13th Biotechnology Congress

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Scientific Tracks & Abstracts

Day 1

Bio America 2016

Akhileshwari Nath et al., J Biotechnol Biomater 2016, 6:8(Suppl)
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Molecular profiling of testis in arsenic induced mice

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Arsenic is a potent environmental toxicant and affects biological system through food chain causing toxicity and disturbs different signaling pathways, thus suppresses immune system and finally causing various diseases. In previous study, extensive survey work has been made in arsenic hit area and drinking water and blood samples were collected. Tissue samples have been collected from cancer patients at S S Hospital and Research Institute. After the confirmation of significant high level of arsenic in drinking water, blood and tissue samples, present study was undertaken. Present study was undertaken to observe the effect of arsenic in testicular cells in mice model and its effect on testicular gene expression. Sodium arsenite was administered into Swiss albino mice as 2 mg/kg body wt. for the different durations. Estimation of arsenic was done by atomic absorption spectrophotometer. TUNEL assay was done to observe the DNA damage and microarray analysis was performed to observe the mRNA expression profile in sodium arsenite administered mice model. High accumulation of arsenic was found in testes of Swiss albino mice. Significant DNA damage was observed in arsenic administered testicular cells of Swiss albino mice. Further, mRNA of few genes shows their altered expression. In the present study, it can be concluded that arsenic affects testicular cells leading to DNA damage and alter testicular gene expression. Thus, our results suggest that mice with high accumulation of arsenic shows altered gene expression.

Biography

Akhileshwari Nath has completed her PhD in 1974 from Patna University, India and did Postdoctoral training on Electron Microscopy at Minneapolis, Minnesota, USA in 1976. She is retired Professor and Head of the Department of Zoology from Patna University, India. She was the Head of Mahavir Cancer Institute & Research Centre, India till January 2015. Presently she is the Head of S S Hospital and Research Institute, India. She has published more than 130 papers in reputed journals and completed 5 major research projects funded by Government of India.

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Jong H Kim et al., J Biotechnol Biomater 2016, 6:8(Suppl)
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Chemobiological approaches for enhancing the efficacy of antifungal intervention

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Control of fungal pathogens, such as causative agents for aspergillosis, candidiasis, cryptococcosis or producers of mycotoxins is problematic since effective antifungal agents are often very limited. Also, the expansion of fungal resistance to conventional drugs or fungicides is a global health or food safety/security issue. Therefore, there is persistent need to improve the drug efficacy or to develop new intervention strategies. Fungal drug resistance frequently involves mutations caused by environmental stressors. In fungi, stress signals resulting from oxidative or cell wall stress are integrated into mitogen-activated protein kinase (MAPK) systems that regulate defense genes countering the stress. Of note, mutations in MAPK signaling system could result in tolerance to antifungal agents. Many natural compounds are promising antifungals or leads due to their ability to disrupt fungal defense systems such as antioxidant pathway. Natural compounds could also serve as chemical probes for identifying new antifungal targets. To enhance drug susceptibility of fungi, the model yeast *Saccharomyces cerevisiae* was used as a tool for identifying cellular targets of natural compounds, where targeting vulnerable components such as antioxidant system effectively disrupted pathogen growth, overcame antifungal tolerance or inhibited mycotoxin production. Finally, chemo-biological approaches enabled the development of novel antifungal chemosensitization which significantly improved the drug susceptibility of fungal pathogens.

Biography

Jong H Kim is a Researcher in the Food-borne Toxin Detection and Prevention Research Unit, Western Regional Research Center, US Department of Agriculture, Albany, California. His research focuses on the development of intervention strategies for control of pathogenic fungi. He provides chemo-biological expertise, particularly in the identification of cellular targets and compound interaction and participates in resistance management in collaboration with industry and academia.

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Notes:

Lmar Babrak, J Biotechnol Biomater 2016, 6:8(Suppl)
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Antibody engineering from hybridoma-derived monoclonal antibodies

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Antibody engineering requires the identification of antigen binding domains (variable regions; VRs) unique to each antibody. This determination can be achieved by sequence analysis of the antibody transcript obtained from the hybridoma as each clonal hybridoma cell line produces in principle a single antigen specific monoclonal antibody (MAb). However, the polyploidy nature of hybridoma cells often results in the added expression of aberrant immunoglobulin-like transcripts or even production of nondescript antibodies. The occurrence of these transcripts confounds identification of the VRs of immunoglobulin heavy and light chains that correspond to the antigen specific antibody. It is the VRs that define the unique antigen binding properties and proper sequence identification is essential for functional performance of a recombinant engineered antibody. To address this problem, we have identified and complied a database of aberrant Ig-like transcripts found in myeloma cell lines (SP2/0-Ag14 and P3X62A8U.1) frequently used in the generation of hybridomas and developed a PCR-based method for the selective amplification of heavy and light chain VRs from a given antigen specific immunoglobulin isotype combined with molecular cloning and DNA based sequence analysis. These methods should increase the certainty regarding the VR sequence structure when evaluating the functional performance of a recombinant antibody. This work serves to facilitate antibody engineering applications with broad interest to biotechnology and pharmaceutical industries.

Biography

Lmar Babrak is currently a Post-doctoral Research Scientist in the laboratory of Dr. Robert Hnasko at the Agricultural Research Service located in Albany, CA. Her research has focused on the development of immunoassays used for the detection of disease causing pathogens, toxins and other agricultural contaminants. She has completed her PhD in Microbiology in 2015 from Oregon State University.

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Notes:

Nivedita Lal et al., J Biotechnol Biomater 2016, 6:8(Suppl)
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Deep sequencing of root endophyte *Piriformospora indica* grown under salt stress

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Piriformospora indica, a filamentous fungus of the order Sebacinales, is able to make symbiotic interaction with root of different plant species and provides better growth and higher yield to the host plant as well as resistance against biotic and abiotic stresses. High soil salinity, excess of NaCl is one of the important environmental factors that limits distribution and productivity of major crops. The need to produce crops with enhanced tolerance to salt stress has been the stimulus for research. *P. indica*-mediated salt tolerance mechanism was found to be linked strongly with increase in antioxidants under salt stress in barley which attenuates the NaCl-induced lipid peroxidation, metabolic heat efflux and fatty acid desaturation in barley leaves. Salt stress studies have indicated promising effect of *P. indica* in barley. Therefore, it is vital to isolate and functionally characterize salinity stress-related genes to elucidate the mechanisms underlying halotolerance and develop salinity stress-tolerant plants. We have compared the transcriptome of *P. indica* growing under high salt conditions (0.5 M NaCl) with salt free conditions as a control. Approximately 30-40 million 76 bp paired-end reads per sample were obtained using an Illumina NextSeq 500. RNA-seq analysis was performed using Bowtie/TopHat/Cufflinks software pipeline. Total 15410 unigenes were generated with N50 value of 3038. A total of 13461 differentially expressed genes (fold change ≥2) were identified and 2646 genes were down-regulated while 2446 genes were up-regulated under high salt condition. We found that the genes involved in different cellular processes, such as metabolism, energy and biosynthetic processes, DNA repair, regulation of protein turnover, transport and salt stress tolerance were changed under high salt condition. RNA-seq and pathway analyses found that salt stressed *P. indica* have significant differences in gene expression. Our results showed the complex mechanism of *P. indica* adaption to salt stress and it was a systematic work for endophyte to cope with the high salinity environmental problems. Thus, these results could be helpful for further investigation of the salt resistance mechanism in microbes.

Biography

Nivedita Lal has completed her PhD in Plant Molecular Biology at the Jawaharlal Nehru University, New Delhi, India. Currently, she is working on her DST young scientist project (*P. indica* interaction under salt stress) as a PI (Postdoctoral Fellow) at Jaima Hamdard, New Delhi. She has participated in various national and international conferences. She is interested in continuing research career in plant-microbe interaction to understand how the plant-microbe relation regulates plant development and defense response against various stresses.

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Inkyu Park, J Biotechnol Biomater 2016, 6:8(Suppl)
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Comparative analysis of complete chloroplast genome sequence of two *Aconitum* species and in the family Ranunculaceae

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Aconitum species are well known herbaceous medicinal ingredient as well as toxic material and has great economic value in Asian countries. However, genomic information is still limited in Ranunculaceae. In this study, we completed chloroplast genome sequence of two *Aconitum* species, *A. coreanum* and *A. carmichaelii*, based on the Illumina MiSeq platform. The gene order, gene content and orientation of two *Aconitum* chloroplast genomes exhibit the general structure of flowering plants and are similar to other *Aconitum* species. The two *Aconitum* chloroplast genomes are 155,880 and 157,040 bp in length, respectively and contain 131 unique functional genes including 86 protein coding gene, 8 rRNA and 37 tRNA. We established genetic relationship of *Aconitum* species and Ranunculaceae through phylogenetic tree based on 71 protein coding genes of 19 angiosperms. Comparison of the chloroplast genome structure and gene order to those of *Aconitum* species revealed general contraction and expansion of the inverted repeat region (IR) and single copy boundary regions. We obtained barcoding target sequence and developed SCAR marker helpful for discrimination of the *Aconitum* species. These results suggest that the sequence variables of chloroplast genome could provide the useful genetic information and development of molecular marker for discrimination to identify *Aconitum* species.

Biography

Inkyu Park is a Senior Research Scientist at the Korea Institute of Oriental Medicine (KIOM), South Korea. He has completed his PhD from Chungnam National University, Republic of Korea. His research has centered upon chloroplast genome study with development molecular marker and plastid evolution.

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Day 2

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Vinod Kumar et al., J Biotechnol Biomater 2016, 6:8(Suppl)
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Production of 1,3-propanediol from glycerol by mutant *Klebsiella pneumoniae* J2B devoid of 2,3-butanediol formation

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The 2,3-butanediol (BDO) is produced as a major byproduct during the production of 1,3- propanediol (PDO) from glycerol under limited aeration conditions by *Klebsiella pneumoniae*. In the present study, The BDO pathway genes, *budA, budB, budC* and budO (whole-*bud* operon), were deleted from *K. pneumoniae* J2B *ΔldhA* and the mutants were studied for glycerol metabolism and alcohols (PDO, BDO) production. Only the *budO* deletion mutant could completely abolish BDO production but it exhibited serious reduction in cell growth and PDO production. By modifying culture medium such as increasing buffering capacity (from 29 mM phosphate to 100 mM phosphate) and adding bicarbonate (50 mM), the performance of the *budO* deletion mutant could be recovered to a similar level of the base strain (91.1 mM PDO under microaerobic condition) on flask scale. However, in fed-batch bioreactor experiment, the *budO* deletion mutant produced significantly less PDO (502 mM) than the base strain (753 mM). In addition, the *budO* deletion mutant produced significant amount of pyruvate (>73 mM) and lactate (>38 mM). The low PDO production in *K. pneumoniae* J2B *ΔldhAΔbudO* was attributed to the accumulation of glycolytic intermediates such as dihydroxyacetone and glyceraldehyde-3-phosphate, which are highly inhibitory to glycerol dehydratase.

Biography

Vinod Kumar is currently working as Marie Curie Fellow at Synthetic Biology Research Centre, The University of Nottingham, UK. He is working in the area of Biorefinery using metabolic engineering and synthetic biology tools for the sustainable production of biofuels and biochemicals through second generation biorefinery. He has published 19 research articles, two book chapters and two review articles. He has completed his PhD in Biochemical Engineering & Biotechnology and MSc in Chemistry from Indian Institute of Technology Delhi, India. He has more than 13 years of research experience including his PhD and 5 year Post-doctoral experience in France, South Korea & UK. He has worked on different biological systems, fungal, yeast and bacterial and carried out research in multidimensional projects aiming at development of low cost, energy efficient and sustainable bioprocesses for production of biofertilizers, biopesticides, biofuels and biochemicals.

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Magnetoliposomes for hyperthermia cancer therapy

Yogita Patil-Sen, Tim Mercer and **Gary Bond**
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Magnetoliposomes, hybrid nanoparticles made of superparamagnetic iron oxide nanoparticles (SPIONs) coated with liposomes, are emerging as new class of bio-nanomaterials due to their potential applications in targeted drug delivery and hyperthermia cancer therapy. Coating SPIONs with liposomes enhances their biocompatibility and dispersibility and therefore their applicability in biomedical applications. The hyperthermia treatment is based on the fact that SPIONs, when subjected to an oscillating magnetic field generate heat and thus can kill tumor cells which are more sensitive to temperature above 41 °C than the normal cells. The amount of heat generated by SPIONs is strongly dependent upon their magnetic properties, which in turn are determined by their physicochemical properties i.e., size and shape as well as coating material. Herein, we report the heating ability of bare SPIONs and core-shell type magnetoliposomes, which was measured using magnetic hyperthermia kit. SPIONs were coated with mixed lipid systems of phospholipids and cholesterol and the anticancer drug doxorubicin was encapsulated in the core-shell structure. The drug loading and release efficiency of bare and lipid coated SPIONs was also investigated. The results suggest that the drug loading efficiency increased upon lipid coating and drug release is much more controlled under the alternating magnetic field which indicates that magnetoliposomes are promising drug delivery vehicles for magnetic hyperthermia based cancer therapy.

Biography

Yogita Patil-Sen has obtained her PhD from the University of Manchester, UK and gained Postdoctoral experience at the University of Manchester and the University of Central Lancashire (UCLan). Currently, she is a Daphne Jackson Fellow at UCLan and her research is jointly funded by the Royal Society of Chemistry and UCLan. Her research interests are in the field of synthesis of different types of nanoparticles for targeted drug delivery and cancer therapy. She has published 9 research articles in high impact factor international journals. She is a Member of the Royal Society of Chemistry and the American Chemical Society.

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Notes:

Varsha Mehra et al., J Biotechnol Biomater 2016, 6:8(Suppl)
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Synergistic antibacterial potential and total bioactive component determination of *Elettaria cardamomum*, *Piper nigrum* and *Syzygium aromaticum*

Varsha Mehra and **Manisha Khatri**
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Spices are considered as rich source of bio-active antimicrobial compounds and are indispensable components of cuisines worldwide. They have been used since long to enhance the flavor and aroma of our foods. Besides, they also produce several medicinal effects and are used in treating various clinical ailments. To provide a scientific basis to traditional uses of *Elletaria cardamomum, Syzygium aromaticum* and *Piper nigrum*, their seed extracts as well as isolated phyto-constituents and combinations were evaluated for their antibacterial and antioxidant potential. Total phenol, flavonoid, condensed tannins and saponin contents were also measured. Organic extracts of all three spices showed good antibacterial activity against all the test strains, which was found to be comparable with standard antibiotics. Minimum inhibitory concentration for aqueous and organic seed extracts ranged from 25 to >50 mg/ml and 2 to 50 mg/ml respectively. Among the different extracts evaluated for DPPH free radical scavenging, ethanolic extract of S. *aromaticum* exhibited the highest inhibition with the IC50 value of 42±7.4 µg/ml. This high radical scavenging activity can be directly correlated with the presence of high total phenolic content (310±6.87 mg GAEs/g extract) possessed by the extract. Inhibitory activity of all the extracts was found to be increased, when used in combination. These findings suggest that these spices enhanced the functionality of the food in which they are used by effectively influencing their antioxidant and antibacterial potential.

Biography

Varsha Mehra has completed her PhD from University of Delhi, India. She is currently an Assistant Professor in the Department of Biomedical Science, Shaheed Rajguru College of Applied Sciences for Women, India. She has a few publications in reputed international journals and currently engaged in research project on finding efficacious plant based drugs against *Mycobacterium tuberculosis*.

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Notes:

Shahram Teimourian, J Biotechnol Biomater 2016, 6:8(Suppl)
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Thwarting PTEN expression by siRNA, augments HL-60 cell differentiation to neutrophil-like cells by DMSO and ATRA and reduces NETosis

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Abnormal cell differentiation in particular suppression of terminal cell differentiation, exist in all tumors. Therapeutic intervention to restore terminal differentiation (differentiation therapy) is a very attractive way to treat cancer, especially leukemia. A variety of chemicals stimulates differentiation of leukemic cells such as dimethyl sulfoxide (DMSO) and all-trans retinoic acid (ATRA). Tumor suppressor genes have a vital role in the gateway to terminal cell differentiation. In this study we inhibited PTEN tumor suppressor gene expression by siRNA to investigate the effect of potentiating cell survival and inhibiting apoptosis on HL-60 cell differentiation by DMSO and ATRA at the same time we looked at NETosis. Our results show that PTEN siRNA increases HL-60 cell differentiation in the presence of DMSO and ATRA. At the same time the presence of siRNA hampered accumulation of apoptotic cells during incubation. PTEN siRNA reduced Net formation by differentiated neutrophils. Our study suggests potential usage of differentiation therapy in PTEN mutated AML leukemia.

Biography

Shaharm Teimourian has completed his PhD from Tehran University and Postdoctoral studies from Oxford University School of Medicine. He is the Director of Medical Genetics and Biotechnology Department. He has published more than 25 papers in reputed journals and has been serving as an Editorial Board Member of *Edorium™ Journal of Molecular Biology* and *World Journal of Hematology.*

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Notes:

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Acceleration of glycolysis and D-lactate production by novel global metabolic engineering in yeast

Ryosuke Yamada, Kazuki Wakita and **Hiroyasu Ogino**
Osaka Prefecture University, Japan

The use of renewable feed-stocks for producing biofuels and bio-based chemicals by engineering metabolic pathways of yeast *Saccharomyces cerevisiae* has recently become an attractive option. Many researchers attempted to accelerate glycolysis by over-expressing some glycolytic enzymes because most target bio-based chemicals are derived through glycolysis. However these attempts have met with little success. In this study, to create a *S. cerevisiae* strain with high glycolytic flux, we used multi-copy integration to develop a novel global metabolic engineering strategy. Then a novel global metabolic engineering strategy was applied for D-lactate production. Among approximately 350 metabolically engineered strains, YPH499/dPdA3-34 exhibited the highest glucose consumption rate. This strain showed 1.3-fold higher cell growth rate and glucose consumption rate than the control strain YPH499/dPdAW. Real-time PCR analysis revealed that transcription levels of glycolysis-related genes such as *HXK2, PFK1, PFK2, PYK2, PGI1* and *PGK1* in YPH499/dPdA3-34 were increased. Besides, by using global metabolic engineering strategy, D-lactate was efficiently produced. This study successfully developed a novel global metabolic engineering strategy for *S. cerevisiae*, improving glucose consumption rate through optimizing the expression of glycolysis-related enzymes. The method detailed here is a promising approach to optimize *S. cerevisiae* metabolic pathways, thereby improving bio-based chemicals production using this organism.

Biography

Ryosuke Yamada has completed his PhD and Postdoctoral studies from Kobe University, Japan. He has then joined as an Assistant Professor at Osaka Prefecture University, Japan. He has published more than 35 papers in journals related to applied microbiology and biochemical engineering.

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Kamna Srivastava, J Biotechnol Biomater 2016, 6:8(Suppl)
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Renin-angiotensin-aldosterone system genomics in essential hypertension

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Objectives: Hypertension is one of the major cardiovascular diseases. Candidate genes encoding the Renin-angiotensin-aldosterone system (RAAS), i.e., Angiotensin Converting Enzyme (ACE), Angiotensinogen, Angiotensin II Type-I receptor, Atrial natriuretic peptide (ANP) and Aldosterone synthase (*CYP11B2*), their expression at genetic and protein levels and their association with essential hypertension, if any, were investigated in a Northern Indian population.

Methods: Genotyping and gene expression at mRNA and protein levels was carried out by PCR-RFLP, Real time PCR and Western blot respectively.

Results: A significant association was found in the AT1R genotypes (AC+CC) with essential hypertension. The expression of angiotensinogen was also up-regulated in patients as compared to controls. The decreased levels of ANP gene expression at mRNA (85%) and protein (72.6%) levels and increased in *CYP11B2* protein expression (1.53 fold) in the patient group as compared to controls were found. The individuals with rare allele in Angiotensinogen gene were found to have significant control in blood pressure with ACE inhibitor, Enalapril.

Conclusion: Our findings suggest the association of candidate gene of RAAS with essential hypertension. The increased expression of Angiotensinogen converting enzyme, Angiotensinogen, Angiotensin II Type-I receptor gene and decreased levels of ANP gene expression at mRNA and protein levels in the patient group as compared to controls were significantly associated with essential hypertension and could be served as a prognostic biomarker for essential hypertension.

Biography

Kamna Srivastava has completed her BPharm, MPharm and PhD from Department of Pharmacology, Institute of Technology, Banaras Hindu University, India. She has held her Post-Doctoral positions in National Institute of Immunology and All India Institute of Medical Sciences, India. Presently, she is an Assistant Professor working in Molecular Cardiology Lab in Dr. B R Ambedkar Centre for Biomedical Research, University of Delhi, India. Her on-going project is focused on identifying the potential biomarkers for cardiovascular diseases. She has more than 30 research publications to her credit and is the recipient of grants from DST, CSIR and ICMR India.

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Day 1




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Optimization of biomass and lipid production from a local *Chlorella* isolates using response surface methodology and artificial neural network

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The exhaustion of the world's fossil fuel supplies and global warming are driving the search for renewable sources of fuel. Microalgae have received great interest as an alternative to fossil fuels due to their fast growth rates and high photosynthetic efficiencies. This study focuses on the optimization of biomass and lipid yield from an indigenous *Chlorella* isolate using the Response Surface Method. The input parameters consisted of $NaNO_3$, $NaHCO_3$ and NaCl within the ranges of 0.05-2.0 g/l, 0.5-3.0 g/l and 0-10 mM respectively. Data from 17 experiments with varied culture conditions was used to develop a polynomial model. Analysis of variance (ANOVA) of the model gave a coefficient of determination (R^2) of 0.72. The predicted optimum conditions for biomass formation were 1.55 g/l $NaNO_3$, 3.0 $NaHCO_3$ and 0 mM NaCl. The response graphs showing the interaction of $NaHCO_3$ and $NaNO_3$ on algal growth revealed that an increase in $NaNO_3$ and $NaHCO_3$ medium concentration enhanced the biomass formation whereas NaCl did not impact on biomass formation. These findings revealed that under optimal conditions the indigenous *Chlorella* isolate could be a potential strain for high biomass formation required for biodiesel production.

Biography

Zanenhlanhla Gumbi has completed her Bachelor of Science degree at the University of KwaZulu Natal and is currently pursuing MSc at the same institution. She is a Member of the Golden Key Honors Society and her key research interests lie in the fields of microalgal biotechnology and renewable energy.

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Preshanthan Moodley, J Biotechnol Biomater 2016, 6:8(Suppl)
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A combined salt and acid pretreatment for enhanced enzymatic saccharification of waste sugarcane leaves

Preshanthan Moodley
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Zinc chloride and sulfuric acid were employed as chemical catalysts to enhance enzymatic pretreatment of waste sugarcane leaves. The effects of salt and acid concentration on the enzymatic digestibility using Novozymes Cellic Ctec 2 were examined at a lab scale. Leaves were pretreated using a combination of 3M $ZnCl_2$ and 1.55% H_2SO_4 (v/v) with a solid loading of 10% (w/v) at 121°C for 60 min. After washing, enzymatic saccharification was conducted with an enzyme and solid loading of 10 FPU and 10% respectively. Preliminary results indicated a glucose yield of 9.5 g/L per gram of dry weight sugarcane leaves. This yield showed an improvement over salt treatment and water treatment by 22% and 98% respectively. The next stage in this work will be to optimize the chemical (salt concentration, acid concentration and solid loading) and enzymatic (enzyme loading, solid loading) pretreatment conditions. These findings illustrate the potential of low-cost chemical pretreatment to enhance glucose recovery from ligncocellulosic materials such as sugarcane leaves.

Biography

Preshanthan Moodley has completed his Master's degree from the University of KwaZulu-Natal in South Africa. His Master's research entailed exploring acidic pretreatment of waste sugarcane leaves for biohydrogen production by dark fermentation. He is currently studying towards his PhD degree with his research focusing on enhancing enzymatic saccharification of lignocellulosic waste towards bioethanol and biodiesel production.

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Notes:

Yeshona Sewsynker, J Biotechnol Biomater 2016, 6:8(Suppl)
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A two-stage hybrid pretreatment for enhanced enzymatic digestibility from corn cobs

Yeshona Sewsynker
University of KwaZulu-Natal, South Africa

This study focused on the effect of a combination of sulfuric acid and zinc chloride on the pretreatment of Corn cobs for sugar recovery and enzymatic digestibility. The first stage was a combination of zinc chloride and sulfuric acid which was autoclaved at 121 °C for 60 min. A solid to liquid ratio of 10% was used. The second stage was enzymatic hydrolysis using Cellic Ctec 2. Preliminary assessment of this hybrid pretreatment technique under a sulfuric acid concentration of 1.5%, zinc chloride concentration of 3M, enzyme loading of 10 FPU and reaction time of 48 hours, resulted in a 75% increase in the glucose recovery compared to a single stage enzymatic hydrolysis. In addition, the two-stage method led to a 100% and 81% increase in the glucose recovery compared to the single stage zinc chloride and sulfuric acid pretreatments, respectively. These results evidently support that the combined ZnCl-H2SO4 with enzymatic pretreatment is an effective and feasible method for processing lignocellulosic biomass.

Biography

Yeshona Sewsynker has completed her MSc from the University of KwaZulu-Natal, South Africa. She is currently pursuing her PhD at the University of KwaZulu-Natal. She has published two of her Master's thesis chapters in peer-reviewed journals with the two chapters.

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New process for copper migration from contaminated soil and bioelectricity generation in soil microbial fuel cells

Hui Wang, Hailing Song, Ran Yu Xian Cao, Zhou Fang and **Xianning Li**
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The soil microbial fuel cell (MFC) is a promising biotechnology for the bioelectricity recovery as well as the remediation soil. Moreover there were no studies on the heavy metal pollution in a soil MFC yet. A soil MFC was constructed to remediate the contaminated soil and the electric field was generated from the oxidation of the acetate at the anode. We demonstrated that the copper migration, the power generation and the pH variation in the soil and the electrodes. The maximal voltage and the power density of 539 mV and 65.77m W/m^2 were obtained in the soil MFC. The chemical fractionation of copper (Cu) was analyzed with a modified BCR sequential extraction method. The soluble Cu form and the total Cu contents from the anode to the cathode increased and the difference between them kept growing over time. The Cu fractions in the soil and the electrodes were converted with the change of the dramatic pH from the anode to the cathode. There was a focusing effect leading to the change of the copper forms and the extractable acid form content increased in the three-fifths where the acid and the alkali fronts met.

Biography

Hui Wang is currently pursuing PhD from Southeast University School of Energy and Environment, China. He has majored in soil science and heavy metal pollution renovation. He has published one paper in reputed journals.

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Simultaneous degradation of refractory organic pesticide and bioelectricity generation in a soil microbial fuel cell with different conditions

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Southeast University School of Energy and Environment, China

In this study, the soil microbial fuel cells (MFCs) were constructed based on sandy soil to remove the refractory organic pesticide hexachlorobenzene (HCB) in top soil by a simple method. The construction of membrane less single-chamber soil MFCs by setting up the cathode and the anode activated carbon, inoculating the sludge and adding the co-substrates can promote HCB removal significantly. The results showed that HCB removal efficiencies in the soils contaminated with 40 mg/kg, 80 mg/kg, and 200 mg/kg were 71.14%, 62.15% and 50.06%, respectively, which were 18.65%, 18.46% and 19.17% higher than in the control, respectively. The electricity generation of soil MFCs in different HCB concentrations was analyzed. The highest power density reached 70.8 mW/m^2 and an internal resistance of approximately 960 Ω was obtained when an external resistance loading of 1000 Ω was connected. Meanwhile, the influences of temperature, substrate species and substrate concentrations on soil MFCs initial electricity production were investigated. The temperature between 25 °C and 30 °C had no influence on the initial electricity production in the soil MFC while the impacts of the substrate concentration were significant. The addition of the anionic surfactant sodium dodecyl sulfate (SDS) into the soil MFCs system contributed to the improvement of HCB removal efficiency.

Biography

Xian Cao is currently pursuing PhD at the Southeast University School of Energy and Environment, China. He has published one paper in reputed journal.

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Chondrogenic and possible pathologic effects of PRP on adipose derived MSCs

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Introduction & Aim: Application of activated Platelet-Rich Plasma (PRP) with its vast range of cytokines and growth factors has achieved a considerable attention for chondrogenic differentiation in tissue engineering fields. Therefore, the aim of this study was to investigate the effects of PRP on human adipose derived MSC chondrogenesis.

Material & Methods: MSCs were differentiated using different PRP concentrations (5% and 15%). Changes in gene expression levels for cartilage and bone specific markers (*COLII, AGC, SMAD2, SOX9*) and (*RUNX*, Osteocalcin), respectively, were appraised by real time PCR. Also chondrogenesis was assessed by measuring secreted glucosaminoglycan in the medium or that kept in cell ECM. The expression of pathologic markers was evaluated by measuring the VEGF, TNFα secretion and alkaline phosphatase activity and calcium deposition.

Results: The most secreted VEGF ($p<0.05$) in 5% and 15% concentration were anti-angiogenesis. The inflammation factor (TNF-α) quantity of 5% PRP was the lowest ($p<0.05$) on 21st day but chemotaxic characteristics of the mentioned group was the highest. The expression levels of *AGC, SOX9, COLII* and *RUNX* were significantly ($p<0.05$) down-regulated while Osteocalcin was up-regulated. In addition, hypertrophy was seen in chondrogenic differentiation.

Conclusion: Due to having vast range of biologic active factors, PRP based chondrogenesis of human adipose derived MSC is dose dependent and the undesired outcomes due to absence of regulatory factors, should be suppressed by further optimizing the formulation of chondrogenic differentiation media.

Biography

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