

Differential mobility spectrometry classification of bacteria

Aim: Rapid identification of bacteria would facilitate timely initiation of therapy and improve cost-effectiveness of treatment. Traditional methods (culture, PCR) require reagents, consumables and hours to days to complete the identification. In this study, we examined whether differential mobility spectrometry could classify most common bacterial species, genera and between Gram status within minutes. **Materials & methods:** Cultured bacterial sample gaseous headspaces were measured with differential mobility spectrometry and data analyzed using k-nearest-neighbor and leave-one-out cross-validation. **Results:** Differential mobility spectrometry achieved a correct classification rate 70.7% for all bacterial species. For bacterial genera, the rate was 77.6% and between Gram status, 89.1%. **Conclusion:** Largest difficulties arose in distinguishing bacteria of the same genus. Future improvement of the sensor characteristics may improve the classification accuracy.

General information

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MoE publication type: A1 Journal article-refereed

Organisations: BioMediTech, Tampere University, Tampere University Hospital, Fimlab Laboratories

Contributors: Hokkinen, L., Kesti, A., Lepomäki, J., Anttalainen, O., Kontunen, A., Karjalainen, M., Aittoniemi, J., Vuento, R., Lehtimäki, T., Oksala, N., Roine, A.

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ASJC Scopus subject areas: Microbiology, Microbiology (medical)

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Research output: [Contribution to journal](#) > [Article](#) > [Scientific](#) > [peer-review](#)

Formation and use of biogenic jarosite carrier for high-rate iron oxidising biofilms

Jarosite precipitates formed in iron oxidising bioreactors have been shown to harbour iron-oxidisers. The aim of this study was to develop an iron oxidising bioprocess where microorganisms are retained solely on biogenic jarosite particles. Based on preliminary experiments using a fluidised-bed bioreactor (FBR), the formed jarosite particles started to disintegrate and wash out at upflow velocities of ≥ 0.21 cm/s. Therefore, the generation and use of biogenic jarosite carrier was studied in an expanded-bed bioreactor (J-EBR) with an upflow velocity of 0.19 cm/s. Inside J-EBR, the jarosite particles formed granules of 0.5–3 mm containing 200–460 mg/g of attached biomass. The performance of J-EBR was compared with an activated carbon biofilm FBR at 0.82 cm/s upflow velocity (AC-FBR). At 35 ± 2 °C with a feed ferrous iron concentration of 10 g/l, the highest obtained iron oxidation rate of J-EBR (6.8 g/l/h) was 33% lower than that of AC-FBR (10.1 g/l/h). This was likely due to the 80% lower recirculation rate and subsequently higher oxygen mass transfer limitation in J-EBR compared to AC-FBR. The present study demonstrates that biogenic jarosite can be used for retainment of iron oxidising biofilms in expanded-bed bioreactors that oxidise iron at high rates.

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Organisations: Research group: Bio- and Circular Economy, Materials Science and Environmental Engineering, Physics, Civil Engineering

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Research output: Contribution to journal > Article > Scientific > peer-review

Spatial variations in bacterial and archaeal abundance and community composition in boreal forest pine mycorrhizospheres

Mycorrhizal fungi have a strong impact on soil biota. In this study, bacterial and archaeal populations in different parts of *Suillus bovinus* - *Pinus sylvestris* mycorrhizospheres in boreal forest were quantified and identified by DNA analysis. The numbers of bacterial and archaeal 16S rRNA gene copies were highest in uncolonized humus and lowest in fruiting bodies. The numbers of bacterial 16S rRNA gene copies varied from 1.3×10^7 to 3.1×10^9 copies g^{-1} fw and archaeal copies from 4.1×10^7 to 9.6×10^8 copies g^{-1} fw. The relatively high number of archaeal 16S rRNA gene copies was likely due to the cold and highly organic habitat. The presence of hyphae appeared to further promote archaeal numbers and the archaea:bacteria ratio was over one in samples containing only fungal material. Most detected archaea belonged to terrestrial Thaumarchaeota. Proteobacteria, Actinobacteria and Acidobacteria were predictably the dominating bacterial taxa in the samples with clear trend of Betaproteobacteria preferring the pine root habitats.

General information

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MoE publication type: A1 Journal article-refereed

Organisations: Materials Science and Environmental Engineering, Research group: Bio- and Circular Economy, University of Helsinki

Contributors: Rinta-Kanto, J. M., Timonen, S.

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ASJC Scopus subject areas: Microbiology, Soil Science, Insect Science

Keywords: Archaea, Bacteria, Ectomycorrhiza, Microbial community, Mycorrhizosphere, Sporocarp

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Research output: Contribution to journal > Article > Scientific > peer-review

Estimating RNA numbers in single cells by RNA fluorescent tagging and flow cytometry

Estimating the statistics of single-cell RNA numbers has become a key source of information on gene expression dynamics. One of the most informative methods of in vivo single-RNA detection is MS2d-GFP tagging. So far, it requires microscopy and laborious semi-manual image analysis, which hampers the amount of collectable data. To overcome this limitation, we present a new methodology for quantifying the mean, standard deviation, and skewness of single-cell distributions of RNA numbers, from flow cytometry data on cells expressing RNA tagged with MS2d-GFP. The quantification method, based on scaling flow-cytometry data from microscopy single-cell data on integer-valued RNA numbers, is shown to readily produce precise, big data on in vivo single-cell distributions of RNA numbers and, thus, can assist in studies of transcription dynamics.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Research group: Laboratory of Biosystem Dynamics-LBD, BioMediTech, Boston University

Contributors: Bahrudeen, M. N., Chauhan, V., Palma, C. S., Oliveira, S. M., Kandavalli, V. K., Ribeiro, A. S.

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Journal: Journal of Microbiological Methods

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Ratings:

Scopus rating (2019): CiteScore 3.2 SJR 0.636 SNIP 0.695

Original language: English

ASJC Scopus subject areas: Microbiology, Molecular Biology, Microbiology (medical)

Keywords: Flow cytometry, MS2d-GFP RNA tagging, Single-cell RNA numbers, Time-lapse microscopy

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Bibliographical note

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Research output: Contribution to journal › Article › Scientific › peer-review

Similar temperature sensitivity of soil mineral-associated organic carbon regardless of age

Most of the carbon (C) stored in temperate arable soils is present in organic matter (OM) intimately associated with soil minerals and with slow turnover rates. The sensitivity of mineral-associated OM to changes in temperature is crucial for reliable predictions of the response of soil C turnover to global warming and the associated flux of carbon dioxide (CO₂) from the soil to the atmosphere. We studied the temperature sensitivity of C in <63 μm fractions rich in mineral-associated organic matter (MOM) and of C in >63 μm fractions rich in particulate organic matter (POM). The fractions were isolated by physical separation of two light-textured arable soils where the C4-plant silage maize had replaced C3-crops 25 years ago. Differences in ¹³C abundance allowed for calculation of the age of C in the soil-size fractions (old C, C3-C > 25 years; recent C, C4-C < 25 years). We incubated bulk soils (<2 mm) and size fractions sequentially at 6, 18, 26 and 34 °C (ramping up and down the temperature scale) and calculated the temperature sensitivity of old and recent C from ¹²CO₂ and ¹³CO₂ evolution rates. The temperature sensitivity was similar or slightly higher for POM than for MOM. Within the POM fraction, old C3-C was more sensitive to changes in temperature than recent C4-C. For the MOM fraction, the temperature sensitivity was unrelated to the age of C. Quantitative PCR analysis indicated that the proportions of bacteria, archaea and fungi did not change during incubation. Our results suggest that while OM stabilizing mechanisms affect the temperature sensitivity of soil C, temperature sensitivity appears unrelated to the age of mineral-associated OM.

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MoE publication type: A1 Journal article-refereed

Organisations: Computing Sciences, University of Helsinki, Finnish Environment Institute, Finnish Museum of Natural History, Aarhus Universitet, Natural Resources Institute Finland (Luke), Finnish Meteorological Institute

Contributors: Karhu, K., Hiltavuori, E., Järvenpää, M., Arppe, L., Christensen, B. T., Fritze, H., Kulmala, L., Oinonen, M., Pitkänen, J. M., Vanhala, P., Heinonsalo, J., Liski, J.

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Original language: English

ASJC Scopus subject areas: Microbiology, Soil Science

Keywords: C natural abundance, Bayesian statistics, Climate change, Decomposition, Soil organic matter, Temperature sensitivity

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Research output: Contribution to journal › Article › Scientific › peer-review

Vertical stratification of bacteria and archaea in sediments of a small boreal humic lake

Although sediments of small boreal humic lakes are important carbon stores and greenhouse gas sources, the composition and structuring mechanisms of their microbial communities have remained understudied. We analyzed the vertical profiles of microbial biomass indicators (PLFAs, DNA and RNA) and the bacterial and archaeal community composition (sequencing of 16S rRNA gene amplicons and qPCR of *mcrA*) in sediment cores collected from a typical small boreal lake. While microbial biomass decreased with sediment depth, viable microbes (RNA and PLFA) were present all through the profiles. The vertical stratification patterns of the bacterial and archaeal communities resembled those in marine sediments with well-characterized groups (e.g. Methanomicrobia, Proteobacteria, Cyanobacteria, Bacteroidetes) dominating in the surface sediment and being replaced by poorly-known groups (e.g. Bathyarchaeota, Aminicenantes and Caldiseica) in the deeper layers. The results also suggested that, similar to marine systems, the deep bacterial and archaeal communities were predominantly assembled by selective survival of taxa able to persist in the low energy conditions. Methanotrophs were rare, further corroborating the role of these methanogen-rich sediments as important methane emitters. Based on their taxonomy, the deep-dwelling groups were putatively organo-heterotrophic, organo-autotrophic and/or acetogenic and thus may contribute to changes in the lake sediment carbon storage.

General information

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MoE publication type: A1 Journal article-refereed

Organisations: Materials Science and Environmental Engineering, Department of Biological and Environmental Science, Jyväskylän yliopisto, University of Eastern Finland

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Publication information

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Original language: English

ASJC Scopus subject areas: Microbiology, Molecular Biology, Genetics

Keywords: 16S rRNA, archaea, bacteria, biomass, lake, sediment

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Research output: Contribution to journal > Article > Scientific > peer-review

Archaea are prominent members of the prokaryotic communities colonizing common forest mushrooms

In this study, the abundance and composition of prokaryotic communities associated with the inner tissue of fruiting bodies of *Suillus bovinus*, *Boletus pinophilus*, *Cantharellus cibarius*, *Agaricus arvensis*, *Lycoperdon perlatum*, and *Piptoporus betulinus* were analyzed using culture-independent methods. Our findings indicate that archaea and bacteria colonize the internal tissues of all investigated specimens and that archaea are prominent members of the prokaryotic community. The ratio of archaeal 16S rRNA gene copy numbers to those of bacteria was >1 in the fruiting bodies of four out of six fungal species included in the study. The largest proportion of archaeal 16S rRNA gene sequences belonged to thaumarchaeotal classes Terrestrial group, Miscellaneous Crenarchaeotic Group (MCG), and Thermoplasmata. Bacterial communities showed characteristic compositions in each fungal species. Bacterial classes Gammaproteobacteria, Actinobacteria, Bacilli, and Clostridia were prominent among communities in fruiting body tissues. Bacterial populations in each fungal species had different characteristics. The results of this study imply that fruiting body tissues are an important habitat for abundant and diverse populations of archaea and bacteria.

General information

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MoE publication type: A1 Journal article-refereed

Organisations: Chemistry and Bioengineering, Department of Microbiology, University of Helsinki, Turku University of Applied Science

Contributors: Rinta-Kanto, J. M., Pehkonen, K., Sinkko, H., Tamminen, M. V., Timonen, S.

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Publication information

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Original language: English

ASJC Scopus subject areas: Microbiology, Immunology, Applied Microbiology and Biotechnology, Molecular Biology, Genetics

Keywords: Archaea, Bacteria, Mushroom, qPCR, Sequencing

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Source ID: 85054057146

Research output: Contribution to journal > Article > Scientific > peer-review

Crawling-induced floor dust resuspension affects the microbiota of the infant breathing zone

Background: Floor dust is commonly used for microbial determinations in epidemiological studies to estimate early-life indoor microbial exposures. Resuspension of floor dust and its impact on infant microbial exposure is, however, little explored. The aim of our study was to investigate how floor dust resuspension induced by an infant's crawling motion and an adult walking affects infant inhalation exposure to microbes. **Results:** We conducted controlled chamber experiments with a simplified mechanical crawling infant robot and an adult volunteer walking over carpeted flooring. We applied bacterial 16S rRNA gene sequencing and quantitative PCR to monitor the infant breathing zone microbial content and compared that to the adult breathing zone and the carpet dust as the source. During crawling, fungal and bacterial levels were, on average, 8-to 21-fold higher in the infant breathing zone compared to measurements from the adult breathing zone. During walking experiments, the increase in microbial levels in the infant breathing zone was far less pronounced. The correlation in rank orders of microbial levels in the carpet dust and the corresponding infant breathing zone sample varied between different microbial groups but was mostly moderate. The relative abundance of bacterial taxa was characteristically distinct in carpet dust and infant and adult breathing zones during the infant crawling experiments. Bacterial diversity in carpet dust and the infant breathing zone did not correlate significantly. **Conclusions:** The microbiota in the infant breathing zone differ in absolute quantitative and compositional terms from that of the adult breathing zone and of floor dust. Crawling induces resuspension of floor dust from carpeted flooring, creating a concentrated and localized cloud of microbial content around the infant. Thus, the microbial exposure of infants following dust resuspension is difficult to predict based on common house dust or bulk air measurements. Improved approaches for the assessment of infant microbial exposure, such as sampling at the infant breathing zone level, are needed.

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MoE publication type: A1 Journal article-refereed

Organisations: Physics, National Public Health Institute, University of Eastern Finland, VTT Technical Research Centre of Finland, Työterveyslaitos, Oulu University of Applied Sciences, University of Helsinki, Purdue University

Contributors: Hyytiäinen, H. K., Jayaprakash, B., Kirjavainen, P. V., Saari, S. E., Holopainen, R., Keskinen, J., Hämeri, K., Hyvärinen, A., Boor, B. E., Täubel, M.

Publication date: 2018

Peer-reviewed: Yes

Publication information

Journal: Microbiome

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Article number: 25

ISSN (Print): 2049-2618

Ratings:

Scopus rating (2018): CiteScore 9.8 SJR 4.466 SNIP 2.633

Original language: English

ASJC Scopus subject areas: Microbiology, Microbiology (medical)

Keywords: 16S rRNA gene sequencing, Indoor microbial exposure, Infant exposure, Particle resuspension, QPCR

Electronic versions:

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URLs:

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Research output: [Contribution to journal](#) > [Article](#) > [Scientific](#) > [peer-review](#)

Microbiological, chemical and sensory spoilage analysis of raw Atlantic cod (*Gadus morhua*) stored under modified atmospheres

During fish spoilage, microbial metabolism leads to the production of volatile organic compounds (VOCs), characteristic off-odors and eventual consumer rejection. The aim of the present study was to contribute to the development of intelligent packaging technologies by identifying and quantifying VOCs that indicate spoilage of raw Atlantic cod (*Gadus morhua*) under atmospheres (%v/v CO₂/O₂/N₂) 60/40/0, 60/5/35 and air. Spoilage was examined by microbiological, chemical and sensory analyses over storage time at 4 or 8 °C. Selected-ion flow-tube mass spectrometry (SIFT-MS) was used for quantifying selected VOCs and amplicon sequencing of the 16S rRNA gene was used for the characterization of the cod microbiota. OTUs classified within the *Photobacterium* genus increased in relative abundance over time under all storage conditions, suggesting that *Photobacterium* contributed to spoilage and VOC production. The onset of exponential VOC concentration increase and sensory rejection occurred at high total plate counts (7–7.5 log). Monitoring of early spoilage thus calls for sensitivity for low VOC concentrations.

General information

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MoE publication type: A1 Journal article-refereed

Organisations: Materials Science, Laboratory of Food Microbiology and Food Preservation, Universiteit Gent, Paper Converting and Packaging Technology

Contributors: Kuuliala, L., Al Hage, Y., Ioannidis, A. G., Sader, M., Kerckhof, F. M., Vanderroost, M., Boon, N., De Baets, B., De Meulenaer, B., Ragaert, P., Devlieghere, F.

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Original language: English

ASJC Scopus subject areas: Food Science, Microbiology

Keywords: Amplicon sequencing, *Photobacterium*, Sensor, SIFT-MS, Volatile organic compound

Electronic versions:

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Source: Scopus

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Research output: [Contribution to journal](#) > [Article](#) > [Scientific](#) > [peer-review](#)

Resistant ammonia-oxidizing archaea endure, but adapting ammonia-oxidizing bacteria thrive in boreal lake sediments receiving nutrient-rich effluents

Climate change along with anthropogenic activities changes biogeochemical conditions in lake ecosystems, modifying the sediment microbial communities. Wastewater effluents introduce nutrients and organic material but also novel microbes to lake ecosystems, simulating forthcoming increases in catchment loadings. In this work, we first used 16s rRNA gene sequencing to study how the overall sediment microbial community responds to wastewater in six boreal lakes. To examine forthcoming changes in the lake biogeochemistry, we focused on the ammonia-oxidizing archaea (AOA) and bacteria (AOB), and examined their functional and compositional community response to wastewater. Although we found the least diverse and least resistant prokaryotic communities from the most wastewater-influenced sediments, the community changed fast toward the natural composition with the diminishing influence of wastewater. Each lake hosted a unique resistant AOA community, while AOB communities were adapting, responding to environmental conditions as well

as receiving new members from WWTPs. In general, AOB dominated in numbers in wastewater-influenced sediments, while the ratio between AOA and AOB increased when moving toward pristine conditions. Our results suggest that although future climate-change-driven increases in nutrient loading and microbial migration might significantly disrupt lake sediment microbiomes, they can promote nitrification through adapting and abundant AOB communities.

General information

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MoE publication type: A1 Journal article-refereed

Organisations: Chemistry and Bioengineering, Research group: Bio- and Circular Economy, Jyväskylän yliopisto, University of Eastern Finland

Contributors: Aalto, S. L., Saarenheimo, J., Mikkonen, A., Rissanen, A. J., Tirola, M.

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Publication information

Journal: Environmental Microbiology

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ISSN (Print): 1462-2912

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Electronic versions:

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Research output: Contribution to journal > Article > Scientific > peer-review

Twin-layer biosensor for real-time monitoring of alkane metabolism

Intracellular metabolic sensors can be used for efficient screening and optimization of microbial cell factories. In particular, the sensors are useful in acquiring information about pathway dynamics and bottlenecks in a straightforward manner. Here, we developed a twin-layer biosensor that functions simultaneously at two levels: Through transcription factor mediated sensing and enzyme-metabolite interaction, providing insights into the dynamics of alkane metabolism. In addition, the sensor can be used for monitoring either alkane degradation or biosynthesis, depending on the used cellular context. Alkanes are monitored using a fluorescent reporter green fluorescent protein placed under a native alkane-inducible promoter, whereas a bacterial luciferase producing bioluminescence signal enzymatically detects a specific metabolic intermediate in the alkane production/degradation pathway. First, we employed the sensor to investigate the native alkane degradation route in *Acinetobacter baylyi* ADP1. The highest fluorescence and luminescence signals were obtained for dodecane. Second, we constructed a non-native alkane synthesis pathway in *A. baylyi* ADP1, of which the functionality was confirmed with the sensor. The twin-layer approach provides convenient means to study and optimize the kinetics and performance of the heterologous pathway and will facilitate the development of an efficient cell factory.

General information

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MoE publication type: A1 Journal article-refereed

Organisations: Chemistry and Bioengineering, Research group: Bio- and Circular Economy

Contributors: Lehtinen, T., Santala, V., Santala, S.

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Publication information

Journal: FEMS Microbiology Letters

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Ratings:

Scopus rating (2017): CiteScore 3.6 SJR 0.79 SNIP 0.605

Original language: English

ASJC Scopus subject areas: Microbiology, Molecular Biology, Genetics

Keywords: Acinetobacter baylyi ADP1, Alkane, Biosensor, GFP, LuxAB, Real-time monitoring

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Twin Sensor_R1

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Research output: Contribution to journal › Article › Scientific › peer-review

Echovirus 1 internalization negatively regulates epidermal growth factor receptor downregulation

We have demonstrated previously that the human picornavirus Echovirus 1 (EV1) triggers an infectious internalization pathway that follows closely, but seems to stay separate, from the epidermal growth factor receptor (EGFR) pathway triggered by epidermal growth factor (EGF). Here, we confirmed by using live and confocal microscopy that EGFR and EV1 vesicles are following intimately each other but are distinct entities with different degradation kinetics. We show here that despite being sorted to different pathways and located in distinct endosomes, EV1 inhibits EGFR downregulation. Simultaneous treatment with EV1 and EGF led to an accumulation of EGFR in cytoplasmic endosomes, which was evident already 15 min p.i. and more pronounced after 2 hr p.i. EV1 treatment led to reduced downregulation, which was proven by increased total cellular amount of EGFR. Confocal microscopy studies revealed that EGFR accumulated in large endosomes, presumably macropinosomes, which were not positive for markers of the early, recycling, or late endosomes/lysosomes. Interestingly, EV1 did not have a similar blocking effect on bulk endosomal trafficking or transferrin recycling along the clathrin pathway suggesting that EV1 did not have a general effect on cellular trafficking pathways. Importantly, EGF treatment increased EV1 infection and increased cell viability during infection. Simultaneous EV1 and EGF treatment seemed to moderately enhance phosphorylation of protein kinase C α . Furthermore, similar phenotype of EGFR trafficking could be produced by phorbol 12-myristate 13-acetate treatment, further suggesting that activated protein kinase C α could be contributing to EGFR phenotype. These results altogether demonstrate that EV1 specifically affects EGFR trafficking, leading to EGFR downregulation, which is beneficial to EV1 infection.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Research group: Data-analytics and Optimization, Research group: Computational Systems Biology, Pori Department, Jyväskylä yliopisto, University of Helsinki

Contributors: Huttunen, M., Turkki, P., Mäki, A., Paavolainen, L., Ruusuvoori, P., Marjomäki, V.

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Publication information

Journal: Cellular Microbiology

Volume: 19

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Ratings:

Scopus rating (2017): CiteScore 8.8 SJR 2.52 SNIP 1.06

Original language: English

ASJC Scopus subject areas: Microbiology, Immunology, Virology

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Research output: Contribution to journal › Article › Scientific › peer-review

Bioluminescence-based system for rapid detection of natural transformation

Horizontal gene transfer plays a significant role in bacterial evolution and has major clinical importance. Thus, it is vital to understand the mechanisms and kinetics of genetic transformations. Natural transformation is the driving mechanism for horizontal gene transfer in diverse genera of bacteria. Our study introduces a simple and rapid method for the investigation of natural transformation. This highly sensitive system allows the detection of a transformation event directly from a bacterial population without any separation step or selection of cells. The system is based on the bacterial luciferase operon from *Photobacterium luminescens*. The studied molecular tools consist of the functional modules luxCDE and luxAB, which involve a replicative plasmid and an integrative gene cassette. A well-established host for bacterial genetic investigations, *Acinetobacter baylyi* ADP1, is used as the model bacterium. We show that natural transformation

followed by homologous recombination or plasmid recircularization can be readily detected in both actively growing and static biofilm-like cultures, including very rare transformation events. The system allows the detection of natural transformation within 1 h of introducing sample DNA into the culture. The introduced method provides a convenient means to study the kinetics of natural transformation under variable conditions and perturbations.

General information

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MoE publication type: A1 Journal article-refereed

Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry

Contributors: Santala, V., Karp, M., Santala, S.

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Journal: FEMS Microbiology Letters

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Scopus rating (2016): CiteScore 3.4 SJR 0.842 SNIP 0.627

Original language: English

ASJC Scopus subject areas: Microbiology, Genetics, Molecular Biology

Keywords: *Acinetobacter baylyi* ADP1, Bacterial luciferase, Bioluminescence, Horizontal gene transfer, In vivo monitoring, Natural transformation

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<http://www.scopus.com/inward/record.url?scp=84977137869&partnerID=8YFLogxK> (Link to publication in Scopus)

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Research output: Contribution to journal > Article > Scientific > peer-review

Robustness of the process of nucleoid exclusion of protein aggregates in *Escherichia coli*

Escherichia coli segregates protein aggregates to the poles by nucleoid exclusion. Combined with cell divisions, this generates heterogeneous aggregate distributions in subsequent cell generations. We studied the robustness of this process with differing medium richness and antibiotics stress, which affect nucleoid size, using multimodal, time-lapse microscopy of live cells expressing both a fluorescently tagged chaperone (IbpA), which identifies in vivo the location of aggregates, and HupA-mCherry, a fluorescent variant of a nucleoid-associated protein. We find that the relative sizes of the nucleoid's major and minor axes change widely, in a positively correlated fashion, with medium richness and antibiotic stress. The aggregate's distribution along the major cell axis also changes between conditions and in agreement with the nucleoid exclusion phenomenon. Consequently, the fraction of aggregates at the midcell region prior to cell division differs between conditions, which will affect the degree of asymmetries in the partitioning of aggregates between cells of future generations. Finally, from the location of the peak of anisotropy in the aggregate displacement distribution, the nucleoid relative size, and the spatiotemporal aggregate distribution, we find that the exclusion of detectable aggregates from midcell is most pronounced in cells with mid-sized nucleoids, which are most common under optimal conditions. We conclude that the aggregate management mechanisms of *E. coli* are significantly robust but are not immune to stresses due to the tangible effect that these have on nucleoid size.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Research group: Laboratory of Biosystem Dynamics-LBD, Department of Signal Processing, Laboratory of Biosystem Dynamics, Instituto de Desenvolvimento de Novas Tecnologias

Contributors: Neeli-Venkata, R., Martikainen, A., Gupta, A., Goncalves, N., Fonseca, J., Ribeiro, A. S.

Number of pages: 9

Pages: 898-906

Publication date: 2016

Peer-reviewed: Yes

Publication information

Journal: Journal of Bacteriology

Volume: 198

Issue number: 6

ISSN (Print): 0021-9193

Ratings:

Scopus rating (2016): CiteScore 6.8 SJR 1.943 SNIP 0.893

Original language: English

ASJC Scopus subject areas: Microbiology, Molecular Biology

DOIs:

10.1128/JB.00848-15. Embargo ended: 4/06/16

Bibliographical note

INT=sgn, "Martikainen, Antti"

Source: Scopus

Source ID: 84960429084

Research output: Contribution to journal > Article > Scientific > peer-review

Changes in global gene expression of *Vibrio parahaemolyticus* induced by cold- and heat-stress

Background: *Vibrio* (*V.*) *parahaemolyticus* causes seafood-borne gastro-intestinal bacterial infections in humans worldwide. It is widely found in marine environments and is isolated frequently from seawater, estuarine waters, sediments and raw or insufficiently cooked seafood. Throughout the food chain, *V. parahaemolyticus* encounters different temperature conditions that might alter metabolism and pathogenicity of the bacterium. In this study, we performed gene expression profiling of *V. parahaemolyticus* RIMD 2210633 after exposure to 4, 15, 20, 37 and 42°C to describe the cold and heat shock response. **Methods:** Gene expression profiles of *V. parahaemolyticus* RIMD 2210633 after exposure to 4, 15, 20, 37 and 42°C were investigated via microarray. Gene expression values and RT-qPCR experiments were compared by plotting the log₂ values. Moreover, volcano plots of microarray data were calculated to visualize the distribution of differentially expressed genes at individual temperatures and to assess hybridization qualities and comparability of data. Finally, enriched terms were searched in annotations as well as functional-related gene categories using the Database for Annotation, Visualization and Integrated Discovery. **Results:** Analysis of 37°C normalised transcriptomics data resulted in differential expression of 19 genes at 20°C, 193 genes at 4°C, 625 genes at 42°C and 638 genes at 15°C. Thus, the largest number of significantly expressed genes was observed at 15 and 42°C with 13.3 and 13 %, respectively. Genes of many functional categories were highly regulated even at lower temperatures. Virulence associated genes (*tdh1*, *tdh2*, *toxR*, *toxS*, *vopC*, *T6SS-1*, *T6SS-2*) remained mostly unaffected by heat or cold stress. **Conclusion:** Along with folding and temperature shock depending systems, an overall temperature-dependent regulation of expression could be shown. Particularly the energy metabolism was affected by changed temperatures. Whole-genome gene expression studies of food related pathogens such as *V. parahaemolyticus* reveal how these pathogens react to stress impacts to predict its behaviour under conditions like storage and transport.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Chemistry and Bioengineering, Department of Signal Processing, Freie Universität Berlin, University of Tampere

Contributors: Urmersbach, S., Aho, T., Alter, T., Hassan, S. S., Autio, R., Huehn, S.

Publication date: 23 Oct 2015

Peer-reviewed: Yes

Publication information

Journal: BMC Microbiology

Volume: 15

Issue number: 1

Article number: 229

ISSN (Print): 1471-2180

Ratings:

Scopus rating (2015): CiteScore 5.1 SJR 1.42 SNIP 1.007

Original language: English

ASJC Scopus subject areas: Microbiology, Microbiology (medical)

Keywords: Gene expression, Thermal shock, *Vibrio parahaemolyticus*

DOIs:

10.1186/s12866-015-0565-7

URLs:

<http://www.scopus.com/inward/record.url?scp=84944883751&partnerID=8YFLogxK> (Link to publication in Scopus)

Bibliographical note

ORG=keb,0.5

ORG=sgn,0.5

Source: Scopus

Source ID: 84944883751

Bioluminescent whole-cell reporter gene assays as screening tools in the identification of antimicrobial natural product extracts

We describe novel tools, bioluminescent whole-cell reporter gene assays, for facilitating the use of natural products in antimicrobial drug discovery. As proof-of-concept, a plant extract library was screened and follow-up experiments were carried out. Primary results can be obtained in 2-4. h with high sensitivity, leading to significant improvements of the process.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Centre for Drug Research, Helsinki University, Division of Pharmaceutical Biosciences

Contributors: Nybond, S., Karp, M., Yrjönen, T., Tammela, P.

Number of pages: 3

Pages: 54-56

Publication date: 1 Jul 2015

Peer-reviewed: Yes

Publication information

Journal: Journal of Microbiological Methods

Volume: 114

ISSN (Print): 0167-7012

Ratings:

Scopus rating (2015): CiteScore 3.5 SJR 0.819 SNIP 0.86

Original language: English

ASJC Scopus subject areas: Microbiology, Molecular Biology, Microbiology (medical), Biotechnology

Keywords: Antibacterial, Bioluminescence, Cell-based assay, Escherichia coli, Natural products, Screening

DOIs:

10.1016/j.mimet.2015.04.014

URLs:

<http://www.scopus.com/inward/record.url?scp=84928920094&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84928920094

Research output: Contribution to journal › Article › Scientific › peer-review

Method with high-throughput screening potential for antioxidative substances using Escherichia coli biosensor katG⁺::lux

A new method is described for the rapid real-time screening of antioxidative properties using a recombinant Escherichia coli DPD2511 biosensor. This microplate technique, without time-consuming pre-incubations and handling, has potential for a high-throughput search of bioactive compounds. Special emphasis was given to obtaining highly reliable and repeatable results.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Research group: Industrial Bioengineering and Applied Organic Chemistry, Department of Chemistry and Bioengineering, Tampere University of Technology, Urban circular bioeconomy (UrCirBio), Natural Resources Institute Finland (Luke), Parkano Research Unit

Contributors: Tienaho, J., Sarjala, T., Franzén, R., Karp, M.

Number of pages: 3

Pages: 78-80

Publication date: 2015

Peer-reviewed: Yes

Publication information

Journal: Journal of Microbiological Methods

Volume: 118

Article number: 4723

ISSN (Print): 0167-7012

Ratings:

Scopus rating (2015): CiteScore 3.5 SJR 0.819 SNIP 0.86

Original language: English

ASJC Scopus subject areas: Microbiology, Molecular Biology, Microbiology (medical)

Keywords: Antioxidative activity, Bacterial biosensor, Bioscreening, Microplate technique

DOIs:

10.1016/j.mimet.2015.08.018

Source: Scopus

Source ID: 84941101607

Research output: Contribution to journal › Article › Scientific › peer-review

Positive association between biotin and the abundance of root-feeding nematodes

Biotin is an essential micronutrient needed but not synthesized by animals. We performed a field experiment where we measured biotin levels and the community composition of nematodes in the rhizosphere of two legumes, the native *Lotus corniculatus* and an invasive alien, *Lupinus polyphyllus*. The relative abundance of root-feeding nematodes and the biotin concentration in nematodes were lower in the rhizosphere of the alien. We are the first to show that biotin levels in indigenous nematode populations are associated with the host plant species, and that the difference may affect nematode community.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Multi-scaled biodata analysis and modelling (MultiBAM), University of Helsinki, Karolinska University Hospital, Adult Stem Cells, School of Management (JKK), Pirkanmaan sairaanhoitopiiri

Contributors: Sinkkonen, A., Laitinen, O. H., Leppiniemi, J., Vauramo, S., Hytönen, V. P., Setälä, H.

Number of pages: 3

Pages: 93-95

Publication date: 2014

Peer-reviewed: Yes

Publication information

Journal: Soil Biology and Biochemistry

Volume: 73

ISSN (Print): 0038-0717

Ratings:

Scopus rating (2014): CiteScore 7 SJR 2.348 SNIP 1.835

Original language: English

ASJC Scopus subject areas: Soil Science, Microbiology

Keywords: Avidins, biotin, Invasiveness, *Lotus corniculatus*, *Lupinus polyphyllus*, Nematode abundance

DOIs:

10.1016/j.soilbio.2014.02.002

URLs:

<http://www.scopus.com/inward/record.url?scp=84896056030&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84896056030

Research output: Contribution to journal › Article › Scientific › peer-review

The haloarchaeal MCM proteins: Bioinformatic analysis and targeted mutagenesis of the β 7- β 8 and β 9- β 10 hairpin loops and conserved zinc binding domain cysteines

The hexameric MCM complex is the catalytic core of the replicative helicase in eukaryotic and archaeal cells. Here we describe the first in vivo analysis of archaeal MCM protein structure and function relationships using the genetically tractable haloarchaeon *Haloferax volcanii* as a model system. Hfx. *volcanii* encodes a single MCM protein that is part of the previously identified core group of haloarchaeal MCM proteins. Three structural features of the N-terminal domain of the Hfx. *volcanii* MCM protein were targeted for mutagenesis: the β 7- β 8 and β 9- β 10 β -hairpin loops and putative zinc binding domain. Five strains carrying single point mutations in the β 7- β 8 β -hairpin loop were constructed, none of which displayed impaired cell growth under normal conditions or when treated with the DNA damaging agent mitomycin C. However, short sequence deletions within the β 7- β 8 β -hairpin were not tolerated and neither was replacement of the highly conserved residue glutamate 187 with alanine. Six strains carrying paired alanine substitutions within the β 9- β 10 β -hairpin loop were constructed, leading to the conclusion that no individual amino acid within that hairpin loop is absolutely required for MCM function, although one of the mutant strains displays greatly enhanced sensitivity to mitomycin C. Deletions of two or four amino acids from the β 9- β 10 β -hairpin were tolerated but mutants carrying larger deletions were inviable. Similarly, it was not possible to construct mutants in which any of the conserved zinc binding cysteines was replaced with alanine, underlining the likely importance of zinc binding for MCM function. The results of these studies demonstrate the feasibility of using Hfx. *volcanii* as a model system for reverse genetic analysis of archaeal MCM protein function and provide important confirmation of the in vivo importance of conserved structural features identified by previous bioinformatic, biochemical and structural studies.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Integrated Technologies for Tissue Engineering Research (ITTE), Kobenhavns Universitet, University of Gothenburg, University of St Andrews

Contributors: Kristensen, T. P., Cherian, R. M., Gray, F. C., MacNeill, S. A.

Publication date: 2014

Peer-reviewed: Yes

Publication information

Journal: *Frontiers in Microbiology*

Volume: 5

Issue number: MAR

Article number: 123

ISSN (Print): 1664-302X

Ratings:

Scopus rating (2014): CiteScore 5.5 SJR 1.879 SNIP 1.14

Original language: English

ASJC Scopus subject areas: Microbiology, Microbiology (medical)

Keywords: Archaea, DNA replication, Haloarchaea, *Haloferax volcanii*, MCM helicase, Reverse genetics, Zinc binding domain

DOIs:

10.3389/fmicb.2014.00123

URLs:

<http://www.scopus.com/inward/record.url?scp=84897941838&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84897941838

Research output: Contribution to journal > Article > Scientific > peer-review

Development of microbial populations in the anaerobic hydrolysis of grass silage for methane production

Six batch leach bed (LB) reactors, installed in parallel and connected to a common upflow anaerobic sludge blanket reactor, were fed with grass silage and operated at 35 (\pm 1) °C. The development and distribution of microorganisms, which firmly and loosely attached to solid materials, and presented in the leachate in the LB reactors, were investigated by 16S rRNA gene-based terminal restriction fragment length polymorphism and clone library analyses. The phylotypes and their relative abundance changed in the respective bacterial community throughout the 49-day run and showed differences between the communities. Large numbers of phylotypes were detected from day 10 onwards. On day 17, the majority of phylotypes in the bacterial community firmly attached to solid residues affiliated to the classes Clostridia and Bacteroidetes. There were high numbers of the phylotypes in the leachate bacterial community. They were closely related to members of classes Clostridia, Bacteroidetes, Betaproteobacteria, Alphaproteobacteria, Gammaproteobacteria, and OP10. The Clostridium-like species clearly dominated the bacterial community. Archaea were only found in the solid residues on day 17 and in the leachate on days 10 and 17. The majority of the Archaea fell within the hydrogenotrophic genus *Methanobacterium*. The organism assigned to the acetoclastic genus *Methanosarcina* was only present in the solid residues.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Jyväskylän yliopisto, Jyväskylä Innovation Ltd., University of Jyväskylä

Contributors: Wang, H., Vuorela, M., Keränen, A. L., Lehtinen, T. M., Lensu, A., Lehtomäki, A., Rintala, J.

Number of pages: 11

Pages: 496-506

Publication date: Jun 2010

Peer-reviewed: Yes

Publication information

Journal: *FEMS Microbiology Ecology*

Volume: 72

Issue number: 3

ISSN (Print): 0168-6496

Ratings:

Scopus rating (2010): SJR 1.735 SNIP 1.248

Original language: English

ASJC Scopus subject areas: Ecology, Applied Microbiology and Biotechnology, Microbiology

Keywords: Cellulose hydrolysis, Clone library, Microbial community, Terminal restriction fragment length polymorphism, Two-stage anaerobic digestion

DOIs:

10.1111/j.1574-6941.2010.00850.x

Source: Scopus

Source ID: 77951955628

Research output: Contribution to journal › Article › Scientific › peer-review

Enumeration of methanotrophic bacteria in the cover soil of an aged municipal landfill

The enumeration of methanotrophic bacteria in the cover soil of an aged municipal landfill was carried out using (1) fluorescent in situ hybridization (FISH) with horseradish peroxidase-labeled oligonucleotide probes and tyramide signal amplification, also known as catalyzed reporter deposition-FISH (CARD-FISH), and (2) most probable number (MPN) method. The number of methanotrophs was determined in cover soil samples collected during April–November 2003 from a point with low CH₄ emission. The number of types I and II methanotrophs obtained by CARD-FISH varied from 15 ± 2 to 56 ± 7 × 10⁸ cells g⁻¹ absolute dry mass (adm) of soil and methanotrophs of type I dominated over type II. The average number of methanotrophs throughout the cover soil profile was highest during May–September when the cover soil temperature was above 13°C. Methanotrophs accounted for about 50% of the total bacterial population in the deepest cover soil layer owing to higher availability of substrate (CH₄). A lower number of methanotrophs (7 × 10² to 17 × 10⁵ cells g⁻¹ adm of soil) was determined by the MPN method compared to the CARD-FISH counts, thus confirming previous results that the MPN method is limited to the estimation of the culturable species that can be grown under the incubation conditions used. The number of culturable methanotrophs correlated with the methane-oxidizing activity measured in laboratory assays. In comparison to the incubation-based measurements, the number of methanotrophs determined by CARD-FISH better reflected the actual characteristics of the environment, such as release and uptake of CH₄, temperature, and moisture, and availability of substrates.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Winogradsky Institute of Microbiology, Russian Academy of Sciences, Jyväskylän yliopisto, University of Tampere Institute of Medical Technology, University of Jyväskylä

Contributors: Kallistova, A. Y., Kevbrina, M. V., Nekrasova, V. K., Shnyrev, N. A., Einola, J. K. M., Kulomaa, M. S., Rintala, J. A., Nozhevnikova, A. N.

Number of pages: 9

Pages: 637–645

Publication date: Nov 2007

Peer-reviewed: Yes

Publication information

Journal: Microbial Ecology

Volume: 54

Issue number: 4

ISSN (Print): 0095-3628

Ratings:

Scopus rating (2007): SJR 1.284 SNIP 1.163

Original language: English

ASJC Scopus subject areas: Aquatic Science, Applied Microbiology and Biotechnology, Ecology, Microbiology

DOIs:

10.1007/s00248-007-9219-0

Source: Scopus

Source ID: 35448949974

Research output: Contribution to journal › Article › Scientific › peer-review

Thermophilic anaerobic treatment of industrial process waters and wastewaters

In many water-intensive industries, high manufacturing temperatures generate hot and concentrated process waters and wastewater fractions. Thermophilic anaerobic treatment offers an attractive alternative to the treatment of these hot streams. Thermophilic treatment could be applied as an external treatment system or as an internal purification unit in closed water circuits combined, e.g., with membranes. The benefits of the thermophilic anaerobic process as compared to the mesophilic one would be an increased loading rate and the avoidance of cooling before treatment and reheating if the water is recirculated. We have conducted laboratory- and pilot-scale studies on thermophilic anaerobic treatment of hot process waters and wastewater streams from the pulp and paper industry and from vegetable processing. These studies have demonstrated a successful startup of thermophilic processes using mesophilic inocula. The performance of the anaerobic processes was stable at 55°C as well as at 70°C. At 55°C, the COD removals were comparable to those in mesophilic processes, while at 70°C the removals were slightly lower. Higher loading rates were achieved at 55°C than at 70°C. Acetate was utilized at temperatures as high as 80°C, while propionate conversion was severely limited or completely inhibited at temperatures ≥70°C. Sulfate reduction occurred readily with acetate both at 55 and 70°C.

General information

Publication status: Published
MoE publication type: A1 Journal article-refereed
Organisations: University of Jyväskylä, Jyväskylän yliopisto
Contributors: Rintala, J. A.
Number of pages: 5
Pages: 583-587
Publication date: 1997
Peer-reviewed: Yes

Publication information

Journal: Microbiology
Volume: 66
Issue number: 5
ISSN (Print): 0026-2617
Original language: English
ASJC Scopus subject areas: Microbiology, Applied Microbiology and Biotechnology
Source: Scopus
Source ID: 0006524771
Research output: Contribution to journal › Article › Scientific › peer-review

A two-stage thermophilic anaerobic process for the treatment of source sorted household solid waste

Hydrolysis and acidification of source sorted household solid waste (SSHSW) at 70°C was studied using continuous stirred tank reactor (CSTR). The soluble COD/total initial COD-ratio of the SSHSW increased from 25 to 35% during the CSTR treatment. A thermophilic (55°C) upflow anaerobic sludge blanket (UASB) reactor removed up to 80% of the COD in the liquid fraction of the SSHSW treated at 70°C.

General information

Publication status: Published
MoE publication type: A1 Journal article-refereed
Organisations: The Anaerobic Microbiology/Biotechnology Group, Department of Environmental Science and Engineering, Danmarks Tekniske Universitet, DTU Informatik
Contributors: Rintala, J. A., Ahring, B. K.
Number of pages: 6
Pages: 1097-1102
Publication date: Oct 1994
Peer-reviewed: Yes

Publication information

Journal: Biotechnology Letters
Volume: 16
Issue number: 10
ISSN (Print): 0141-5492
Original language: English
ASJC Scopus subject areas: Microbiology, Applied Microbiology and Biotechnology, Bioengineering, Biotechnology
DOIs:
10.1007/BF01022410
Source: Scopus
Source ID: 0028036651
Research output: Contribution to journal › Article › Scientific › peer-review

Thermophilic anaerobic digestion of source-sorted household solid waste: the effects of enzyme additions

Thermophilic (55°C) methanation of source-sorted household solid waste (HSW) was studied in batch and in continuous experiments. Furthermore, the effects of additions of xylanase, lipase, protease and a mixture of these on the methanation were tested. In the batch studies, comparative assays with active and inactive enzymes were used to elucidate the role of the added enzymes. The results showed that the HSW was readily digestible, up to 400-590 mlCH₄·g⁻¹ volatile solids (VS) was produced. Only with protease added, at a concentration of 1.1 Anson protease units·kg⁻¹ VS was a higher specific methanogenic activity found with active enzymes compared to inactive (autoclaved) enzymes or without enzyme addition. The methane yield by conversion of the HSW in the batch assays and in the reactor studies was not increased by enzyme additions (enzyme mixture).

General information

Publication status: Published
MoE publication type: A1 Journal article-refereed
Organisations: The Anaerobic Microbiology/Biotechnology Group, Department of Biotechnology, Danmarks Tekniske Universitet, DTU Informatik

Contributors: Rintala, J. A., Ahring, B. K.

Number of pages: 4

Pages: 916-919

Publication date: Feb 1994

Peer-reviewed: Yes

Publication information

Journal: Applied Microbiology and Biotechnology

Volume: 40

Issue number: 6

ISSN (Print): 0175-7598

Original language: English

ASJC Scopus subject areas: Microbiology (medical), Microbiology, Bioengineering, Biotechnology

DOIs:

10.1007/BF00173999

Source: Scopus

Source ID: 0028258804

Research output: Contribution to journal › Article › Scientific › peer-review