, Prevotella brevis, Prevotella bryantii, Prevotella ruminicola 23, 16S rDNA library, Cytophaga/Flexibacter/Bacteroides phylum, Genetic diversity, Ruminal bacterium, Microbiology, Sequence-Analysis, Bacteroides-Ruminicola, Phylogenetic Analysis, Rumen, DNA, Identification, Strains, ruminal bacterium, genetic diversity, Europe Palearctic region, Japan Palearctic region, bacterial genetic diversity analysis, clusters, microbial ecology, Anaerobic Gram-Negative Rods Eubacteria Bacteria Microorganisms (Bacteria, Eubacteria, Microorganisms) - Bacteroidaceae [06901] Bacteroides, Artiodactyla Mammalia Vertebrata Chordata Animalia (Animals, Artiodactyls, Chordates, Mammals, Nonhuman Vertebrates, Nonhuman Mammals, Vertebrates) - Bovidae [85715] cattle, Cytophagales Nonfruiting Gliding Bacteria Eubacteria Bacteria Microorganisms (Bacteria, Eubacteria, Microorganisms) - Cytophaga, Microorganisms (Bacteria, Eubacteria, Microorganisms) - Bacteria [05000] bacteria ruminal bacterium, Nonfruiting Gliding Bacteria Eubacteria Bacteria Microorganisms (Bacteria, Eubacteria, Microorganisms) - Cytophagales [08510] Flexibacter, 03502, Genetics - General, 03506, Genetics - Animal, 07502, Ecology: environmental biology - General and methods, 07508, Ecology: environmental biology - Animal, 10062, Biochemistry studies - Nucleic acids, purines and pyrimidines, 14004, Digestive system - Physiology and biochemistry, 29500, Microorganisms - General, 30000, Bacteriology, general and systematic, 31000, Physiology and biochemistry of bacteria, 31500, Genetics of bacteria and viruses, Biochemistry and Molecular Biophysics, Ingestion and Assimilation, rumen digestive system, PCR polymerase chain reaction DNA amplification, in-situ recombinant gene expression detection, molecular genetic method,
Rumen bacterial diversity as determined by sequence analysis of 16S rDNA libraries

Molecular diversity of rumen bacteria was analyzed by PCR amplification and sequencing of 16S rDNA clone libraries prepared from the rumen content of Holstein cows fasted for 16 h. A total of 84 clones, containing almost full size 16S rDNA sequences (about 1.5 kb long), were completely sequenced and subjected to an on line similarity search. Four sequences from the 84 clones closely resembled that of Butyrivibro fibrisolvens and one clone was found to be related to Treponema bryanti. For 38% of the sequences, the similarity with database sequences was in the range of 90%-98% and for the remaining 56% the similarity was less than 90%. The bacterial community structure was also revealed by phylogenetic placement of sequences in relation to different fractions of rumen content. In the library from the rumen fluid, the sequences were affiliated with the following major phyla: low G+C Gram-positive bacteria (52.4%), Cytophaga-Flexibacter-Bacteroides (38.1%), Proteobacteria (4.7%) and Spirochaetes (2.4%). 2.4% had an uncertain affiliation. The vast majority of sequences from the rumen solids were found to be related to low G+C Gram-positive bacteria (71.4%) and the remaining sequences were placed within the Cytophaga-Flexibacter-Bacteroides (26.2%) and Spirochaetes (2.4%) phyla. (C) 1999 Federation of European Microbiological Societies. Published by Elsevier Science B.V. All rights reserved.

General information
State: Published
Organisations: STAFF-Institute
Authors: Tajima, K. (Ekstern), Aminov, R. (Intern), Nagamine, T. (Ekstern), Ogata, K. (Ekstern), Nakamura, M. (Ekstern), Matsui, H. (Ekstern), Benno, Y. (Ekstern)
Number of pages: 11
Pages: 159-169
Publication date: 1999
Main Research Area: Technical/natural sciences

Publication information
Journal: F E M S Microbiology Ecology
Volume: 29
Issue number: 2
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Biased 16S rDNA PCR amplification caused by interference from DNA flanking the template region

General information
State: Published
Organisations: Department of Systems Biology, Center for Systems Microbiology
Authors: Hansen, M. C. (Intern), Tolker-Nielsen, T. (Intern), Givskov, M. C. (Intern), Molin, S. (Intern)
Pages: 141-149
Publication date: 1998
Main Research Area: Technical/natural sciences

Publication information
Journal: F E M S Microbiology Ecology
Volume: 26
ISSN (Print): 0168-6496

Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
A total of 100 Aeromonas caviae strains isolated from river waters (38 isolates), raw sewage (30 isolates) and effluents of stabilisation ponds (i.e. treated sewage; 32 isolates) in Marrakech, Morocco, were tested for the presence of putative virulence factors to delineate differences, if any, in their enteropathogenic potential in relation to the source of isolation. A number of A. caviae isolates were able to elaborate at least one of the tested virulence factors. Of the 100 strains tested, 27 were capable of producing haemolysins, 19 produced cytotoxin, 24 produced cytotonic toxin, while 18 of the isolates possessed the capacity to adhere to HenLe 407 human intestinal cells with more than five bacteria adhering per cell. In order to assess the virulence potential of A. caviae isolates in relation to the source of isolation, we suggest the potential virulence index (PVI) as a tool for comparison. It is calculated as $\text{PVI} = \frac{x}{ny}$, where $x$ is the number of positive occurrence of virulence factors in a population $y$, and $n$ is the number of suitable virulence factors used for the calculation of the PVI. Accordingly, in this study A. caviae strains isolated from treated sewage samples showed a higher PVI ($= 0.406$) than those isolated from raw sewage ($\text{PVI} = 0.175$) or those from river waters ($\text{PVI} = 0.09$). These results suggest that stabilisation pond systems used for sewage purification under arid climate conditions in Marrakech, may have selected potentially enteropathogenic A. caviae strains.
Anaerobic microbiology of an alkaline Icelandic hot spring

General information
State: Published
Organisations: Department of Environmental Science and Engineering
Authors: Sonne-Hansen, J. (Intern), Ahring, B. K. (Intern)
Pages: 31 - 38
Publication date: 1997
Main Research Area: Technical/natural sciences

Publication information
Journal: F E M S Microbiology Ecology
Volume: 23
Issue number: 1
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Conjugal transfer at natural population densities in a microcosm simulating an estuarine environment

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Barkay, T. (Ekstern), Kroer, N. (Ekstern), Rasmussen, L. D. (Intern), Sørensen, S. J. (Ekstern)
Pages: 43-54
Publication date: 1996
Main Research Area: Technical/natural sciences

Publication information
Journal: FEMS Microbiology Ecology
Volume: 16
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Limiting Factors for Microbial Fe(III)-Reduction In a Landfill Leachate Polluted Aquifer (Vejen, Denmark)

Aquifer sediment samples from two locations within the anaerobic leachate plume of a municipal landfill were compared with respect to microbiology (especially Fe(III)-reduction) and geochemistry. The samples close to the landfill were characterized by low contents of Fe(III), whereas samples from the more distant cluster were rich in Fe(III)-oxides. The active microbial population seemed to be less dense in samples more distant from the landfill (measured by ATP and phospholipid fatty acids (PLFA)), but the microbial communities were very similar in the two sample clusters according to the composition of PLFA. Very little, if any, Fe(III)-reduction was observed close to the landfill, but all the more distant samples showed evident microbially mediated Fe(III)-reduction. After amendment with both acetate and Fe(III), all the samples showed a potential for Fe(III)-reduction, and the in situ Fe(III)-reduction seemed to be limited by the lack of Fe(III)-availability. It was suggested, that Fe(III)-reducing populations might be facultative, surviving by use of other electron-acceptors than Fe(III), when Fe(II) is not available for reduction.
Survival of Rhizobium leguminosarum in Soil after Addition as Inoculant

General information
State: Published
Organisations: Risø National Laboratory for Sustainable Energy
Authors: Jensen, E. (Intern), Sørensen, L. (Ekstern)
Publication date: 1987
Main Research Area: Technical/natural sciences

Publication information
Journal: F E M S Microbiology Ecology
ISSN (Print): 0168-6496
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.85
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 3.77
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 3.8
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.15
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.78
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.63