Den traditionelle metode til rensning af spildevand er baseret på aktivt slam. Metoden er effektiv overfor letnedbrydelige lægemidler, men ineffektiv overfor middelsvære og svært nedbrydelige lægemidler.

Teknologien med biofilm er testet i laboratorieskala og i pilot-skala på dels råspildevand med koncentreret indhold af lægemidler fra en kræftafdeling, dels blandet råspildevand fra et hospital, dels almindeligt råspildevand fra Herning Vand, og dels på udløbsvand fra Viby reseanlæg. Over 95% af den samlede belastning med lægemidler i miljøet kommer i dag fra almindeligt husspildevand, både fra håndkøbsmedicin og fra patienter i ambulant behandling.

Projektet gennemførte således en benchmarking af lægemiddelfjernelse på forskellige typer af spildevand, og kunne på den baggrund demonstrere, at en biofilm-baseret teknologi er langt mere effektiv end den konventionelle aktiv slam behandling, som bruges i dag. Bl.a. viser projektet, at teknologien med fordel kan anvendes til at efterpolere allerede renset spildevand, og at driftsomkostningerne til teknologien er relativt lave.

Resultaterne af projektet er så lovende, at de allerede er anvendt til at starte et nyt MUDP-projekt, MerEff, der tester teknologien til at efterpolere renset spildevand i større skala på Herning Vands reseanlæg.
Fast Inscription of Long Period Gratings in Microstructured Polymer Optical Fibers

We demonstrate 20 dB long period grating (LPG) fast inscription in microstructured polymer optical fibers (mPOFs) using a point-by-point technique obtaining an LPG total length of 25 mm. Two 248 nm UV laser pulses of 15 ns duration have been employed for every inscription point, which means a time reduction by over 21 times compared with the fastest inscription time already reported in literature. The device has been fabricated in a single-mode mPOF with a core that has been doped with benzyl dimethyl ketal for photosensitivity enhancement. Moreover, we characterize the strain and temperature responses and the stability of the fabricated gratings response under different conditions in order to assess the viability for different applications.

General information
State: Published
Organisations: Department of Photonics Engineering, Fiber Sensors and Supercontinuum Generation, Universidad Politecnica de Valencia, University of Aveiro
Authors: Min, R. (Ekstern), Marques, C. (Ekstern), Nielsen, K. (Intern), Bang, O. (Intern), Ortega, B. (Ekstern)
Pages: 1919-1923
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Scopus rating (2016): CiteScore 3.12 SJR 0.706 SNIP 1.689
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.684 SNIP 1.908 CiteScore 2.85
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.799 SNIP 1.934 CiteScore 2.5
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.666 SNIP 1.811 CiteScore 2.6
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.602 SNIP 1.445 CiteScore 2.09
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.572 SNIP 1.421 CiteScore 2.13
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.533 SNIP 1.077
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.631 SNIP 1.351
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.641 SNIP 1.371
Direct whole-genome sequencing of Plasmodium falciparum specimens from dried erythrocyte spots

Background: Plasmodium falciparum malaria remains a major health burden and genomic research represents one of the necessary approaches for continued progress towards malaria control and elimination. Sample acquisition for this purpose is troublesome, with the majority of malaria-infected individuals living in rural areas, away from main infrastructure and the electrical grid. The aim of this study was to describe a low-tech procedure to sample P. falciparum specimens for direct whole genome sequencing (WGS), without use of electricity and cold-chain. Methods: Venous blood samples were collected from malaria patients in Bandim, Guinea-Bissau and leukocyte-depleted using Plasmodipur filters, the enriched parasite sample was spotted on Whatman paper and dried. The samples were stored at ambient temperatures and subsequently used for DNA-extraction. Ratios of parasite:human content of the extracted DNA was assessed by qPCR, and five samples with varying parasitaemia, were sequenced. Sequencing data were used to analyse the sample content, as well as sample coverage and depth as compared to the 3d7 reference genome. Results: qPCR revealed that 73% of the 199 samples were applicable for WGS, as defined by a minimum ratio of parasite:human DNA of 2:1. WGS revealed an even distribution of sequence data across the 3d7 reference genome, regardless of parasitaemia. The acquired read depths varied from 16 to 99×, and coverage varied from 87.5 to 98.9% of the 3d7 reference genome. SNP-analysis of six genes, for which amplicon sequencing has been performed previously, confirmed the reliability of the WGS-data. Conclusion: This study describes a simple filter paper based protocol for sampling P. falciparum from malaria patients for subsequent direct WGS, enabling acquisition of samples in remote settings with no access to electricity.
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.001 SNIP 1.326 CiteScore 3.07
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.112 SNIP 1.276 CiteScore 3.56
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.855 SNIP 1.32 CiteScore 3.61
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.764 SNIP 1.303 CiteScore 3.56
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.783 SNIP 1.252
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.511 SNIP 1.276
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.373 SNIP 1.123
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.213 SNIP 0.995
Scopus rating (2006): SJR 1.05 SNIP 1.161
Scopus rating (2005): SJR 0.84 SNIP 0.502
Scopus rating (2004): SJR 0.541 SNIP 0.392
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Publication: Research › peer-review › Journal article – Annual report year: 2018

**Transportvaneundersøgelsen, Variabeldeklaration dataset TU0617v1**

**General information**
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Organisations: Department of Management Engineering, Transport DTU
Authors: Christiansen, H. (Intern), Warnecke, M. (Intern)
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**Determining Biodegradation Kinetics of Hydrocarbons at Low Concentrations: Covering 5 and 9 Orders of Magnitude of Kow and Kaw**
A partitioning-based experimental platform was developed and applied to determine primary biodegradation kinetics of 53 hydrocarbons at ng/L to μg/L concentrations covering C8-C20, 11 structural classes, and several orders of magnitude in hydrophobicity and volatility: (1) Passive dosing from a loaded silicone donor was used to set the concentration of each hydrocarbon in mixture stock solutions; (2) these solutions were combined with environmental water samples in gastight
auto sampler vials for 1-100 days incubation, and (3) automated solid phase microextraction (SPME) coupled to GC-MS was applied directly on these test systems for measuring primary biodegradation relative to abiotic controls. First order biodegradation kinetics were obtained for 40 hydrocarbons in activated sludge filtrate, 18 in seawater, and 21 in lake water. Water phase half-lives in seawater and lake water were poorly related to hydrophobicity and volatility but were, with a few exceptions, within a factor of 10 or shorter than BioHCwin predictions. The most persistent hydrocarbons, 1,1,4,4,6-pentamethyldecalin, perhydropyrene, 1,2,3,6,7,8-hexahydropyrene, and 2,2,4,4,6,8,8-heptamethylnonane, showed limited or inconsistent degradation in all three environmental media. This biodegradation approach can cover a large chemical space at low substrate concentrations, which makes it highly suited for optimizing predictive models for environmental biodegradation.

**General information**
State: Published
Organisations: Department of Environmental Engineering, Environmental Fate & Effect of Chemicals
Authors: Birch, H. (Intern), Høst Hammershøj, R. (Intern), Mayer, P. (Intern)
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Scopus rating (2016): CiteScore 6.26 SJR 2.538 SNIP 1.889
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 2.584 SNIP 1.828 CiteScore 5.61
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.777 SNIP 2.017 CiteScore 5.5
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 2.956 SNIP 2.103 CiteScore 5.52
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.146 SNIP 2.056 CiteScore 5.17
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.178 SNIP 1.953 CiteScore 5.16
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 2.964 SNIP 1.729
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 2.835 SNIP 1.803
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 2.943 SNIP 1.942
Web of Science (2008): Indexed yes
Prevalence and risk factors for CTX-M gram-negative bacteria in hospitalized patients at a tertiary care hospital in Kilimanjaro, Tanzania

Emergence and spread of extended spectrum beta-lactamase (ESBL)-producing gram-negative bacteria, mainly due to CTX-M, is a major global public health problem. Patients infected with ESBL-producing gram-negative bacteria have an increased risk of treatment failure and death. We investigated the prevalence and risk factors for CTX-M gram-negative bacteria isolated from clinical specimens of patients hospitalized at a tertiary care hospital in Kilimanjaro, Tanzania. Isolated gram-negative bacteria from inpatients admitted at Kilimanjaro Christian Medical Centre (KCMC) between August 2013 and August 2015 were fully genome sequenced. The prevalence of ESBL-producing gram-negative bacteria was determined based on the presence of blaCTX-M. The odds ratio (OR) and risk factors for ESBL-producing gram-negative bacteria due to CTX-M were assessed using logistic regression models. The overall CTX-M prevalence (95% CI) was 13.6% (10.1–18.1). Adjusted for other factors, the OR of CTX-M gram-negative bacteria for patients previously hospitalized was 0.26 (0.08–0.88), p = 0.031; the OR for patients currently on antibiotics was 4.02 (1.29–12.58), p = 0.017; the OR for patients currently on ceftriaxone was 0.14 (0.04–0.46), p = 0.001; and the OR for patients with wound infections was 0.24 (0.09–0.61), p = 0.003. The prevalence of ESBL-producing gram-negative bacteria due to CTX-M in this setting is relatively low compared to other previous reports in similar settings. However, to properly stop further spread in the hospital, we recommend setting up a hospital surveillance system that takes full advantage of the available next-generation sequencing facility to routinely screen for all types of bacterial resistance genes.

General information

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Organisations: Department of Bio and Health Informatics, Genomic Epidemiology, National Food Institute, Research Group for Genomic Epidemiology, Kilimanjaro Christian Medical Centre, Kilimanjaro Christian Medical University College, University of Copenhagen, East African Health Research Commission
Authors: Sonda, T. (Ekstern), Kumburu, H. (Ekstern), van Zwetselaar, M. (Ekstern), Alifrangis, M. (Ekstern), Mmbaga, B. T. (Ekstern), Lund, O. (Intern), Møller Aarestrup, F. (Intern), Kibiki, G. (Ekstern)
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We demonstrate a robust, compact, portable and efficient upconversion detector (UCD) for a differential absorption lidar (DIAL) system designed for range-resolved methane (CH4) atmospheric sensing. The UCD is built on an intracavity pump system that mixes a 1064 nm pump laser with the lidar backscatter signal at 1646 nm in a 25-mm long periodically poled lithium niobate crystal. The upconverted signal at 646 nm is detected by a photomultiplier tube (PMT). The UCD with a noise equivalent power around 127 fW/Hz1/2 outperforms a conventional InGaAs based avalanche photodetector when both are used for DIAL measurements. Using the UCD, CH4 DIAL measurements have been performed yielding differential absorption optical depths with relative errors of less than 11% at ranges between 3 km and 9 km.
General information
State: Published
Organisations: Department of Photonics Engineering, Optical Sensor Technology, German Aerospace Center (DLR), NLIR ApS
Authors: Meng, L. (Intern), Fix, A. (Ekstern), Wirth, M. (Ekstern), Høgstedt, L. (Ekstern), Tidemand-Lichtenberg, P. (Intern), Pedersen, C. (Intern), Rodrigo, P. J. (Intern)
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Scopus rating (2016): CiteScore 3.48 SJR 1.487 SNIP 1.589
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.976 SNIP 1.755 CiteScore 3.78
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.349 SNIP 2.166 CiteScore 4.18
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 2.358 SNIP 2.226 CiteScore 4.38
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.587 SNIP 2.145 CiteScore 3.85
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 2.579 SNIP 2.606 CiteScore 4.04
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 2.943 SNIP 2.466
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.092 SNIP 2.669
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.195 SNIP 2.393
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 3.27 SNIP 2.032
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 3.233 SNIP 2.326
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 3.334 SNIP 2.379
Web of Science (2005): Indexed yes
Multiplex PCR for detection of plasmid-mediated colistin resistance determinants, mcr-1, mcr-2, mcr-3, mcr-4 and mcr-5 for surveillance purposes

Background and aim: Plasmid-mediated colistin resistance mechanisms have been identified worldwide in the past years. A multiplex polymerase chain reaction (PCR) protocol for detection of all currently known transferable colistin resistance genes (mcr-1 to mcr-5, and variants) in Enterobacteriaceae was developed for surveillance or research purposes.

Methods: We designed four new primer pairs to amplify mcr-1, mcr-2, mcr-3 and mcr-4 gene products and used the originally described primers for mcr-5 to obtain a stepwise separation of ca 200 bp between ampli-cons. The primer pairs and amplification conditions allow for single or multiple detection of all currently described mcr genes and their variants present in Enterobacteriaceae. The protocol was validated testing 49 European Escherichia coli and Salmonella isolates of animal origin. Results: Multiplex PCR results in bovine and porcine isolates from Spain, Germany, France and Italy showed full concordance with whole genome sequence data. The method was able to detect mcr-1, mcr-3 and mcr-4 as singletons or in different combinations as they were present in the test isolates. One new mcr-4 variant, mcr-4.3, was also identified. Conclusions: This method allows rapid identification of mcr-positive bacteria and overcomes the challenges of phenotypic detection of colistin resistance. The multiplex PCR should be particularly interesting in settings or laboratories with limited resources for performing genetic analysis as it provides information on the mechanism of colistin resistance without requiring genome sequencing.

General information
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Authors: Rebelo, A. R. (Intern), Bortolaia, V. (Intern), Kjeldgaard, J. S. (Intern), Karlsmose Pedersen, S. (Intern), Leekitcharoenphon, P. (Intern), Hansen, I. M. (Intern), Guerra, B. (Ekstern), Malorny, B. (Ekstern), Borowiak, M. (Ekstern), Hammerl, J. A. (Ekstern), Battisti, A. (Ekstern), Franco, A. (Ekstern), Alba, P. (Ekstern), Perrin-Guyomard, A. (Ekstern), Granier, S. A. (Ekstern), de Frutos, C. (Ekstern), Escobar (Ekstern), Malhotra-Kumar, S. (Ekstern), Villa, L. (Ekstern), Carattoli, A. (Ekstern), Hendriksen, R. S. (Intern)
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Web of Science (2018): Indexed yes
Experimentally validated dispersion tailoring in a silicon strip waveguide with alumina thin-film coating

We propose a silicon strip waveguide structure with alumina thin-film coating in-between the core and the cladding for group-velocity dispersion tailoring. By carefully designing the core dimension and the coating thickness, a spectrally-flattened near-zero anomalous group-velocity dispersion within the telecom spectral range is obtained, which is predicted to significantly broaden the bandwidth of four-wave mixing. We validate this by characterizing the wavelength conversion in a waveguide sample by atomic layer deposition technology, which to our best knowledge is the first experimental demonstration of the proposed structure. Due to the alumina thin-film coating, the wavelength conversion bandwidth reaches $58\text{ nm}$, an increase by a factor of 1.3 compared to the corresponding structure without coating. This method can also be applied to other material platforms and applications requiring accurate group-velocity dispersion control.

General information
State: Published
Organisations: Department of Photonics Engineering, Fiber Optics, Devices and Non-linear Effects, Centre of Excellence for Silicon Photonics for Optical Communications, Diode Lasers and LED Systems, Nanophotonic Devices, High-Speed Optical Communication, National University of Defense Technology, Technical University of Denmark
Authors: Guo, K. (Ekstern), Christensen, J. B. (Intern), Shi, X. (Ekstern), Christensen, E. N. (Intern), Lin, L. (Intern), Ding, Y. (Intern), Ou, H. (Intern), Rottwitt, K. (Intern)
Number of pages: 9
Publication date: 6 Feb 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: IEEE Photonics Journal
Volume: 10
Mid-IR hyperspectral imaging for label-free histopathology and cytology

Mid-infrared (MIR) imaging has emerged as a valuable tool to investigate biological samples, such as tissue histological sections and cell cultures, by providing non-destructive chemical specificity without recourse to labels. While feasibility studies have shown the capabilities of MIR imaging approaches to address key biological and clinical questions, these techniques are still far from being deployable by non-expert users. In this review, we discuss the current state of the art of MIR technologies and give an overview on technical innovations and developments with the potential to make MIR imaging systems more readily available to a larger community. The most promising developments over the last few years are discussed here. They include improvements in MIR light sources with the availability of quantum cascade lasers and supercontinuum IR sources as well as the recently developed upconversion scheme to improve the detection of MIR radiation. These technical advances can substantially speed up data acquisition of multispectral or hyperspectral datasets thus providing the end user with vast amounts of data when imaging whole tissue areas of many mm². Therefore, effective data analysis is of tremendous importance, and progress in method development is discussed with respect to the specific biomedical context.

General information

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Organisations: Department of Photonics Engineering, Optical Sensor Technology, University of Exeter, Humboldt-Universitat zu Berlin, Gloucestershire Hospitals NHS Foundation Trust
Cryogenic Preamplifiers for Magnetic Resonance Imaging

Pursuing the ultimate limit of detection in magnetic resonance imaging (MRI) requires cryogenics to decrease the thermal noise of the electronic circuits. As cryogenic coils for MRI are slowly emerging cryogenic preamplifiers are required to fully exploit their potential. A cryogenic preamplifier operated at 77 K is designed and implemented for C imaging at 3 T (32.13 MHz), using off-the-shelves components. The design is based on a high electron mobility transistor (ATF54143) in a common source configuration. Required auxiliary circuitry for optimal cryogenic preamplifier performance is also presented consisting of a voltage regulator (noise free supply voltage and optimal power consumption), switch, and trigger (for active detuning during transmission to protect the preamplifier). A gain of 18 dB with a noise temperature of 13.7 K is achieved. Performing imaging experiments in a 3 T scanner showed an 8% increased signal-to-noise ratio from 365 to 399 when lowering the temperature of the preamplifier from 296 to 77 K while keeping the coil at room temperature. This paper thus enables the merger of cryogenic coils and preamplifiers in the hopes of reaching the ultimate limit of detection for MRI.
Column leaching from a Danish forest soil amended with wood ashes: fate of major and trace elements

Application of wood ashes onto two Danish forest soil horizons (A- and O-horizons) was investigated through a series of column experiments for ash dosages of 3, 9 and 30 Mg ha$^{-1}$. Developments in the composition of the percolating soil solutions were investigated both in a short-term (below 0.5 m$^3$ m$^{-2}$ of infiltrating water) and long-term perspective (until 2.0 m$^3$ m$^{-2}$ of infiltrating water). The higher the ash dosage, the higher the percolation of readily soluble elements (K, Cl, Mg and S) occurred within a short-term perspective. This initial washout of soluble elements resulted in the exchange of ions in the soil, thereby causing other soil bound elements to be released and the pH to decrease temporarily. Wood ash application also promoted an increase in the long-term leaching of As, Cu, K, P and Si beyond the O-horizon layer (until $\sim$2.0 m$^3$ m$^{-2}$), while the migration of trace elements through this soil horizon appeared to be of limited concern compared with Danish groundwater quality criteria. Relatively similar effects were observed for both the use of 3 and 9 Mg ha$^{-1}$ dosages on the composition of the percolating soil solutions. Low mobility of Cd, Co, Cr, Cu, Mo, Ni, Pb, Se, V and Zn was observed. The released amounts were generally limited to a few percentage points of their total contents in the columns. The potential accumulation of trace elements within the forest soil should be evaluated with respect to the specific case, if high ash dosages are intended for spreading.
Occurrence of cyclic imines in European commercial seafood and consumers risk assessment

Cyclic imines constitute a quite recently discovered group of marine biotoxins that act on neural receptors and that bioaccumulate in seafood. They are grouped together due to the imino group functioning as their common pharmacore, responsible for acute neurotoxicity in mice. Cyclic imines (CIs) have not been linked yet to human poisoning and are not regulated in the European Union (EU), although the European Food Safety Authority (EFSA) requires more data to perform conclusive risk assessment for consumers. Several commercial samples of bivalves including raw and processed samples from eight countries (Italy, Portugal, Slovenia, Spain, Ireland, Norway, The Netherlands and Denmark) were obtained over 2 years. Emerging cyclic imine concentrations in all the samples were analysed on a LC-3200QTRAP and LC-HRMS QExactive mass spectrometer. In shellfish, two CIs, pinnatoxin G (PnTX-G) and 13-desmethylspirolide C (SPX-1) were found at low concentrations (0.1–12 µg/kg PnTX-G and 26–66 µg/kg SPX-1), while gymnodimines and pteriatoxins were not detected in commercial (raw and processed) samples. In summary, SPX-1 (n: 47) and PnTX-G (n: 96) were detected in 9.4% and 4.2% of the samples, respectively, at concentrations higher than the limit of quantification (LOQ), and in 7.3% and 31.2% of the samples at concentrations lower than the LOQ (25 µg/kg for SPX-1 and 3 µg/kg for PnTX-G), respectively. For the detected cyclic imines, the average exposure and the 95th percentile were calculated. The results obtained indicate that it is unlikely that a potential health risk exists through the seafood diet for CIs in the EU. However, further information about CIs is necessary in order to perform a conclusive risk assessment.

General information
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Organisations: National Food Institute, Research Group for Analytical Food Chemistry, IRTA - Institute of Agrifood Research and Technology, Norwegian Veterinary Institute, National Research Council of Canada, Ghent University, I.P. (IPMA), Aeiforia s.r.l, University of Maribor, Wageningen University & Research, AquaTT
Aberrant intestinal microbiota in individuals with prediabetes

Aims/hypothesis: Individuals with type 2 diabetes have aberrant intestinal microbiota. However, recent studies suggest that metformin alters the composition and functional potential of gut microbiota, thereby interfering with the diabetes-related microbial signatures. We tested whether specific gut microbiota profiles are associated with prediabetes (defined as fasting plasma glucose of 6.1–7.0 mmol/l or HbA1c of 42–48 mmol/mol [6.0–6.5%]) and a range of clinical biomarkers of poor metabolic health. Methods: In the present case–control study, we analysed the gut microbiota of 134 Danish adults with prediabetes, overweight, insulin resistance, dyslipidaemia and low-grade inflammation and 134 age- and sex-matched individuals with normal glucose regulation. Results: We found that five bacterial genera and 36 operational taxonomic units (OTUs) were differentially abundant between individuals with prediabetes and those with normal glucose regulation. At the genus level, the abundance of Clostridium was decreased (mean log2 fold change −0.64 (SEM 0.23), \(p_{\text{adj}} = 0.0497\)), whereas the abundances of Dorea, \([\text{Ruminococcus}]\), Sutterella and Streptococcus were increased (mean log2 fold change 0.51 (SEM 0.12), \(p_{\text{adj}} = 5 \times 10^{-4}\); 0.51 (SEM 0.11), \(p_{\text{adj}} = 1 \times 10^{-4}\); 0.60 (SEM 0.21), \(p_{\text{adj}} = 0.0497\); and 0.92 (SEM 0.21), \(p_{\text{adj}} = 4 \times 10^{-4}\), respectively). The two OTUs that differed the most were a member of the order Clostridiales (OTU 146564) and Akkermansia muciniphila, which both displayed lower abundance among individuals with prediabetes (mean log2 fold change −1.74 (SEM 0.41), \(p_{\text{adj}} = 2 \times 10^{-3}\) and −1.65 (SEM 0.34), \(p_{\text{adj}} = 4 \times 10^{-4}\), respectively). Faecal transfer from donors with prediabetes or screen-detected, drug-naive type 2 diabetes to germfree Swiss Webster or conventional C57BL/6 J mice did not induce impaired glucose regulation in recipient mice. Conclusions/interpretation: Collectively, our data show that individuals with prediabetes have aberrant intestinal microbiota characterised by a decreased abundance of the genus Clostridium and the mucin-degrading bacterium A. muciniphila. Our findings are comparable to observations in overt chronic diseases characterised by low-grade inflammation.

General information
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Organisations: National Food Institute, Research Group for Gut Microbiology and Immunology, Copenhagen Center for Health Technology, Department of Mechanical Engineering, University of Copenhagen, University of Gothenburg, Research Centre for Prevention and Health, Aalborg University, Novo Nordisk AS, Lund University, Umeå University, Harvard University, Syddansk Universitet, Aarhus University
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Main Research Area: Technical/natural sciences
Linking secondary metabolites to gene clusters through genome sequencing of six diverse Aspergillus species

The fungal genus of Aspergillus is highly interesting, containing everything from industrial cell factories, model organisms, and human pathogens. In particular, this group has a prolific production of bioactive secondary metabolites (SMs). In this work, four diverse Aspergillus species (A. campestris, A. novofumigatus, A. ochraceoroseus, and A. steynii) have been whole-genome PacBio sequenced to provide genetic references in three Aspergillus sections. A. taichungensis and A. candidus also were sequenced for SM elucidation. Thirteen Aspergillus genomes were analyzed with comparative genomics to determine phylogeny and genetic diversity, showing that each presented genome contains 15–27% genes not found in other sequenced Aspergilli. In particular, A. novofumigatus was compared with the pathogenic species A. fumigatus. This suggests that A. novofumigatus can produce most of the same allergens, virulence, and pathogenicity factors as A. fumigatus, suggesting that A. novofumigatus could be as pathogenic as A. fumigatus. Furthermore, SMs were linked to gene clusters based on biological and chemical knowledge and analysis, genome sequences, and predictive algorithms. We thus identify putative SM clusters for aflatoxin, chlorflavonin, and ochrindol in A. ochraceoroseus, A. campestris, and A. steynii, respectively, and novofumigatonin, ent-cycloechinulin, and epi-asazonalenins in A. novofumigatus. Our study delivers six fungal genomes, showing the large diversity found in the Aspergillus genus; highlights the potential for discovery of beneficial or harmful SMs; and supports reports of A. novofumigatus pathogenicity. It also shows how biological, biochemical, and genomic information can be combined to identify genes involved in the biosynthesis of specific SMs.

General information

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Organisations: Department of Biotechnology and Biomedicine, Network Engineering of Eukaryotic Cell factories, Fungal Chemodiversity, Natural Product Discovery, Department of Biotechnology, Eukaryotic Molecular Cell Biology, U.S. Department of Energy, University of Manchester
Fast and stable gratings inscription in POFs made of different materials with pulsed 248 nm KrF laser

This paper presents fiber Bragg grating (FBG) inscription with a pulsed 248 nm UV KrF laser in polymer optical fibers (POFs) made of different polymers, namely polymethyl methacrylate (PMMA), cyclic-olefin polymer and co-polymer, and Polycarbonate. The inscribed gratings and the corresponding inscription parameters are compared with grating inscribed in POFs made of the aforementioned materials but with the hitherto most used laser for inscription, which is a continuous wave 325 nm UV HeCd laser. Results show a reduction of the inscription time of at least 16 times. The maximum time reduction is more than 130 times. In addition, a reflectivity and a bandwidth close to or higher than the ones with the 325 nm laser were obtained. The polymer optical fiber Bragg gratings (POFBGs) inscribed with the 248 nm laser setup present high stability with small variations in their central wavelength, bandwidth, and reflectivity after 40 days.

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Formalization of the Resolution Calculus for First-Order Logic
I present a formalization in Isabelle/HOL of the resolution calculus for first-order logic with formal soundness and completeness proofs. To prove the calculus sound, I use the substitution lemma, and to prove it complete, I use Herbrand interpretations and semantic trees. The correspondence between unsatisfiable sets of clauses and finite semantic trees is formalized in Herbrand's theorem. I discuss the difficulties that I had formalizing proofs of the lifting lemma found in the literature, and I formalize a correct proof. The completeness proof is by induction on the size of a finite semantic tree. Throughout the paper I emphasize details that are often glossed over in paper proofs. I give a thorough overview of formalizations of first-order logic found in the literature. The formalization of resolution is part of the IsaFoL project, which is an effort to formalize logics in Isabelle/HOL.

General information
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Radiative MRI Coil Design Using Parasitic Scatterers: MRI Yagi

Conventionally, radiofrequency (RF) coils used for magnetic resonance imaging (MRI) are electrically small and designed for nearfield operation. Therefore, existing antenna design techniques are mostly irrelevant for RF coils. However, the use of higher frequencies in ultrahigh field (UHF) MRI allows for antenna design techniques to be adapted to RF coil designs. This study proposes the use of parasitic scatterers to improve the performance of an existing 7T MRI coil called the single-sided adapted dipole (SSAD) antenna. The results reveal that scatterers arranged in a Yagi fashion can be applied to reduce local specific absorption rate (SAR) maxima of a reference SSAD by 40% with only a 6% decrease in the propagated $B_1^+$ field at the tissue depth of 15 cm. The higher directivity of the proposed design also decreasing the coupling with additional elements, making this antenna suitable for use in high density arrays. These findings show the potential of parasitic scatterers as an effective method to improve the performance of existing radiative MRI coils.

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Approximation of ruin probabilities via Erlangized scale mixtures

In this paper, we extend an existing scheme for numerically calculating the probability of ruin of a classical Cramér–Lundberg reserve process having absolutely continuous but otherwise general claim size distributions. We employ a dense class of distributions that we denominate Erlangized scale mixtures (ESM) that correspond to nonnegative and absolutely continuous distributions which can be written as a Mellin–Stieltjes convolution $\Pi^\ast G$ of a nonnegative distribution.
Π with an Erlang distribution G. A distinctive feature of such a class is that it contains heavy-tailed distributions. We suggest a simple methodology for constructing a sequence of distributions having the form Π•G with the purpose of approximating the integrated tail distribution of the claim sizes. Then we adapt a recent result which delivers an explicit expression for the probability of ruin in the case that the claim size distribution is modeled as an Erlangized scale mixture. We provide simplified expressions for the approximation of the probability of ruin and construct explicit bounds for the error of approximation. We complement our results with a classical example where the claim sizes are heavy-tailed.