Two-step bioleaching of copper and gold from discarded printed circuit boards (PCB)

An effective strategy for environmentally sound biological recovery of copper and gold from discarded printed circuit boards (PCB) in a two-step bioleaching process was experimented. In the first step, chemolithotrophic acidophilic Acidithiobacillus ferrivorans and Acidithiobacillus thiooxidans were used. In the second step, cyanide-producing heterotrophic Pseudomonas fluorescens and Pseudomonas putida were used. Results showed that at a 1% pulp density (10. g/L PCB concentration), 98.4% of the copper was bioleached by a mixture of A. ferrivorans and A. thiooxidans at pH 1.0-1.6 and ambient temperature (23. ±. 2. °C) in 7. days. A pure culture of P. putida (strain WCS361) produced 21.5 (±1.5). mg/L cyanide with 10. g/L glycine as the substrate. This gold complexing agent was used in the subsequent bioleaching step using the Cu-leached (by A. ferrivorans and A. thiooxidans) PCB material, 44.0% of the gold was mobilized in alkaline conditions at pH 7.3-8.6, and 30. °C in 2. days. This study provided a proof-of-concept of a two-step approach in metal bioleaching from PCB, by bacterially produced lixiviants.

General information

State: Published
Ministry of Education publication type: A1 Journal article-refereed
Authors: Işildar, A., van de Vossenberg, J., Rene, E. R., van Hullebusch, E. D., Lens, P. N. L.
Pages: 149–157
Publication date: Nov 2016
Peer-reviewed: Yes

Publication information

Journal: Waste Management
Volume: 57
ISSN (Print): 0956-053X
Ratings:
Scopus rating (2016): CiteScore 4 SJR 1.354 SNIP 2.044
Scopus rating (2015): SJR 1.739 SNIP 2.256 CiteScore 4.33
Scopus rating (2014): SJR 1.777 SNIP 2.482 CiteScore 3.43
Scopus rating (2013): SJR 1.822 SNIP 2.435 CiteScore 3.39
Scopus rating (2012): SJR 1.611 SNIP 2.184 CiteScore 2.91
Scopus rating (2011): SJR 1.698 SNIP 2.085 CiteScore 2.99
Scopus rating (2010): SJR 1.555 SNIP 1.78
Scopus rating (2009): SJR 1.502 SNIP 1.899
Scopus rating (2008): SJR 1.378 SNIP 2.13
Scopus rating (2007): SJR 1.035 SNIP 1.767
Scopus rating (2006): SJR 1.046 SNIP 1.749
Scopus rating (2005): SJR 1.059 SNIP 1.65
Scopus rating (2004): SJR 1.289 SNIP 1.939
Scopus rating (2003): SJR 0.847 SNIP 1.269
Scopus rating (2002): SJR 0.561 SNIP 0.874
Scopus rating (2001): SJR 0.456 SNIP 0.696
Scopus rating (2000): SJR 0.271 SNIP 0.451
Scopus rating (1999): SJR 0.262 SNIP 0.479
Original language: English
ASJC Scopus subject areas: Waste Management and Disposal
Keywords: Bioleaching, Copper, Gold, PCB, Secondary resource, Two-step, WEEE
DOIs:
10.1016/j.wasman.2015.11.033
Source: Scopus
Source-ID: 84950236733
Research output: Scientific - peer-review Article

Thermo-catalytic decomposition of methane: The effect of reaction parameters on process design and the utilization possibilities of the produced carbon

The study presents a path for selecting the reaction and reactor parameters of a process applying thermo-catalytic decomposition of methane (TDM). Temperature and catalyst are the main reaction parameters affecting the type of TDM carbon and defining the reaction’s theoretical heat requirement. Secondly, the reaction parameters affect the reactor design including the selection of reactor type and heating source as well as the reactor dimensioning. The reactor dimensioning is discussed by highlighting the methane residence time requirement at different reaction conditions. Finally, the economic value of the TDM products is analyzed. According to the analyses, the reaction temperature and catalyst
have a significant effect on reactor design and on the value and utilization possibilities of the TDM carbon. The prices of carbon products vary greatly as does the global demand of these. The utilization possibilities of carbon highly affect the overall viability of the TDM process and therefore should be carefully considered during process design.

**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 Photorhabdus 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**

State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry
Microbial electrochemical technologies with the perspective of harnessing bioenergy: Maneuvering towards upscaling

Microbial electrochemical technologies have gained much attention in the recent years during which basic research has been carried out to provide proof of concept by utilizing microorganisms for generating bioenergy in an electro redox active environment. However, these bio-electrocatalyzed systems pose significant challenges towards up-scaling and practical applications. Various parameters viz., electrodes, materials, configuration, biocatalyst, reaction kinetics, fabrication and operational costs, resistance for electron transfer etc. will critically govern the performance of microbial catalyzed electrochemical systems. Majorly, the surface area of electrode materials, biofilm coverage on the electrode surface, enrichment of electrochemically active electrode respiring bacteria and reduction reactions at cathode will aid in increasing the reaction kinetics towards the upscaling of microbial electrochemical technologies. Enrichment of electroactive microbial community on anode electrode can be promoted with electrode pretreatment, controlled anode potential or electrical current, external resistance, optimal operation temperature, chemical additions and bioaugmentation. Inhibition of the growth of methanogens also increases the columbic efficiency, an essential parameter that determines the efficacy of bioelectricity generation. Considering the practical implementation of these microbial electrochemical technologies, the current review addresses the challenges and strategies to improve the performance of bio-electrocatalyzed systems with respect to the operational, physico-chemical and biological factors towards scale up. Besides, the feasibility for long term operation, the scope for future research along with the operational and maintenance costs are discussed to provide a broad spectrum on the role of the system components for the implementation of these bio-electrochemical technologies for practical utility.
A study on raw, torrefied, and steam-exploded wood: Fine grinding, drop-tube reactor combustion tests in N\textsubscript{2}/O\textsubscript{2} and CO\textsubscript{2}/O\textsubscript{2} atmospheres, particle geometry analysis, and numerical kinetics modelling

The purpose of this study was to compare the fine grinding properties and combustion behavior of three wood pellet products: raw, torrefied, and steam-exploded wood. The energy required to fine grind the pellets was tested, and so was the geometry and size distribution of the resulting ground products. Out of all the samples the steam-exploded wood pellet required the most energy for grinding. However, it also produced more sphere-like particles compared to the other two types of samples. The combustion behavior of the samples was tested in a laminar drop-tube reactor (DTR). The samples were preground and the particles were sieved with vibration sieves with an opening of 112–125 μm. The pyrolysis process was examined separately at a temperature range of 973–1173 K. The combined pyrolysis and combustion tests were carried out at a reactor temperature of 1123 K. The O\textsubscript{2} concentrations used in the measurements were 3–21 vol-% in either N\textsubscript{2} or CO\textsubscript{2} atmospheres. The initial size distribution of the sample particles as well as their diameter evolution during pyrolysis and combustion was studied by using optical techniques. The surface temperature of the combusting particles was measured with a two-color pyrometer from within the DTR. The density, specific surface area, and pore diameter were measured from the ground samples with a mercury porosimeter. The chemical kinetic parameters, which describe the pyrolysis and char oxidation rates of the samples, were determined by using the data from the measurements.
Chemical and bacterial leaching of metals from a smelter slag in acid solutions

The purpose of this study was to assess the dissolution of Si, Fe, Cu and Zn from a smelter slag sample under acidic chemical and bacterial leaching conditions. The Cu-containing solid phases were Cu-sulfides (57% distribution), fayalite (18%) and metallic Cu (16%). Zn was mostly associated with fayalite, magnetite and Na-silicate phases (Σ94%). Two mixed cultures (HB1 and HB2) were enriched from samples taken from the slag lagoon site at the smelter location. Comparable results of metal dissolution were obtained with the two mixed cultures. The enrichment culture HB1 was characterized further by denaturing gradient gel electrophoresis (DGGE) of polymerase chain reaction amplified 16S rRNA genes. Based on the 16S rRNA gene sequences, culture HB1 contained at least Acidithiobacillus ferrivorans and Alicyclobacillus cycloheptanicus, with sequences of three DGGE bands matching distantly with Alicyclobacillus tolerans and Alicyclobacillus herbarium in the database. Alicyclobacillus spp. have not been previously associated with slag lagoons or slag bioleaching. Approximately 80% Cu and 25% Zn were dissolved from the slag (10% pulp) in shake flasks when S\textsuperscript{0} was provided for the bacteria to produce H\textsubscript{2}SO\textsubscript{4}. Bioleaching in stirred tanks was conducted at controlled pH values and was practiced at pH levels promoting metal dissolution and suppressing iron and silicate solubilization from fayalite and Na-silicate. Chemical leaching at pH 2.3-4.0 did not yield substantial dissolution of valuable metals.
Clashing coalitions: A discourse analysis of an artificial groundwater recharge project in Finland

The purpose of this paper is to increase understanding of the dynamics of knowledge production in the context of large-scale environmental projects causing local conflict. In particular, the paper analyses the discourse coalitions that formed around an artificial groundwater recharge project for the Turku Region in Finland. The material for this study consists of over 400 articles and opinion pieces which were collected from local and regional newspapers between 1999 and 2010. The articles were analysed by using Hajer's [1995. The politics of environmental discourse. Ecological modernisation and the policy process. Oxford, UK: Clarendon] discursive framework, and the analysis was complemented with the concept of knowledge coalition by Van Buuren and Edelenbos [2004. Conflicting knowledge. Why is joint knowledge production such a problem? Science and Public Policy, 31 (4), 289–299]. Results of the study indicate that knowledge coalitions were formed among the researchers, lay residents, and policy-makers, and they all utilised similar expertise-based factual arguments to support their cause. Thus, the paper participates in the academic discussion on the use and interpretation of expert knowledge in environmental policy-making by reshaping the division between experts and lay residents.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Turun Kauppakorkeakoulu
Authors: Kurki, V., Takala, A., Vinnari, E.
Pages: 1317-1331
Publication date: 2016
Peer-reviewed: Yes
Preferential adsorption of Cu in a multi-metal mixture onto biogenic elemental selenium nanoparticles

Preferential adsorption of Cu in wastewaters is desirable as the Cu can then be reprocessed and reused more easily. In this study, biogenic elemental selenium nanoparticles (BioSeNPs) were assessed for their ability to preferentially adsorb Cu from an equimolar mixture containing Cu, Cd and Zn. Variations in metal to BioSeNPs ratios and initial metal solution pH improved the preferential adsorption capacity of BioSeNPs toward Cu, with the ratio of Cu adsorbed to combined Cd and Zn adsorbed varying from 2.3 to 6.6. More than 78% of the added Cu was adsorbed at an initial metal solution pH of 5.2 and metal to BioSeNPs ratio of 0.21mgmg⁻¹ when the ratio of Cu adsorbed to the sum of Cd and Zn adsorbed was 2.3. Infrared spectroscopy revealed that the Cu, Cd and Zn were interacting with the hydroxyl and carboxyl surface functional groups of the BioSeNPs. The modeling of BioSeNPs' acid-base titration revealed the presence of high concentrations of carboxylic groups (C=60.3molkg⁻¹) with a pKₐ of 3.9, providing further evidence of their interaction with Cu. The adsorption of Cu resulted in a lower colloidal stability of the BioSeNPs as indicated by more than 99% retention of added BioSeNPs after adsorption of heavy metals and filtration. BioSeNPs showed a good preferential adsorption capacity toward Cu as compared to other adsorbent. This study provides a proof-of-concept for the preferential adsorption of Cu onto BioSeNPs which are present in the effluent of a bioreactor treating selenium oxyanions containing wastewater.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Tampere University of Technology, Research group: Industrial Bioengineering and Applied Organic Chemistry, Université Paris-Est
Authors: Jain, R., Dominic, D., Jordan, N., Rene, E. R., Weiss, S., van Hullebusch, E. D., Hübner, R., Lens, P. N. L.
Pages: 917–925
Publication date: 2016
Peer-reviewed: Yes
Early online date: 1 Jan 2015

Publication information
Journal: Chemical Engineering Journal
Lignocellulosic biomass has been considered as an important and sustainable source of renewable energy. Cellulose constitutes the major component of the lignocellulosic biomass and also offers maximum recalcitrance towards its fullest utilization. The enzymatic breakdown of cellulose is achieved through cellulases. Diverse forms of microbes including fungi, bacteria, actinomycetes and yeast are known to produce cellulases that have found extensive application in various industries. Due to the current global political unrest over oil prices and the threat of global warming following combustion of fossil fuels, the paradigm of research is now focused on biofuel production from plant biomass. Conventional approaches have not been economically feasible for meeting the demands of the industry. This review provides an update regarding the status of present microbial cellulase production technologies and research with special reference to solid state fermentation and different molecular techniques such as mutagenesis, metabolic engineering and heterologous gene expression of cellulases from different microbial domains with improved catalytic and stability properties. Metagenomic and genomic studies for mining of novel cellulase genes in addition to screening of culturable strains using conventional methods have been advanced. In addition the bottlenecks associated with cellulase production and how the future research needs to be directed to provide a comprehensive technology for the production of cellulases with novel traits for application at an industrial level without economic constraints are discussed.
Our aim was to study the biomass growth of microalga Chlorella vulgaris using diluted human urine as a sole nutrient source. Batch cultivations (21 days) were conducted in five different urine dilutions (1:25-1:300), in 1:100-diluted urine as such and with added trace elements, and as a reference, in artificial growth medium. The highest biomass density was obtained in 1:100-diluted urine with and without additional trace elements (0.73 and 0.60 g L(-1), respectively). Similar biomass growth trends and densities were obtained with 1:25- and 1:300-diluted urine (0.52 vs. 0.48 g VSS L(-1)) indicating that urine at dilution 1:25 can be used to cultivate microalgal based biomass. Interestingly, even 1:300-diluted urine contained sufficiently nutrients and trace elements to support biomass growth. Biomass production was similar despite pH-variation from < 5 to 9 in different incubations indicating robustness of the biomass growth. Ammonium formation did not inhibit overall biomass growth. At the beginning of cultivation, the majority of the biomass consisted of living algal cells, while towards the end, their share decreased and the estimated share of bacteria and cell debris increased.
Mesophilic anaerobic digestion of pulp and paper industry biosludge-long-term reactor performance and effects of thermal pretreatment

The pulp and paper industry wastewater treatment processes produce large volumes of biosludge. Limited anaerobic degradation of lignocellulose has hindered the utilization of biosludge, but the processing of biosludge using anaerobic digestion has recently regained interest. In this study, biosludge was used as a sole substrate in long-term (400 d) mesophilic laboratory reactor trials. Nine biosludge batches collected evenly over a period of one year from a pulp and paper industry wastewater treatment plant had different solid and nutrient (nitrogen, phosphorus, trace elements) characteristics. Nutrient characteristics may vary by a factor of 2-11, while biomethane potentials (BMPs) ranged from 89 to 102 NL CH$_4$ kg$^{-1}$ VS between batches. The BMPs were enhanced by 39-88% with thermal pretreatments at 105-134 °C. Despite varying biosludge properties, stable operation was achieved in reactor trials with a hydraulic retention time (HRT) of 14 d. Hydrolysis was the process limiting step, ceasing gas production when the HRT was shortened to 10 days. However, digestion with an HRT of 10 days was feasible after thermal pretreatment of the biosludge (20 min at 121 °C) due to enhanced hydrolysis. The methane yield was 78 NL CH$_4$ kg$^{-1}$ VS for untreated biosludge and was increased by 77% (138 NL CH$_4$ kg$^{-1}$ VS) after pretreatment.

General information

State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Urban circular bioeconomy (UrCirBio)
Authors: Kinnunen, V., Ylä-Outinen, A., Rintala, J.
Number of pages: 7
Pages: 105-111
Publication date: 15 Dec 2015
Peer-reviewed: Yes
Early online date: 5 Sep 2015

Publication information
Journal: Water Research
Volume: 87
Article number: 11500
ISSN (Print): 0043-1354
Ratings:
Scopus rating (2016): CiteScore 7.49 SJR 2.629 SNIP 2.558
Scopus rating (2015): SJR 2.689 SNIP 2.507 CiteScore 6.63
Scopus rating (2014): SJR 2.957 SNIP 2.727 CiteScore 6.13
Scopus rating (2013): SJR 2.956 SNIP 2.693 CiteScore 6.02
Scopus rating (2012): SJR 2.966 SNIP 2.456 CiteScore 5.15
Fluorescent Protein Toolbox: Protein Engineering Broadens the Range of in vitro and in vivo Applications of Fluorescent Proteins

In the last two decades, fluorescent proteins have become one of the most widely studied and exploited proteins in biochemistry and cell biology. Fluorescent protein is a protein that upon excitation at low wavelength light emits fluorescence at higher wavelength. Its ability to generate high intracellular visibility together with the stable internal fluorophore and non-invasive measurement technologies made it the finest tool to monitor cellular processes and molecular events in living cells at its normal physiological conditions. Protein engineering and identification of novel fluorescent proteins have resulted in the development of color variants ranging from the blue to near-infrared region of the spectrum. Protein engineering has also led to the development of highly stable fluorescent proteins with improved photochemical properties and sensing abilities.

The fluorescent proteins have made a strong impact in cell biology research due to its ability to participate in energy transfer interactions, such as Fluorescence resonance energy transfer (FRET) and thus allowing to measure and study molecular-scale distances and dynamics through changes in fluorescence. Development of novel FRET based techniques, FRET sensors and FRET pairs will provide opportunity to understand the cellular processes and dynamics with high precision at nano-scale level. This thesis focusses on FRET studies by developing novel FRET based sensor, novel FRET pairs and analyzing intramolecular FRET. The study also focuses on analyzing the potential of fluorescent proteins in sensing applications outside the cell environment, an area which has not yet been exploited. This was accomplished by protein engineering of fluorescent proteins with specific objectives followed by steady-state and time-resolved fluorescence spectroscopy measurements.

In one of the specific objective, intramolecular FRET in fluorescent proteins was studied by demonstrating FRET between fluorescent protein and conjugated chemical fluorophores whereby FRET occurs from inside to outside of the protein and vice versa. For this study, novel FRET pairs MDCC–Citrine and Citrine– Alexafluor 568 was generated. FRET analyzed using steady-state and ultra-fast time-resolved spectroscopy measurements revealed strong intramolecular FRET with high efficiencies. To my knowledge, this is the first and only study on bidirectional FRET between fluorescent protein and conjugated chemical labels. This study was made possible by genetically engineering Citrine to incorporate cysteine residues on the surface of the protein and this enabled site-specific bioconjugation of the labels to the fluorescent protein.

The surface exposed cysteine on the fluorescent protein was also exploited in this study to generate self-assembled monolayer (SAM) of Citrine on the surface of etched optical fibers (EOF). The conjugation of Citrine to the surface of EOF demonstrated a proof-of-concept for the use of this bio-conjugated protein in in vitro bio-sensing applications. To the best of our knowledge, this is the first and only study on the formation of fluorescent protein SAM on EOF. Steady-state and fluorescence lifetime measurements confirm the formation of SAM on EOF and revealed that the bioconjugation is site-specific and covalent in nature. The study also demonstrates that the proteins retains its photochemical properties on
bioconjugation and are stable at physiological conditions.

The engineered surface exposed cysteine was further used in this study for the development of a FRET based redox sensor. This was developed aiming to overcome the disadvantages of the current FRET based redox sensors which includes low FRET efficiency and dynamic range, and to monitor the redox status in bacteria. For the sensor development, fluorescent proteins Citrine and Cerulean were genetically engineered to expose reactive cysteine residues on the protein surface. The proteins were fused using a biotinylation domain as a linker to generate the FRET sensor. The redox titrations and the fluorescence measurements confirmed the redox response and reversibility of the sensor. The FRET sensor exhibited high FRET efficiency and dynamic range in intensity based measurements. Intracellular studies with Escherichia coli revealed the capability of the FRET sensor in detecting real-time redox variations at single cell level.

In the final study, novel FRET pairs were developed aiming at improved fluorescence lifetime dynamic range and high FRET efficiency for the use in fluorescence lifetime imaging microscopy (FLIM) studies. The fluorescent protein with the longest reported fluorescence lifetime NowGFP was used as a FRET donor and various red-fluorescent protein variants were screened for the optimal FRET acceptor. Among the FRET pairs screened, NowGFP-tdTomato and NowGFP-mRuby2 were found to be superior FRET pairs with high lifetime dynamic range and FRET efficiency. NowGFP-tdTomato pair was found to have the highest reported Förster radius and fluorescence lifetime dynamic range for any fluorescent protein based FRET pairs yet used in biological studies.

In summary, we have developed novel FRET based tools and in vitro techniques using fluorescent proteins which can assist in deepening the knowledge on intracellular environment and dynamics, and also in developing novel fluorescent protein based sensors which can be used outside the cellular environment.

General information
State: Published
Ministry of Education publication type: G5 Doctoral dissertation (article)
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry
Authors: George Abraham, B.
Number of pages: 92
Publication date: 4 Dec 2015

Publication information
Publisher: Tampere University of Technology
Original language: English

Publication series
Name: Tampere University of Technology. Publication
Publisher: Tampere University of Technology
Volume: 1351
ISSN (Print): 1459-2045
Electronic versions:
george_abraham_1351
Links:

Bibliographical note
Awarding institution: Tampere University of Technology
Research output: Collection of articles › Doctoral Thesis

Metabolic engineering of Acinetobacter baylyi ADP1 for removal of Clostridium butyricum growth inhibitors produced from lignocellulosic hydrolysates
Background: Pretreatment of lignocellulosic biomass can produce inhibitory compounds that are harmful for microorganisms used in the production of biofuels and other chemicals from lignocellulosic sugars. Selective inhibitor removal can be achieved with biodetoxification where microorganisms catabolize the inhibitors without consuming the sugars. We engineered the strictly aerobic Acinetobacter baylyi ADP1 for detoxification of lignocellulosic hydrolysates by removing the gene for glucose dehydrogenase, gcd, which catalyzes the first step in its glucose catabolism. Results: The engineered A. baylyi ADP1 strain was shown to be incapable of consuming the main sugar components of lignocellulosic hydrolysates, i.e., glucose, xylose, and arabinose, but rapidly utilized acetate and formate. Formate was consumed during growth on acetate and by stationary phase cells, and this was enhanced in the presence of a common aromatic inhibitor of lignocellulosic hydrolysates, 4-hydroxybenzoate. The engineered strain tolerated glucose well up to 70 g/l, and the consumption of glucose, xylose, or arabinose was not observed in prolonged cultivations. The engineered strain was applied in removal of oxygen, a gaseous inhibitor of anaerobic fermentations. Co-cultivation with the A. baylyi ADP1 gcd knockout strain under initially aerobic conditions allowed the strictly anaerobic Clostridium butyricum to grow and produce
hydrogen (H₂) from sugars of the enzymatic rice straw hydrolysate. Conclusions: We demonstrated that the model organism of bacterial genetics and metabolism, A. baylyi ADP1, could be engineered to be an efficient biodetoxification strain of lignocellulosic hydrolysates. Only one gene knockout was required to completely eliminate sugar consumption and the strain could be used in production of anaerobic conditions for the strictly anaerobic hydrogen producer, C. butyricum. Because of these encouraging results, we believe that A. baylyi ADP1 is a promising candidate for the detoxification of lignocellulosic hydrolysates for bioprocesses.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Urban circular bioeconomy (UrCirBio), Rhodes University
Authors: Kannisto, M. S., Mangayil, R. K., Shrivastava-Bhattacharya, A., Pletschke, B. I., Karp, M. T., Santala, V. P.
Publication date: 1 Dec 2015
Peer-reviewed: Yes

Publication information
Journal: Biotechnology for Biofuels
Volume: 8
Issue number: 1
Article number: 198
ISSN (Print): 1754-6834
Ratings:
Scopus rating (2016): SJR 1.969 SNIP 1.65 CiteScore 5.89
Scopus rating (2015): SJR 2.409 SNIP 1.89 CiteScore 6.79
Scopus rating (2014): SJR 2.414 SNIP 1.722 CiteScore 5.86
Scopus rating (2013): SJR 2.17 SNIP 1.815 CiteScore 6.21
Scopus rating (2012): SJR 2.15 SNIP 1.849 CiteScore 5.7
Scopus rating (2011): SJR 2.249 SNIP 2.168 CiteScore 6.1
Scopus rating (2010): SJR 1.774 SNIP 1.745
Scopus rating (2009): SJR 1.317 SNIP 1.74
Original language: English
Keywords: Acinetobacter baylyi, Biodetoxification, Biohydrogen, Clostridium butyricum, Metabolic engineering, Rice straw hydrolysate
ASJC Scopus subject areas: Energy(all), Management, Monitoring, Policy and Law, Biotechnology, Applied Microbiology and Biotechnology, Renewable Energy, Sustainability and the Environment
DOI: 10.1186/s13068-015-0389-6
Source: Scopus
Source-ID: 84956930091
Research output: Scientific - peer-review › Article

Preparation and antimicrobial characterization of silver-containing packaging materials for meat
In food technology, antimicrobial packaging materials could inhibit or limit the growth of spoilage bacteria and thus improve the shelf life of packaged products. The present study provides new insights into the preparation and antimicrobial characterization of silver-containing packaging materials and their efficacy against typical meat spoilage bacteria. Antimicrobial efficacy of packaging films produced by coextrusion or liquid flame spray process was determined by bioluminescence imaging and conventional antimicrobial assay. Fresh pork sirloin was packaged in selected films and composition of meat microbiota was analyzed by 16S rRNA amplicon sequencing. Shelf life of meat was not affected by any of the silver-containing packaging films, even though meat microbiota mostly consisted of bacteria that were inhibited or retarded in vitro by nanoscale silver coating. This may be due to different release dynamics of silver ions on meat surfaces compared to the circumstances in the antimicrobial assay or interactions between silver and amino acids.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Materials Science, Research group: Paper Converting and Packaging, Department of Chemistry and Bioengineering, Engineering materials science and solutions (EMASS), Urban circular bioeconomy (UrCirBio), University of Helsinki, Department of Food Hygiene and Environmental Health
Authors: Kuuliala, L., Pippuri, T., Hultman, J., Auvinen, S., Kolppo, K., Nieminen, T., Karp, M., Björkroth, J., Kuusipalo, J., Jääskeläinen, E.
Number of pages: 8
Pages: 53-60
Publication date: 1 Dec 2015
Production of Oleaginous Microbial Biomass by Reusing Wastewaters

Global energy demand continues to increase, which raises the question regarding how to solve the energy crisis caused by diminishing fossil fuels. There is no single alternative energy source that could substitute the fossil fuels, but microbial single cell oils (SCO) could be part of the solution. SCOs can be produced by cultivating microorganisms in wastewater in which nutrients and carbon from the wastewater are used for biomass production. In optimized conditions, microorganisms begin to accumulate lipids, and these lipids can be further refined for the production of biodiesel or renewable diesel. The lipid accumulation of the microorganisms may be enhanced by culturing the microorganisms under stressful conditions. The most commonly used strategy for enhancing lipid accumulation is nitrogen starvation, but it is even more effective when combined with another stress factor, such as moderately increased salinity. In microbial lipid production, the major cost factor is often the substrate needed for the microorganisms. Therefore, utilizing inexpensive substrates and waste materials for the cultivation of oleaginous microorganisms is very desirable. Various wastewaters from municipalities, agriculture, and industrial sources have been studied, and many of these wastewaters have shown the potential for lipid-rich biomass production. Unfortunately, most of the studies have been conducted using sterilized wastewater. In large-scale applications, the sterilization of the wastewater is not cost-effective; therefore, lipid-accumulating microorganisms able to compete with the indigenous microorganisms of the wastewater need to be further studied. The aim of this work was to sustainably produce oleaginous biomass by reusing the carbon and nutrients from wastewaters. This work included an evaluation of the suitability of various wastewaters for lipid-rich biomass production (Paper I), the isolation of yeasts and fungi, which could possibly accumulate lipids by utilizing wastewater as substrate (Paper II), and the determination of the ability of the isolated microorganisms to accumulate lipids by comparing them with known lipid accumulating yeasts (Paper II). Unlike yeasts and fungi, microalgae are able to use an inorganic carbon source for their growth. This feature enables the combination of wastewater and flue gas treatment. Therefore, the growth and lipid accumulation of three microagal species were compared (Paper III), and the suitability of the most potential microagal species for accumulating lipids in sterilized and non-sterilized wastewater was studied (Paper III & IV). Based on the results of this study, palm oil mill effluent (POME) has more potential for lipid production than chemithermomechanical pulp mill effluent (CTMP) or municipal wastewater (MWW) (Paper I). The residual lipids and solids of POME obstructed the analyses of the microbial SCOs. Eukaryotes isolated from POME with agar plates were genetically identified as Candida silvae NRRL Y-6725 (with 100% similarity), Galactomyces geotrichum LMA-20 (with 99.8% similarity), Lecythophora hoffmannni CBS245.38T (with 96.7% similarity), and Graphium penicillioides JCM9300 (with 99.3% similarity) (Paper II). The fungus Graphium penicillioides had a great potential for lipid accumulation based on the comparison study with well-known oleaginous yeast strains (Yarrowia lipolytica DSMZ8212, Cryptococcus curvatus DSMZ70022, & Cryptococcus albicus DSMZ701097) in a synthetic medium (Paper II). Unlike yeasts and fungi, microalgae are able to use an inorganic carbon source for their growth. This feature enables the combination of wastewater and flue gas treatment. Therefore, the growth and lipid accumulation of three microagal species were compared (Paper III), and the suitability of the most potential microagal species for accumulating lipids in sterilized and non-sterilized wastewater was studied (Paper III & IV). Based on the results of this study, palm oil mill effluent (POME) has more potential for lipid production than chemithermomechanical pulp mill effluent (CTMP) or municipal wastewater (MWW) (Paper I). The residual lipids and solids of POME obstructed the analyses of the microbial SCOs. Eukaryotes isolated from POME with agar plates were genetically identified as Candida silvae NRRL Y-6725 (with 100% similarity), Galactomyces geotrichum LMA-20 (with 99.8% similarity), Lecythophora hoffmannni CBS245.38T (with 96.7% similarity), and Graphium penicillioides JCM9300 (with 99.3% similarity) (Paper II). The fungus Graphium penicillioides had a great potential for lipid accumulation based on the comparison study with well-known oleaginous yeast strains (Yarrowia lipolytica DSMZ8212, Cryptococcus curvatus DSMZ70022, & Cryptococcus albicus DSMZ701097) in a synthetic medium (Paper II). The lipid content per dry weight was higher with G. penicillioides compared to C. curvatus after 15 days of incubation (29.1±3.0 wt% vs 20.2±2.9 wt%, Paper II). Unfortunately, the overall lipid concentration was lower due to a lower biomass concentration. G. penicillioides contained more than 20% lipids, so it can be called oleaginous. From the three microalgae isolated from a Taiwanese freshwater area (Chlorella sorokiniana CY1, Chlorella vulgaris CY5, & Chlamydomonas sp. JSC-04), C. vulgaris accumulated more lipids when various media, nitrogen sources, and nitrogen concentrations were studied (Paper III). The C. vulgaris in the BG-11 medium, initially containing 0.38 g NaNO3/L, produced 3.8 g/L biomass and 57.5 wt% lipids after 12 days of incubation. The most suitable wastewater dilution for the lipid accumulation of C. vulgaris on sterilized anaerobically treated piggery wastewater was 5x dilution, which resulted in initial chemical oxygen demand and total
Kjeldahl nitrogen of 75.4 mg/L and 57.4 mg/L, respectively. C. vulgaris was suitable for accumulating lipids on both sterilized and non-sterilized anaerobically treated piggery wastewater (PW) (Paper IV). The highest lipid content and productivity with the non-sterilized wastewater were rather promising (32.5±3.2 wt%, 71.2±2.2 g/L/d). However, under the conditions of these experiments, C. vulgaris excreted dissolved organic carbon (Paper III & IV), and the aim in wastewater treatment is the removal of organic carbon. In summary, this work demonstrates the potential of indigenous eukaryotic microorganisms for lipid-rich biomass production. G. penicillioides isolated from POME has the potential for lipid-rich biomass production in a synthetic medium, which has not been previously reported. Similarly, C. vulgaris has the potential for lipid-rich biomass production in non-sterilized piggery wastewater, while most of the studies in the literature on C. vulgaris and wastewater have been conducted using sterilized wastewater. To enable simultaneous accumulation of lipids and efficient treatment of wastewater, special attention should be focused on the growth conditions.

General information
State: Published
Ministry of Education publication type: G5 Doctoral dissertation (article)
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry
Authors: Marjakangas, J.
Number of pages: 58
Publication date: 28 Nov 2015

Publication information
Publisher: Tampere University of Technology
Original language: English

Publication series
Name: Tampere University of Technology. Publication
Publisher: Tampere University of Technology
Volume: 1348
ISSN (Print): 1459-2045
Electronic versions:
marjakangas_1348
Links:

Bibliographical note
Awarding institution:Tampere University of Technology
Research output: Collection of articles › Doctoral Thesis

Organic Chromophores in Self-Assembled Monolayers and Supramolecular Arrays
Large aromatic chromophores, e.g. phthalocyanines or perylene derivatives are widely used in modern photonic applications. For these systems, well-organized films of the chromophores are very important. One of the ways to ensure the order on molecular level is to bind the organic dyes covalently to a solid substrate with a suitable anchor group. Expanding the concept, multilayered supramolecular assemblies can be built on surfaces as well.

In the present Thesis various chromophores with a capability to anchor onto a solid surface were prepared. Synthesized molecules were porphyrins, phthalocyanines, and perylene mono- and diimides with different substituents. The anchor-surface pairs were of several types, and the chromophores were attached to a surface by one- or two-step methods.

Two of the perylene monoimide derivatives were found to be a perfect basement for construction of multilayered films. Using a metal-ligand interaction it was possible to prepare stable double layers, as well ten molecules thick stable deeply colored multilayer films. The developed approach is versatile and will allow in future to expand the capabilities of molecular film architecture.

General information
State: Published
Ministry of Education publication type: G5 Doctoral dissertation (article)
Organisations: Department of Chemistry and Bioengineering, Research group: Supramolecular photochemistry
Authors: Sariola-Leikas, E.
Number of pages: 58
Publication date: 20 Nov 2015

Publication information
Publisher: Tampere University of Technology
Simultaneous nutrient removal and lipid production with Chlorella vulgaris on sterilized and non-sterilized anaerobically pretreated piggery wastewater

Piggery wastewater is a potent nutrient source for microalgal lipid production. Wastewater has been usually sterilized when used for microalgal cultivation. This is uneconomical in large-scale applications. Therefore, lipid productivity of Chlorella vulgaris CY5 using sterilized and non-sterilized diluted anaerobically pretreated piggery wastewater was studied in batch reactors. The maximum average lipid productivity was obtained after 12 days of incubation and it was higher with the sterilized wastewater than with the non-sterilized one (117g/L/d vs. 91.3g/L/d), due to the higher biomass concentration. Because of the unexpected increase of dissolved organic carbon (DOC) in the cultures, second experiment was conducted to characterize the composition of produced DOC in non-sterilized wastewater. Carbohydrate content increased in the liquid phase but decreased in the biomass after nitrogen had been exhausted. After 12 days of incubation, soluble chemical oxygen demand (COD) was 414±56mg/L, biomass production was 2.8±0.15g/L, and lipid content was 30.3±1.2wt%. Average lipid productivity from day zero to day 12 was 70.5±1.1g/L/d. C. vulgaris removed nutrients from the non-sterilized wastewater and produced oleaginous biomass, although the lipid productivity was higher with sterilized wastewater.
Power generation in fed-batch and continuous up-flow microbial fuel cell from synthetic wastewater

Up-flow bioreactors have the advantages of retaining very high cell density and having high mass transfer efficiency. The recirculation rate could improve the up-flow rate in up-flow bioreactor. A two-chamber UFMFC (up-flow microbial fuel cell) is constructed with flat graphite electrodes and anion exchange membrane for electricity generation. The anode chamber is seeded with compost culture enriched on xylose and operated on synthetic wastewater with 0.5 g/L xylose, external resistance of 100 Ω, at pH 7.0 and 37 °C in fed-batch mode. The cathode chamber in the top of the UFMFC is filled with potassium ferricyanide (pH 7.0) as the electron acceptor. The effects of different recirculation rates of 1.2, 2.4, 4.8 and 7.2 RV (reactor-volumes)/h to increase the mass transfer and electricity production are determined in fed-batch mode. At a recirculation rate of 4.8 RV/h, a power density of 356 ± 24 mW/m² with CE (coulombic efficiency) of 21.3 ± 1.0% is obtained. Decreasing HRT (hydraulic retention time) could improve the electricity production performance of UFMFC in continuous mode. The power generation is increased to 372 ± 20 mW/m², while CE remains at 13.4 ± 0.5% with HRT of 1.7 d and optimum recirculation rate of 4.8 RV/h on continuous mode. Microbial communities were characterized with PCR (polymerase chain reaction) - DGGE (denaturing gradient gel electrophoresis). In the end of the experiment, the biofilm contained both fermenting and exoelectrogenic bacteria, while fermenting and nitrate-reducing bacteria were mainly present in the anodic solutions. Moreover, some changes occurred in the microbial communities of the anodic solutions when the MFCs were switched from fed-batch to continuous mode, while the differences were minor between different recirculation rates in fed-batch mode.
Cultivation of Nannochloropsis for eicosapentaenoic acid production in wastewaters of pulp and paper industry

The eicosapentaenoic acid (EPA) containing marine microalga Nannochloropsis oculata was grown in an effluent from anaerobic digestion of excess activated sludge from a wastewater treatment plant serving a combination of a pulp and a paper mill and a municipality (digester effluent, DE), mixed with the effluent of the same wastewater treatment plant. The maximum specific growth rate and photosynthesis of N. oculata were similar in the DE medium and in artificial sea water medium (ASW) but after 7 days, algae grown in the DE medium contained seven times more triacylglycerols (TAGs) per cell than cells grown in ASW, indicating mild stress in the DE medium. However, the volumetric rate of EPA production was similar in the ASW and DE media. The results suggest that N. oculata could be used to produce EPA, utilizing the nutrients available after anaerobic digestion of excess activated sludge of a pulp and paper mill.

General Information

State: Published
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Urban circular bioeconomy (UrCirBio), University of Turku, Department of Biochemistry/Molecular Plant Biology, Department of Biochemistry/Food Chemistry and Food Development
Authors: Polishchuk, A., Valev, D., Tarvainen, M., Mishra, S., Kinnunen, V., Antal, T., Yang, B., Rintala, J., Tyystjärvi, E.
Number of pages: 8
Pages: 469-476
Publication date: 1 Oct 2015
Peer-reviewed: Yes
Early online date: 2 Jul 2015

Publication Information
Journal: Bioresource Technology
Volume: 193
ISSN (Print): 0960-8524
Ratings:
Scopus rating (2016): CiteScore 5.94 SJR 2.191 SNIP 1.91
Scopus rating (2015): SJR 2.255 SNIP 1.908 CiteScore 5.47
Scopus rating (2014): SJR 2.41 SNIP 2.104 CiteScore 5.3
Scopus rating (2013): SJR 2.412 SNIP 2.503 CiteScore 5.97
Scopus rating (2012): SJR 2.389 SNIP 2.465 CiteScore 5.25
Scopus rating (2011): SJR 2.314 SNIP 2.508 CiteScore 5.56
Scopus rating (2010): SJR 2.086 SNIP 2.355
Scopus rating (2009): SJR 1.912 SNIP 2.231
Scopus rating (2008): SJR 1.734 SNIP 2.732
Scopus rating (2007): SJR 1.529 SNIP 2.423
Scopus rating (2006): SJR 1.315 SNIP 1.98
Measuring the green color of vegetables from digital images using image analysis

When analyzing the color of foods, a measurement device consisting of a digital camera and image analysis software is an attractive alternative to traditional instruments such as spectrophotometers, colorimeters and sensory evaluations. The device enables the measuring of the surface of a sample pixel-by-pixel and offers versatile possibilities for new imaging-based analysis strategies for food research. Our objective was to evaluate if this apparatus could detect differences in colors existing in green vegetables. We showed that the device separated batches of green vegetables and detected color differences that existed in vegetables with different degrees of green color. We demonstrated that this device could measure the color change of green vegetables during heat treatments. We conclude that this experimental setup has the potential to evaluate the healthiness of a diet by analyzing the proportion and quality of green vegetables for use in a serving at a buffet table or dinner plate.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Turun Yliopisto/Turun Biomateriaalikeskus, University of Oslo, Faculty of Medicine, 22.10.2010, University of Turku, Functional Foods Forum
Authors: Manninen, H., Paakki, M., Hopia, A., Franzén, R.
Number of pages: 7
Pages: 1184-1190
Publication date: 1 Oct 2015
Peer-reviewed: Yes
Early online date: 14 Apr 2015

Publication information
Journal: LWT: Food Science and Technology
Volume: 63
Issue number: 2
ISSN (Print): 0023-6438
Ratings:
Scopus rating (2016): SJR 1.323 SNIP 1.534 CiteScore 3.31
Scopus rating (2015): SJR 1.298 SNIP 1.572 CiteScore 3.11
Scopus rating (2014): SJR 1.348 SNIP 1.8 CiteScore 3.12
Scopus rating (2013): SJR 1.365 SNIP 1.824 CiteScore 3.11
Scopus rating (2012): SJR 1.574 SNIP 2.013 CiteScore 3.12
Scopus rating (2011): SJR 1.442 SNIP 1.877 CiteScore 3.18
Scopus rating (2010): SJR 1.347 SNIP 1.508
Scopus rating (2009): SJR 1.171 SNIP 1.223
Scopus rating (2008): SJR 1.087 SNIP 1.209
Scopus rating (2007): SJR 0.874 SNIP 1.21
Scopus rating (2006): SJR 0.767 SNIP 1.204
Scopus rating (2005): SJR 0.51 SNIP 0.967
Effects of anode potentials on bioelectrogenic conversion of xylose and microbial community compositions

The results on the effects of different anode potentials on current densities, coulombic efficiencies and microbial communities are contradictory and have not been studied with xylose, an important constituent of lignocellulosic materials. In this study, the effects of different anode potentials (+0.2, 0 and -0.2V vs. Ag/AgCl) on current generation, xylose degradation and microbial communities were examined with an exoelectrogenic enrichment culture originating from anaerobic sludge. Anode potential of +0.2V (vs. Ag/AgCl) resulted in the highest current density and coulombic efficiency of 1.5±0.2A/m² and 62±11%, respectively, and there was no accumulation of soluble metabolites. With anode potentials of 0 and -0.2V the current densities remained low and acetate, butyrate and propionate were detected in the end of batch runs. Different anode potentials resulted in substantial differences in the anodic bacterial species. At more positive anode potentials, Ochrobactrum intermedium reported to be capable of direct electron transfer dominated. At more negative anode potentials, a known mediator-producer, Alcaligenes faecalis, and Desulfitobacterium hafniense, that has been reported to use mediated electron transfer, were detected. This study shows that the anode potential has a substantial effect on microbial communities and on xylose metabolism.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Urban circular bioeconomy (UrCirBio)
Authors: Kokko, M. E., Mäkinen, A. E., Sulonen, M. L. K., Puhakka, J. A.
Number of pages: 5
Pages: 248-252
Publication date: 5 Sep 2015
Peer-reviewed: Yes
Early online date: 24 Jun 2015

Publication information
Journal: Biochemical Engineering Journal
Volume: 101
ISSN (Print): 1369-703X
Ratings:
Scopus rating (2016): CiteScore 3.16 SJR 0.893 SNIP 1.181
Scopus rating (2015): SJR 0.955 SNIP 1.063 CiteScore 2.75
Scopus rating (2014): SJR 1.059 SNIP 1.226 CiteScore 2.72
Scopus rating (2013): SJR 1.068 SNIP 1.326 CiteScore 3.03
Scopus rating (2012): SJR 1.218 SNIP 1.727 CiteScore 3.15
Scopus rating (2011): SJR 1.21 SNIP 1.347 CiteScore 2.95
Scopus rating (2010): SJR 1.248 SNIP 1.452
Scopus rating (2009): SJR 1.048 SNIP 1.253
Scopus rating (2008): SJR 1.014 SNIP 1.269
Scopus rating (2007): SJR 0.894 SNIP 1.223
Scopus rating (2006): SJR 0.816 SNIP 1.342
Scopus rating (2005): SJR 0.673 SNIP 1.258
Vibrio (V.) parahaemolyticus is an aquatic bacterium capable of causing foodborne gastroenteritis. In the environment or the food chain, V. parahaemolyticus cells are usually forced into the stationary phase, the common phase for bacterial survival in the environment. So far, little is known about whole genomic expression of V. parahaemolyticus in the early stationary phase compared with the exponential growth phase. We performed whole transcriptomic profiling of V. parahaemolyticus cells in both phases (exponential and early stationary phase). Our data showed in total that 172 genes were induced in early stationary phase, while 61 genes were repressed in early stationary phase compared with the exponential phase. Three functional categories showed stable gene expression in the early stationary phase. Eleven functional categories showed that up-regulation of genes was dominant over down-regulation in the early stationary phase. Although genes related to endogenous metabolism were repressed in the early stationary phase, massive regulation of gene expression occurred in the early stationary phase, indicating the expressed gene set of V. parahaemolyticus in the early stationary phase impacts environmental survival.
Searching for a robust strategy for minimizing alkali chlorides in fluidized bed boilers during burning of high SRF-energy-share fuel

To meet the increasing volume of waste to be treated via energy recovery, high SRF-energy-share fuel is being fired in conventional waste-to-energy facilities. In this work, corrosion related risk during firing of 70 e-% share (target fuel) is studied and compared against the base case fuel containing 50 e-% share. Cl and S concentration is highest in the target fuel as a direct result of increasing the proportion of SRF in the fuel mixture. Br, Zn and Pb showed the same trend. Meanwhile, the concentration of Na, K, Al and Si are highly dependent on the type of the SRF fired. The corrosion risk of the base and target fuels are analyzed using the composition of the fine aerosol fraction and deposit samples measured near the vicinity of the superheater. Surprisingly aerosols for the target fuel are less risky - having less Cl and more S, than that of the base fuel. The effects of sulfur based additives - elemental sulfur and sulfate injection, and fuel substitution on the risk of superheater corrosion are likewise analyzed. All these strategies can reduce the concentration of Cl in the aerosols, however it is concluded that sulfate injection is considered as a robust strategy for mitigating alkali chloride formation. Sulfate injection is able to reduce Cl in the aerosols and deposits regardless of the quality of the fuel mixture. Robust strategies are important in ensuring the boiler performance during high SRF-energy share firing. An attempt of linking the quality of the deposits and the properties of the flue gas and aerosols around the superheater using partial least squares regression is also presented.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio), University of Jyväskylä, Valmet Technologies Oy, VTT Technical Research Centre of Finland, Department of Chemistry, Renewable Natural Resources and Chemistry of Living Environment, Stora Enso
Authors: Bajamundi, C. J. E., Vainikka, P., Hedman, M., Silvennoinen, J., Heinanen, T., Taipale, R., Konttinen, J.
Number of pages: 12
Pages: 25-36
Publication date: 1 Sep 2015
Peer-reviewed: Yes

Publication information
Journal: Fuel
Volume: 155
ISSN (Print): 0016-2361
Ratings:
Scopus rating (2016): CiteScore 4.9 SJR 1.744 SNIP 2.179
Scopus rating (2015): SJR 1.809 SNIP 2.125 CiteScore 4.46
Scopus rating (2014): SJR 1.667 SNIP 2.331 CiteScore 4.14
Scopus rating (2013): SJR 1.811 SNIP 2.595 CiteScore 4.31
Scopus rating (2012): SJR 1.852 SNIP 2.465 CiteScore 3.99
Scopus rating (2011): SJR 2.093 SNIP 2.427 CiteScore 4.1
Scopus rating (2010): SJR 1.984 SNIP 2.319
Scopus rating (2009): SJR 2.012 SNIP 2.277
Scopus rating (2008): SJR 1.635 SNIP 2.184
Selecting an indigenous microalgal strain for lipid production in anaerobically treated piggery wastewater

The aim of this study was to select a potential microalgal strain for lipid production and to examine the suitability of anaerobically treated piggery wastewater as a nutrient source for production of lipid-rich biomass with the selected microalgae. Biomass and lipid productivity of three microalgal strains (Chlorella sorokiniana CY1, Chlorella vulgaris CY5 and Chlamydomonas sp. JSC-04) were compared by using different media, nitrogen sources, and nitrogen concentrations. The highest lipid content and productivity (62.5 wt%, 162 mg/L/d) were obtained with C. vulgaris with BG-11 with 62 mg N/L. Secondly, C. vulgaris was cultivated in sterilized, diluted (1–20×), anaerobically treated piggery wastewater. Biomass production decreased and lipid content increased, when wastewater was more diluted. The highest lipid content of 54.7 wt% was obtained with 20× dilution, while the highest lipid productivity of 100.7 mg/L/d with 5× dilution. Piggery wastewater is a promising resource for mass production of oleaginous microalgal biomass.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Urban circular bioeconomy (UrCirBio)
Number of pages: 8
Pages: 369-376
Publication date: Sep 2015
Peer-reviewed: Yes

Publication information
Journal: Bioresource Technology
Volume: 191
ISSN (Print): 0960-8524
Ratings:
Scopus rating (2016): CiteScore 5.94 SJR 2.191 SNIP 1.91
Scopus rating (2015): SJR 2.255 SNIP 1.908 CiteScore 5.47
Scopus rating (2014): SJR 2.41 SNIP 2.104 CiteScore 5.3
Scopus rating (2013): SJR 2.412 SNIP 2.503 CiteScore 5.97
Scopus rating (2012): SJR 2.389 SNIP 2.465 CiteScore 5.25
Scopus rating (2011): SJR 2.314 SNIP 2.508 CiteScore 5.56
Scopus rating (2010): SJR 2.086 SNIP 2.355
Scopus rating (2009): SJR 1.912 SNIP 2.231
Scopus rating (2008): SJR 1.734 SNIP 2.732
Scopus rating (2007): SJR 1.529 SNIP 2.423
Scopus rating (2006): SJR 1.315 SNIP 1.98
Scopus rating (2005): SJR 1.269 SNIP 2.006
Fe2O3-TiO2 nanosystems by a hybrid PE-CVD/ALD approach: controllable synthesis, growth mechanism, and photocatalytic properties

Supported Fe2O3-TiO2 nanocomposites are fabricated by an original vapor phase synthetic strategy, consisting of the initial growth of Fe2O3 nanosystems on fluorine-doped tin oxide substrates by plasma enhanced-chemical vapor deposition, followed by atomic layer deposition of TiO2 overlayers with variable thickness, and final thermal treatment in air. A thorough characterization of the target systems is carried out by X-ray diffraction, atomic force microscopy, field emission-scanning electron microscopy, energy dispersive X-ray spectroscopy, transmission electron microscopy, and X-ray photoelectron spectroscopy. High purity nanomaterials characterized by the co-presence of Fe2O3 (hematite) and TiO2 (anatase), with an intimate Fe2O3-TiO2 contact, are successfully obtained. In addition, photocatalytic tests demonstrate that, whereas both single-phase oxides do not show appreciable activity, the composite systems are able to degrade methyl orange aqueous solutions under simulated solar light, and even visible light, with an efficiency directly dependent on TiO2 overlayer thickness. This finding opens attractive perspectives for eventual applications in wastewater treatment.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Supramolecular photochemistry, Padova University, Padova University and INSTM, Department of Physics and Astronomy, University of Turku, Univ Antwerp, University of Antwerp, EMAT, CNR-IENI and INSTM, Department of Chemistry, Department of Chemical and Pharmaceutical Sciences, ICCOM-CNR Trieste Research Unit - INSTM Research Unit, Trieste University
Authors: Barreca, D., Carraro, G., Warwick, M. E. A., Kaunisto, K., Gasparotto, A., Gombac, V., Sada, C., Turner, S., Van Tendeloo, G., Maccato, C., Fornasier, P.
Number of pages: 8
Pages: 6219-6226
Publication date: 28 Aug 2015
Peer-reviewed: Yes

Publication information
Journal: CrystEngComm
Volume: 17
Issue number: 32
ISSN (Print): 1466-8033
Ratings:
Scopus rating (2016): SJR 1.043 SNIP 0.904 CiteScore 3.37
Scopus rating (2015): SJR 1.063 SNIP 0.999 CiteScore 3.83
Scopus rating (2014): SJR 1.131 SNIP 1.11 CiteScore 3.97
Scopus rating (2013): SJR 1.079 SNIP 1.11 CiteScore 3.81
Scopus rating (2012): SJR 1.253 SNIP 1.142 CiteScore 3.83
Scopus rating (2011): SJR 1.174 SNIP 1.191 CiteScore 3.87
Scopus rating (2010): SJR 1.233 SNIP 1.229
Scopus rating (2009): SJR 1.227 SNIP 1.257
Scopus rating (2008): SJR 1.297 SNIP 1.183
Scopus rating (2007): SJR 1.42 SNIP 1.704
Scopus rating (2006): SJR 1.296 SNIP 1.406
Fluorescent Protein Based FRET Pairs with Improved Dynamic Range for Fluorescence Lifetime Measurements

Fluorescence Resonance Energy Transfer (FRET) using fluorescent protein variants is widely used to study biochemical processes in living cells. FRET detection by fluorescence lifetime measurements is the most direct and robust method to measure FRET. The traditional cyan-yellow fluorescent protein based FRET pairs are getting replaced by green-red fluorescent protein variants. The green-red pair enables excitation at a longer wavelength which reduces cellular autofluorescence and phototoxicity while monitoring FRET. Despite the advances in FRET based sensors, the low FRET efficiency and dynamic range still complicates their use in cell biology and high throughput screening. In this paper, we utilized the higher lifetime of NowGFP and screened red fluorescent protein variants to develop FRET pairs with high dynamic range and FRET efficiency. The FRET variations were analyzed by proteolytic activity and detected by steady-state and time-resolved measurements. Based on the results, NowGFP-tdTomato and NowGFP-mRuby2 have shown high potentials as FRET pairs with large fluorescence lifetime dynamic range. The in vitro measurements revealed that the NowGFP-tdTomato has the highest Forster radius for any fluorescent protein based FRET pairs yet used in biological studies. The developed FRET pairs will be useful for designing FRET based sensors and studies employing Fluorescence Lifetime Imaging Microscopy (FLIM).

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Supramolecular photochemistry, Research group: Industrial Bioengineering and Applied Organic Chemistry, Frontier Photonics, Urban circular bioeconomy (UrCirBio)
Authors: George Abraham, B., Sarkisyan, K. S., Mishin, A. S., Santala, V., Tkachenko, N. V., Karp, M.
Number of pages: 15
Publication date: 3 Aug 2015
Peer-reviewed: Yes

Publication information
Journal: PLoS One
Volume: 10
Issue number: 8
Article number: e013443
ISSN (Print): 1932-6203

Ratings:
Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092
Scopus rating (2015): SJR 1.414 SNIP 1.131 CiteScore 3.32
Scopus rating (2014): SJR 1.545 SNIP 1.141 CiteScore 3.54
Scopus rating (2013): SJR 1.74 SNIP 1.147 CiteScore 3.94
Scopus rating (2012): SJR 1.945 SNIP 1.142 CiteScore 4.15
Scopus rating (2011): SJR 2.369 SNIP 1.23 CiteScore 4.58
Scopus rating (2010): SJR 2.631 SNIP 1.161
Scopus rating (2009): SJR 2.473 SNIP 0.985
Scopus rating (2008): SJR 2.323 SNIP 0.96
Scopus rating (2007): SJR 1.289 SNIP 0.525
Original language: English
Keywords: RESONANCE ENERGY-TRANSFER, IMAGING MICROSCOPY, FORSTER DISTANCES, MONOMERIC RED, LIVING CELLS, LIVE CELLS, BIOSENSORS, SENSOR, FLIM, ENVIRONMENT
Electricity production by a microbial fuel cell fueled by brewery wastewater and the factors in its membrane deterioration

Electricity production from brewery wastewater using dual-chamber microbial fuel cells (MFCs) with a tin-coated copper mesh in the anode was investigated by changing the hydraulic retention time (HRT). The MFCs were fed with wastewater samples from the inlet (inflow, MFC-1) and outlet (outflow, MFC-2) of an anaerobic digester of a brewery wastewater treatment plant. Both chemical oxygen demand removal and current density were improved by decreasing HRT. The best MFC performance was with an HRT of 0.5 d. The maximum power densities of 8.001 and 1.843 µW/cm<sup>2</sup> were obtained from reactors MFC-1 and MFC-2, respectively. Microbial diversity at different conditions was studied using PCR-DGGE profiling of 16S rRNA fragments of the microorganisms from the biofilm on the anode electrode. The MFC reactor had mainly Geobacter, Shewanella, and Clostridium species, and some bacteria were easily washed out at lower HRTs. The fouling characteristics of the MFC Nafion membrane and the resulting degradation of MFC performance were examined. The ion exchange capacity, conductivity, and diffusivity of the membrane decreased significantly after fouling. The morphology of the Nafion membrane and MFC degradation were studied using scanning electron microscopy and attenuated total reflection-Fourier transform infrared spectroscopy.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Portland State University, Department of Civil and Environmental Engineering, Yildiz Technical University
Authors: Çetinkaya, A. Y., Köroğlu, E. O., Demir, N. M., Baysoy, D. Y., Özkaya, B., Çakmakçi, M.
Number of pages: 9
Pages: 1068-1076
Publication date: 20 Jul 2015
Peer-reviewed: Yes

Publication information
Journal: Chinese Journal of Catalysis
Volume: 36
Issue number: 7
ISSN (Print): 0253-9837
Ratings:
Scopus rating (2016): SJR 0.7 SNIP 0.812 CiteScore 2.56
Scopus rating (2015): SJR 0.585 SNIP 0.809 CiteScore 2.24
Scopus rating (2014): SJR 0.514 SNIP 0.735 CiteScore 1.6
Scopus rating (2013): SJR 0.41 SNIP 0.674 CiteScore 1.39
Scopus rating (2012): SJR 0.373 SNIP 0.73 CiteScore 1.32
Scopus rating (2011): SJR 0.373 SNIP 0.69 CiteScore 1.28
Scopus rating (2010): SJR 0.345 SNIP 0.477
Scopus rating (2009): SJR 0.335 SNIP 0.555
Scopus rating (2008): SJR 0.293 SNIP 0.582
Scopus rating (2007): SJR 0.253 SNIP 0.378
Scopus rating (2006): SJR 0.216 SNIP 0.339
Scopus rating (2005): SJR 0.29 SNIP 0.488
Scopus rating (2004): SJR 0.245 SNIP 0.395
Scopus rating (2003): SJR 0.166 SNIP 0.287
Scopus rating (2002): SJR 0.157 SNIP 0.276
Scopus rating (2001): SJR 0.139 SNIP 0.131
Scopus rating (2000): SJR 0.117 SNIP 0.135
Scopus rating (1999): SJR 0.134 SNIP 0.203
Original language: English
ASJC Scopus subject areas: Catalysis, Chemistry(all)
Keywords: Anaerobic processes, Biofilm, Microbial community, Microbial fuel cell, Wastewater treatment
DOIs:
10.1016/S1872-2067(15)60833-6
Column leaching of low-grade sulfide ore from Zijinshan copper mine

Abstract Copper and iron dissolution of Zijinshan low-grade copper sulfide ores was investigated in ore-packed columns. At 60 °C and pH 1.0, 37.1 g Fe(III) L⁻¹ permitted effective copper dissolution and inhibited the activity of iron-oxidizing microorganisms. At 30 °C, microorganisms stimulated Fe(II) and pyrite oxidation, resulting in 85 and 54% of copper and pyrite extraction yields, respectively. Bacteria belonging to the genera Acidithiobacillus and Leptospirillum were dominant as observed by real-time PCR assay. Aeration and inoculation of columns were not necessary. Solutions had a higher pH of 1.7 in the columns operated without recirculation. Under these conditions, copper extraction was not affected and Fe(III) precipitated as jarosite, indicating a novel method for iron control in Zijinshan copper mine.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Urban circular bioeconomy (UrCirBio), Shanghai Institute of Ceramics Chinese Academy of Sciences, Zijin Mining Group Co., Ltd., Institute of Process Engineering, Chinese Academy of Sciences
Authors: Zou, G., Papirio, S., Lai, X., Wu, Z., Zou, L., Puhakka, J., Ruan, R.
Number of pages: 6
Pages: 11-16
Publication date: 15 Jul 2015
Peer-reviewed: Yes

Publication information
Journal: International Journal of Mineral Processing
Volume: 139
Article number: 2730
ISSN (Print): 0301-7516

Ratings:
Scopus rating (2016): SJR 0.795 SNIP 1.518 CiteScore 2.03
Scopus rating (2015): SJR 0.811 SNIP 1.578 CiteScore 1.78
Scopus rating (2014): SJR 0.896 SNIP 1.847 CiteScore 1.8
Scopus rating (2013): SJR 1.145 SNIP 2.272 CiteScore 2.02
Scopus rating (2012): SJR 0.939 SNIP 2.104 CiteScore 1.8
Scopus rating (2011): SJR 0.888 SNIP 1.875 CiteScore 1.74
Scopus rating (2010): SJR 0.936 SNIP 1.348
Scopus rating (2009): SJR 1.066 SNIP 1.856
Scopus rating (2008): SJR 0.769 SNIP 1.395
Scopus rating (2007): SJR 0.822 SNIP 1.18
Scopus rating (2006): SJR 0.926 SNIP 1.384
Scopus rating (2005): SJR 1.14 SNIP 1.693
Scopus rating (2004): SJR 0.738 SNIP 1.736
Scopus rating (2003): SJR 1.203 SNIP 2.233
Scopus rating (2002): SJR 0.7 SNIP 1.418
Scopus rating (2001): SJR 0.545 SNIP 1.182
Scopus rating (2000): SJR 0.447 SNIP 1.175
Scopus rating (1999): SJR 0.831 SNIP 1.188

Original language: English
ASJC Scopus subject areas: Geotechnical Engineering and Engineering Geology, Geochemistry and Petrology
Keywords: Chalcocite, Column bioleaching, Ferric leaching, Jarosite, Temperature

DOI: 10.1016/j.minpro.2015.04.005
Links:
http://www.scopus.com/inward/record.url?scp=84928725349&partnerID=8YFLogxK (Link to publication in Scopus)
Source: Scopus
Source-ID: 84928725349
Lipid production by eukaryotic microorganisms isolated from palm oil mill effluent

Microbial oil production combined with wastewater management is one option for a more sustainable future. Micrographs of microbial cultures enriched from palm oil mill effluent (POME) showed lipid inclusion in the eukaryotic cells, indicating the cells can accumulate lipids. However, enriching the culture did not increase the total lipids. Therefore, eukaryotic microorganisms were isolated from POME to investigate whether these microorganisms are potential lipid producers. Four strains were isolated, and their lipid synthesis capabilities were compared with known oleaginous yeasts in a synthetic oil-free medium. Two strains (identified as Galactomyces geotrichum and Graphium penicillioides) had the potential to accumulate lipid accumulation based on the increase in triacylglycerol content. G. penicillioides was the most promising strain for lipid production as this strain accumulated more lipids than the well-known oleaginous yeast Cryptococcus curvatus (29.1 ± 3.0. wt% vs. 20.2 ± 2.9. wt%). To our knowledge, oil synthesis and accumulation by G. penicillioides have not previously been reported.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Urban circular bioeconomy (UrCirBio), National Cheng Kung University, Center of Bioscience and Biotechnology, Research Center for Energy Technology and Strategy, Neste Oil Oyj
Authors: Marjakangas, J. M., Lakaniemi, A. M., Koskinen, P. E. P., Chang, J. S., Puhakka, J. A.
Number of pages: 7
Pages: 48-54
Publication date: 5 Jul 2015
Peer-reviewed: Yes

Publication information
Journal: Biochemical Engineering Journal
Volume: 99
ISSN (Print): 1369-703X
Ratings:
- Scopus rating (2016): CiteScore 3.16 SJR 0.893 SNIP 1.181
- Scopus rating (2015): SJR 0.955 SNIP 1.063 CiteScore 2.75
- Scopus rating (2014): SJR 1.059 SNIP 1.226 CiteScore 2.72
- Scopus rating (2013): SJR 1.068 SNIP 1.326 CiteScore 3.03
- Scopus rating (2012): SJR 1.218 SNIP 1.727 CiteScore 3.15
- Scopus rating (2011): SJR 1.21 SNIP 1.347 CiteScore 2.95
- Scopus rating (2010): SJR 1.248 SNIP 1.452
- Scopus rating (2009): SJR 1.048 SNIP 1.253
- Scopus rating (2008): SJR 1.014 SNIP 1.269
- Scopus rating (2007): SJR 0.894 SNIP 1.223
- Scopus rating (2006): SJR 0.816 SNIP 1.342
- Scopus rating (2005): SJR 0.673 SNIP 1.258
- Scopus rating (2004): SJR 0.762 SNIP 1.214
- Scopus rating (2003): SJR 0.486 SNIP 1.069
- Scopus rating (2002): SJR 0.549 SNIP 0.88
- Scopus rating (2001): SJR 0.346 SNIP 0.873
- Scopus rating (2000): SJR 0.3 SNIP 0.83
- Scopus rating (1999): SJR 0.316 SNIP 0.684

Original language: English
ASJC Scopus subject areas: Biotechnology, Bioengineering, Biomedical Engineering, Environmental Engineering
Keywords: Filamentous fungi, Lipid accumulation, Microbial growth, Palm oil mill effluent, Physiology, Yeast
DOI: 10.1016/j.bej.2015.03.006
Links:
http://www.scopus.com/inward/record.url?scp=84924943977&partnerID=8YFLogxK (Link to publication in Scopus)
Source: Scopus
Source-ID: 84924943977
Research output: Scientific - peer-review > Article
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.

Selenium biomineralization for biotechnological applications

Selenium (Se) is not only a strategic element in high-tech electronics and an essential trace element in living organisms, but also a potential toxin with low threshold concentrations. Environmental biotechnological applications using bacterial biomineralization have the potential not only to remove selenium from contaminated waters, but also to sequester it in a reusable form. Selenium biomineralization has been observed in phylogenetically diverse microorganisms isolated from pristine and contaminated environments, yet it is one of the most poorly understood biogeochemical processes. Microbial respiration of selenium is unique because the microbial cells are presented with both soluble (SeO₄²⁻ and SeO₃²⁻) and insoluble (Se) forms of selenium as terminal electron acceptor. Here, we highlight selenium biomineralization and the
potential biotechnological uses for it in bioremediation and wastewater treatment.

Characteristics and agronomic usability of digestates from laboratory digesters treating food waste and autoclaved food waste

Digestate characteristics such as organic and nutrient content, hygienic quality and stability are valuable measures when evaluating the use of food waste (FW) digestate as organic fertiliser. This study compared the characteristics of FW and autoclaved (160 °C, 6.2 bar) FW and their digestates from laboratory-scale reactors. Decreased ammonification and low ammonium nitrogen content were observed in the digestate from an autoclaved FW reactor due to autoclave treatment of FW, which affected the nitrogen-containing molecules by formation of Maillard compounds. The methane potential of autoclaved FW and its digestate was decreased by 40% due to reduced microbial activity as microbes were not able to adapt to the conditions within a reactor fed with autoclaved FW. Both studied materials were suitable for agricultural use in terms of their nutrient content, hygienic quality and stability, and thus the decrease in ammonium nitrogen in digestate from an autoclaved FW reactor supported the use of digestate as soil amendment rather than fertiliser.
Gene expression profiles of Vibrio parahaemolyticus in viable but non-culturable state

Viable but non-culturable (VBNC) state is referred to as a dormant state of non-spore-forming bacteria enhancing the survival in adverse environments. To our knowledge, only few studies have been conducted on whole genomic expression of Vibrio parahaemolyticus VBNC state. Since a degradation of nucleic acids in V. vulnificus non-culturable state has been detected, we hypothesize that gene regulation of VBNC cells is highly reduced, downregulation of gene expression is dominant and only metabolic functions crucial for survival are kept on a sustained basis. Hence, we performed the whole transcriptomic profiles of V. parahaemolyticus in three phases (exponential, early stationary phase and VBNC state).

Compared with exponential and early stationary phase, in V. parahaemolyticus VBNC cells we found 509 induced genes and 309 repressed by more than 4-fold among 4820 investigated genes. Upregulation was dominant in most of non-metabolism functional categories, while five metabolism-related functional categories revealed downregulation in VBNC state. To our knowledge, this is the first study of comprehensive transcriptomic analyses of three phases of V. parahaemolyticus RIMD2210633. Although the mechanism of VBNC state is not yet clear, massive regulation of gene expression occurs in VBNC state compared with expression in other two phases, indicating VBNC cells are active.

General information

State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Urban circular bioeconomy (UrCirBio), Natural Resources Institute Finland (Luke)
Authors: Tampio, E., Ervasti, S., Rintala, J.
Number of pages: 7
Pages: 86-92
Publication date: 1 May 2015
Peer-reviewed: Yes
Developing Synthetic Biology Tools and Model Chassis: Production of Bioenergy and High-Value Molecules

One of the aims of synthetic biology is the sustainable production of high-value compounds and bioenergy molecules. Synthetic biologists exploit fundamental engineering principles, such as DNA component standardization, modular genetic circuits, and de novo design, to create novel production pathways and products. A well-characterized host cell serves as the chassis for the system construction; generally, the model bacterium Escherichia coli is applied. However, the metabolism and characteristics of E. coli are not ideal for all applications. Furthermore, many E. coli based systems are patent protected which restricts the use in forthcoming application. Acinetobacter baylyi ADP1 is a potential alternative host for synthetic biology. The metabolism and genetics of the strain are well-understood, and the engineering of its genome is technically straight-forward. The versatile and unusual metabolic pathways, including those producing long chain hydrocarbons, can be rerouted, modified, and integrated into novel ones. I exploited A. baylyi ADP1 as a model host for the production of high-value hydrocarbons, triacylglycerols and wax esters. I employed metabolic engineering, novel molecular monitoring tools, and synthetic pathway design to improve the production, and to demonstrate the utility of ADP1 as a synthetic biology host. In particular, the production of triacylglycerols was improved over 5-folds by targeted gene deletions which resulted in redirected carbon flux towards the product and elimination of competitive pathways. The long-chain hydrocarbon metabolism, including alcohol and wax ester biosynthesis, is not yet fully understood. These pathways are regulated through several mechanisms sensitive to specific environmental conditions and the cellular states. However, the lack of robust and straight-forward analysis tools has restricted the studies of lipid metabolism and
production kinetics. I developed a simple in vivo tool for the investigation of the long chain hydrocarbon metabolism in real-time. The tool is based on a light-producing reporter enzyme, bacterial luciferase. The enzyme utilizes a specific intermediate of the hydrocarbon synthesis pathway as a substrate for bioluminescence production. Initially, the tool was applied for monitoring the wax ester metabolism of A. baylyi ADP1. Subsequently, I modified the monitoring tool for studying the degradation of alkanes. The studies suggest that the tool can be applied for production optimization in different hosts and for a variety of products. I also reconstructed the wax ester synthesis pathway of A. baylyi ADP1 by replacing a natural key enzyme with an alternative well-characterized component, enabling a regulated production of unnatural wax esters. Bioprocess control and scale-up of production systems are challenging. Multispecies cultures are suggested to improve the robustness and performance of bacterial production processes. I exploited the metabolic versatility of A. baylyi ADP1 to construct a rationally engineered synthetic coculture with E. coli. The designed coculture exhibited improved biomass and recombinant protein production compared to the pure culture of E. coli. To conclude, I have shown that the strain ADP1 is a suitable host for synthetic biology applications, especially for long-chain hydrocarbon production, the development of novel tools for metabolic studies, and for exploiting the existing unusual metabolic networks of the cell. Thus, further studies of the remaining challenges related to ADP1 bioprocess and as-of-yet uncharacterized cell mechanisms, are warranted.
and interactive effects on microbial growth, metabolism and hydrogenase enzyme. Hydrogenases are metalloenzymes that reversibly catalyzes proton reduction to $H_2$, and are divided into three classes based on the metal cofactor at the active site, [Fe-Fe], [Ni-Fe] and [Fe] hydrogenase. Among the hydrogenase classes, [Fe-Fe] hydrogenases exhibit highest catalytic activity involving mostly in $H_2$ production. Apart from their pivotal role in fermentative $H_2$ production, [Fe-Fe] hydrogenases promise an alternative catalyst choice in fuel cells. However, in spite of their preference towards $H_2$ production, [Fe-Fe] hydrogenases are extremely prone to catalytic inactivation upon oxygen exposure. This is the major challenge, at the protein level, that hinders a cost-effective approach for biotechnological applications and suggests the requirement of targeted tools to investigate the inactivation process at the molecular level. The purpose of the present study was to investigate bio$H_2$ production in protein to community level perspective. More specifically the aims were to (1) establish an anaerobic biopanning procedure to enrich antibody binders specific against clostridial [Fe-Fe] hydrogenase protein, (2) develop and standardize a novel enrichment system, (3) implement the enrichment technique to enrich functional inoculum capable of degrading complex substrates, (4) enrich crude glycerol fermenting microbial community and finally, (5) optimize the physico-chemical factors influencing fermentative $H_2$ production for efficient bioprocess. In the present study, biopanning with synthetic ‘mixed’ single chain variable fragment (scFv) libraries against active and inactive clostridial [Fe-Fe] hydrogenases aided the enrichment of anti-hydrogenase antibodies. Out of ninety four (from inactive hydrogenase) and ninety two (from active hydrogenase) random clones screened, nine potential antibody clones with recognition specificity towards Clostridium acetobutylicum [Fe-Fe] hydrogenase were selected. The enriched binders also recognized [Fe-Fe] hydrogenase from C. butyricum. Based on the results from this study, it could be reasoned that the binders with generic specificity against closely related clostridial [Fe-Fe] hydrogenases can be used as novel molecular tools for quantitative monitoring [Fe-Fe] hydrogenases at the protein level. Another of note observation was the specificity of the antibody binders towards active and inactive hydrogenases. Preliminary experiments indicated 7Ac binder (enriched against active hydrogenase) specificity towards the catalytically active [Fe-Fe] hydrogenase rather to the inactive state and 48In (enriched against inactive hydrogenase) recognized both catalytic states. These findings indicate the possibility to apply the isolated antibody clones for functional detection of clostridial [Fe-Fe] hydrogenases. The study progresses in investigating bio$H_2$ production in perspective of microbial community. The novel microbial enrichment system was developed and the proof-of-principle experiments conducted using artificial mixed microbial community and varied selection criteria allowed the enrichment of the best $H_2$ producer. The system was implemented in enriching cellulosic degrading $H_2$ producer from an environmental sample. The bacterial strain isolated by spread plate technique on agar plates containing CMC was affiliated with Citrobacter sp. and named as Citrobacter sp. CMC-1. Citrobacter sp. CMC-1 utilized glucose, cellubiose and CMC and followed mixed-acid fermentation profile producing $H_2$ and carbon dioxide ($CO_2$) as gaseous metabolites and acetate, formate, lactate and ethanol as liquid metabolites. At optimized values of cultivation conditions ($pH$ 6.0 and 34 $˚C$) the $H_2$ yield was 1.82 mol-$H_2$/mol-glucose. The isolate efficiently fermented monomeric hemi-cellulose sugars to $H_2$ (mol-$H_2$/mol-substrate): Galactose, 1.18; Mannose, 1.23; Xylose, 1.22; Arabinose, 0.94 and Rhamnose, 1.01. Except for arabinose, an increase in cultivation period improved the biomass and $H_2$ yield (mol-$H_2$/mol-substrate): Galactose, 1.68; Mannose, 1.93 and Xylose, 1.63) followed with observations of reduced formate accumulation in the medium, indicating that Citrobacter sp. CMC-1 produced $H_2$ from formate breakdown via the FHL complex. Microbial community pre-dominated with Clostridium spp. enriched from activated sludge fermented crude glycerol mainly to $H_2$, $CO_2$, acetate, butyrate and ethanol. Optimal bioprocess conditions for the enriched inoculum were experimentally observed to be $pH$ 6.5, 40 $˚C$ and 1g/L crude glycerol. The $H_2$ yield from raw glycerol at optimal cultivation conditions was 1.1 mol-$H_2$/mol-glycerol consumed. At elevated crude glycerol concentrations, substrate utilization and $H_2$ production were limited due to the presence of impurities in the crude glycerol fraction. The bioconversion of crude glycerol to $H_2$ was further improved by statistical optimization of the growth medium composition. Initial screening with Plackett – Burman design identified $NH_4Cl$, $K_2HPO_4$ and $KH_2PO_4$ with individual and interactive effects on $H_2$ yield. Among the three identified media components, $NH_4Cl$ and $KH_2PO_4$ imparted the maximal significance and were optimized in scrutiny. A series of statistical models identified the optimal media composition for improved $H_2$ production from crude glycerol fermentations and were successful in improving the $H_2$ yield by 29% (1.42 mol-$H_2$/mol-glycerol consumed ) in comparison to previously reported value (1.1 mol-$H_2$/mol-glycerol consumed ).
Fluidized-bed denitrification of mining water tolerates high nickel concentrations

This study revealed that fluidized-bed denitrifying cultures tolerated soluble Ni concentrations up to 500mg/L at 7-8 and 22°C. From 10 to 40mg/L of feed Ni, denitrification resulted in complete nitrate and nitrite removal. The concomitant reduction of 30mg/L of sulfate produced 10mg/L of sulfide that precipitated nickel, resulting in soluble effluent Ni below 22mg/L. At this stage, Dechloromonas species were the dominant denitrifying bacteria. From 60 to 500mg/L of feed Ni, nickel remained in solution due to the inhibition of sulfate reduction. At soluble 60mg/L of Ni, denitrification was partially inhibited prior to recover after 34days of enrichment by other Ni-tolerant species (including Delftia, Zoogloea and Azospira) that supported Dechloromonas. Subsequently, the FBR cultures completely removed nitrate even at 500mg/L of Ni. Visual Minteq speciation model predicted the formation of NiS, NiCO3 and Ni3(PO4)2, whilst only Ni3(PO4)2 was detected by XRD.

General information

State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Urban circular bioeconomy (UrCirBio), Université Paris-Est, Laboratoire Géomatériaux et Environnement (EA 4508), UPEM
Authors: Zou, G., Papirio, S., van Hullebusch, E. D., Puhakka, J. A.
Number of pages: 7
Pages: 284-290
Publication date: 1 Mar 2015
Peer-reviewed: Yes

Publication information

Journal: Bioresource Technology
Volume: 179
ISSN (Print): 0960-8524
Ratings:
- Scopus rating (2016): CiteScore 5.94 SJR 2.191 SNIP 1.91
- Scopus rating (2015): SJR 2.255 SNIP 1.908 CiteScore 5.47
- Scopus rating (2014): SJR 2.41 SNIP 2.104 CiteScore 5.3
- Scopus rating (2013): SJR 2.412 SNIP 2.503 CiteScore 5.97
- Scopus rating (2012): SJR 2.389 SNIP 2.465 CiteScore 5.25
- Scopus rating (2011): SJR 2.314 SNIP 2.508 CiteScore 5.56
- Scopus rating (2010): SJR 2.086 SNIP 2.355
- Scopus rating (2009): SJR 1.912 SNIP 2.231
- Scopus rating (2008): SJR 1.734 SNIP 2.732
- Scopus rating (2007): SJR 1.529 SNIP 2.423
- Scopus rating (2006): SJR 1.315 SNIP 1.98
- Scopus rating (2005): SJR 1.269 SNIP 2.006
- Scopus rating (2004): SJR 1.197 SNIP 1.659
- Scopus rating (2003): SJR 0.948 SNIP 1.639
Improved bioconversion of crude glycerol to hydrogen by statistical optimization of media components

Bioconversion of crude glycerol to hydrogen has gained importance as it addresses both sustainable energy production and waste disposal issues. Until recently, statistical optimizations of crude glycerol bioconversion to hydrogen have been greatly focused on pure strains. In this study, biohydrogen production from crude glycerol by an enriched microbial culture (predominated with Clostridium species) was improved by statistical optimization of media components. Plackett-Burman design identified MgCl\textsubscript{2}.6H\textsubscript{2}O and KCl with negative effect on hydrogen production and selected NH\textsubscript{4}Cl, K\textsubscript{2}HPO\textsubscript{4} and KH\textsubscript{2}PO\textsubscript{4} as significant variables. Box-Behnken design indicated the optimal region beyond design area and studies were continued by ridge analysis. Central composite face centered design envisaged a maximal hydrogen yield of 1.41mol-H\textsubscript{2}/mol-glycerol\textsubscript{consumed} at concentrations 4.40g/L and 2.27g/L for NH\textsubscript{4}Cl and KH\textsubscript{2}PO\textsubscript{4} respectively. Confirmation experiment with the optimized media (NH\textsubscript{4}Cl, 4.40g/L; K\textsubscript{2}HPO\textsubscript{4}, 1.6g/L; KH\textsubscript{2}PO\textsubscript{4}, 2.27g/L; MgCl\textsubscript{2}, 6H\textsubscript{2}O, 1.0g/L; KCl, 1.0g/L; Na-acetate, 3H\textsubscript{2}O, 1.0g/L and tryptone, 2.0g/L) revealed an excellent correlation between predicted and experimental hydrogen yield. Optimization of media components by design of experiments enhanced hydrogen yield by 29%.

General information

State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Tampere University of Technology, Department of Signal Processing, Urban circular bioeconomy (UrCirBio)
Authors: Mangayil, R., Aho, T., Karp, M., Santala, V.
Number of pages: 7
Pages: 583-589
Publication date: 1 Mar 2015
Peer-reviewed: Yes

Publication information
Journal: Renewable Energy
Volume: 75
ISSN (Print): 0960-1481
Ratings:
Scopus rating (2016): CiteScore 4.83 SJR 1.697 SNIP 2.044
Scopus rating (2015): SJR 1.845 SNIP 2.118 CiteScore 4.51
Scopus rating (2014): SJR 1.983 SNIP 2.687 CiteScore 4.51
Scopus rating (2013): SJR 2.066 SNIP 2.767 CiteScore 4.63
Scopus rating (2012): SJR 1.852 SNIP 2.745 CiteScore 3.97
Scopus rating (2011): SJR 1.688 SNIP 2.404 CiteScore 3.9
Scopus rating (2010): SJR 1.494 SNIP 2.215
Scopus rating (2009): SJR 1.305 SNIP 1.945
Scopus rating (2008): SJR 1.449 SNIP 1.867
Scopus rating (2007): SJR 1.214 SNIP 1.65
Scopus rating (2006): SJR 1.137 SNIP 1.486
Scopus rating (2005): SJR 1.215 SNIP 1.26
Scopus rating (2004): SJR 0.76 SNIP 1.154
Scopus rating (2003): SJR 0.965 SNIP 0.948
Integrated in vitro-in silico screening strategy for the discovery of antibacterial compounds

Multidrug-resistant bacterial infections are an increasing source of healthcare problems, and the research for new antibiotics is currently unable to respond to this challenge. In this work, we present a screening strategy that integrates cell-based high-throughput screening (HTS) with in silico analogue search for antimicrobial small-molecule drug discovery. We performed an HTS on a diverse chemical library by using an assay based on a bioluminescent Escherichia coli K-12 (pTetLux1) strain. The HTS yielded eight hit compounds with >50% inhibition. These hits were then used for structural similarity-based virtual screening, and of the 29 analogues selected for in vitro testing, four compounds displayed potential activity in the pTetLux1 assay. The 11 most active compounds from combined HTS and analogue search were further assessed for antimicrobial activity against clinically important strains of E. coli and Staphylococcus aureus and for in vitro cytotoxicity against human cells. Three of the compounds displayed antibacterial activity and low human cell cytotoxicity. Additionally, two compounds of the set fully inhibited S. aureus growth after 24 h, but also exhibited human cell cytotoxicity in vitro.
Glycerol as an Efficient Medium for the Petasis Borono-Mannich Reaction

The multicomponent Petasis borono-Mannich (PBM) reaction is a useful tool for the preparation of complex molecules in a single step from boronic acids, aldehydes/ketones, and amines. Here, we describe the use of glycerol in the PBM reaction of salicylaldehydes or 2-pyridinecarbaldehyde with several boronic acids and secondary amines. From these readily available starting materials, alkylaminophenols, 2-substituted pyridines, and 2H-chromenes were prepared in reasonable to good yields. Glycerol was compared with other solvents, and in some cases, it provided the reaction product in higher yield. Crude glycerol, as generated by the biodiesel industry, was evaluated and found to be a suitable solvent for the PBM reaction, successfully expanding the potential use of this industry by-product. Based on density functional theory (DFT) calculations and the obtained experimental results, the involvement of glycerol-derived boronic esters in the reaction mechanism is suggested to be competitive with the free boronic acid pathway. Similar Gibbs free energies for the aryl migration from the boronate species to the iminium were determined for both mechanisms.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Research group: Industrial Bioengineering and Applied Organic Chemistry, Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio), Univ Lisbon, Fac Farm, Inst Invest Medicamento iMed ULisboa
Authors: Rosholm, T., Gois, P. M. P., Franzen, R., R. Candeias, N.
Number of pages: 8
Pages: 39-46
Publication date: Feb 2015
Peer-reviewed: Yes

Publication information
Journal: Chemistryopen
Volume: 4
Issue number: 1
ISSN (Print): 2191-1363
Ratings:
Scopus rating (2016): SJR 1.034 SNIP 0.66 CiteScore 2.54
Scopus rating (2015): SJR 1.278 SNIP 0.742 CiteScore 3.23
Scopus rating (2014): SJR 0.913 SNIP 0.775 CiteScore 2.72
Scopus rating (2013): SJR 0.111 SNIP 0
Original language: English
Keywords: amines, boron, glycerol, multicomponent reactions, sustainable chemistry, CROSS-COUPLING REACTIONS, ALPHA-AMINO-ACIDS, ONE-POT, ORGANOBORONIC ACIDS, SOLVENT, DERIVATIVES, ALDEHYDES, HYDROGEN, SALICYLALDEHYDES, 2H-CHROMENES
DOIs:
10.1002/open.201402066

Bibliographical note
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Source: WOS
Source-ID: 000349953300006
Research output: Scientific - peer-review › Article

Aryl end-capped quaterthiophenes applied as anode interfacial layers in inverted organic solar cells
Four aryl end-capped quaterthiophene derivatives were synthesized and their material properties were studied by computational, spectroscopic, electrochemical, and thermoanalytical methods. Compounds were applied as interfacial
layers between the bulk heterojunction active layer and Ag anode in inverted organic solar cells. Results show that p-
cyanophenyl end-capped quaterthiophene with hexyl side chains increases both the short circuit current density and
power conversion efficiency notably compared to reference interlayer material, tris-(8-hydroxyquinoline)aluminum. The
improved cell performance was attributed to the optimal positions of the highest occupied molecular orbital and the lowest
occupied molecular orbital (LUMO) of this material, relative to those of the photactive electron donor poly(3-
hexylthiophene) and Ag anode, and evenly distributed LUMO. In addition, the use of these materials as an anode
interfacial layer increases the absorption of the solar cell, which could contribute to the formation of excitons and additional
current production by the cell.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Supramolecular photochemistry, Frontier Photonics, University of Oulu, Department of Chemistry and Mathematics, Faculty of Petroleum and Mining Engineering, Suez University
Number of pages: 11
Pages: 196-206
Publication date: 1 Jan 2015
Peer-reviewed: Yes

Publication Information
Journal: Thin Solid Films
Volume: 574
ISSN (Print): 0040-6090
Ratings:
Scopus rating (2016): CiteScore 1.83 SJR 0.64 SNIP 0.897
Scopus rating (2015): SJR 0.705 SNIP 0.98 CiteScore 1.84
Scopus rating (2014): SJR 0.73 SNIP 1.115 CiteScore 1.94
Scopus rating (2013): SJR 0.818 SNIP 1.215 CiteScore 2
Scopus rating (2012): SJR 0.899 SNIP 1.162 CiteScore 1.86
Scopus rating (2011): SJR 0.995 SNIP 1.337 CiteScore 2.13
Scopus rating (2010): SJR 1.141 SNIP 1.235
Scopus rating (2009): SJR 1.142 SNIP 1.221
Scopus rating (2008): SJR 1.191 SNIP 1.282
Scopus rating (2006): SJR 1.147 SNIP 1.318
Scopus rating (2005): SJR 1.173 SNIP 1.246
Scopus rating (2004): SJR 1.188 SNIP 1.308
Scopus rating (2003): SJR 1.231 SNIP 1.282
Scopus rating (2002): SJR 1.175 SNIP 1.14
Scopus rating (2001): SJR 1.032 SNIP 1.032
Scopus rating (2000): SJR 0.99 SNIP 0.924
Scopus rating (1999): SJR 0.914 SNIP 0.862
Original language: English
Keywords: Anode interfacial layer, Bulk heterojunction, Computational research, Inverted organic solar cell, Oligothiophene, Spectroscopy, Suzuki-Miyaura
ASJC Scopus subject areas: Electronic, Optical and Magnetic Materials, Materials Chemistry, Metals and Alloys, Surfaces, Coatings and Films, Surfaces and Interfaces
DOIs:
10.1016/j.tsf.2014.12.007
Links:
http://www.scopus.com/inward/record.url?scp=84921286591&partnerID=8YFLogxK (Link to publication in Scopus)
Source: Scopus
Source-ID: 84921286591
Research output: Scientific - peer-review › Article

Biological Nitrogen Removal from Acidic, Heavy-metal Containing Waters
Chemolithotrophic denitrification in biofilm reactors

Chemolithotrophic denitrification is an inexpensive and advantageous process for nitrate removal and represents a promising alternative to classical denitrification with organics. Chemolithotrophic denitrifiers are microorganisms able to reduce nitrate and nitrite using inorganic compounds as source of energy. Ferrous iron, sulfur-reduced compounds (e.g. hydrogen sulfide, elemental sulfur and thiosulfate), hydrogen gas, pyrite and arsenite have been used as inorganic electron donors resulting in diverse outcomes. In the last 40 years, a large number of engineered systems have been used to maintain chemolithothrophic denitrification and improve rate and efficiency of the process. Among them, biofilm reactors proved to be robust and high-performing technologies. Packed bed reactors are particularly suitable for the removal of low nitrate concentrations, since high retention times are required to complete denitrification. Fluidized bed and membrane biofilm reactors result in the highest denitrification rates (>20kg N-NO₃/m³d) when hydrogen gas and sulfur reduced compounds are used as electron donors. Hydrogen gas pressure and current intensity rule the performance of membrane biofilm and biofilm electrode reactors, respectively. Biofouling is the most common and detrimental issue in biofilm reactors. Bed fluidization and hydrogen supply limitation are convenient and effective solutions to mitigate biofouling.
Combination of a novel electrode material and artificial mediators to enhance power generation in an MFC

This study focuses on two main aspects: developing a novel cost-effective electrode material and power production from domestic wastewater using three different mediators. Methylene blue (MB), neutral red (NR) and 2-hydroxy-1,4-naphthoquinone (HNQ) were selected as electrode mediators with different concentrations. A tin-coated copper mesh electrode was tested as anode electrode. Maximum power density of the microbial fuel cell (MFC) with 300 μM MB was 636 mW/m². Optimal mediator concentrations with respect to the achieved maximum power output for MB, NR and HNQ were 300 μM, 200 μM and 50 μM, respectively. The results demonstrate that tin-coated copper mesh showed a higher biocompatibility and electrical conductivity.
Metal laden wastes and contamination pose a threat to ecosystem well being and human health. Metal containing waste streams are also a valuable resource for recovery of precious and scarce elements. Although biological methods are inexpensive and effective for treating metal wastewaters and in situ bioremediation of metal(loid) contamination, little progress has been made towards metal(loid) recovery. Bioelectrochemical systems are emerging as a new technology platform for removal and recovery of metal ions from metallurgical wastes, process streams and wastewaters. Biodegradation of organic matter by electroactive biofilms at the anode has been successfully coupled to cathodic reduction of metal ions. Until now, leaching of Co(II) from LiCoO$_2$ particles, and removal of metal ions i.e. Co(II/III), Cr(VI), Hg(II), Ag(I), Se(IV), and Cd(II) from aqueous solutions has been demonstrated. This article reviews the state of art research of bioelectrochemical systems for removal and recovery of metal(loid) ions and pertaining removal mechanisms.

**General information**

State: Published
Ministry of Education publication type: A2 Review article in a scientific journal
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Urban circular bioeconomy (UrCirBio), CSIR-Indian Institute of Chemical Technology, Bhabha Atomic Research Centre
Authors: Nancharaiah, Y. V., Venkata Mohan, S., Lens, P.
Number of pages: 13
Pages: 102-114
Publication date: 2015
Peer-reviewed: Yes
Early online date: 17 Jun 2015

**Publication information**

Journal: Bioresource Technology
Volume: 195
ISSN (Print): 0960-8524
Ratings:
Scopus rating (2016): CiteScore 5.94 SJR 2.191 SNIP 1.91
Scopus rating (2015): SJR 2.255 SNIP 1.908 CiteScore 5.47
Scopus rating (2014): SJR 2.41 SNIP 2.104 CiteScore 5.3
Scopus rating (2013): SJR 2.412 SNIP 2.503 CiteScore 5.97
Scopus rating (2012): SJR 2.389 SNIP 2.465 CiteScore 5.25
Scopus rating (2011): SJR 2.314 SNIP 2.508 CiteScore 5.56
Scopus rating (2010): SJR 2.086 SNIP 2.355
Scopus rating (2009): SJR 1.912 SNIP 2.231
Scopus rating (2008): SJR 1.734 SNIP 2.732
Scopus rating (2007): SJR 1.529 SNIP 2.423
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.
Rationally engineered synthetic coculture for improved biomass and product formation

In microbial ecosystems, bacteria are dependent on dynamic interspecific interactions related to carbon and energy flow. Substrates and end-metabolites are rapidly converted to other compounds, which protects the community from high concentrations of inhibitory molecules. In biotechnological applications, pure cultures are preferred because of the more straightforward metabolic engineering and bioprocess control. However, the accumulation of unwanted side products can limit the cell growth and process efficiency. In this study, a rationally engineered coculture with a carbon channeling system was constructed using two well-characterized model strains Escherichia coli K12 and Acinetobacter baylyi ADP1. The directed carbon flow resulted in efficient acetate removal, and the coculture showed symbiotic nature in terms of substrate utilization and growth. Recombinant protein production was used as a proof-of-principle example to demonstrate the coculture utility and the effects on product formation. As a result, the biomass and recombinant protein titers of E. coli were enhanced in both minimal and rich medium simple batch cocultures. Finally, harnessing both the strains to the production resulted in enhanced recombinant protein titers. The study demonstrates the potential of rationally engineered cocultures for synthetic biology applications.
Biohydrogen production in extreme conditions: A comprehensive study of the fermentative metabolism of a polyextremophilic bacterium

Dark fermentation is a potential carbon neutral process that exploits fermentative microorganisms to convert renewable organic substrates (e.g., lignocellulosic biomass and wastes) to H2, a non-fuel commodity and an ideal and clean energy carrier for replacing fossil fuels in the future. In the quest for developing a robust and efficient dark fermentative process for H2 production at industrial scale, the organism(s) selected to carry out the bioconversion is crucial. Thermophilic anaerobic bacteria have been drawing attention because they come close to meet the features that an ideal H2-producing organism should possess, including efficient breakdown and conversion of complex organic substrates to H2. In this study, a novel microorganism, Caloramator celer (former Thermobrachium celere), was evaluated for its potential to produce H2 from organic substrates. C. celer is a strict anaerobic, alkalitolerant, thermophilic bacterium capable of converting glucose to H2, CO2, acetate, ethanol and formate by mixed acid fermentation. In addition, C. celer shows remarkable features such as an extremely elevated growth rates (doubling time of 10 minutes) and the ability to grow in extreme conditions (Topt= 67 °C; pH67°Copt= 8.2). For these reasons C. celer may be of industrial interest for the conversion of organic waste material to H2 in an open (non-sterile) bioprocess system. However, for a biotechnological exploitation of this bacterium for H2 production it is crucial to understand the factors that regulate carbon and electron flux and therefore the final distribution of metabolites to channel the metabolic flux towards the desired product. The general goal of this study is to investigate the fermentative and energy metabolism of C. celer in order to understand how factors pertaining to the fermentation process can alter the metabolic fluxes. This is achieved by determining the relationship between fermentation conditions, physiological state, genome content, gene expression, metabolic fluxes and end-product yields through the combination of multiple methodologies such as conventional one-factor-at-a-time optimization, batch fermentations, comparative and functional genomics, transcription analysis and metabolic flux analysis. The final goal is to identify the optimal process conditions and metabolic state that maximize the H2 production from C. celer. In this study, glucose fermentation of C. celer was characterized in controlled and non-controlled cultivations and the effect of several parameters on growth and fermentation of C. celer was investigated to identify the optimal conditions for H2 production. In addition, the inhibitory effect of high concentrations of substrate and soluble end-products on growth and H2 production was studied to assess the robustness of C. celer. The whole genome sequence provided valuable information for interpretation of experimental results and for directing experimental design. Genomic data were employed to design transcriptional analysis, construct a stoichiometric model employed in metabolic flux analysis (MFA), and infer the network topology and possible regulatory mechanisms that dictate metabolic fluxes. End-product synthesis profiles, and consequently H2 production, changed in response to several modifications of the culture conditions namely growth rate, growth phase, iron content in the medium, substrate availability and nutrient content, presence of soluble metabolites, pH and H2 concentration. The distribution of the fluxes at key metabolic nodes was found to be a function of thermodynamics as well as several physiological factors including genome content, growth and glycolytic rate, need for maintaining intracellular redox and pH homeostasis and only to some extent control of gene expression. The synthesis of formate and ethanol, two products of the branched metabolism of C. celer, was found to compete with H2-evolving reactions for the disposal of reducing equivalents. Ethanol and formate production served as an alternative to H2 production for regulating the redox state when hydrogenases were inhibited. Moreover, formate synthesis was strictly linked to the growth rate suggesting its possible role in anabolic metabolism. Low growth rates, low substrate availability and nutrient content, high iron availability, presence of subinhibitory concentration of acetate and ethanol, slightly acidic pH and low H2 concentrations minimized the redirection of carbon and electron flow to ethanol and formate synthesis and thus favored efficient H2 production. Kinetics of growth and H2 production were inhibited, albeit to different degrees, by high concentration of substrate and soluble end-products, whereas H2 yields remained marginally affected even in presence of considerable concentration of inhibitors. Acetate, the main soluble metabolite of the fermentation, inhibited H2 productivity due to the increasing ionic strength in the medium, rather than the uncoupling effect of the undissociated form. The critical substrate and salt concentration estimated for C. celer suggests that this organism is not particularly osmotolerant. In conclusion, this study provides valuable information on the capabilities of C. celer to efficiently produce H2 as well as on its limitations through a comprehensive investigation of its fermentative and energy metabolism. C. celer showed a great metabolic flexibility that allows redistribution of fluxes at key metabolic nodes to simultaneously control redox state and efficiently harvest energy from substrate even under unfavorable conditions. Understanding how fermentation conditions control the metabolic fluxes contributes to expand the knowledge of the thermophilic dark fermentative H2 production process.

General information
State: Published
Ministry of Education publication type: G5 Doctoral dissertation (article)
Organisations: Department of Chemistry and Bioengineering
Authors: Ciranna, A.
Number of pages: 220
Publication date: 29 Aug 2014

Publication information
Place of publication: Tampere
Publisher: Tampere University of Technology
ISBN (Print): 978-952-15-3328-0
Bioprocessing of enhanced cellulase production from a mutant of Trichoderma asperellum RCK2011 and its application in hydrolysis of cellulose

A mutant strain of Trichoderma asperellum RCK2011 was developed through UV-irradiation for enhanced cellulase production and lower catabolite repression. The production of FPase, CMCase and β-glucosidase was optimized under solid state fermentation; up to 20 mM of glucose did not inhibit cellulase production. The mutant strain T. asperellum SR1-7 produced FPase (2.2 IU/gds), CMCase (13.2 IU/gds), and β-glucosidase (9.2 IU/gds) under optimized conditions, which is, 1.4, 1.3, 1.5-fold higher than the wild type. The wild as well as mutant strain produced the cellulases at pH range, 4.0-10.0. Saccharification of pretreated corn cob, wheat straw, and sugarcane bagasse by cellulase from mutant strain SR1-7 resulted in release of reducing sugar at the rate of 530.0 mg/g, 290.0 mg/g, and 335.0 mg/g of substrate, respectively; this is 1.6-fold higher than the wild type strain. © 2014 Published by Elsevier Ltd.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Tampere University of Technology, Urban circular bioeconomy (UrCirBio), Department of Microbiology, University of Delhi South Campus, Lignocellulose Biotechnology Laboratory
Authors: Raghuwanshi, S., Deswal, D., Karp, M., Kuhad, R. C.
Number of pages: 7
Pages: 183-189
Publication date: 15 May 2014
Peer-reviewed: Yes

Publication information
Journal: Fuel
Volume: 124
ISSN (Print): 0016-2361
Ratings:
Scopus rating (2016): CiteScore 4.9 SJR 1.744 SNIP 2.179
Scopus rating (2015): SJR 1.809 SNIP 2.125 CiteScore 4.46
Scopus rating (2014): SJR 1.667 SNIP 2.331 CiteScore 4.14
Scopus rating (2013): SJR 1.811 SNIP 2.595 CiteScore 4.31
Scopus rating (2012): SJR 1.852 SNIP 2.465 CiteScore 3.99
Scopus rating (2011): SJR 2.093 SNIP 2.427 CiteScore 4.1
Scopus rating (2010): SJR 1.984 SNIP 2.319
Scopus rating (2009): SJR 2.012 SNIP 2.277
Scopus rating (2008): SJR 1.635 SNIP 2.184
Scopus rating (2007): SJR 1.383 SNIP 1.86
Scopus rating (2006): SJR 1.278 SNIP 1.64
Scopus rating (2005): SJR 1.623 SNIP 1.73
Scopus rating (2004): SJR 1.273 SNIP 1.883
Scopus rating (2003): SJR 1.103 SNIP 1.481
Scopus rating (2002): SJR 1.13 SNIP 1.301
Inhibitory effects of substrate and soluble end products on biohydrogen production of the alkalithermophile Caloramator celer: Kinetic, metabolic and transcription analyses

In this study the tolerance of the alkalithermophile Caloramator celer towards substrate (glucose) and soluble end product (acetate, formate and ethanol) inhibition was assessed employing nonlinear inhibition models. In addition, the effects of subinhibitory concentrations of end products on fermentative metabolism and regulation of 12 key genes involved in pyruvate catabolism were studied. Optimal growth and H₂ production were found at 50 mM of glucose and the critical substrate concentration was observed at 290-360 mM. Two inhibition models revealed that ethanol had a higher inhibitory effect on growth rate, whereas H₂ production kinetics was more sensitive towards increasing concentrations of acetate and formate. Acetate, the main soluble metabolite of the fermentation, inhibited the H₂ production by increasing the ionic strength in the medium. Subinhibitory concentrations of soluble end products induced changes in the metabolite profile of C. celer, specifically exogenous acetate (80 mM) and ethanol (40 mM) slightly increased the H₂ yield by 4 and 7%, respectively. However, despite the observed metabolic shifts, gene regulation was minimal and not always in agreement with the measured product yields. Overall, the results suggest that further optimization of the H₂ production process from C. celer should focus on methods to evolve adapted osmotolerant strains and/or remove soluble metabolites, especially acetate, from the culture. Copyright © 2014, Hydrogen Energy Publications, LLC. Published by Elsevier Ltd. All rights reserved.
Assessment of metabolic flux distribution in the thermophilic hydrogen producer Caloramator celer as affected by external pH and hydrogen partial pressure

Background: Caloramator celer is a strict anaerobic, alkalitolerant, thermophilic bacterium capable of converting glucose to hydrogen (H$_2$), carbon dioxide, acetate, ethanol and formate by a mixed acid fermentation. Depending on the growth conditions C. celer can produce H$_2$ at high yields. For a biotechnological exploitation of this bacterium for H$_2$ production it is crucial to understand the factors that regulate carbon and electron fluxes and therefore the final distribution of metabolites to channel the metabolic flux towards the desired product.

Results: Combining experimental results from batch fermentations with genome analysis, reconstruction of central carbon metabolism and metabolic flux analysis (MFA), this study shed light on glucose catabolism of the thermophilic alkalitolerant bacterium C. celer. Two innate factors pertaining to culture conditions have been identified to significantly affect the metabolic flux distribution: culture pH and partial pressures of H$_2$ ($P_{H2}$). Overall, at alkaline to neutral pH the rate of biomass synthesis was maximized, whereas at acidic pH the lower growth rate and the less efficient biomass formation are accompanied with more efficient energy recovery from the substrate indicating high cell maintenance possibly to sustain intracellular pH homeostasis. Higher H$_2$ yields were associated with fermentation at acidic pH as a consequence of the lower synthesis of other reduced by-products such as formate and ethanol. In contrast, $P_{H2}$ did not affect the growth of C. celer on glucose. At high $P_{H2}$ the cellular redox state was balanced by rerouting the flow of carbon and electrons to ethanol and formate production allowing unaltered glycolytic flux and growth rate, but resulting in a decreased H$_2$ synthesis.

Conclusion: C. celer possesses a flexible fermentative metabolism that allows redistribution of fluxes at key metabolic nodes to simultaneously control redox state and efficiently harvest energy from substrate even under unfavorable conditions (i.e. low pH and high $P_{H2}$). With the H$_2$ production in mind, acidic pH and low $P_{H2}$ should be preferred for a high yield-oriented process, while a high productivity-oriented process can be achieved at alkaline pH and high $P_{H2}$. © 2014 Ciranna et al.; licensee BioMed Central Ltd.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Tampere University of Technology, Urban circular bioeconomy (UrCirBio), Lunds Universitet / Lunds Tekniska Högskola, Lund Univ, Lund University, Department of Applied Microbiology
Authors: Ciranna, A., Pawar, S. S., Santala, V., Karp, M., van Niel, E. W. J.
Publication date: 28 Mar 2014
Peer-reviewed: Yes

Publication information
Journal: Microbial Cell Factories
Volume: 13
Issue number: 1
Article number: 48
ISSN (Print): 1475-2859
Ratings:
Rewiring the wax ester production pathway of acinetobacter baylyi ADP1

Wax esters are industrially relevant high-value molecules. For sustainable production of wax esters, bacterial cell factories are suggested to replace the chemical processes exploiting expensive starting materials. However, it is well recognized that new sophisticated solutions employing synthetic biology toolbox are required to improve and tune the cellular production platform to meet the product requirements. For example, saturated wax esters with alkanol chain lengths C12 or C14 that are convenient for industrial uses are rare among bacteria. Acinetobacter baylyi ADP1, a natural producer of wax esters, is a convenient model organism for studying the potentiality and modifiability of wax esters in a natural host by means of synthetic biology. In order to establish a controllable production platform exploiting well-characterized biocomponents, and to modify the wax ester synthesis pathway of A. baylyi ADP1 in terms product quality, a fatty acid reductase complex LuxCDE with an inducible arabinose promoter was employed to replace the natural fatty acyl-CoA reductase acr1 in ADP1. The engineered strain was able to produce wax esters by the introduced synthetic pathway. Moreover, the fatty alkanol chain length profile of wax esters was found to shift toward shorter and more saturated carbon chains, C16:0 accounting for most of the alkanols. The study demonstrates the potentiality of recircuiting a biosynthesis pathway in a natural producer, enabling a regulated production of a customized bioproduct. Furthermore, the LuxCDE complex can be potentially used as a well-characterized biopart in a variety of synthetic biology applications involving the production of long-chain hydrocarbons. © 2014 American Chemical Society.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Research area: Design, Development and LCM, Urban circular bioeconomy (UrCirBio), Neste Oil Oyj
Authors: Santala, S., Efimova, E., Koskinen, P., Karp, M. T., Santala, V.
Number of pages: 7
Pages: 145-151
Publication date: 21 Mar 2014
Peer-reviewed: Yes

Publication information
Journal: ACS Synthetic Biology
Volume: 3
Issue number: 3
ISSN (Print): 2161-5063
Anaerobic digestion of autoclaved and untreated food waste

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Tampio, E., Ervasti, S., Paavola, T., Heaven, S., Banks, C., Rintala, J.
Number of pages: 8
Pages: 370-377
Publication date: 2014
Peer-reviewed: Yes

Publication information
Journal: Waste Management
Volume: 34
Issue number: 2
ISSN (Print): 0956-053X

Ratings:
Scopus rating (2016): CiteScore 4.7
Scopus rating (2015): SJR 2.736 SNIP 1.024 CiteScore 4.41
Scopus rating (2014): SJR 3.783 SNIP 1.219 CiteScore 3.84
Scopus rating (2013): SJR 1.796 SNIP 0.859 CiteScore 3.42
Original language: English
ASJC Scopus subject areas: Biochemistry, Genetics and Molecular Biology (miscellaneous), Biomedical Engineering, Medicine(all)
Keywords: Acinetobacter baylyi ADP1, fatty-acyl CoA reductase, long chain aldehyde, luxCDE, recircuiting, wax ester
DOIs:
10.1012/sb4000788
Links:
http://www.scopus.com/inward/record.url?scp=84896925324&partnerID=8YFLogxK (Link to publication in Scopus)

Bibliographical note
Contribution: organisation=keb,FACT1=1<br/>Portfolio EDEND: 2014-02-15<br/>Publisher name: American Chemical Society
Source: researchoutputwizard
Source-ID: 1454
Research output: Scientific - peer-review › Article
Bacterial and chemical leaching of chalcopyrite concentrates as affected by the redox potential and ferric/ferrous iron ratio at 22 °C

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Bevilaqua, D., Lahti-Tommila, H., Garcia Jr., O., Puhakka, J. A., Tuovinen, O. H.
Number of pages: 7
Pages: 1-7
Publication date: 2014
Peer-reviewed: Yes

Publication information
Journal: International Journal of Mineral Processing
Volume: 132
ISSN (Print): 0301-7516
Ratings:
Scopus rating (2016): SJR 0.795 SNIP 1.518 CiteScore 2.03
Scopus rating (2015): SJR 0.811 SNIP 1.578 CiteScore 1.78
Scopus rating (2014): SJR 0.896 SNIP 1.847 CiteScore 1.8
Scopus rating (2013): SJR 1.145 SNIP 2.272 CiteScore 2.02
Scopus rating (2012): SJR 0.939 SNIP 2.104 CiteScore 1.8
Scopus rating (2011): SJR 0.888 SNIP 1.875 CiteScore 1.74
Scopus rating (2010): SJR 0.936 SNIP 1.348
Scopus rating (2009): SJR 1.066 SNIP 1.856
Scopus rating (2008): SJR 0.769 SNIP 1.395
Scopus rating (2007): SJR 0.822 SNIP 1.18
Scopus rating (2006): SJR 0.926 SNIP 1.384
Scopus rating (2005): SJR 1.14 SNIP 1.693
Scopus rating (2004): SJR 0.738 SNIP 1.736
Scopus rating (2003): SJR 1.203 SNIP 2.233
Scopus rating (2002): SJR 0.7 SNIP 1.418
Scopus rating (2001): SJR 0.545 SNIP 1.182
Scopus rating (2000): SJR 0.447 SNIP 1.175
Scopus rating (1999): SJR 0.831 SNIP 1.188
Original language: English
DOI: 10.1016/j.minpro.2014.08.008

Bibliographical note
Contribution: organisation=keb,FACT1=1
Portfolio EDEND: 2014-09-22
Publisher name: Elsevier BV
Source: researchoutputwizard
Source-ID: 165
Research output: Scientific - peer-review » Article

Biosensors, Antibiotics and Food

General information
State: Published
Ministry of Education publication type: A3 Part of a book or another research book
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Urban circular bioeconomy (UrCirBio)
Dark fermentative hydrogen production from lignocellulosic hydrolyzates - A review

Authors: Nissilä, M. E., Lay, C., Puhakka, J. A.
Number of pages: 15
Pages: 145-159
Publication date: 2014

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Nissilä, M. E., Lay, C., Puhakka, J. A.
Number of pages: 15
Pages: 145-159
Publication date: 2014
Peer-reviewed: Yes

Publication information
Journal: Biomass & Bioenergy
Volume: 67
ISSN (Print): 0961-9534
Ratings:
Scopus rating (2016): CiteScore 3.71 SJR 1.188 SNIP 1.368
Scopus rating (2015): SJR 1.521 SNIP 1.615 CiteScore 4.03
Scopus rating (2014): SJR 1.888 SNIP 1.985 CiteScore 4.36
Scopus rating (2013): SJR 1.678 SNIP 1.823 CiteScore 4.42
Scopus rating (2012): SJR 1.545 SNIP 1.743 CiteScore 3.66
Scopus rating (2011): SJR 1.793 SNIP 2.283 CiteScore 4.74
Scopus rating (2010): SJR 1.931 SNIP 2.254
Scopus rating (2009): SJR 1.743 SNIP 2.187
Scopus rating (2008): SJR 1.609 SNIP 2.073
Scopus rating (2007): SJR 1.454 SNIP 1.77
Scopus rating (2006): SJR 1.292 SNIP 1.954
Scopus rating (2005): SJR 1.226 SNIP 1.398
Scopus rating (2004): SJR 1.037 SNIP 1.637
Scopus rating (2003): SJR 0.693 SNIP 1.312
Scopus rating (2002): SJR 0.442 SNIP 0.764
Scopus rating (2001): SJR 0.468 SNIP 0.994
Scopus rating (2000): SJR 0.429 SNIP 0.903
Dynamics of microbial communities in untreated and autoclaved food waste anaerobic digesters

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Blasco, L., Kahala, M., Tampio, E., Ervasti, S., Paavola, T., Rintala, J., Joutsjoki, V.
Number of pages: 7
Pages: 3-9
Publication date: 2014
Peer-reviewed: Yes

Publication information
Journal: Anaerobe
Volume: 29
ISSN (Print): 1075-9964
Ratings:
Scopus rating (2016): SJR 0.958 SNIP 0.94 CiteScore 2.75
Scopus rating (2015): SJR 1.109 SNIP 1.002 CiteScore 2.77
Scopus rating (2014): SJR 1.015 SNIP 1.173 CiteScore 2.77
Scopus rating (2013): SJR 1.094 SNIP 1.074 CiteScore 2.68
Scopus rating (2012): SJR 0.98 SNIP 0.943 CiteScore 2.48
Scopus rating (2011): SJR 0.899 SNIP 0.95 CiteScore 2.48
Scopus rating (2010): SJR 0.872 SNIP 1.052
Scopus rating (2009): SJR 0.674 SNIP 0.852
Scopus rating (2008): SJR 0.601 SNIP 0.724
Scopus rating (2007): SJR 0.623 SNIP 0.736
Scopus rating (2006): SJR 0.388 SNIP 0.564
Scopus rating (2005): SJR 0.32 SNIP 0.443
Scopus rating (2004): SJR 0.428 SNIP 0.524
Scopus rating (2003): SJR 0.349 SNIP 0.449
Scopus rating (2002): SJR 0.259 SNIP 0.264
Scopus rating (2001): SJR 0.399 SNIP 0.375
Scopus rating (2000): SJR 0.485 SNIP 0.831
Scopus rating (1999): SJR 0.528 SNIP 0.469
Original language: English
DOIs:
10.1016/j.anaerobe.2014.04.011

Bibliographical note
Contribution: organisation=keb,FACT1=1<br/>Portfolio EDEND: 2014-06-27<br/>Publisher name: Academic Press; Anaerobe Society of the Americas, Inc.
Source: researchoutputwizard
Source-ID: 178
Research output: Scientific - peer-review › Article

Effect of arsenic on nitrification of simulated mining water

General information
Fluidized-bed denitrification for mine waters. Part II: effects of Ni and Co

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Zou, G., Papirio, S., Ylinen, A., Di Capua, F., Lakaniemi, A., Puhakka, J.
Number of pages: 7
Pages: 417-423
Publication date: 2014
Peer-reviewed: Yes

Publication information
Journal: BIODEGRADATION
Volume: 25
ISSN (Print): 0923-9820
Ratings:
Scopus rating (2016): SJR 0.804 SNIP 1.069 CiteScore 2.41
Fluorescent protein-based FRET sensor for intracellular monitoring of redox status in bacteria at single cell level

Monitoring of intracellular redox status in a bacterial cell provides vital information about the physiological status of the cell, which can be exploited in several applications such as metabolic engineering and computational modeling. Fluorescent protein-based genetically encoded sensors can be used to monitor intracellular oxidation/reduction status. This study reports the development of a redox sensor for intracellular measurements using fluorescent protein pairs and the phenomenon of Förster resonance energy transfer (FRET). For the development of the sensor, fluorescent proteins Citrine and Cerulean were genetically modified to carry reactive cysteine residues on the protein surface close to the chromophore and a constructed FRET pair was fused using a biotinylation domain as a linker. In oxidized state, the FRET pairs are in close proximity by labile disulfide bond formation resulting in higher FRET efficiency. In reducing environment, the FRET is diminished due to the increased distance between FRET pairs providing large dynamic measurement range to the sensor. Intracellular studies in Escherichia coli mutants revealed the capability of the sensor in detecting real-time redox variations at single cell level. The results were validated by intensity based and time resolved measurements. The functional immobilization of the fluorescent protein-based FRET sensor at solid surfaces for in vitro applications was also demonstrated. [Figure not available: see fulltext.]
Mesophilic and thermophilic anaerobic laboratory-scale digestion of Nannochloropsis microalga residues

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Kinnunen, H., Koskinen, P., Rintala, J.
Number of pages: 9
Pages: 314-322
Publication date: 2014
Peer-reviewed: Yes

Publication information
Journal: Bioresource Technology
Volume: 155
ISSN (Print): 0960-8524
Ratings:
Scopus rating (2016): CiteScore 5.94 SJR 2.191 SNIP 1.91
Scopus rating (2015): SJR 2.255 SNIP 1.908 CiteScore 5.47
Scopus rating (2014): SJR 2.41 SNIP 2.104 CiteScore 5.3
Scopus rating (2013): SJR 2.412 SNIP 2.503 CiteScore 5.97
Scopus rating (2012): SJR 2.389 SNIP 2.465 CiteScore 5.25
Scopus rating (2011): SJR 2.314 SNIP 2.508 CiteScore 5.56
Scopus rating (2010): SJR 2.086 SNIP 2.355
Scopus rating (2009): SJR 1.912 SNIP 2.231
Scopus rating (2008): SJR 1.734 SNIP 2.732
Scopus rating (2007): SJR 1.529 SNIP 2.423
Scopus rating (2006): SJR 1.315 SNIP 1.98
Scopus rating (2005): SJR 1.269 SNIP 2.006
Metabolic engineering of Acinetobacter baylyi ADP1 for improved growth on gluconate and glucose

A high growth rate in bacterial cultures is usually achieved by optimizing growth conditions, but metabolism of the bacterium limits the maximal growth rate attainable on the carbon source used. This limitation can be circumvented by engineering the metabolism of the bacterium. Acinetobacter baylyi has become a model organism for studies of bacterial metabolism and metabolic engineering due to its wide substrate spectrum and easy-to-engineer genome. It produces naturally storage lipids, such as wax esters, and has a unique gluconate catabolism as it lacks a gene for pyruvate kinase. We engineered the central metabolism of A. baylyi ADP1 more favorable for gluconate catabolism by expressing the pyruvate kinase gene (pykF) of Escherichia coli. This modification increased growth rate when cultivated on gluconate or glucose as a sole carbon source in a batch cultivation. The engineered cells reached stationary phase on these carbon sources approximately twice as fast as control cells carrying an empty plasmid and produced similar amount of biomass. Furthermore, when grown on either gluconate or glucose, pykF expression did not lead to significant accumulation of overflow metabolites and consumption of the substrate remained unaltered. Increased growth rate on glucose was not accompanied with decreased wax ester production, and the pykF-expressing cells accumulated significantly more of these storage lipids with respect to cultivation time.
Murein lytic enzyme TgaA of Bifidobacterium bifidum MIMBb75 modulates dendritic cell maturation through its cysteine- and histidine-dependent amidohydrolase/peptidase (CHAP) amidase domain

Bifidobacteria are Gram-positive inhabitants of the human gastrointestinal tract that have evolved close interaction with their host and especially with the host's immune system. The molecular mechanisms underlying such interactions, however, are largely unidentified. In this study, we investigated the immunomodulatory potential of Bifidobacterium bifidum MIMBb75, a bacterium of human intestinal origin commercially used as a probiotic. Particularly, we focused our attention on TgaA, a protein expressed on the outer surface of MIMBb75's cells and homologous to other known bacterial immunomodulatory proteins. TgaA is a peptidoglycan lytic enzyme containing two active domains: lytic murein transglycosylase (LT) and cysteine- and histidine-dependent amidohydrolase/peptidase (CHAP). We ran immunological experiments stimulating dendritic cells (DCs) with the B. bifidum MIMBb75 and TgaA, with the result that both the bacterium and the protein activated DCs and triggered interleukin-2 (IL-2) production. In addition, we observed that the heterologous expression of TgaA in Bifidobacterium longum transferred to the bacterium the ability to induce IL-2. Subsequently, immunological experiments performed using two purified recombinant proteins corresponding to the single domains LT and CHAP demonstrated that the CHAP domain is the immune-reactive region of TgaA. Finally, we also showed that TgaA-dependent activation of DCs requires the protein CD14, marginally involves TRIF, and is independent of Toll-like receptor 4 (TLR4) and MyD88. In conclusion, our study suggests that the bacterial CHAP domain is a novel microbe-associated molecular pattern actively participating in the cross talk mechanisms between bifidobacteria and the host's immune system. © 2014, American Society for Microbiology.
Novel design of a multitube microbial fuel cell (UM2FC) for energy recovery and treatment of membrane concentrates

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering
Authors: Köroglu, E. O., Yilmaz Baysoy, D., Cetinkaya, A. Y., Özkaya, B., Cakmakci, M.
Number of pages: 8
Pages: 58-65
Publication date: 2014
Peer-reviewed: Yes

Publication information
Journal: Biomass & Bioenergy
Volume: 69
ISSN (Print): 0961-9534
Ratings:
Scopus rating (2016): CiteScore 3.71 SJR 1.188 SNIP 1.368
Scopus rating (2015): SJR 1.521 SNIP 1.615 CiteScore 4.03
Scopus rating (2014): SJR 1.888 SNIP 1.985 CiteScore 4.36
Scopus rating (2013): SJR 1.678 SNIP 1.823 CiteScore 4.42
Scopus rating (2012): SJR 1.545 SNIP 1.743 CiteScore 3.66
Scopus rating (2011): SJR 1.793 SNIP 2.283 CiteScore 4.74
Scopus rating (2010): SJR 1.931 SNIP 2.254
Scopus rating (2009): SJR 1.743 SNIP 2.187
Scopus rating (2008): SJR 1.609 SNIP 2.073
Scopus rating (2007): SJR 1.454 SNIP 1.77
Scopus rating (2006): SJR 1.292 SNIP 1.954
Scopus rating (2005): SJR 1.226 SNIP 1.398
Scopus rating (2004): SJR 1.037 SNIP 1.637
Novel metabolic features in Acinetobacter baylyi ADP1 revealed by a multiomics approach

**General information**
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering
Authors: Stuani, L., Lechaplais, C., Salminen, A. V., Segurens, B., Durot, M., Castelli, V., Pinet, A., Labadie, K., Cruveiller, S., Weissenbach, J., de Berardinis, V., Salanoubat, M., Perret, A.
Number of pages: 16
Publication date: 2014
Peer-reviewed: Yes

**Publication information**
Journal: Metabolomics
ISSN (Print): 1573-3882
Ratings:
Scopus rating (2016): SJR 1.119 SNIP 1.042 CiteScore 3.66
Scopus rating (2015): SJR 1.283 SNIP 1.156 CiteScore 3.49
Scopus rating (2014): SJR 1.272 SNIP 1.145 CiteScore 3.74
Scopus rating (2013): SJR 1.113 SNIP 1.022 CiteScore 4.03
Scopus rating (2012): SJR 1.223 SNIP 1.194 CiteScore 4.37
Scopus rating (2011): SJR 1.362 SNIP 1.172 CiteScore 4.48
Scopus rating (2010): SJR 1.15 SNIP 0.927
Scopus rating (2009): SJR 1.264 SNIP 0.82
Scopus rating (2008): SJR 1.195 SNIP 0.784
Scopus rating (2007): SJR 0.8 SNIP 0.631
Scopus rating (2006): SJR 0.824 SNIP 0.418
Original language: English
DOIs: 10.1007/s11306-014-0662-x

**Bibliographical note**
Published online: 29 April 2014
Portfolio EDEND: 2014-05-19
Publisher name: Springer New York LLC; Metabolomics Society
Source-ID: 1558

Stabilization of fine fraction from landfill mining in leach bed reactor

**General information**
State: Published
Ministry of Education publication type: B3 Non-refereed article in conference proceedings
Organisations: Department of Chemistry and Bioengineering, Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry
Authors: Mönkäre, T., Palmroth, M., Rintala, J.
**TgaA, a VirB1-like component belonging to a putative type IV secretion system of Bifidobacterium bifidum MIMBb75**

Bifidobacterium bifidum MIMBb75 is a human intestinal isolate demonstrated to be interactive with the host and efficacious as a probiotic. However, the molecular biology of this microorganism is yet largely unknown. For this reason, we undertook wholegenome sequencing of B. bifidum MIMBb75 to identify potential genetic factors that would explain the metabolic and probiotic attributes of this bacterium. Comparative genomic analysis revealed a 45-kb chromosomal region that comprises 19 putative genes coding for a potential type IV secretion system (T4SS). Thus, we undertook the initial characterization of this genetic region by studying the putative virB1-like gene, named tgaA. Gene tgaA encodes a peptidoglycan lytic enzyme containing two active domains: lytic murein transglycosylase (LT, cd00254.3) and cysteine- and histidine-dependent amidohydrolase/peptidase (CHA, pfam05257.4). By means of several in vitro assays, we experimentally confirmed that protein TgaA, consistent with its computationally assigned role, has peptidoglycan lytic activity, which is principally associated to the LT domain. Furthermore, immunofluorescence and immunogold labeling showed that the protein TgaA is abundantly expressed on the cell surface of B. bifidum MIMBb75. According to the literature, the T4SSs, which have not been characterized before in bifidobacteria, can have important implications for bacterial cell-to-cell communication as well as cross talk with host cells, justifying the interest for further studies aimed at the investigation of this genetic region. © 2014, American Society for Microbiology.
Non-sterile process for biohydrogen and 1,3-propanediol production from raw glycerol

Raw glycerol is a tempting substrate for fermentations, but contains impurities that can be inhibitory for organisms. In this study, raw glycerol tolerance and contamination risk of pure bacterial culture at hypersaline process conditions were evaluated. The inhibitory effect of raw glycerol was similar on a halophilic (Halanaerobium saccharolyticum) and a non-halophilic (Clostridium butyricum) bacterium implying the inhibition originating from methanol or other impurities rather than salt. The hypersaline process conditions decreased efficiently contaminations and no growth of contaminants was observed at and above 125 g/l NaCl. Halophilic H₂ and 1,3-PD production from raw glycerol were studied separately as 1-stage processes and jointly as 2-stage process in non-sterile conditions. Non-sterile conditions were successfully applied and the highest production yields obtained were 3.0 mol H₂/mol glycerol and 0.66 mol 1,3-PD/mol glycerol (1-stage processes), whereas the highest cumulative production was 74 mmol H₂/l culture and 31 mmol 1,3-PD/l culture (2-stage process). © 2013, Hydrogen Energy Publications, LLC. Published by Elsevier Ltd. All rights.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Tampere University of Technology, Urban circular bioeconomy (UrCirBio)
Authors: Kivistö, A., Santala, V., Karp, M.
Number of pages: 7
Pages: 11749-11755
Publication date: 10 Sep 2013
Peer-reviewed: Yes

Publication information
Volume: 38
Issue number: 27
ISSN (Print): 0360-3199
Ratings:
Scopus rating (2016): CiteScore 3.74 SJR 1.142 SNIP 1.286
Scopus rating (2015): SJR 1.294 SNIP 1.319 CiteScore 3.46
Scopus rating (2014): SJR 1.212 SNIP 1.494 CiteScore 3.54
Scopus rating (2013): SJR 1.278 SNIP 1.467 CiteScore 3.38
Scopus rating (2012): SJR 1.515 SNIP 1.729 CiteScore 3.96
Scopus rating (2011): SJR 1.456 SNIP 1.837 CiteScore 4.42
Scopus rating (2010): SJR 1.589 SNIP 1.871
Scopus rating (2009): SJR 1.333 SNIP 1.885
Scopus rating (2008): SJR 1.401 SNIP 2.096
Scopus rating (2007): SJR 1.279 SNIP 2.201
Scopus rating (2006): SJR 1.073 SNIP 2.161
Scopus rating (2005): SJR 1.107 SNIP 1.787
Scopus rating (2004): SJR 1.225 SNIP 1.626
Prospecting hydrogen production of Escherichia coli by metabolic network modeling

Genome-scale model was applied to analyze the anaerobic metabolism of Escherichia coli. Three different methods were used to find deletions affecting fermentative hydrogen production: flux balance analysis (FBA), algorithm for blocking competing pathways (ABCP), and manual selection. Based on these methods, 81 E. coli mutants possessing one gene deletion were selected and cultivated in batch experiments. Experimental results of H₂ and biomass production were compared against the results of FBA. Several gene deletions enhancing H₂ production were found. Correctness of gene essentiality predictions of FBA for the selected genes was 78% and 77% in glucose and galactose media, respectively. 33% of the mutations that were predicted by FBA to increase H₂ production had a positive effect in experiments. Batch cultivation is a simple and straightforward experimental way to screen improvements in H₂ production. However, the ability of FBA to predict the H₂ production rate cannot be evaluated by batch experiments. Metabolic network models provide a method for gaining broader understanding of the complicated metabolic system of a cell and can aid in prospecting suitable gene deletions for enhancing H₂ production. © 2013, Hydrogen Energy Publications, LLC. Published by Elsevier Ltd. All rights.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Tampere University of Technology, Department of Signal Processing, Prostate cancer research center (PCRC), Urban circular bioeconomy (UrCirBio), Aalto University
Authors: Seppälä, J. J., Larjo, A., Aho, T., Yli-Harja, O., Karp, M. T., Santala, V.
Number of pages: 10
Pages: 11780-11789
Publication date: 10 Sep 2013
Peer-reviewed: Yes

Publication information
Volume: 38
Issue number: 27
ISSN (Print): 0360-3199
Ratings:
- Scopus rating (2016): CiteScore 3.74 SJR 1.142 SNIP 1.286
- Scopus rating (2015): SJR 1.294 SNIP 1.319 CiteScore 3.46
- Scopus rating (2014): SJR 1.212 SNIP 1.494 CiteScore 3.54
- Scopus rating (2013): SJR 1.278 SNIP 1.467 CiteScore 3.38
- Scopus rating (2012): SJR 1.515 SNIP 1.729 CiteScore 3.96
- Scopus rating (2011): SJR 1.456 SNIP 1.837 CiteScore 4.42
- Scopus rating (2010): SJR 1.589 SNIP 1.871
- Scopus rating (2009): SJR 1.333 SNIP 1.885
- Scopus rating (2008): SJR 1.401 SNIP 2.096
Bioprocess data mining using regularized regression and random forests

Background: In bioprocess development, the needs of data analysis include (1) getting overview to existing data sets, (2) identifying primary control parameters, (3) determining a useful control direction, and (4) planning future experiments. In particular, the integration of multiple data sets causes that these needs cannot be properly addressed by regression models that assume linear input-output relationship or unimodality of the response function. Regularized regression and random forests, on the other hand, have several properties that may appear important in this context. They are capable, e.g., in handling small number of samples with respect to the number of variables, feature selection, and the visualization of response surfaces in order to present the prediction results in an illustrative way.

Results: In this work, the applicability of regularized regression (Lasso) and random forests (RF) in bioprocess data mining was examined, and their performance was benchmarked against multiple linear regression. As an example, we used data from a culture media optimization study for microbial hydrogen production. All the three methods were capable in providing a significant model when the five variables of the culture media optimization were linearly included in modeling. However, multiple linear regression failed when also the multiplications and squares of the variables were included in modeling. In this case, the modeling was still successful with Lasso (correlation between the observed and predicted yield was 0.69) and RF (0.91).

Conclusion: We found that both regularized regression and random forests were able to produce feasible models, and the latter was efficient in capturing the non-linearity in the data. In this kind of a data mining task of bioprocess data, both methods outperform multiple linear regression.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Signal Processing, Research group: Laboratory of Bysystem Dynamics-LBD, Research group: Computational Systems Biology, Research group: Industrial Bioengineering and Applied Organic Chemistry, Department of Chemistry and Bioengineering, Research group: Vision, Research Community on Data-to-Decision (D2D), Urban circular bioeconomy (UrCirBio)
Authors: Hassan, S. S., Farhan, M., Mangayil, R., Huttunen, H., Aho, T.
Number of pages: 7
Publication date: 12 Aug 2013
Peer-reviewed: Yes

Publication information
Journal: BMC Systems Biology
Volume: 7
Issue number: Suppl 1
Article number: 5
ISSN (Print): 1752-0509
Screening pretreatment methods to enhance thermophilic anaerobic digestion of pulp and paper mill wastewater treatment secondary sludge

The effect of hydrothermal (150°C for 10min and 70°C for 40min), enzymatic (Accelerase 1500, 0.07g/g volatile solids (VS)), ultrasound (45kHz for 30min) and chemical pretreatments (HNO₃ at pH3 and NaOH at pH12) alone or in combination on the chemical composition and methane yield of the pulp and paper mill secondary sludge was studied in batch assays at 55°C. In total, 12 different pretreatment combinations were compared. Chemical analyses showed that all pretreatments except for HNO₃ and ultrasound pretreatments improved the organic matter solubilization. Among the studied pretreatments, hydrothermal (150°C, 10min) pretreatment alone or in combination with enzymatic and/or ultrasound pretreatment had the highest impact on sludge solubilization and methane yield. The increase in methane yield was 31% (from 108ml/g VSoriginal to 141ml/g VSoriginal). In addition, enzymatic pretreatment also improved the methane yields but only when combined with hydrothermal pretreatment at 150°C or ultrasound+hydrothermal pretreatment at 150°C. On the other hand, ultrasound pretreatment did not improve the methane yields while acid and alkaline pretreatments resulted in lower methane yields than control. Improved hydrolysis and higher methane production rates noticed in assays subjected to hydrothermal pretreatment alone or in combination with enzymes and/or ultrasound could make these treatments more attractive in reducing the retention times required during full-scale anaerobic digestion of pulp and paper mill wastewater sludges. © 2013 Elsevier B.V.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Tampere University of Technology, Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio), Jyväskylän Yliopisto, University of Jyväskylä
Authors: Bayr, S., Kaparaju, P., Rintala, J.
Number of pages: 8
Pages: 479-486
Publication date: 1 May 2013
Peer-reviewed: Yes
Hydrogen and methane production in extreme thermophilic conditions in two-stage (upflow anaerobic sludge bed) UASB reactor system

Two-stage hydrogen and methane production in extreme thermophilic (70 °C) conditions was demonstrated for the first time in UASB-reactor system. Inoculum used in hydrogen and methane reactors was granular sludge from mesophilic internal circulation reactor and was first acclimated for extreme thermophilic conditions. In hydrogen reactor, operated with hydraulic retention time (HRT) of 5 h and organic loading rate (OLR) of 25.1 kg COD/m³/d, hydrogen yield was 0.73 mol/mol glucose added. Methane was produced in second stage from hydrogen reactor effluent. In methane reactor operated with HRT of 13 h and OLR of 7.8 kg COD/m³/d, methane yield was 117.5 ml/g COD added. These results prove that hydrogen and methane can be produced in extreme thermophilic temperatures, but as batch experiments confirmed, for methane production lower temperature would be more efficient. Copyright © 2013, Hydrogen Energy Publications, LLC. Published by Elsevier Ltd. All rights reserved.
Anaerobic conversion of microalgal biomass to sustainable energy carriers - A review

General information
State: Published
Ministry of Education publication type: A2 Review article in a scientific journal
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Lakaniemi, A., Tuovinen, O. H., Puhakka, J. A.
Number of pages: 10
Pages: 222-231
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Bioresource Technology
Volume: 135
Issue number: May
ISSN (Print): 0960-8524
Ratings:
Scopus rating (2016): CiteScore 5.94 SJR 2.191 SNIP 1.91
Scopus rating (2015): SJR 2.255 SNIP 1.908 CiteScore 5.47
Scopus rating (2014): SJR 2.41 SNIP 2.104 CiteScore 5.3
Scopus rating (2013): SJR 2.412 SNIP 2.503 CiteScore 5.97
Scopus rating (2012): SJR 2.389 SNIP 2.465 CiteScore 5.25
Scopus rating (2011): SJR 2.314 SNIP 2.508 CiteScore 5.56
Scopus rating (2010): SJR 2.086 SNIP 2.355
Scopus rating (2009): SJR 1.912 SNIP 2.231
Scopus rating (2008): SJR 1.734 SNIP 2.732
Scopus rating (2007): SJR 1.529 SNIP 2.423
Scopus rating (2006): SJR 1.315 SNIP 1.98
Scopus rating (2005): SJR 1.269 SNIP 2.006
Scopus rating (2004): SJR 1.197 SNIP 1.659
Scopus rating (2003): SJR 0.948 SNIP 1.639
Scopus rating (2002): SJR 0.882 SNIP 1.3
Scopus rating (2001): SJR 0.541 SNIP 1.208
Scopus rating (2000): SJR 0.464 SNIP 1.049
Scopus rating (1999): SJR 0.669 SNIP 1.061
An in vitro study of composites of poly(L-lactide-co-ε-caprolactone), β-tricalcium phosphate and ciprofloxacin intended for local treatment of osteomyelitis

Osteomyelitis is a bacterial disease that can become chronic, and treatment often includes a surgical operation to remove infected bone. The aim of this study was to develop and investigate in vitro bone filling composite materials that release ciprofloxacin to kill any remaining bacteria and contain bioceramic to help the bone to heal. Three composites of poly(L-lactide-co-ε-caprolactone), β-tricalcium phosphate and ciprofloxacin were compounded using twin-screw extrusion and sterilized by gamma irradiation. Drug release and degradation of the composites were investigated in vitro for 52 weeks. The composite with 50 wt% of β-TCP had the most promising ciprofloxacin release profile. The ceramic component accelerated the drug release that occurred in three phases obeying first-order kinetics. Inhibition zone testing using bioluminescence showed that the released ciprofloxacin had effect in eradicating a common osteomyelitis causing bacteria Pseudomonas aeruginosa. During the in vitro degradation test series, molar weight of the polymer matrix of the composites decreased rapidly. Additionally, 1H-NMR analysis showed that the polymer had blocky structure and the comonomer ratio changed during hydrolysis. The tested composites showed great potential to be developed into bone filler materials for the treatment of osteomyelitis or other bone related infections.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Electronics and Communications Engineering, Department of Chemistry and Bioengineering, Frontier Photonics
Authors: Ahola, N., Männistö, N., Veiranto, M., Karp, M., Rich, J., Efimov, A., Seppälä, J., Kellomäki, M.
Number of pages: 13
Pages: 1-13
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Biomatter
Volume: 3
Issue number: 2
Article number: e23162
ISSN (Print): 2159-2527
Ratings:
Scopus rating (2016): SJR 0.579 SNIP 3.262 CiteScore 1.92
Scopus rating (2015): SJR 0.627 SNIP 1.402 CiteScore 2.67
Scopus rating (2014): SJR 0.632 SNIP 0.47 CiteScore 2.39
Scopus rating (2013): SJR 0.329 CiteScore 1.2
Scopus rating (2012): SJR 0.143
Original language: English
Electronic versions:
ahola_an_in_vitro_study_of_composites.pdf
DOI:s:
10.4161/biom.23162
Links:
http://www.landesbioscience.com/journals/biom/article/23162/
http://urn.fi/URN:NBN:fi:tty-201401301067

Bibliographical note
Contribution: organisation=elt,FACT1=0.7<br/>Contribution: organisation=keb,FACT2=0.3<br/>Portfolio EDEND: 2013-07-29<br/>Publisher name: Landes Bioscience
Source: researchoutputwizard
Source-ID: 1886
Research output: Scientific - peer-review › Article
Antimicrobial assay optimization and validation for HTS in 384-well format using a bioluminescent E. coli K-12 strain

This report describes the optimization and validation of an antimicrobial assay based on the genetically modified bacterial strain Escherichia coli K-12 (pTetux1). The use of this particular strain enables an inducible cell-based bioluminescent assay for high-throughput screening (HTS) of antimicrobial agents, which shows a pronounced detection of compounds targeting transcriptional and translational events in protein synthesis. The optimizations in 96-well format led to several improvements in assay conditions, such as reduction of the pre-incubation time before luminescence induction by half. The threshold for DMSO tolerability was concluded to be up to 1%. Assay protocol was further miniaturized into 384-well format and the liquid handling was automated using a robotic workstation. The use of compound pre-plating into 384-well plates as a part of the process was evaluated, and the total assay volume was further downscaled from 50 μl to 30 μl. With this approach, the amount of test compound needed per well was reduced to nanoliter volumes. Using the miniaturized protocol a pilot screen of 2000 known drugs and bioactives was performed. The assay performance was evaluated by calculating known assay quality parameters, the Z’ factor having a mean value of 0.8 during the compound library screening indicated an excellent performance. Of the assay positives, 54 compounds showed high inhibitions (60-100%), of which the majority (89%) were known antibacterial agents. Of the actives showing >60% inhibition, 16 compounds were identified as known transcriptional and translational inhibitors. The screening results demonstrated that the miniaturized assay is well suited for identification of antimicrobial compounds in HT screening, and that the assay is specifically sensitive towards bacterial transcription and translation inhibitors. © 2013 Elsevier B.V.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Industrial Bioengineering and Applied Organic Chemistry, Tampere University of Technology, Urban circular bioeconomy (UrCirBio), Centre for Drug Research, Faculty of Pharmacy, Helsinki University
Authors: Nybond, S., Karp, M., Tammela, P.
Number of pages: 8
Pages: 782-789
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: European Journal of Pharmaceutical Sciences
Volume: 49
Issue number: 4
ISSN (Print): 0928-0987
Ratings:
Scopus rating (2016): CiteScore 4.2 SJR 1.223 SNIP 1.499
Scopus rating (2015): SJR 1.156 SNIP 1.415 CiteScore 4.04
Scopus rating (2014): SJR 0.994 SNIP 1.247 CiteScore 3.48
Scopus rating (2013): SJR 1.038 SNIP 1.287 CiteScore 3.47
Scopus rating (2012): SJR 1.254 SNIP 1.425 CiteScore 3.6
Scopus rating (2011): SJR 1.236 SNIP 1.428 CiteScore 3.57
Scopus rating (2010): SJR 1.289 SNIP 1.283
Scopus rating (2009): SJR 1.169 SNIP 1.465
Scopus rating (2008): SJR 1.015 SNIP 1.265
Scopus rating (2007): SJR 0.927 SNIP 1.137
Scopus rating (2006): SJR 0.775 SNIP 1.039
Scopus rating (2005): SJR 0.93 SNIP 1.409
Scopus rating (2004): SJR 0.873 SNIP 1.367
Scopus rating (2003): SJR 0.964 SNIP 1.4
Scopus rating (2002): SJR 0.791 SNIP 1.167
Scopus rating (2001): SJR 0.694 SNIP 0.969
Scopus rating (2000): SJR 0.445 SNIP 0.901
Scopus rating (1999): SJR 0.388 SNIP 0.79
Original language: English
ASJC Scopus subject areas: Pharmaceutical Science
Keywords: Bioluminescence, Cell-based assay, High-throughput screening, Miniaturization, Transcription, Translation
DOIs:
10.1016/j.ejps.2013.05.024
Bioelectricity production on xylose with a compost enrichment culture

Bibliographical note
Contribution: organisation=keb,FACT1=1<br/>Portfolio EDEND: 2013-09-29<br/>Publisher name: Elsevier BV
Source: researchoutputwizard
Source-ID: 3025
Research output: Scientific - peer-review › Article

Bioelectricity production on xylose with a compost enrichment culture

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Mäkinen, A. E., Lay, C., Nissilä, M. E., Puhakka, J. A.
Number of pages: 7
Pages: 15606-15612
Publication date: 2013
Peer-reviewed: Yes

Publication information
Volume: 38
Issue number: 35
ISSN (Print): 0360-3199
Ratings:
Scopus rating (2016): CiteScore 3.74 SJR 1.142 SNIP 1.286
Scopus rating (2015): SJR 1.294 SNIP 1.319 CiteScore 3.46
Scopus rating (2014): SJR 1.212 SNIP 1.494 CiteScore 3.54
Scopus rating (2013): SJR 1.278 SNIP 1.467 CiteScore 3.38
Scopus rating (2012): SJR 1.515 SNIP 1.729 CiteScore 3.96
Scopus rating (2011): SJR 1.456 SNIP 1.837 CiteScore 4.42
Scopus rating (2010): SJR 1.589 SNIP 1.871
Scopus rating (2009): SJR 1.333 SNIP 1.885
Scopus rating (2008): SJR 1.401 SNIP 2.096
Scopus rating (2007): SJR 1.279 SNIP 2.201
Scopus rating (2006): SJR 1.073 SNIP 2.161
Scopus rating (2005): SJR 1.107 SNIP 1.787
Scopus rating (2004): SJR 1.225 SNIP 1.626
Scopus rating (2003): SJR 1.003 SNIP 1.319
Scopus rating (2002): SJR 0.763 SNIP 1.157
Scopus rating (2001): SJR 0.487 SNIP 1.185
Scopus rating (2000): SJR 0.518 SNIP 0.866
Scopus rating (1999): SJR 0.382 SNIP 0.897
Original language: English
DOIs:
10.1016/j.ijhydene.2013.04.137

Bibliographical note
Available online 2 June 2013<br/>Contribution: organisation=keb,FACT1=1<br/>Portfolio EDEND: 2013-11-29<br/>Publisher name: Elsevier Ltd
Source: researchoutputwizard
Source-ID: 2864
Research output: Scientific - peer-review › Article

Biomethane production from maize and liquid cow manure - Effect of share of maize, post-methanation potential and digestate characteristics

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Seppälä, M., Pyykkönen, V., Väisänen, A., Rintala, J.
Number of pages: 8
Pages: 209-216
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Fuel
Volume: 107
ISSN (Print): 0016-2361
Ratings:
Scopus rating (2016): CiteScore 4.9 SJR 1.744 SNIP 2.179
Scopus rating (2015): SJR 1.809 SNIP 2.125 CiteScore 4.46
Scopus rating (2014): SJR 1.667 SNIP 2.331 CiteScore 4.14
Scopus rating (2013): SJR 1.811 SNIP 2.595 CiteScore 4.31
Scopus rating (2012): SJR 1.852 SNIP 2.465 CiteScore 3.99
Scopus rating (2011): SJR 2.093 SNIP 2.427 CiteScore 4.1
Scopus rating (2010): SJR 1.984 SNIP 2.319
Scopus rating (2009): SJR 2.012 SNIP 2.277
Scopus rating (2008): SJR 1.635 SNIP 2.184
Scopus rating (2007): SJR 1.383 SNIP 1.86
Scopus rating (2006): SJR 1.278 SNIP 1.64
Scopus rating (2005): SJR 1.623 SNIP 1.73
Scopus rating (2004): SJR 1.273 SNIP 1.883
Scopus rating (2003): SJR 1.103 SNIP 1.481
Scopus rating (2002): SJR 1.13 SNIP 1.301
Scopus rating (2001): SJR 1.136 SNIP 1.264
Scopus rating (2000): SJR 1.047 SNIP 1.272
Scopus rating (1999): SJR 1.117 SNIP 1.157
Original language: English
DOIs: 10.1016/j.fuel.2012.12.069

Bibliographical note
Contribution: organisation=keb,FAC1=1
Portfolio EDEND: 2013-11-29
Publisher name: Elsevier Ltd
Source: researchoutputwizard
Source-ID: 3399
Research output: Scientific - peer-review › Article

Column bioleaching of low grade copper sulfide ore at extreme conditions for most mineral processing bacteria

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering
Authors: Zou, G., Zengling, W., Xiaokang, L., Laichang, Z., Renman, R., Papirio, S., Puhakka, J.
Number of pages: 4
Pages: 318-321
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Advanced Materials Research
Volume: 825
ISSN (Print): 1022-6680
Ratings:
Scopus rating (2016): SJR 0.12 SNIP 0.154
Draft genome sequence of the hydrogen- and ethanol-producing anaerobic alkalithermophilic bacterium *Caloramator celer*.

**General information**
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Signal Processing, Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Ciranna, A., Larjo, A., Kivistö, A., Santala, V., Roos, C., Karp, M.
Number of pages: 2
Pages: 1-2
Publication date: 2013
Peer-reviewed: Yes

**Publication information**
Journal: Genome Announcements
Volume: 1
Issue number: 4
ISSN (Print): 2169-8287
Ratings:
Scopus rating (2016): SJR 0.217 SNIP 0.233 CiteScore 0.41
Scopus rating (2015): SJR 0.199 SNIP 0.077
Scopus rating (2014): SJR 0.218 SNIP 0.089
Original language: English
DOIs:
10.1128/genomeA.00471-13

**Bibliographical note**
Contribution: organisation=keb,FACT1=1
Contribution: organisation=sgn,FACT2=0.2
Portfolio EDEND: 2013-11-29
Publisher name: American Society for Microbiology
Source: researchoutputwizard
Source-ID: 2047
Research output: Scientific - peer-review › Article

Effect of NA-chloride on the bioleaching of a chalcopyrite concentrate in shake flasks and stirred tank bioreactors

**General information**
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Electricity generation from young landfill leachate in a microbial fuel cell with a new electrode material

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering
Authors: Özkaya, B., Cetinkaya, A. Y., Cakmakci, M., Karadag, D., Sahinkaya, E.
Pages: 399-405
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Bioprocess and Biosystems Engineering
Volume: 36
Issue number: 4
ISSN (Print): 1615-7591
Ratings:
Scopus rating (2016): SJR 0.628 SNIP 0.956 CiteScore 1.96
Scopus rating (2015): SJR 0.687 SNIP 0.887 CiteScore 1.97
Scopus rating (2014): SJR 0.699 SNIP 0.968 CiteScore 1.95
Enrichment of electrogens on xylose from anaerobi digester sample

General information
State: Published
Ministry of Education publication type: A4 Article in a conference publication
Organisations: Department of Chemistry and Bioengineering
Authors: Nissilä, M., Sulonen, M., Puhakka, J.
Number of pages: 4
Publication date: 2013

Host publication information
Title of host publication: Proceedings of 13th World Congress on Anaerobic Digestion, 25th-28th June 2013, Santiago de Compostela, Spain
Publisher: IWA International Water Association

Publication series
Name: Anaerobic Digestion World Congress

Bibliographical note
SPB16 (IWA-10806) on page 124<br/>Contribution: organisation=keb,FACT1=1<br/>Portfolio EDEND: 2013-07-29<br/>Publisher name: IWA International Water Association
Source: researchoutputwizard
Source-ID: 3000
Research output: Scientific - peer-review › Conference contribution

Fluidized-bed denitrification for mine waters. Part I: low pH and temperature operation

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Papirio, S., Ylinen, A., Zou, G., Peltola, M., Esposito, G., Puhakka, J.
Number of pages: 11
Pages: 1-11
Publication date: 2013
Peer-reviewed: Yes
Fluorescence properties of the chromophore-binding domain of bacteriophytochrome from Deinococcus radiodurans

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Research group: Supramolecular photochemistry, Frontier Photonics
Authors: Lehtivuori, H., Rissanen, I., Takala, H., Bamford, J., Tkachenko, N. V., Ihalainen, J. A.
Pages: 11049-11057
Publication date: 2013
Peer-reviewed: Yes
Genome Sequence of Halanaerobium saccharolyticum subsp. saccharolyticum Strain DSM 6643T, a Halophilic Hydrogen-Producing Bacterium

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Signal Processing, Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Kivistö, A., Larjo, A., Ciranna, A., Santala, V., Roos, C., Karp, M.
Number of pages: 2
Pages: 1-2
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Genome Announcements
Volume: 1
Issue number: 2
ISSN (Print): 2169-8287
Ratings:
Scopus rating (2016): SJR 0.217 SNIP 0.233 CiteScore 0.41
Scopus rating (2015): SJR 0.199 SNIP 0.077
Scopus rating (2014): SJR 0.218 SNIP 0.089
Original language: English
DOIs:
10.1128/genomeA.00187-13

Bibliographical note
Contribution: organisation=keb,FACT1=0.8<br/>Contribution: organisation=sgn,FACT2=0.2<br/>Portfolio EDEND: 2013-09-29<br/>Publisher name: American Society for Microbiology
Source: researchoutputwizard
Source-ID: 2575
Research output: Scientific - peer-review › Article

Impact of heavy metals on denitrification of simulated mining wastewaters

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Zou, G., Ylinen, A., Di Capua, F., Papirio, S., Lakaniemi, A., Puhakka, J.
Number of pages: 4

Bibliographical note
Contribution: organisation=keb,FACT1=1<br/>Portfolio EDEND: 2013-10-29<br/>Publisher name: American Chemical Society
Source: researchoutputwizard
Source-ID: 2752
Research output: Scientific - peer-review › Article
Lipid profile characterization of wastewaters from different origins

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Efimova, E., Marjakangas, J., Lakaniemi, A., Koskinen, P., Puhakka, J.
Number of pages: 10
Pages: 2505-2514
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Water Science and Technology
Volume: 68
Issue number: 11
ISSN (Print): 0273-1223
Ratings:

1. Scopus rating (2016): SJR 0.394 SNIP 0.621 CiteScore 1.3
2. Scopus rating (2015): SJR 0.466 SNIP 0.599 CiteScore 1.19
3. Scopus rating (2014): SJR 0.587 SNIP 0.685 CiteScore 1.14
4. Scopus rating (2013): SJR 0.568 SNIP 0.7 CiteScore 1.3
5. Scopus rating (2012): SJR 0.601 SNIP 0.669 CiteScore 1.13
6. Scopus rating (2011): SJR 0.591 SNIP 0.626 CiteScore 1.25
7. Scopus rating (2010): SJR 0.522 SNIP 0.602
8. Scopus rating (2009): SJR 0.589 SNIP 0.686
9. Scopus rating (2008): SJR 0.579 SNIP 0.697
10. Scopus rating (2007): SJR 0.749 SNIP 0.781
11. Scopus rating (2006): SJR 0.693 SNIP 0.796
12. Scopus rating (2005): SJR 0.763 SNIP 0.85
13. Scopus rating (2004): SJR 0.877 SNIP 0.904
14. Scopus rating (2003): SJR 0.882 SNIP 0.902
15. Scopus rating (2002): SJR 0.903 SNIP 0.888
16. Scopus rating (2001): SJR 0.759 SNIP 0.967
17. Scopus rating (2000): SJR 0.76 SNIP 0.885
18. Scopus rating (1999): SJR 0.889 SNIP 0.936

Original language: English
DOIs:
10.2166/wst.2013.538
Modification of the Escherichia coli metabolic model LAF1260 based on anaerobic experiments

General information
State: Published
Ministry of Education publication type: A4 Article in a conference publication
Organisations: Department of Signal Processing, Department of Chemistry and Bioengineering
Authors: Seppälä, J., Larjo, A., Aho, T., Kivistö, A., Karp, M., Santala, V.
Pages: 80-86
Publication date: 2013

Host publication information
Title of host publication: The 10th International Workshop on Computational Systems Biology, WCSB 2013, June 10-12, Tampere, Finland
Editors: Autio, R., Shmulevich, I., Strimmer, K., Wiuf, C., Sarbu, S., Yli-Harja, O.

Publication series
Name: International Workshop on Computational Systems Biology
ISSN (Print): 1456-2774
Links:

Molecular weight distribution of a full-scale landfill leachate treatment by membrane bioreactor and nanofiltration membrane

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering
Authors: Campagna, M., Cakmakci, M., Busra Yaman, F., Özkaya, B.
Number of pages: 5
Pages: 866-870
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Waste Management
Volume: 33
Issue number: 4
ISSN (Print): 0956-053X
Ratings:
Scopus rating (2016): CiteScore 4 SJR 1.354 SNIP 2.044
Scopus rating (2015): SJR 1.739 SNIP 2.256 CiteScore 4.33
Scopus rating (2014): SJR 1.777 SNIP 2.482 CiteScore 3.43
Scopus rating (2013): SJR 1.822 SNIP 2.435 CiteScore 3.39
Scopus rating (2012): SJR 1.611 SNIP 2.184 CiteScore 2.91
Scopus rating (2011): SJR 1.698 SNIP 2.085 CiteScore 2.99
Scopus rating (2010): SJR 1.555 SNIP 1.78
Screening of novel plants for biogas production in northern conditions

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Seppälä, M., Laine, A., Rintala, J.
Number of pages: 8
Pages: 355-362
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Bioresource Technology
Volume: 139
ISSN (Print): 0960-8524
Ratings:
Scopus rating (2016): CiteScore 5.94 SJR 2.191 SNIP 1.91
Scopus rating (2015): SJR 2.255 SNIP 1.908 CiteScore 5.47
Scopus rating (2014): SJR 2.41 SNIP 2.104 CiteScore 5.3
Scopus rating (2013): SJR 2.412 SNIP 2.503 CiteScore 5.97
Scopus rating (2012): SJR 2.389 SNIP 2.465 CiteScore 5.25
Scopus rating (2011): SJR 2.314 SNIP 2.508 CiteScore 5.56
Scopus rating (2010): SJR 2.086 SNIP 2.355
Scopus rating (2009): SJR 1.912 SNIP 2.231
Scopus rating (2008): SJR 1.734 SNIP 2.732
Scopus rating (2007): SJR 1.529 SNIP 2.423
Scopus rating (2006): SJR 1.315 SNIP 1.98
Scopus rating (2005): SJR 1.269 SNIP 2.006
Scopus rating (2004): SJR 1.197 SNIP 1.659
Scopus rating (2003): SJR 0.948 SNIP 1.639
Scopus rating (2002): SJR 0.882 SNIP 1.3
Scopus rating (2001): SJR 0.541 SNIP 1.208
Scopus rating (2000): SJR 0.464 SNIP 1.049
Scopus rating (1999): SJR 0.669 SNIP 1.061
Original language: English
DOIs:
S-Layer protein mediates the stimulatory effect of lactobacillus helveticus MIMLh5 on innate immunity

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Number of pages: 11
Pages: 1221-1231
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Applied and Environmental Microbiology
Volume: 79
Issue number: 4
ISSN (Print): 0099-2240
Ratings:
Scopus rating (2016): SJR 1.691 SNIP 1.243 CiteScore 4.08
Scopus rating (2015): SJR 1.896 SNIP 1.351 CiteScore 4.14
Scopus rating (2014): SJR 1.862 SNIP 1.402 CiteScore 4.02
Scopus rating (2013): SJR 1.909 SNIP 1.41 CiteScore 4.25
Scopus rating (2012): SJR 1.967 SNIP 1.427 CiteScore 4.29
Scopus rating (2011): SJR 1.91 SNIP 1.453 CiteScore 4.12
Scopus rating (2010): SJR 1.885 SNIP 1.431
Scopus rating (2009): SJR 1.975 SNIP 1.529
Scopus rating (2008): SJR 2.168 SNIP 1.574
Scopus rating (2007): SJR 2.045 SNIP 1.652
Scopus rating (2006): SJR 2.054 SNIP 1.594
Scopus rating (2005): SJR 2.078 SNIP 1.646
Scopus rating (2004): SJR 2.123 SNIP 1.641
Scopus rating (2003): SJR 2.108 SNIP 1.806
Scopus rating (2002): SJR 2.044 SNIP 1.739
Scopus rating (2001): SJR 2 SNIP 1.737
Scopus rating (2000): SJR 1.958 SNIP 1.75
Scopus rating (1999): SJR 2.316 SNIP 1.723
Original language: English
DOI's:
10.1128/AEM.03056-12

Bibliographical note
Contribution: organisation=keb,FACT1=1
Portfolio EDEND: 2013-06-29
Publisher name: American Society for Microbiology
Source: researchoutputwizard
Source-ID: 3518
Research output: Scientific - peer-review > Article

Suppression of methanogenesis in cellulose-fed microbial fuel cells in relation to performance, metabolite formation, and microbial population

General information
Energy Demands of Nitrogen Supply in Mass Cultivation of Two Commercially Important Microalgal Species, Chlorella vulgaris and Dunaliella tertiolecta

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Hulatt, C. J., Lakaniemi, A., Puhakka, J. A., Thomas, D. N.
Pages: 669-684
Publication date: 2012
Peer-reviewed: Yes

Publication information
Journal: BioEnergy Research
Volume: 5
Issue number: 3
ISSN (Print): 1939-1234
Ratings:
Scopus rating (2016): SJR 0.943 SNIP 0.932 CiteScore 2.64
Scopus rating (2015): SJR 1.317 SNIP 1.285 CiteScore 3.35
Scopus rating (2014): SJR 1.453 SNIP 1.344 CiteScore 3.64
Scopus rating (2013): SJR 1.162 SNIP 1.384 CiteScore 3.66
Scopus rating (2012): SJR 1.362 SNIP 1.645 CiteScore 4.23
Scopus rating (2011): SJR 1 SNIP 1.435 CiteScore 3.16
Scopus rating (2010): SJR 0.458 SNIP 0.671
Original language: English
DOIs: 10.1007/s12155-011-9175-x
Eukaryotic and prokaryotic microbial communities during microalgal biomass production

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Lakaniemi, A., Hulatt, C. J., Wakeman, K. D., Thomas, D. N., Puhakka, J. A.
Pages: 387-393
Publication date: 2012
Peer-reviewed: Yes

Publication information
Journal: Bioresource Technology
Volume: 124
Issue number: November
ISSN (Print): 0960-8524
Ratings:
Scopus rating (2016): CiteScore 5.94 SJR 2.191 SNIP 1.91
Scopus rating (2015): SJR 2.255 SNIP 1.908 CiteScore 5.47
Scopus rating (2014): SJR 2.41 SNIP 2.104 CiteScore 5.3
Scopus rating (2013): SJR 2.412 SNIP 2.503 CiteScore 5.97
Scopus rating (2012): SJR 2.389 SNIP 2.465 CiteScore 5.25
Scopus rating (2011): SJR 2.314 SNIP 2.508 CiteScore 5.56
Scopus rating (2010): SJR 2.086 SNIP 2.355
Scopus rating (2009): SJR 1.912 SNIP 2.231
Scopus rating (2008): SJR 1.734 SNIP 2.732
Scopus rating (2007): SJR 1.529 SNIP 2.423
Scopus rating (2006): SJR 1.315 SNIP 1.98
Scopus rating (2005): SJR 1.269 SNIP 2.006
Scopus rating (2004): SJR 1.197 SNIP 1.659
Scopus rating (2003): SJR 0.948 SNIP 1.639
Scopus rating (2002): SJR 0.882 SNIP 1.3
Scopus rating (2001): SJR 0.541 SNIP 1.208
Scopus rating (2000): SJR 0.464 SNIP 1.049
Scopus rating (1999): SJR 0.669 SNIP 1.061
Original language: English
DOIs:
10.1016/j.biortech.2012.08.048

Fluidized-bed bioreactor applications for the treatment of metal-, sulfate- and nitrate-contaminated mine waters

General information
State: Published
Ministry of Education publication type: G4 Doctoral dissertation (monograph)
Organisations: Department of Chemistry and Bioengineering
Authors: Papirio, S.
Publication date: 2012
Growth of Chlorella vulgaris and associated bacteria in photobioreactors

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Lakaniemi, A., Intihar, V. M., Tuovinen, O. H., Puhakka, J. A.
Pages: 69-78
Publication date: 2012
Peer-reviewed: Yes

Publication information
Journal: Microbial Biotechnology
Volume: 5
Issue number: 1
ISSN (Print): 0964-7562
Ratings:
Scopus rating (2016): SJR 1.207 SNIP 0.992 CiteScore 3.56
Scopus rating (2015): SJR 1.382 SNIP 1.124 CiteScore 3.59
Scopus rating (2014): SJR 1.37 SNIP 1.18 CiteScore 3.19
Scopus rating (2013): SJR 1.19 SNIP 0.985 CiteScore 3
Scopus rating (2012): SJR 1.152 SNIP 0.978 CiteScore 2.7
Scopus rating (2011): SJR 0.919 SNIP 0.761 CiteScore 1.92
Scopus rating (2010): SJR 0.856 SNIP 0.76
Scopus rating (2009): SJR 0.768 SNIP 0.661
Original language: English
DOIs: 10.1111/j.1751-7915.2011.00298.x

Bibliographical note
Contribution: organisation=keb bio,FACT1=1<br/>Publisher name: Wiley-Blackwell Publishing Ltd
Source: researchoutputwizard
Source-ID: 4643
Research output: Scientific - peer-review › Article

Growth of Dunaliella tertiolecta and associated bacteria in photobioreactors

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Lakaniemi, A., Intihar, V. M., Tuovinen, O. H., Puhakka, J. A.
Pages: 1357-1365
Publication date: 2012
Peer-reviewed: Yes

Publication information
Journal: Journal of Industrial Microbiology and Biotechnology
Volume: 39
Production of Electricity and Butanol from Microalgal Biomass in Microbial Fuel Cells

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Lakaniemi, A., Tuovinen, O. H., Puhakka, J. A.
Pages: 481-491
Publication date: 2012
Peer-reviewed: Yes

Publication information
Journal: BioEnergy Research
Volume: 5
Issue number: 2
ISSN (Print): 1939-1234
Ratings:
Scopus rating (2016): SJR 0.943 SNIP 0.932 CiteScore 2.64
Scopus rating (2015): SJR 1.317 SNIP 1.285 CiteScore 3.35
Scopus rating (2014): SJR 1.453 SNIP 1.344 CiteScore 3.64
Scopus rating (2013): SJR 1.162 SNIP 1.384 CiteScore 3.66
Scopus rating (2012): SJR 1.362 SNIP 1.645 CiteScore 4.23
Scopus rating (2011): SJR 1 SNIP 1.435 CiteScore 3.16
Scopus rating (2010): SJR 0.458 SNIP 0.671
Original language: English
DOIs:
10.1007/s12155-012-9186-2
Biogenic hydrogen and methane production from Chlorella vulgaris and Dunaliella tertiolecta biomass

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Lakaniemi, A., Hulatt, C. J., Thomas, D. N., Tuovinen, O. H., Puhakka, J. A.
Number of pages: 12
Pages: 1-12
Publication date: 2011
Peer-reviewed: Yes

Publication information
Journal: Biotechnology for Biofuels
Volume: 4
Issue number: 1
Article number: 34
ISSN (Print): 1754-6834
Ratings:
Scopus rating (2016): SJR 1.969 SNIP 1.65 CiteScore 5.89
Scopus rating (2015): SJR 2.409 SNIP 1.89 CiteScore 6.79
Scopus rating (2014): SJR 2.414 SNIP 1.722 CiteScore 5.86
Scopus rating (2013): SJR 2.17 SNIP 1.815 CiteScore 6.21
Scopus rating (2012): SJR 2.15 SNIP 1.849 CiteScore 5.7
Scopus rating (2011): SJR 2.249 SNIP 2.168 CiteScore 6.1
Scopus rating (2010): SJR 1.774 SNIP 1.745
Scopus rating (2009): SJR 1.317 SNIP 1.74
Original language: English
DOIs:
10.1186/1754-6834-4-34

Biological note
Contribution: organisation=keb bio,FACT1=1
Source: researchoutputwizard
Source-ID: 4645
Research output: Scientific - peer-review › Article

Biogenic hydrogen and methane production from reed canary grass

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Department of Chemistry and Bioengineering, Urban circular bioeconomy (UrCirBio)
Authors: Lakaniemi, A., Koskinen, P. E., Nevatalo, L. M., Kaksonen, A. H., Puhakka, J. A.
Pages: 773-780
Publication date: 2011
Peer-reviewed: Yes

Publication information
Journal: Biomass & Bioenergy
Volume: 35
Issue number: 2
ISSN (Print): 0961-9534
Ratings:
Scopus rating (2016): CiteScore 3.71 SJR 1.188 SNIP 1.368
Scopus rating (2015): SJR 1.521 SNIP 1.615 CiteScore 4.03
A luminescent Escherichia coli biosensor for the high throughput detection of beta-lactams

A group-specific bioluminescent Escherichia coli strain for studying the action of beta-lactam antibiotics is described. The strain contains a plasmid, pBlaLux1, in which the luciferase genes from Photorhabdus luminescens are inserted under the control of the beta-lactam-responsive element ampR/ampC from Citrobacter freundii. In the presence of beta-lactams, the bacterial cells are induced to express the luciferase enzyme and three additional enzymes generating the substrate for the luciferase reaction. This biosensor for beta-lactams does not need any substrate or cofactor additions, and the bioluminescence can be measured very sensitively in real time by using a luminometer. Basic parameters affecting the light production and induction in the gram-negative model organism E. coli SN0301/pBlaLux1 by various beta-lactams were studied. The dose-response curves were bell shaped, indicating toxic effects for the sensor strain at high concentrations of beta-lactams. Various beta-lactams had fairly different assay ranges: ampicillin, 0.05-1.0 µg/ml; piperacillin, 0.0025-25 µg/ml; imipenem, 0.0025-0.25 µg/ml; cephapirin, 0.025-2.5 µg/ml; cefoxitin, 0.0025-1.5 µg/ml; and oxacillin, 25-500 µg/ml. Also, the induction coefficients (signal over background noninduced control) varied considerably from 3 to 158 in a 2-hour assay. Different non-beta-lactam antibiotics did not cause induction. Because the assay can be automated using microplate technologies, the approach may be suitable for higher throughput analysis of beta-lactam action.
Comparison of the total mercury content in sediment samples with a mercury sensor bacteria test and Vibrio fischeri toxicity test

The suitability of a luminescent bacterial sensor strain Escherichia coli MC1061(pTOO11) [Virta, M.; Lampinen, J.; Karp, M. Anal Chem 1995, 67, 667-669] for the measuring of mercury from sediment samples was evaluated. The sensor strain is based on the control of expression of a reporter gene, firefly luciferase, by a mercury sensitive regulation unit. The sensor responds to mercury by increased luminescence as a consequence of increased production of the reporter protein luciferase. The method is simple to perform since the luminescence is recorded with a portable luminometer and the sensor bacteria are freeze-dried. The results obtained from river sediment samples were compared with the total mercury content of the samples, which was measured by atomic absorption spectrometry and Leco(R) Mercury analyzer and the modified photobacteria luminescence inhibition test (Lappalainen, J.; Juvonen, R.; Vaajasaari, K.; Karp, M. Chemosphere 1999, 38, 1069-1083). The correlation between the bacterial sensor results with the total mercury content, ranging from 0.01 mg/kg to 16 mg/kg, was significant with 32 samples tested (R-2 UP to 0.8115). There was no correlation between the total mercury content and toxicity measured with Vibrio fischeri in this sample panel, (C) 2000 by John Wiley & Sons, Inc.
Detecting bioavailable toxic metals and metalloids from natural water samples using luminescent sensor bacteria

We have generated microbial sensors for analyzing the presence of various metals or metalloids by recombinant DNA technology. The strains are based on strictly regulated promoters controlling the expression of the firefly luciferase gene in microbial cells. The regulator-reporter constructs are located in shuttle plasmids capable of replicating in gram-negative or -positive microbial organisms. The sensors developed are real-time indicators of metal responsive gene expression giving results in approximately 30 min, with optimal induction times ranging from 60 to 240 min. We describe here the performance of these metal sensing bacteria for the assessment of different water samples spiked with lead, arsenic, mercury or cadmium. We show that these bacteria are sensitive detectors of metal bioavailability, which is difficult or even impossible to measure by traditional analytical chemistry methods. All measurements were done using freeze-dried bacteria, which makes these sensors reagent-like and also easy to use in field conditions. (C) 2000 Elsevier Science Ltd. All rights reserved.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: Univ Turku, University of Turku, Dept Biotechnol
Authors: Tauriainen, S. M., Virta, M. P. J., Karp, M. T.
Number of pages: 6
Pages: 2661-2666
Publication date: Jul 2000
Peer-reviewed: Yes

Publication information
Journal: Water Research
Volume: 34
Issue number: 10
ISSN (Print): 0043-1354
Ratings:
Scopus rating (2016): CiteScore 7.49 SJR 2.629 SNIP 2.558
Scopus rating (2015): SJR 2.689 SNIP 2.507 CiteScore 6.63
Scopus rating (2014): SJR 2.957 SNIP 2.727 CiteScore 6.13
Scopus rating (2013): SJR 2.956 SNIP 2.693 CiteScore 6.02
Scopus rating (2012): SJR 2.966 SNIP 2.456 CiteScore 5.15
Scopus rating (2011): SJR 2.867 SNIP 2.374 CiteScore 5.43
Scopus rating (2010): SJR 2.582 SNIP 2.196
Scopus rating (2009): SJR 2.319 SNIP 2.225
Scopus rating (2008): SJR 2.065 SNIP 2.19
Scopus rating (2007): SJR 1.994 SNIP 2.208
Scopus rating (2006): SJR 1.895 SNIP 2.214
Scopus rating (2005): SJR 2.114 SNIP 2.337
Fractionation of DNA with Sephacryl S-1000(R)

In this study the application of gel filtration for purification of heterogeneous DNA is described. The fractionation of partial restriction enzyme digests of bacterial chromosomal DNA on a Sephacryl S-1000-column is easy and rapid. Simultaneously intact chromosomal DNA and low molecular weight substances are eliminated in the run. The method is also applicable to the purification of plasmid DNA, as has been previously reported (3). Thus we are able to get pure DNA with yields over 80%.

**General information**

State: Published

Ministry of Education publication type: A1 Journal article-refereed

Organisations: University of Turku

Authors: Suominen, A. I., Karp, M. T., Mäntsälä, P. I.

Number of pages: 7

Pages: 209-215

Publication date: Feb 1984

Peer-reviewed: Yes

**Publication Information**

Journal: Biochemistry Research International

Volume: 8

Issue number: 2

ISSN (Print): 2090-2247

Keywords: acrylic resins, chromatography, gel, DNA, bacterial, Escherichia coli, genes, bacterial, Geobacillus stearothermophilus, plasmids

Source: PubMed

Source-ID: 6383398

Research output: Scientific - peer-review Article

Time-resolved europium fluorescence in enzyme activity measurements: a sensitive protease assay

A method for incorporating into proteins a nonradioactive Eu3+ label, which exhibits fluorescence of a long decay time in the presence of suitable ligands, is described. As an example of the use of this label the method has been developed to work as a sensitive protease assay. By hydrolyzing the Eu3+-labeled casein, bound to an insoluble matrix (Sepharose 4B or Affi-Gel 10), with proteases and measuring the Eu3+ released with a pulsed time-resolved fluorometer it was possible to detect as low as 2.5, 1.0, or 1.0 ng of alpha-chymotrypsin, trypsin, or subtilisin, respectively.

**General information**

State: Published

Ministry of Education publication type: A1 Journal article-refereed

Organisations: University of Turku
Simultaneous extraction and combined bioluminescent assay of NAD+ and NADH

A new method for extracting pyridine nucleotides from tissue samples at room temperature that allows the simultaneous extraction of both the oxidized and reduced nucleotide when using a 70% buffered ethanol solution as the extractant has been developed. The extraction efficiencies for NAD+ and NADH were 91 and 102%, respectively. The extraction method was followed by a combined bioluminescent assay of both nucleotides. A bacterial bioluminescent system, which included luciferase and low levels of a NADH-specific oxidoreductase, was used to produce a constant light intensity directly proportional to the amount of NADH in the tissue extract sample. When the NADH had been measured, the NAD+ present in the extract was enzymatically converted to NADH by the addition of alcohol dehydrogenase, after which the second increase in light level was recorded. The sensitivity of the bioluminescent assay presented here is 5 X 10(-14) mol NADH or NAD+ per assay.

General information
State: Published
Ministry of Education publication type: A1 Journal article-refereed
Organisations: University of Turku
Authors: Karp, M. T., Raunio, R. P., Lövgren, T. N.
Number of pages: 6
Pages: 175-180
Publication date: Jan 1983
Peer-reviewed: Yes