17th EURO BIOTECHNOLOGY CONGRESS

September 25-27, 2017 Berlin, Germany

Scientific Tracks & Abstracts

Day 1

Sessions:

Environmental Biotechnology | Industrial and Microbial Biotechnology | Plant and Agriculture Biotechnology

Session Chair
Fuad Fares
University of Haifa, Israel

Session Co-Chair
Elizabeth E Hood
Arkansas State University, USA

Session Introduction

Title: **Early phase value scan for biotechnology innovation**
Mark JC Nuijten, A2M, Netherlands

Title: **Identification and cytogenetic characteristics of oat DH lines obtained by wide crossing with maize**
Tomasz Warzecha, Agricultural University of Kraków, Poland

Title: **Mapping and detection of phylloxera in vineyards using UAVs, hyperspectral remote sensing and artificial intelligence**
Felipe Gonzalez, Queensland University of Technology, Australia

Title: **Molecular cloning and characterization of the small heat shock protein family in the spruce budworm, Choristoneura fumiferana**
Guoxing Quan, Great Lakes Forestry Centre, Canada

Title: **Kinetic parameters of adsorption of pesticides in an organic matrix with agro-industrial and lignocellulosic residues for a bio-purification system**
Maria Cristina Diez, University of La Frontera, Chile

Title: **Hyper cellulase-producing fungus *Talaromyces pinophilus* EMM development through random mutagenesis and genetic engineering**
Anli Geng, BioEnergy Society of Singapore, Singapore

Mark Nuijten, J Biotechnol Biomater 2017, 7:3(Suppl)
DOI: 10.4172/2155-952X-C1-076

Early phase value scan for biotechnology innovation

Mark Nuijten
A2M, Netherlands

Background: Registration of a medicinal product by EMA or FDA used to be the main determinant for the future sales forecast of the product and would justify a higher valuation of the share of the company, especially for a biotech company with only a limited number of products. Contrary, new emerging requirements for reimbursement authorities, payers and drug policy changes are increasingly going to determine the actual future sales and the actual post-launch costs. The current most important criteria for coverage decisions are effectiveness, cost-effectiveness and budgetary impact, which are taken into consideration to make a value for money decision. As the future financial performance of a pharmaceutical company is directly related to the free cash flow of a new drug, an appropriate assessment of the potential sales forecast of a portfolio of forthcoming new drugs is an important predictor of the economic value of a pharmaceutical company. Today, such an assessment should include the estimated effects of the new emerging requirements for reimbursement authorities, payers and the effects of other pharma policy changes, as pay-for-performance based financial agreements.

Objective: This presentation aims to provide a strategic value scan for biotechnology products at the early onset of the development program considering the emerging hurdles for market access. The application of the early phase scan will be based on a hypothetical new innovative drug in breast cancer.

Methods: The outcomes of the strategic value scan are determined by the key decision criteria: efficacy and safety, cost-effectiveness, budget impact and additional criteria may be included depending on the disease area. The input of the strategic scan is based on a sales forecast model, a cost-effectiveness model, and a pricing model, which are interacted and executed simultaneously. The strategic value scan will provide guidance on the position of the new product in the treatment pattern for each scenario and the expected comparators in each position. The cost-effectiveness model and pricing model will provide upper limits for the pricing potential for each scenario and the expected comparators in each position. These outcomes can be linked with a discounted cash flow model to optimize the economic value of the biotechnology company taken into considerations the hurdles for reimbursement and market access. The value scan includes various scenarios (e.g. negative, base case and optimistic) for the expected clinical profile of the new product and the positioning of the new product in the treatment pattern (e.g. 1-line, 2-line, 3-line treatment). It is important to predict the incremental benefit of the new product versus the relevant expected comparators at each possible position. Changes in design of the forthcoming clinical trial or positioning of the new product may increase the economic value of the company. For example, health economic data (effectiveness and resource utilisation) may be collected alongside the forthcoming clinical trial, which may be used as input for the health economic models.

Conclusion: We present a novel approach for the early phase valuation of biotechnology products from a broader perspective by bridging concepts from health economics, market access, pricing and the economics of business economic valuation.

Biography

Mark Nuijten trained as a Physician and worked in clinical practice before completing an international MBA from Erasmus University, Rotterdam. He completed his PhD in Health Economics at the Erasmus University, Rotterdam, in 2003 and the thesis entitled as "In search of more confidence in health economic modeling". He was Board Director of ISPOR (2002-2004) and Chair of the Management Board of Value in Health (2002-2004). He is a pioneer in the field of Healthcare Innovation in Biotechnology and Nutrition, and has been the first classical health economist successfully applying and developing sales forecast methodologies for valuation of biotechnology companies. Prior to setting up A2M, he was a partner with MEDTAP International. As a VP Business Development for Europe, he established global Pricing and Reimbursement Consultancy Services for MEDTAP. Before MEDTAP, he was a Managing Director of the Quintiles office in the Netherlands.

mark@a2m.nl

Tomasz Warzecha et al., J Biotechnol Biomater 2017, 7:3(Suppl)
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Identification and cytogenetic characteristics of oat DH lines obtained by wide crossing with maize

Tomasz Warzecha[1], Dominika Idziak-Helmcke[2], Magdalena Rojek[2], Marta Hosiawa-Barańska[2], Agnieszka Sutkowska[1], Angelika Noga[3], Izabela Marcińska[3], Ilona Czyczyło-Mysza[3], Marzena Warchoł[3], Kinga Dziurka[3] and **Edyta Skrzypek[3]**

[1]Agricultural University of Kraków, Poland

[2]University of Silesia in Katowice, Poland

[3]The Franciszek Górski Institute of Plant Physiology-Polish Academy of Sciences, Poland

One of the most effective ways to generate oat DH lines is to perform a wide crossing with maize. An elevated level of homozygosity possessed by DH lines is a feature desirable for the durability of certain characteristics of new autogamous cultivars. Unlike other cereals, oat can form stable and fertile partial hybrids after pollinating with maize, since oat is able to retain one or more maize chromosomes without a lethal effect. The identification of an oat-maize addition lines could help in the selection of partial hybrids and describing the impact of additional chromosomes on the morphological and agricultural features of oat. The aim of the study was to detect maize DNA introgression into the oat genome using the PCR technique. To establish whether maize genomic DNA was present in oat DH lines, a fragment of maize-specific retro-transposon Grande1 (500 bp) was amplified and was detected after an electrophoresis in an agarose gel. All DH lines with detected fragments of retro-transposon Grande1 were analyzed with genomic in situ hybridization to detect and visualize maize chromosomes. Among the 94 oat DH lines that were obtained, 47 retained the maize chromatin, as inferred from the presence of a fragment of the Grande1 retro-transposon. Fertile lines that produced grains underwent GISH analysis, which revealed from 1 to 4 maize additional chromosomes. Aside from whole maize chromosomes, a banding pattern was also observed in most cases, which presumably co-localized with 25S rDNA sites. Additional hybridization signals were detected in 2-3 chromosome pairs depending on the analyzed line. These signals might correspond to oat's 5S rDNA sites, although it cannot be eliminated that these sequences originated from the maize genome and were inserted into oat chromosomes.

Acknowledgement: Research funded by National Centre for Research and Development, No. PBS3/B8/17/2015

Biography

Tomasz Warzecha has completed his PhD in 2001 from Agricultural University in Kraków, Poland. He has participated at the International Postgraduate Course on Biotechnology in Agriculture, Plants and Microorganisms at the Hebrew University of Jerusalem. Additionally completed the Pedagogical Studium, majored in Biology and Chemistry at Jagiellonian University in Krakow, Poland. He has worked in a project focused to examine natural variation in the recombination pathways in maize at the Department of Plant Breeding and Genetics at Cornell University, Ithaca, USA.

rrwarzec@cyf-kr.edu.pl

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Felipe Gonzalez et al., J Biotechnol Biomater 2017, 7:3(Suppl)
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Mapping and detection of phylloxera in vineyards using UAVs, hyperspectral remote sensing and artificial intelligence

Felipe Gonzalez[1,2], **Fernando Vanegas**[1,2], **Dmitry Bratanov**[1], **John Weiss**[2,3] and **Kevin S Powell**[2,4]
[1]Queensland University of Technology, Brisbane, Australia
[2]Plant Biosecurity Cooperative Research Centre, Australia
[3]AgriBio Centre, Australia
[4]Agriculture Victoria, Rutherglen, Australia

The use of unmanned aerial vehicles (UAVS) or drones in agriculture and plant biosecurity is rapidly increasing. Grape phylloxera (*Daktulsphaira vitifoliae* Fitch) is a serious economically important invasive insect pest of European grapevine (*Vitis vinifera* L). Although widely present in most grape-growing countries worldwide, its distribution within Australia is limited, mainly due to strict biosecurity measures in place at farm, regional and state levels. As the insect is very small, and primarily lives underground on the roots of the grapevines, it is very hard to detect until the symptoms of infestation appear (slow stunted growth and premature yellowing of leaves), usually after 2-3 years (although in some instances this can be longer). This research, part of a Plant Biosecurity CRC project on "Optimising plant biosecurity surveillance protocols for remote sensing using unmanned aerial systems", evaluates the use of UAV based high resolution RBG, thermal, multi- and hyper-spectral imagery at detecting symptoms of phylloxera infestation at two different vineyards, multi-variety grapevines, at two separate time periods and under different levels of phylloxera infestation. Early detection of phylloxera within the first year would allow vineyard managers to implement phytosanitary measures to restrict or slow the spread of the pest and reduce future costs and losses in production. Previous research indicated that early infection of grapevines by phylloxera can be detected with hand-held spectro-radiometers and changes in leaf and canopy level reflectance were associated with changes in leaf chemistry. Datasets from each imagery type are compared to existing phylloxera detection practices; visual inspection, ground-based insect traps, soil DNA probes as well as being overlain with EM38 ground conductivity survey data. The ultimate aim of this study is to move towards a more targeted integrated approach for phylloxera detection and is the first study of its type to focus on a soil borne pest of biosecurity significance.

Biography

Felipe Gonzalez is an Associate Professor in the Science and Engineering Faculty, Australia and team Leader for Integrated Intelligent Airborne Sensing Laboratory at the Queensland University of Technology, Australia. He holds a BE (Mech) and a PhD from the University of Sydney. His research explores bioinspired optimization, uncertainty based UAV path planning and UAVs for environmental monitoring. He leads the CRC plant biosecurity project evaluating unmanned aerial systems for deployment in plant biosecurity and the CRC PB 2135 optimizing surveillance protocols using unmanned aerial systems and developing pest risk models of buffel grass using unmanned aerial systems and statistical methods. He is a Chartered Professional Engineer and member of Professional Organizations including the RAeS, IEEE and AIAA.

felipe.gonzalez@qut.edu.au

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Guoxing Quan, J Biotechnol Biomater 2017, 7:3(Suppl)
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Molecular cloning and characterization of the small heat shock protein family in the spruce budworm, *Choristoneura fumiferana*

Guoxing Quan
Great Lakes Forestry Centre, Canada

Small heat shock proteins are a superfamily of molecular chaperones and are characterized by the presence of a conserved α-crystallin domain. They exhibit ATP-independent chaperone-like activity by assisting in the correct folding of nascent and stress-accumulated misfolded protein to prevent irreversible protein aggregation. Unlike HSPs of large molecular weight, the sHSPs display structural and functional diversity among different insect species. Some sHSPs may contribute to stress tolerance, enhancing insect survival in severe environmental conditions. As such, studying SHSPs may lead to a better understanding of how pest insect survives in unfavorable environments and how the changing climate affects their distribution and outbreaks. The spruce budworm, *C. fumiferana* is a destructive native forest defoliator in North America. In the past few hundred years, periodic outbreaks are known to have occurred across tens of millions of square kilometers of forest. Here, we report the identification of 15 sHSP genes from the spruce budworm transcriptome. Examination of the mRNA expression profiles of the sHSPs revealed that the levels varied according to the developmental stage and tissue as well as whether the insects were reared under normal and stress conditions. Nine sHSP genes were sensitive to heat shock stress. Some, but not all, sHSPs may play a vital role during diapause.

Biography

Guoxing Quan received his PhD degree in 1998 from Tokyo University of Agriculture and Technology, Japan. He worked as a Postdoctoral Fellow in Japan and Canada for several years. Currently, he is a Research Scientist working at Great Lakes Forestry Centre, Sault Ste. Marie, Ontario. He has published more than 20 papers and been a reviewer for many scientific journals. He has worked on transgenic silkworm, RNAi and owns three patents. His current research focuses on the identification of genes involved in adapting to unfavorable environmental conditions and how the changing climate affects insect distribution and outbreaks.

guoxing.quan@canada.ca

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M Cristina Diez et al., J Biotechnol Biomater 2017, 7:3(Suppl)
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Kinetic parameters of adsorption of pesticides in an organic matrix with agro-industrial and lignocellulosic residues for a bio-purification system

M Cristina Diez[1,2], **Bárbara Leiva**[2] and **Felipe Gallardo**[1,2]
[1]University of La Frontera, Chile
[2]CIBAMA-BIOREN, Chile

Bio-purification system is used to adsorb and degrade pesticide spills during handling of products before its application. The PBS has an organic matrix (biomix) composed of soil, commercial peat and wheat straw (1:1:2). We evaluated the adsorption capacity of different agro-industrial and lignocellulosic residues, as components of the biomix of the BPS, to treat water contaminated with pesticides. Sawdust, barley husk, compost and biochar were used in this process. Each biomix and individual components were characterized, and biomixes were formulated with partial replacement of 50% wheat straw or peat, moistened at 60-70% water holding capacity (WHC) and pre-incubated for 30 days at 20-25 °C. For kinetic studies, biomixes were contaminated with atrazine (ATZ), chlorpyrifos (CHL) and iprodione (IPR) at a concentration of 5 mg/L and to attain ionic strength, 0.01 M $CaCl_2$ was added to it. Adsorption at 30, 60, 300, 600, 1080 and 1140 min of incubation at 22 ± 1 °C was evaluated. The adsorption isotherms were carried out with different amounts of biomix and concentration of pesticides for 24 hrs. It was observed that the highest adsorption capacity was achieved in biochar based biomixes, independent of the type of pesticide. CHL presents the highest adsorption rate, ATZ presents a constant and linear saturation for other biomezclas not presenting greater difference, and IPR differs its adsorption for each particular biomix. The Freundlich and Langmuir models were used to describe the kinetics of the adsorption process in the biomixes.

Biography

M Cristina Diez has completed her PhD in 1993 at Universidad Estadual de Campinas, Brazil. She is a Professor in Chemical Engineering Department and, the Director of Biotechnological Research Center Applied to the Environment (CIBAMA-BIOREN) of La Frontera University. She has published more than 115 papers in reputed journals. She is a member of FONDECYT's technology board. She is serving as an Editorial Board Member of the *Journal of Soil Science and Plant Nutrition.*

cristina.diez@ufrontera.cl

Notes:

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Hyper cellulase-producing fungus *Talaromyces pinophilus* EMM development through random mutagenesis and genetic engineering

Anli Geng[1], Zunsheng Wang[1], Rupali Rahul Manglekar[1], Fen Liu[1,2], Zhiyi Zhou[1,2], Huirong Zhang[1,2] and **Youhong Zhang[2]**
[1]Ngee Ann Polytechnic, Singapore
[2]Wuhan Institute of Technology, China

Talaromyces pinophilus UTA1 and EMM are cellulase hyper-producing mutants that originated from *T. pinophilus* OPC4-1 through UV irradiation and chemical mutagenesis by NTG and EMS. Full genome sequencing of these two mutants and the parent strain was conducted and 73 genes were identified with either SNPs or InDels. Functions of the 73 genes were identified using NCBI GenBank database. Among the 73 genes, 3 transcription factors were identified. They might be responsible for the enhancement of cellulase activity in mutant strains, UTA1 and EMM. Genes encoding the 3 transcription factors were successfully cloned to further confirm their enhancement in cellulase and hemicellulase production in mutant strains. Further genetic engineering of the mutant strain EMM was conducted to further enhance its enzyme production. A uracil auxotroph strain *T. pinophilus* EMU was isolated through random mutagenesis. A wild-type *pyrF* gene encoding orotate phosphoribosyl transferase (OPRTase, EC 2.4.2.10) isolated from *T. pinophilus* OPC4-1, the parent strain can be used as the selection marker for genetic engineering of strain *T. pinophilus* EMM. A marker recycle system was developed and was used for the knock-out of creA gene, the gene mediating catabolite repression. A creA gene knock-out strain, A creA 21 was successfully isolated. It demonstrated enhanced cellulase and xylanase production and higher resistance to the increased glucose concentration. The genetic engineering tools were successfully developed for strain *T. pinophilus* EMM and disruption of creA gene in strain EMM was effective for enhanced enzyme production.

Figure 1: Zone of clearance generated by creA knock-out mutant of *T. pinophilus* EMM

Biography

Anli Geng is currently an Assistant Director of Life Sciences and Chemical Technology of Ngee Ann Polytechnic. She currently holds the President position in BioEnergy Society of Singapore (BESS). She is also the Co-founder and Director of Sunvisiae Biotech Pte Ltd, a Singapore-based industrial biotechnology company. Prior to joining Ngee Ann Polytechnic, she was working at Institute of Environmental Science and Engineering (IESE) as a Research Scientist. She has more than 25 years of R&D experience, working extensively in environmental biotechnology, green energy technology and industrial biotechnology. She has more than 30 journal publications and her work has been presented in many international conferences. Her current research focuses on developing novel microorganisms to produce industrial enzymes, chemicals and fuels, novel nutraceuticals and cosmetics ingredients at Ngee Ann Polytechnic. She obtained Ngee Ann Polytechnic Staff Excellence Award and IChemE Award on Sustainable Technology in 2012.

Geng_Anli@np.edu.sg

Notes:

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Special Session

Day 2

John B Carrigan, J Biotechnol Biomater 2017, 7:3(Suppl)
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John B Carrigan

SOSV-Penrose Wharf, Ireland

The first steps in becoming a biotech entrepreneur; why it's easier and more cost efficient than you think?

SOSV is a cork-based global bio accelerator initiative, which is dedicated to funding and building start-ups for aiding humanity and having founded the world's first life sciences accelerator in Cork in 2014. SOSV now operates two accelerator programs, IndieBio based in San Francisco and RebelBio again based in Cork. These accelerators are responsible for establishing many synthetic biology start-ups around the world including Perfect Day Foods, Memphis Meats, Microsynbiotix and the German based Saphium Biotech. We provide the mechanism by which young scientists, entrepreneurs and tinkerers can shape their own destiny and make something that matters. RebelBio provides seed funding and mentorship to drive the transition of science to a business in only four months, before launching its graduate companies into the world of biotechnology to make their fortune, buffered by the company's many alumni, partners and partner investors.

Biography

John B Carrigan has completed his PhD in 2005 at University College Dublin and carried out Postdoctoral studies both in Dublin and in Copenhagen. He has been involved with several start-ups, most recently bio-based advanced materials company and Cellulac Ltd. He is the CSO in SOSV responsible for scientific due diligence, recruitment, product development analysis in addition to other work. He has published several papers in protein engineering, enzymology, metabolomics and cellulosic biofuels.

john.carrigan@sosv.com

Notes:

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Scientific Tracks & Abstracts

Day 2

Sessions:

Day 2 September 26, 2017

Biotechnology in Medical and Healthcare | Pharmaceutical Biotechnology

Session Chair
Tomasz Warzecha
Agricultural University of Kraków, Poland

Session Co-Chair
Emmanuel Loeb
Patho-Logica, Scientific Park Ness Ziona, Israel

Session Introduction

Title: **Free floating brain sections for immunofluorescence markers: A technical and scientific approach**
Emmanuel Loeb, Patho-Logica, Scientific Park Ness Ziona, Israel

Title: **Biotechnologically produced D-lactic acid – starting material for biopolymers**
Anja Kuenz, Thünen-Institute of Agricultural Technology, Germany

Title: **Assessment of invasive grasses using unmanned aerial vehicles: A machine learning approach**
Felipe Gonzalez, Queensland University of Technology, Australia

Title: **Application of laccase during the attainment of PVA hydrogels reticulated with ferulic acid**
Andreia de Araújo Morandim-Giannetti, Centro Universitário da FEI, Brazil

Young Research Forum

Session Chair
Fuad Fares
University of Haifa, Israel

Title: **Atrazine degradation by *Arthrobacter* sp. ZXY-2: Kinetics, pathway, gene expression response and genomic characterization**
Xinyue Zhao, Harbin Institute of Technology, China

Title: **Improved lipid biosynthesis in *E. coli* through heterologous expression of a plant thioesterase**
David Bolonio, Universidad Politécnica de Madrid, Spain

Title: **Characterizing constitutive promoters in yeast**
Sabrina Schulze, University of Potsdam, Germany

Title: **Orthogonal regulation of gene expression in yeast using plant-derived transcription factors**
Gita Naseri, University of Potsdam, Germany

Emmanuel Loeb, J Biotechnol Biomater 2017, 7:3(Suppl)
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Free floating brain sections for immunofluorescence markers: A technical and scientific approach

Emmanuel Loeb
Patho-Logica, Scientific Park Ness Ziona, Israel

Free floating sections is regarded as a new histological method that can be used for immune fluorescence staining. This method is clearly the best way to go for optimal Ab expression in the tissue. Furthermore, staining of thick sections can later on be used for a confocal microscopical analysis. This presentation covers the technical work pattern of the method starting with the tissue preparation and conservation, threw brain accurate dissection and staining. The method is very suitable for morphometry quantification of histological data, here method of image analysis will be presented and the scientific value will be discussed. Furthermore, examples are presented of projects that had combined the method such as stroke and Parkinson models in lab animals. Finally a discussion will be presented were the advantages of the current method will be pointed compared to the classical immunohistochemistry methods.

Biography

Emmanuel Loeb is a graduate from School of Veterinary Medicine, Utrecht University, Netherlands and a qualified expert, Veterinary Pathologist with published papers. He has 12 years of experience in Experimental Pathology and is constantly improving his skills through continuous profession development. In his work, he takes part in annual professional meetings such as the ESVP and follows The Society of Toxicologic Pathology recommendations. He established new methods in the laboratory such as "free floating sections" for immunofluorescence staining, and developed translation tools from pathological hallmarks to histological end point. He is also teaching pathology at the Veterinary School of Koret (Hebrew University).

e.loeb@patho-logica.com

Anja Kuenz et al., J Biotechnol Biomater 2017, 7:3(Suppl)
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Biotechnologically produced D-lactic acid – starting material for biopolymers

Anja Kuenz, S Klotz, N Kaufmann, U Prüße and **K D Vorlop**
Thünen-Institute of Agricultural Technology, Germany

Biopolymers from D- and L-lactic acid represent an alternative to petrochemical plastics, e.g., in the packaging and food industry, and can be produced from renewable resources. In the last 20 years L-lactic acid gained importance as starting material for the poly L-lactic acid (PLLA). This plastic is a promising material, but the softening point is too low for a variety of applications. Whereas, the melting point of the stereocomplex of PLLA and poly D-lactic acid (PDLA) is about 50 °C higher than that of single polymers. In contrast to L-lactic acid, there is no large-scale process for the biotechnological production of D-lactic acid. Thus, the development of an effective biotechnological production process of enantiomerically pure D-lactic acid is required. Therefore, two strains from the genus *Sporolactobacillus* were characterized. In the majority of biotechnological processes yeast extract is used as a complex nitrogen source which is expensive and influences the cultivation in an undefined way. To replace yeast extract, 61 different nutrient sources were fully analyzed for its constituents. The analytical data in combination with cultivation experiments as well as successfully tested immobilized cells were used in bioreactor scale to achieve the aim of converting inexpensive raw materials. Rapeseed meals were used as replacement of yeast extract and thin juice from sugar beet production as substrate. Successfully 153 g/L D-lactic acid with a yield of 91% and maximum productivity of 4.67 g/(Lh) were produced biotechnologically with an enantiomeric excess of ≥99% ee within 48 hours using inexpensive raw materials.

Biography

Anja Kuenz has completed her PhD with the theme "Itaconic acid production based on renewable resources to replace petrochemical acrylic acid" from Thünen-Institute of Agricultural Technology, Braunschweig, Germany. She is a Senior Scientist at the Thünen-Institute of Agricultural Technology and she is working in the fields of biotechnology, immobilisation and the biotechnical conversion of renewable resources. She has more than 35 papers and conference contributions in those fields.

anja.kuenz@thuenen.de

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Assessment of invasive grasses using unmanned aerial vehicles: A machine learning approach

Felipe Gonzalez[1,2] and **Ed Puig Garcia**[1,2]
[1]Queensland University of Technology, Australia
[2]Plant Biosecurity Cooperative Research Centre, Australia

Invasive weeds are responsible for irreversible environmental damage, millions of dollars in crop losses and management costs every year. In order to implement optimal site-specific treatments and reduce control costs, new methods to accurately monitor and assess weed and pest damage need to be investigated. In this paper, we explore the combination of unmanned aerial vehicles (UAV), remote sensing, sensors and machine learning techniques as a promising technology to address this challenge. The deployment of UAVs as a sensor platform is a rapidly growing field of study for biosecurity and precision agriculture applications. In this experiment, we use grass as a case study. A data collection campaign was performed at two different locations covered by Buffel grass and other vegetation (eg. Green Panic, Spinifex scarab). The first site is at cattle farm Chinchilla, QLD, Australia. The Second locations are two sites at Cape Range National Park, WA. In this study, we describe the UAV platform deployed to collect high-resolution RGB and hyperspectral imagery as well as the image processing pipeline implemented to create an ortho-image and machine which results in two or five classifications of the vegetation abundance maps. The aim of the approach is to simplify the image analysis step by minimizing user input requirements and avoiding the manual data labelling necessary in supervised learning approaches. The methodology presented in this paper represents a venue for further research towards automated invasive grass assessments and biosecurity surveillance.

Biography

Felipe Gonzalez is an Associate Professor in the Science and Engineering Faculty, Australia and Team Leader for Integrated Intelligent Airborne Sensing Laboratory at Queensland University of Technology, Australia. He holds a BE (Mech) and a PhD degree from the University of Sydney. His research explores bioinspired optimization, uncertainty based UAV path planning and UAVs for environmental monitoring. He leads the CRC plant biosecurity project evaluating unmanned aerial systems for deployment in plant biosecurity and the CRC PB 2135 optimizing surveillance protocols using unmanned aerial systems and developing pest risk models of buffel grass using unmanned aerial systems and statistical methods. He is a Chartered Professional Engineer and member of professional organizations including the RAeS, IEEE and AIAA.

felipe.gonzalez@qut.edu.au

Notes:

Andreia de Araújo Morandim-Giannetti et al., J Biotechnol Biomater 2017, 7:3(Suppl)
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Application of laccase during the attainment of PVA hydrogels reticulated with ferulic acid

Andreia de Araújo Morandim-Giannetti[1], Victor Hugo Escobar[1], Fernando dos Santos Ortega[1], Octaviano Magalhães Junior[2], Paulo Schor[2] and **Patrícia Alessandra Bersanetti[2]**
[1]Centro Universitário da FEI, Brazil
[2]Escola Paulista de Medicina, Brazil

Many researches have been aiming at obtaining new possible vitreous humor substitutes. Therefore, we performed studies related to obtain hydrogels enzymatically cross-linked with ferulic acid. The hydrogels were obtained by varying PVA mass, enzyme concentration and the mass of ferulic acid, to obtain the best condition to have a material with similar characteristics in terms of density (1.0053 to 1.0089 g/mL), kinematic viscosity (greater than 4mm2/cm) and refractive index (between 1.3345 and 1.3348). The data was analysed using the Statistica 12.0 software, and it was possible to determine the best condition for obtaining the material: mPVA=12.05% (m/m), laccase concentration=836 (µg/mL) and ferulic acid concentration=1.95 (mM). Hydrogels were obtained under the best condition and on analyzing by DSC, confirmed the presence of crosslinks in the hydrogels and reinforced the hypothesis of the presence of crosslinks due to the action of the Laccase enzyme. This was justified due to a reduction of the glass transition temperature (69.99 and 74.49 °C), melt temperature (216.48 and 220.26 °C) and crystallization temperature (181.82 and 184.62 °C), as well as the degree of crystallinity (29.18 and 29.74 %) for the hydrogel obtained with and without PVA, ferulic acid and laccase, respectively. In this case, it is possibly attributed to the greater intensity of the hydrogen bonds between the PVA chains, which makes it difficult to move and pack the chains into crystallites.

Biography

Andreia de Araújo Morandim Giannetti has completed her PhD and Postdoctoral studies from Paulista State University (UNESP). She is a teacher at FEI University Center. She has published more than 18 papers in reputed journals and has been serving as a reviewer in several renowned journals.

preamorandim@fei.edu.br

Notes:

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Young Research Forum

Day 2

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Atrazine degradation by *Arthrobacter* sp. ZXY-2: Kinetics, pathway, gene expression response and genomic characterization

Xinyue Zhao[1,2], **Jixian Yang**[1], **Li Wang1** and **Fang Ma**[1]
[1]Harbin Institute of Technology, China
[2]Delft University of Technology, Netherlands

Isolation of atrazine-degrading microorganisms with specific characteristics is significant for the bio-augmentation to deal with atrazine wastewater. However, lacking the investigation of specific characteristics will hinder the further understanding of bio-augmentation. A strain *Arthrobacter* sp. ZXY-2 with strong capacity of atrazine degradation has been isolated and suggested a potential candidate for bio-augmentation. In this study, we identified the factors that might be relevant to the biodegradation capacity of strain ZXY-2, and reveal how these factors might contribute to the future understanding of bio-augmentation. The growth pattern of strain ZXY-2 followed Haldane-Andrew model with the inhibition constant (Ki) of 52.76 mg/L obtained, indicating that the strain ZXY-2 offered a possibility of bio-augmenting wastewater with the concentration of atrazine below 52.76 mg/L. The Real-time quantitative PCR (RT-qPCR) results showed a positive correlation between atrazine degradation and the expression levels of functional genes (trzN, atzB and atzC), which provided a basis data that could help to distinguish the role strain ZXY-2 played in the bio-augmentation. Moreover, the multiple copies of atzB gene, found via genome sequencing, might account for the highest expression levels among three genes. Meanwhile, the multiple copies of atzB gene might also provide a compensation mechanism to ensure the smooth work of strain ZXY-2 in future bio-augmentation.

Biography

Xinyue Zhao completed her Master's degree in Environmental Microbiology at Harbin Institute of Technology (HIT) in July 2014. Then, she continued her PhD research, majored in Environmental Science and Engineering as a visiting scholar-PhD student from September 2016 at Delft University of Technology. She has published six papers during her PhD study.

mary900410@126.com

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Improved lipid biosynthesis in *E. coli* through heterologous expression of a plant thioesterase

David Bolonio, Angela Contreras, Alvaro Vinuesa, Laureano Canoira and **Luis Gómez**
Universidad Politécnica de Madrid, Spain

Advanced biodiesel is an alternative fuel prepared from renewable non-food sources of biomass. It is non-toxic, non-flammable, biodegradable, and compatible with current vehicles and infrastructure. Most efforts to develop advanced biodiesel have focused on the metabolic engineering of microorganisms able to efficiently convert lignocellulosic and waste biomass into fuel molecules. The enterobacterial, *Escherichia coli* is well suited for this purpose owing to its exceptional amenability for genetic manipulation. Indeed, it has already been used for commercial synthesis of a wide array of chemicals. This work addresses two key steps for biodiesel production in E. coli: (i) increasing the total yields of free fatty acids (FAA) and (ii) improving FAA length and unsaturation from an applied standpoint. These properties must be carefully optimized in order to obtain optimum engine performance once FAAs are converted into esters or biodiesel. To this end, *E. coli* cells were genetically modified to express in an inducible fashion, a leaderless version of the enzyme thioesterase I (tesA), which cleaves the fatty acyl-carrier protein and deregulates the tight product inhibition typical of fatty acid synthesis, the transcription factor FadR, which down-regulates several genes in the fatty acid degradation pathway and increases fatty acid unsaturation; and a plant acyl-ACP thioesterase (FatA) showing higher hydrolytic activity towards oleoyl-ACP than the endogenous bacterial enzyme. As a result of the above manipulations we report here a 6-fold increase in FAA yield and a significant improvement of one of the most important properties of biodiesel: The cold flow performance.

Biography

David Bolonio is a third year PhD student. He graduated in Mining Engineering at Universidad Politécnica de Madrid (Spain) and holds a Master's Degree in Environmental Research and Modeling and Risk Assessment from the same university. He has performed research at the School of Chemistry of the University of Graz (Austria) and the Joint Bioenergy Institute of the Lawrence Berkeley National Laboratory (USA). His results have been presented in seven peer-reviewed conferences and four research papers published in international journals.

david.bolonio@upm.es

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Characterizing constitutive promoters in yeast

Sabrina Schulze
University of Potsdam, Germany

Design and establishment of new biosynthetic pathways in yeast are important goals in synthetic biology. Therefore, promoters with predictable and reproducible protein expression levels independent of the protein of interest are needed. Data presented here show a library of constitutive promoters expressing two different fluorescent proteins in diverse conditions. We compare expression levels for episomal and chromosomal location, different growth media and different growth times. GFP and RFP are quantified via fluorescence spectroscopy and flow cytometry.

Biography

Sabrina Schulze completed her PhD in Medical Sciences at the University of Aberdeen (UK) followed by a Postdoctoral Associate position at the University of Pittsburgh (USA). In 2017, she joined the group for synthetic biosystems at Potsdam University (Germany).

saschulz@uni-potsdam.de

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Orthogonal regulation of gene expression in yeast using plant-derived transcription factors

Gita Naseri
University of Potsdam, Germany

Central goal for synthetic biology is the regulated expression of genes for establishing complex protein expression systems. Artificial transcription factors are one possibility for regulation of gene expression in an orthogonal control system. Presented data show the use of plant-derived artificial transcription factors to establish orthogonal regulators in yeast. The library consists of more than 100 members build from different DNA-binding sites, activation domains and corresponding synthetic promoters. Functionality of the library members is shown by GFP expression and its flow cytometric quantitation.

Biography

Gita Naseri completed her Master's degree in Plant Biotechnology from University of Guilan (Iran) followed by several years as Technical Manager in laboratories of the Rice Research Center (Rasht, Iran) and the laboratory of Plant Protection Clinic (Fouman, Iran). In 2013, she joined the group for synthetic biosystems at Potsdam University (Germany) as a PhD student. She has published first data of her thesis in *ACS Syn Biol* in 2017.

naseri@uni-potsdam.de

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