Broad host range ProUSER vectors enable fast characterization of inducible promoters and optimization of p-coumaric acid production in *Pseudomonas putida* KT2440

*Pseudomonas putida* KT2440 has gained increasing interest as a host for the production of biochemicals. Because of the lack of a systematic characterization of inducible promoters in this strain, we generated ProUSER broad-host-expression plasmids that facilitate fast uracil-based cloning. A set of ProUSER-reporter vectors was further created to characterize different inducible promoters. The PrhaB and Pm promoters were orthogonal and showed titratable, high, and homogeneous expression. To optimize the production of p-coumaric acid, *P. putida* was engineered to prevent degradation of tyrosine and p-coumaric acid. Pm and PrhaB were used to control the expression of a tyrosine ammonia lyase or ArG* and TyrA* involved in tyrosine production, respectively. Pathway expression was optimized by modulating inductions, resulting in small-scale p-coumaric acid production of 1.2 mM, the highest achieved in *Pseudomonads* under comparable conditions. With broad-host-range compatibility, the ProUSER vectors will serve as useful tools for optimizing gene expression in a variety of bacteria.
One of the great challenges facing society is how to sustainably produce food, chemicals and other commodities required to maintain and develop our current lifestyle. To compete with and ultimately replace existing petrochemical-based manufacturing processes, the development of innovative and effective solutions is needed.

In this project we have explored the possibility of using designed consortiums for the covalorization of the main carbon sources in lignocellulosic biomass (xylose, glucose, arabinose, and acetic acid). In one study we have used pre-processing simulations, constraint-based modelling, and state-of-the-art metabolic engineering tools to develop a consortium of cells capable of efficient valorization of synthetic hemicellulosic hydrolysate. Stable co-existence and effective covalorization was achieved through niche-differentiation, auxotrophy, and adaptive evolution. In another study, stable consortia based fermentation was achieved through niche partitioning, syntrophy (auxotrophy combined with removal of inhibitory side product), and CRISPRi mediated gene silencing. The achieved results demonstrate that consortium based approaches for valorizing complex biomass and waste related carbon sources can be an attractive alternative to the design of a so-called "superbug" and can thereby add significant value to biorefineries.
Enhanced protein and biochemical production using CRISPRi-based growth switches

Production of proteins and biochemicals in microbial cell factories is often limited by carbon and energy spent on excess biomass formation. To address this issue, we developed several genetic growth switches based on CRISPR interference technology. We demonstrate that growth of *Escherichia coli* can be controlled by repressing the DNA replication machinery, by targeting *dnaA* and *oriC*, or by blocking nucleotide synthesis through *pyrF* or *thyA*. This way, total GFP-protein production could be increased by up to 2.2-fold. Single-cell dynamic tracking in microfluidic systems was used to confirm functionality of the growth switches. Decoupling of growth from production of biochemicals was demonstrated for mevalonate, a precursor for isoprenoid compounds. Mass yield of mevalonate was increased by 41%, and production was maintained for more than 45 h after activation of the *pyrF*-based growth switch. The developed methods represent a promising approach for increasing production yield and titer for proteins and biochemicals.

General information
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Organisations: Novo Nordisk Foundation Center for Biosustainability, Research Groups, Forschungszentrum Julich (FZJ)
Authors: Li, S. (Intern), Jendresen, C. B. (Intern), Grünberger, A. (Ekstern), Ronda, C. (Intern), Ingemann Jensen, S. (Intern), Noack, S. (Ekstern), Nielsen, A. T. (Intern)
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Scopus rating (2014): SJR 3.381 SNIP 2.034 CiteScore 7.23
Web of Science (2014): Indexed yes
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Scopus rating (2013): SJR 4.004 SNIP 2.185 CiteScore 8.43
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Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.032 SNIP 1.858 CiteScore 6.72
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
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ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
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Scopus rating (2010): SJR 2.373 SNIP 1.802
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.575 SNIP 1.421
Small proteins of fifty amino acids or less have been understudied due to difficulties that impede their annotation and detection. In order to obtain information on small open reading frames (sORFs) in P. putida, bioinformatic and proteomic approaches were used to identify putative small open reading frames (sORFs) in the well-characterized strain KT2440. A plasmid-based system was established for sORF validation, enabling expression of C-terminal sequential peptide affinity (SPA) tagged variants and their detection via protein immunoblotting. Out of 22 tested putative sORFs, the expression of fourteen sORFs was confirmed, where all except one are novel. All of the validated sORFs except one are located adjacent to annotated genes on the same strand and three are in close proximity to genes with known functions. These include an ABC transporter operon and the two transcriptional regulators Fis and CysB involved in biofilm formation and cysteine biosynthesis, respectively. The work sheds light on the P. putida small proteome and small protein identification, a necessary first step towards gaining insights into their functions and possible evolutionary implications.
Predictable tuning of protein expression in bacteria

We comprehensively assessed the contribution of the Shine-Dalgarno sequence to protein expression and used the data to develop EMOPEC (Empirical Model and Oligos for Protein Expression Changes; http://emopec.biosustain.dtu.dk). EMOPEC is a free tool that makes it possible to modulate the expression level of any *Escherichia coli* gene by changing only a few bases. Measured protein levels for 91% of our designed sequences were within twofold of the desired target level.

General information

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Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 20.9 SNIP 6.131 CiteScore 15.62
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
The Ssr protein (T1E_1405) from *Pseudomonas putida* DOT-T1E enables oligonucleotide-based recombineering in platform strain *P. putida* EM42

Some strains of the soil bacterium *Pseudomonas putida* have become in recent years platforms of choice for hosting biotransformations of industrial interest. Despite availability of many genetic tools for this microorganism, genomic editing of the cell factory *P. putida* EM42 (a derivative of reference strain KT2440) is still a time-consuming endeavor. In this work we have investigated the in vivo activity of the Ssr protein encoded by the open reading frame T1E_1405 from *Pseudomonas putida* DOT-T1E, a plausible functional homologue of the β protein of the Red recombination system of λ phage of *Escherichia coli*. A test based on the phenotypes of pyrF mutants of *P. putida* (the yeast's URA3 ortholog) was developed for quantifying the ability of Ssr to promote invasion of the genomic DNA replication fork by synthetic oligonucleotides. The efficiency of the process was measured by monitoring the inheritance of the changes entered into pyrF by oligonucleotides bearing mutated sequences. Ssr fostered short and long genomic deletions/insertions as well as single-base swaps not affected by mismatch repair. These results not only demonstrate the feasibility of recombineering in *P. putida*, but they also enable a suite of multiplexed genomic manipulations in this biotechnologically important bacterium.

**General information**

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Organisations: Novo Nordisk Foundation Center for Biosustainability, Bacterial Cell Factory Optimization, Research Groups, CSIC
Authors: Aparicio, T. (Ekstern), Ingemann Jensen, S. (Intern), Nielsen, A. T. (Intern), Victor de Lorenzo, V. D. (Ekstern), Martínez-García, E. (Ekstern)
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**Publication information**
Identification and validation of small proteins in *Pseudomonas putida* KT–2440

General information
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Organisations: Novo Nordisk Foundation Center for Biosustainability, Bacterial Cell Factory Optimization, iLoop
Authors: Yang, X. (Intern), Ingemann Jensen, S. (Intern), Wulff, T. (Intern), Harrison, S. J. (Intern), Long, K. S. (Intern)
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Seven gene deletions in seven days: fast generation of *Escherichia coli* strains tolerant to acetate and osmotic stress

Generation of multiple genomic alterations is currently a time consuming process. Here, a method was established that enables highly efficient and simultaneous deletion of multiple genes in *Escherichia coli*. A temperature sensitive plasmid containing arabinose inducible lambda Red recombineering genes and a rhamnose inducible flippase recombinase was constructed to facilitate fast marker-free deletions. To further speed up the procedure, we integrated the arabinose inducible lambda Red recombineering genes and the rhamnose inducible FLP into the genome of *E. coli* K-12 MG1655. This system enables growth at 37°C, thereby facilitating removal of integrated antibiotic cassettes and deletion of additional genes in the same day. Phosphorothioated primers were demonstrated to enable simultaneous deletions during one round of electroporation. Utilizing these methods, we constructed strains in which four to seven genes were deleted in *E. coli* W and *E. coli* K-12. The growth rate of an *E. coli* K-12 quintuple deletion strain was significantly improved in the presence of high concentrations of acetate and NaCl. In conclusion, we have generated a method that enables efficient and simultaneous deletion of multiple genes in several *E. coli* variants. The method enables deletion of up to seven genes in as little as seven days.
The molecular dimension of microbial species: 1. Ecological distinctions among, and homogeneity within, putative ecotypes of *Synechococcus* inhabiting the cyanobacterial mat of Mushroom Spring, Yellowstone National Park

Based on the Stable Ecotype Model, evolution leads to the divergence of ecologically distinct populations (e.g., with different niches and/or behaviors) of ecologically interchangeable membership. In this study, pyrosequencing was used to provide deep sequence coverage of *Synechococcus* psaA genes and transcripts over a large number of habitat types in the Mushroom Spring microbial mat. Putative ecological species [putative ecotypes (PEs)], which were predicted by an evolutionary simulation based on the Stable Ecotype Model (Ecotype Simulation), exhibited distinct distributions relative to temperature-defined positions in the effluent channel and vertical position in the upper 1 mm-thick mat layer. Importantly, in most cases variants predicted to belong to the same PE formed unique clusters relative to temperature and depth in the mat in canonical correspondence analysis, supporting the hypothesis that while the PEs are ecologically distinct, the members of each ecotype are ecologically homogeneous. PEs responded differently to experimental perturbations of temperature and light, but the genetic variation within each PE was maintained as the relative abundances of PEs changed, further indicating that each population responded as a set of ecologically interchangeable individuals. Compared to PEs that predominate deeper within the mat photic zone, the timing of transcript abundances for selected genes differed for PEs that predominate in microenvironments closer to upper surface of the mat with spatiotemporal differences in light and O₂ concentration. All of these findings are consistent with the hypotheses that *Synechococcus* species in hot spring mats are sets of ecologically interchangeable individuals that are differently adapted, that these adaptations control their distributions, and that the resulting distributions constrain the activities of the species in space and time.

The molecular dimension of microbial species: 2. An ecological and genomic analysis of the cyanobacterial mat of Mushroom Spring, Yellowstone National Park

This study provides a comprehensive analysis of the ecological and genomic diversity of the cyanobacterial mat of Mushroom Spring, Yellowstone National Park. It uses a combination of high-throughput sequencing and classical ecological techniques to characterize the biodiversity and ecological structure of the mat. The results highlight the importance of understanding the evolutionary and ecological dynamics of microbial communities in extreme environments such as hot springs.
Temporal metatranscriptomic patterning in phototrophic Chloroflexi inhabiting a microbial mat in a geothermal spring.

Filamentous anoxygenic phototrophs (FAPs) are abundant members of microbial mat communities inhabiting neutral and alkaline geothermal springs. Natural populations of FAPs related to Chloroflexus spp. and Roseiflexus spp. have been well characterized in Mushroom Spring, where they occur with unicellular cyanobacteria related to Synechococcus spp. strains A and B'. Metatranscriptomic sequencing was applied to the microbial community to determine how FAPs regulate their gene expression in response to fluctuating environmental conditions and resource availability over a diel period. Transcripts for genes involved in the biosynthesis of bacteriochlorophylls (BChls) and photosynthetic reaction centers were much more abundant at night. Both Roseiflexus spp. and Chloroflexus spp. expressed key genes involved in the 3-hydroxypropionate (3-OHP) carbon dioxide fixation bi-cycle during the day, when these FAPs have been thought to perform primarily photoheterotrophic and/or aerobic chemoorganotrophic metabolism. The expression of genes for the synthesis and degradation of storage polymers, including glycogen, polyhydroxyalkanoates and wax esters, suggests that FAPs produce and utilize these compounds at different times during the diel cycle. We summarize these results in a proposed conceptual model for temporal changes in central carbon metabolism and energy production of FAPs living in a natural environment. The model proposes that, at night, Chloroflexus spp. and Roseiflexus spp. synthesize BChl, components of the photosynthetic apparatus, polyhydroxyalkanoates and wax esters in concert with fermentation of glycogen. It further proposes that, in daytime, polyhydroxyalkanoates and wax esters are degraded and used as carbon and electron reserves to support photomixotrophy via the 3-OHP bi-cycle.
"Candidatus Thermochlorobacter aerophilum": an aerobic chlorophototrophic member of the phylum Chlorobi defined by metagenomics and metatranscriptomics

An uncultured member of the phylum Chlorobi, provisionally named "Candidatus Thermochlorobacter aerophilum", occurs in the microbial mats of alkaline siliceous hot springs at the Yellowstone National Park. "Ca. T. aerophilum" was investigated through metagenomic and metatranscriptomic approaches. "Ca. T. aerophilum" is a member of a novel, family-level lineage of Chlorobi, a chlorophototroph that synthesizes type-1 reaction centers and chlorosomes similar to cultivated relatives among the green sulfur bacteria, but is otherwise very different physiologically. "Ca. T. aerophilum" is proposed to be an aerobic phototroph that cannot oxidize sulfur compounds, cannot fix N2, and does not fix CO2 autotrophically. Metagenomic analyses suggest that "Ca. T. aerophilum" synthesizes bacteriochlorophyll (BChl) d, and thus it occupies a different ecological niche than other chlorosome-containing chlorophototrophs in the mat. Transcription profiling throughout a diel cycle revealed distinctive gene expression patterns. Although "Ca. T. aerophilum" probably photoassimilates organic carbon sources and synthesizes most of its cell materials during the day, it mainly transcribes genes for BChl synthesis during late afternoon and early morning, and it synthesizes and assembles its photosynthetic apparatus during the night. The ISME Journal (2012) 6, 1869-1882; doi:10.1038/ismej.2012.24; published online 29 March 2012

General information
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Organisations: Montana State University, J. Craig Venter Institute, University of Copenhagen, Pennsylvania State University
Authors: Liu, Z. (Ekstern), Klatt, C. G. (Ekstern), Ludwig, M. (Ekstern), Rusch, D. B. (Ekstern), Ingemann Jensen, S. (Intern), Kühl, M. (Ekstern), Ward, D. M. (Ekstern), Bryant, D. A. (Ekstern)
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Publication information
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Volume: 6
Fine-Scale Distribution Patterns of Synechococcus Ecological Diversity in Microbial Mats of Mushroom Spring, Yellowstone National Park

Past analyses of sequence diversity in high-resolution protein-encoding genes have identified putative ecological species of unicellular cyanobacteria in the genus Synechococcus, which are specialized to 60°C but not 65°C in Mushroom Spring microbial mats. Because these studies were limited to only two habitats, we studied the distribution of Synechococcus sequence variants at 1°C intervals along the effluent flow channel and at 80-tim vertical-depth intervals throughout the upper photic layer of the microbial mat. Diversity at the psaA locus, which encodes a photosynthetic reaction center protein (PsaA), was sampled by PCR amplification, cloning, and sequencing methods at 60, 63, and 65°C sites. The evolutionary simulation programs Ecotype Simulation and AdaptML were used to identify putative ecologically distinct populations (ecotypes). Ecotype Simulation predicted a higher number of putative ecotypes in cases where habitat variation was limited, while AdaptML predicted a higher number of ecologically distinct phylogenetic clades in cases where habitat variation was high. Denaturing gradient gel electrophoresis was used to track the distribution of dominant sequence variants of ecotype populations relative to temperature variation and to °2’ pH, and spectral irradiance variation, as measured using microsensors. Different distributions along effluent channel flow and vertical gradients, where temperature, light, and O2 concentrations are known to vary, confirmed the ecological distinctness of putative ecotypes.
In situ dynamics of O$_2$, pH and cyanobacterial transcripts associated with CCM, photosynthesis and detoxification of ROS.

The relative abundance of transcripts encoding proteins involved in inorganic carbon concentrating mechanisms (CCM), detoxification of reactive oxygen species (ROS) and photosynthesis in the thermophilic cyanobacterium Synechococcus OS-B' was measured in hot spring microbial mats over two diel cycles, and was coupled with in situ determinations of incoming irradiance and microenvironmental dynamics of O(2) and pH. Fluctuations in pH and O(2) in the mats were largely driven by the diel cycle of solar irradiance, with a pH variation from \(\approx 7.0\) to \(\approx 9.5\), and O(2) levels ranging from anoxia to supersaturation during night and day, respectively. Levels of various transcripts from mat cyanobacteria revealed several patterns that correlated with incident irradiance, O(2) and pH within the mat matrix. Transcript abundances for most genes increased during the morning dark-light transition. Some transcripts remained at a near constant level throughout the light period, whereas others showed an additional increase in abundance as the mat underwent transition from low-to-high light (potentially reflecting changes in O(2) concentration and pH), followed by either a decreased abundance in the early afternoon, or a gradual decline during the early afternoon and into the evening. One specific transcript, psbA1, was the lowest during mid-day under high irradiance and increased when the light levels declined. We discuss these complex in situ transcriptional patterns with respect to environmental and endogenous cues that might impact and regulate transcription over the diel cycle.

General information
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Organisations: University of Copenhagen, The Carnegie Institution for Science, Centre National de la Recherche Scientifique
Authors: Ingemann Jensen, S. (Intern), Steunou, A. (Ekstern), Bhaya, D. (Ekstern), Kühl, M. (Ekstern), Grossman, A. R. (Ekstern)
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Publication date: 2011
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Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
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Scopus rating (2013): SJR 4.71 SNIP 2.175 CiteScore 8.62
ISI indexed (2013): ISI indexed yes
Regulation of nif gene expression and the energetics of N2 fixation over the diel cycle in a hot spring microbial mat.

Nitrogen fixation, a prokaryotic, O2-inhibited process that reduces N2 gas to biomass, is of paramount importance in biogeochemical cycling of nitrogen. We analyzed the levels of nif transcripts of Synechococcus ecotypes, NifH subunit and nitrogenase activity over the diel cycle in the microbial mat of an alkaline hot spring in Yellowstone National Park. The results showed a rise in nif transcripts in the evening, with a subsequent decline over the course of the night. In contrast, immunological data demonstrated that the level of the NifH polypeptide remained stable during the night, and only declined when the mat became oxic in the morning. Nitrogenase activity was low throughout the night; however, it exhibited two peaks, a small one in the evening and a large one in the early morning, when light began to stimulate cyanobacterial photosynthetic activity, but O2 consumption by respiration still exceeded the rate of O2 evolution. Once the irradiance increased to the point at which the mat became oxic, the nitrogenase activity was strongly inhibited. Transcripts for proteins associated with energy-producing metabolisms in the cell also followed diel patterns, with fermentation-related transcripts accumulating at night, photosynthesis- and respiration-related transcripts accumulating during the day and late afternoon, respectively. These results are discussed with respect to the energetics and regulation of N2 fixation in hot spring mats and factors that can markedly influence the extent of N2 fixation over the diel cycle.
Different bacterial communities associated with the roots and bulk sediment of the seagrass Zostera marina

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

General information
State: Published
Organisations: University of Copenhagen
Authors: Ingemann Jensen, S. (Intern), Kuehl, M. (Ekstern), Prieme, A. (Ekstern)
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Publication date: 2007
Main Research Area: Technical/natural sciences
Oxic microzones and radial oxygen loss from roots of Zostera marina

Oxygen microelectrodes and planar oxygen optodes were used to map the microdistribution of oxygen and the radial oxygen loss (ROL) from roots of Zostera marina kept in natural sediment. Substantial heterogeneity in the oxygen distribution was seen along the roots, with oxygen mainly leaking out from the root tips. Maximum oxygen levels at the root surface reached 19 to 80 % of air saturation in the light and the oxygenated zone extended 1 to 2 mm away from the root tip. The oxygen concentration at the root surface decreased to 0-5 % of air saturation at positions 3 to 6 mm behind the root apex. The high oxygen levels at the root tip surface were due to an effective barrier to ROL on the older part of the roots and the presence of an effective gas-transport system in the plant, with numerous intercellular spaces extending...
very close to the apical meristem of the root. Radial diffusion of oxygen from the root surface created a dynamic 0 to 1 mm-wide oxic microzone around the similar to 0.3 mm wide roots of Z. marina that varied with irradiance and distance from the root tip. Rootsurface oxygen concentrations and ROL measured 2 mm behind the apex increased with increasing irradiance until ROL saturation was reached at irradiances > 400 mu mol photons m(-2) s(-1). The ROL increased from 16.2 nmol O-2 cm(-2) h(-1) in darkness to 21.6, 28.8 and 36.0 nmol O-2 cm(-2) h(-1) at incident irradiances of 25, 111 and 467 mu mol photons m(-2) s(-1), respectively. Based on measured steady-state radial oxygen profiles, the total oxygen export from one 6 cm long root of the first actively growing root bundle with a total surface area of 0.56 cm(2) was estimated to be 6.0 to 6.7 nmol O-2 h(-1) in saturating light. The total subsurface input of plant-mediated oxygen was estimated to be only in the order of 2 to 14 % of the total diffusive oxygen uptake (DOU) across the sediment-water interface. The local input of oxygen from the root tip was, however, similar to the DOU at the primary sediment-water interface, and 35 to 43 % of the total oxygen loss occurred from the outermost 0 to 3.5 mm of the root tip. The roots of Z. marina grow similar to 5 mm d(-1), and significant oxygen levels will therefore only be present at a given spot for less than 24 h during root growth. The rhizosphere of Z. marina is thus characterised by a constantly changing mosaic of ephemeral oxic microniches in the reduced sulphidic sediment, leaving behind an anoxic but oxidised zone around the more mature parts of the roots.

General information
State: Published
Organisations: University of Copenhagen
Authors: Ingemann Jensen, S. (Intern), Kühl, M. (Ekstern), Glud, R. N. (Ekstern), Jørgensen, L. B. (Ekstern), Prieme, A. (Ekstern)
Pages: 49-58
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Main Research Area: Technical/natural sciences

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- Web of Science (2015): Indexed yes
- Scopus rating (2014): CiteScore 2.75
- Web of Science (2014): Indexed yes
- Scopus rating (2013): CiteScore 2.79
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- Web of Science (2013): Indexed yes
- Scopus rating (2012): CiteScore 2.9
- ISI indexed (2012): ISI indexed no
- Web of Science (2012): Indexed yes
- Scopus rating (2011): CiteScore 2.85
- ISI indexed (2011): ISI indexed no
- Web of Science (2011): Indexed yes
- Web of Science (2010): Indexed yes
- Web of Science (2009): Indexed yes
- Web of Science (2008): Indexed yes
- Web of Science (2007): Indexed yes
- Web of Science (2006): Indexed yes
- Web of Science (2005): Indexed yes
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**COPL - COnsortia based Production of biochemicals from Lignocellulosic biomass**

Novo Nordisk Foundation Center for Biosustainability

**Bacterial Cell Factory Optimization**

*Period:* 01/07/2017 → 30/06/2020

*Number of participants:* 2

*Acronym:* COPL

*Project participant:*

Ingemann Jensen, Sheila (Intern)

*Other:*

Kjiproski, Darko (Intern)

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**Activities:**

**Sustain-ATV Conference 2016**

*Period:* 30 Nov 2016

Sheila Ingemann Jensen (Speaker)

Novo Nordisk Foundation Center for Biosustainability

Bacterial Cell Factory Optimization

**Description**

Consortia based production of biochemicals

**Related event**

**Sustain-ATV Conference 2016**

30/11/2016 → 30/11/2016

Kgs. Lyngby, Denmark

Activity: Talks and presentations › Conference presentations

**DMS Congress 2016**

*Period:* 14 Nov 2016

Sheila Ingemann Jensen (Speaker)

Novo Nordisk Foundation Center for Biosustainability

Bacterial Cell Factory Optimization

**Description**

Consortia based production of biochemicals

**Related event**

**DMS Congress 2016**

14/11/2016 → 14/11/2016

Copenhagen, Denmark

Activity: Talks and presentations › Conference presentations
IDTU advanced course - 2016
Sheila Ingemann Jensen (Participant)
Novo Nordisk Foundation Center for Biosustainability
Bacterial Cell Factory Optimization

Related event

2016 Annual NNF-CFB Seminar
Period: 28 Sep 2016 → 29 Sep 2016
Sheila Ingemann Jensen (Speaker)
Novo Nordisk Foundation Center for Biosustainability
Bacterial Cell Factory Optimization

Description
Consortia-based production of biochemicals

Related event

Informations medieskole
Period: 26 Sep 2016 → 5 Dec 2016
Sheila Ingemann Jensen (Participant)
Novo Nordisk Foundation Center for Biosustainability
Bacterial Cell Factory Optimization

Description
Informations Medieskole

Related event

Novozymes Prize Symposium
Period: 19 Nov 2015
Sheila Ingemann Jensen (Participant)
Bacterial Cell Factory Optimization
Novo Nordisk Foundation Center for Biosustainability

Related event

Novozymes Prize Symposium: Carbohydrate-active enzyme discovery, characterization and engineering
19/11/2015 → 19/11/2015
Hellerup, Denmark
Activity: Participating in or organising an event › Participating in or organising workshops, courses, seminars etc.
Basic innovation course
Period: 29 Jun 2015 → 1 Jul 2015
Sheila Ingemann Jensen (Participant)
Bacterial Cell Factory Optimization
Novo Nordisk Foundation Center for Biosustainability

Related event

Basic innovation course
29/06/2015 → 01/07/2015
Denmark
Activity: Participating in or organising an event › Participating in or organising workshops, courses, seminars etc.

Sådan skriver du en succesfuld ansøgning til Horizon 2020
Period: 2 Jun 2015
Sheila Ingemann Jensen (Participant)
Bacterial Cell Factory Optimization
Novo Nordisk Foundation Center for Biosustainability

Related event

Sådan skriver du en succesfuld ansøgning til Horizon 2020
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Denmark
Activity: Participating in or organising an event › Participating in or organising workshops, courses, seminars etc.

Novo Nordisk Foundation Conference Cell Factories and Biosustainability
Sheila Ingemann Jensen (Participant)
Bacterial Cell Factory Optimization
Novo Nordisk Foundation Center for Biosustainability

Related event

Novo Nordisk Foundation Conference Cell Factories and Biosustainability
17/05/2015 → 21/05/2015
Denmark
Activity: Participating in or organising an event › Participating in or organising workshops, courses, seminars etc.

Reviewer for NILS Science & Sustainability programme
Period: 27 Nov 2014
Sheila Ingemann Jensen (Reviewer)
Bacterial Cell Factory Optimization
Novo Nordisk Foundation Center for Biosustainability
Activity: Other › Other (prizes, external teaching and other activities) - Other

THE NOVO NORDISK PRIZE 2014
Period: 28 Apr 2014
Sheila Ingemann Jensen (Participant)
Novo Nordisk Foundation Center for Biosustainability
Bacterial Cell Factory Optimization

Description
Microbial Life Style Disease, The Novo Nordisk Prize 2014
Related event

**THE NOVO NORDISK PRIZE 2014**
28/04/2014 → 28/04/2014
Lyngby, Denmark
Activity: Participating in or organising an event › Participating in or organising workshops, courses, seminars etc.

**2013 Congress of The Danish Microbiological Society**
Period: 18 Nov 2013
Sheila Ingemann Jensen (Participant)
Bacterial Cell Factory Optimization
Novo Nordisk Foundation Center for Biosustainability

**Biomedical science week**
Period: 28 May 2013
Sheila Ingemann Jensen (Participant)
Novo Nordisk Foundation Center for Biosustainability
Bacterial Cell Factory Optimization

**2012 Symposium of The Danish Microbiological Society**
Period: 15 Nov 2012
Sheila Ingemann Jensen (Participant)
Bacterial Cell Factory Optimization
Novo Nordisk Foundation Center for Biosustainability

**Symposium in Marine Microbial Biotechnology**
Period: 15 Nov 2012 → 16 Nov 2012
Sheila Ingemann Jensen (Participant)
Novo Nordisk Foundation Center for Biosustainability
Bacterial Cell Factory Optimization

**Symposium in Marine Microbial Biotechnology**
15/11/2012 → 16/11/2012
Denmark
Activity: Participating in or organising an event › Participating in or organising workshops, courses, seminars etc.

14th International Symposium on Microbial Ecology
Sheila Ingemann Jensen (Participant)
Bacterial Cell Factory Optimization
Novo Nordisk Foundation Center for Biosustainability

Related event

14th International Symposium on Microbial Ecology: The Power of the Small
19/08/2012 → 24/08/2012
Copenhagen, Denmark
Activity: Participating in or organising an event › Participating in or organising workshops, courses, seminars etc.

2011 Symposium The Danish Microbiological Society
Period: 7 Nov 2011
Sheila Ingemann Jensen (Participant)
Bacterial Cell Factory Optimization
Novo Nordisk Foundation Center for Biosustainability

Related event

2011 Symposium The Danish Microbiological Society
07/11/2011 → …
Copenhagen, Denmark
Activity: Participating in or organising an event › Participating in or organising workshops, courses, seminars etc.

3rd Congress of European Microbiologists
Sheila Ingemann Jensen (Speaker)
Bacterial Cell Factory Optimization
Novo Nordisk Foundation Center for Biosustainability

Related event

3rd Congress of European Microbiologists
28/06/2009 → 02/07/2009
Goteborg, Sweden
Activity: Talks and presentations › Conference presentations

ISME-11 Meeting
Sheila Ingemann Jensen (Participant)
Bacterial Cell Factory Optimization
Novo Nordisk Foundation Center for Biosustainability

Related event

ISME-11 Meeting
01/01/2006 → …
Vienna, Austria.
Activity: Participating in or organising an event › Participating in or organising workshops, courses, seminars etc.