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International Conference and Summit on

# Industrial & Pharmaceutical Microbiology

October 17-18, 2016 Kuala Lumpur, Malaysia

## Scientific Tracks & Abstracts (Day 1)



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## Diverse microbes inhabiting livestock feed resources

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The safety of animal feed resources is of global importance in livestock sector. Knowledge of the function and diversity of microorganisms dwelling in animal feed habitats is essentially required beforehand for the safe management of feed resources. Microorganisms are not only beneficial organisms in natural feed resources but are also key players in spoilage processes changing feed quality. Depending on moisture and nutrient contents, diverse microbes are differentially inhabiting in various feed resources such as barley, soybean curd residue, brewer's grain, rice bran, spent mushroom substrates, pig feed, broiler feed, milking cow feed and corn silage etc. However, to date, microorganisms inhabiting naturally in feed resources were little reported. In this study, about 100 strains of both bacteria and fungi were isolated from various feed resources and then identified by 16S rDNA sequencing. Beneficial microorganisms include *Bacillus amyloliquefaciens*, *Lactobacillus plantarum*, *Lactococcus lactis* and *Leuconostoc citreum*, etc. Harmful microorganisms include *Burkholderia vietnamiensis*, *Enterococcus casseliflavus*, *Staphylococcus saprophyticus*, *Enterococcus durans* and *Pantoea agglomerans*, etc. Many other isolated strains were unclear for a safety as well as function. We will mention the strains of harmful microorganism involved in feed spoilage and pathogen by literature review. Enzyme activities related on nutrient digestion, drug resistance and antimicrobial activity were also investigated on the isolated strains.

### Biography

Soo-Ki Kim has completed his PhD in Osaka University and Postdoctoral studies in Department of Biology of Purdue University. He is a Professor in Department of Animal Science and Technology of Konkuk University in South Korea. He has published research papers in the field of basic microbiology and development of animal feed additives. He has contributed as a President of Korean Agricultural Microbiology Research Association from 2013 to 2015.

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## Stable isotope probing coupled Raman microscopy: An efficient way to study single cell biochemistry

Hemanth Nag Noothalapati Venkata  
Shimane University, Japan

Lipid droplets have been hypothesized to be intimately associated with intracellular proteins. However, there is little direct evidence for both spatiotemporal and functional relations between lipid droplets and proteins provided by molecular-level studies on intact cells. To elucidate the interplay between them at the single cell level, Raman microscopy was coupled with a very powerful strategy, namely, stable isotope labeling. Here, I present *in vivo* time lapse Raman imaging, coupled with stable-isotope ( $^{13}\text{C}$ ) labeling, of single living *Schizosaccharomyces pombe* cells. Our results show that the proteins newly synthesized from incorporated  $^{13}\text{C}$ -substrate are localized specifically to lipid droplets as the lipid concentration within the cell increases. Lipids, which help to store energy in a compact form, have variety of roles in biological systems and their metabolism is central to life. Here, we show that combination of stable isotope probing (SIP), Raman micro-spectroscopy and multivariate curve resolution analysis can serve as a valuable approach in metabolomics research. We studied ergosterol biosynthesis in single living fission yeast cells, grown in mixtures of normal ( $^{12}\text{C}$ ) and  $^{13}\text{C}$ -glucose as the sole carbon source. By carefully looking into the biosynthetic pathways and by comparing the observed peak positions with calculation results on isotope-substituted ergosterol, it is possible to understand how  $^{13}\text{C}$  is incorporated in the conjugated C=C moiety of the molecule. The multivariate spectral data analysis revealed intrinsic spectra and their relative abundances of all isotopomers.

### Biography

Hemanth Nag Noothalapati Venkata has completed his PhD from National Chiao Tung University, Taiwan. During his PhD, he studied spatio-temporal relationship between proteome and lipid droplet in single fission yeast cells *in vivo* by Raman microscopy. He has then developed methods to study single cell biochemistry utilizing carbon isotopes during his Post-doctorate at Ultimate Spectroscopy and Imaging Laboratory, NCTU. Later he moved to Shimane University, Japan as an Assistant Professor and has been actively working on medical and biological applications of Raman microspectroscopy.

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## Morphological traits of some actinobacteria and their importance in the genomic era

Luis A Maldonado<sup>1,2</sup> and Erika T. Quintana<sup>3</sup><sup>1</sup>Universidad Autonoma Metropolitana, Mexico<sup>2</sup>Universidad Nacional Autonoma de Mexico, Mexico<sup>3</sup>Instituto Politécnico Nacional (IPN), Mexico

Microbes still are a vast and fully unexplored source for novel biologically active compounds and the actinobacteria subgroup (Gram positive bacteria with a 40 to 60% GC content) accounts for nearly 80% of the current medically employed antibiotics. Among the actinobacteria, members of the genus *Salinispora* are a promising source for novel compounds due to their unique ability to solely grow on the presence of sea water, a fact which supports their adeptness to the marine ecosystem. *Salinispora* are still difficult to isolate and characterize as strains usually undergo several chameleonic morphological states. In this study, a collection of 66 isolates recovered from a national resource and assigned to the genus *Salinispora* were screened for their metabolic profiles coupled to both genotypic and morphological properties. Evaluation of the enzymatic profile of the strains for amylases, cellulases, lipases and proteases indicated that all the strains produced amylases and lipases whereas only 7.5% produced proteases; no cellulase activity was found. Also, the 66 strains showed antimicrobial activity against clinical isolates of *Staphylococcus epidermidis*. It is therefore, proposed that genome sequencing, single gene oriented phylogenies and morphological properties should be used in conjunction to construct a robust system to fully comprehend and exploit the biotechnological potential of *Salinispora* since several of the isolates from this study contained sequences not-related to previously reported Rifamycin clusters from *Salinispora* recovered from other regions of the world.

### Biography

Luis A Maldonado has completed his PhD at the University of Newcastle, UK in 2002, followed by a Postdoctoral position in Biodiversity and Biogeography of Marine Actinomycetes. He has published more than 30 papers and/or book chapters in the actinobacteria field that have been cited over 1250 times. He is PLOS ONE Academic Editor, constantly reviews manuscripts for other journals and grant funding agencies. He is also a co-author on the latest edition of the *Bergey's Manual* for the genera *Gordonia*, *Nocardia* and *Salinispora*. His research interests are in improving selective isolation strategies for industrially important actinobacteria notably *Micromonospora*, *Salinispora* and rare *Streptomyces* while exploring their biotechnological applications.

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## Development of cost-effective fermentation media for biobutanol production from lignocellulosic biomass

Huang Miao, Saraswathi Narayanasamy, Kit Lun Chan, Martin Hui Cai, Lei Shi, Feng Tian and Boon Keat Tay  
Temasek Polytechnic, Singapore

Biobutanol as biofuel is superior to bioethanol as it can be used wholly in petrol engines and does not require any modification to the existing infrastructure for its transport and distribution. Biobutanol from lignocellulosic feedstock is an environmentally sustainable solution to energy crisis as it is renewable and does not compete with the world's increasing population for food. Various types of lignocellulosic biomass have been studied for biobutanol production. In all these studies, pre-treatment is an essential step to disrupt the highly-ordered cellulose structure and the lignin-carbohydrate complex and ultimately hydrolyze cellulose and hemicellulose to simple sugars. Unfortunately, this process increases the entire cost of lignocellulosic biobutanol production. In this study, a cost-effective fermentation media was developed for biobutanol production using *Clostridium beijerinckii* strains. This optimized fermentation media were prepared with less energy input and no supplementation of extra carbon source or expensive nitrogen source to reduce cost for large scale industrial applications. The developed media could support satisfactory microbial growth without concentration or detoxification procedures. Knowledge shared in this study will also be beneficial for the lignocellulosic bio-refinery industry overall.

### Biography

Huang Miao has completed her PhD from School of Biological Science, Nanyang Technological University (NTU) in Singapore and Postdoctoral studies from School of Civil and Environmental Engineering in NTU. She is currently a Research Scientist in Temasek Polytechnic, Singapore. She is interested in industrial and environmental microbiology, where the various microorganisms with their unique genetic makeup play important roles.

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## Seclusion and depiction of microorganisms responsible for spoilage of fruits and vegetables

**Anju Dhiman**

Maharshi Dayanand University, India

Fruits and vegetables are the main dietary source of nutrients, micronutrients, vitamins and fiber for human, which are consumed widely. However, they are contaminated with diverse range of bacterias and their spores through reproductive cells. Fruits and vegans samples were collected from four different places viz. Bhalout (Rohtak, India), Chandpur (Jind, India), Chang (Bhiwani) and Ganaur (Sonipat). Test samples were processed to identify total viable cells (cfu/ml). The highest total viable count was found in tomato followed by lemon. *Bacillus*, *Micrococcus*, *Staphylococcus*, *Klebsiella*, *Escherichia coli*, *Pseudomonas* and Enterobacter species were isolated and identified on the basis of morphology (Gram staining and cell morphology), biochemical tests (indole production test, methyl-red test, Voges-Proskauer test and citrate utilization test) and growth on selective cum differential culture media (such as MacConkey agar and mannitol salt agar media). It was found that *Bacillus*, *Klebsiella*, *E. coli*, *E. aerogenes* and *Pseudomonas* were dominating species in the spoilage of every category of fruits and vegan samples. The bacteria particularly Gram negative, was key responsible for food spoilage. Proper handling of fruits and vegetables, hygiene transportation and appropriate storage is necessary to avoid microbial food spoilage and related health risks.

### Biography

Anju Dhiman has completed her PhD from Maharshi Dayanand University and presently serving as an Assistant Professor since 2006. She has published more than 35 papers in reputed journals and serving as an Editorial Board Member of reputed pharmacy journals.

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## Chlorflavonin, a flavone-type fungal metabolite with potent and selective antitubercular activity

Georgios Daletos, Peter Proksch, Sergi H Akone and Rainer Kalscheuer  
Heinrich Heine University, Germany

*Mycobacterium tuberculosis*, the etiologic agent of tuberculosis (TB), is one of the leading causes of mortality and morbidity caused by pathogenic microorganisms. Treatment of TB is currently facing serious problems due to the emergence of multidrug-resistant (MDR) and extensively drug-resistant (XDR) *M. tuberculosis* strains. The latter is practically untreatable with the currently available anti-TB drugs on the market and thus that there is an urgent need for novel antibiotics against TB. During our ongoing search for new potential anti-TB drug leads, we investigated the endophytic fungus *Mucor irregularis*, which was isolated from the Cameroonian medicinal plant *Moringa stenopetala*. The ethyl acetate extract of *M. irregularis* yielded two flavonoid-type derivatives, chlorflavonin and dechlorflavonin, the latter only differing by the absence of a chlorine atom in the B ring. In contrast to dechlorflavonin, chlorflavonin exhibited strong growth inhibitory activity against *M. tuberculosis*, indicating that chlorination plays an important role for anti-TB activity. Importantly, chlorflavonin showed no cytotoxicity against the human fibroblast (MRC-5) and macrophage-like human acute monocytic leukemia (THP-1) cell lines up to concentrations of 100  $\mu$ M. Mapping of resistance-mediating mutations revealed that chlorflavonin specifically inhibits the acetohydroxyacid synthase IIVB1, which mediates the first step in branched chain amino acids and pantothenic acid biosynthesis. Chlorflavonin displayed synergistic effects in combination with the first-line antibiotic isoniazid leading to a complete sterilization and no resistance in liquid culture during combination treatment. Moreover, chlorflavonin exhibited potent activity against XDR *M. tuberculosis* strains, which highlights the potential of this compound as a promising anti-TB agent.

### Biography

Georgios Daletos obtained his Diploma and Graduate Diploma of Specialization (GDS) degrees in Pharmacy and Pharmacognosy at the University of Patras (Greece), in 2007 and 2010, respectively. He completed his Doctorate (Ph.D.) degree in Pharmacy from the Institute of Pharmaceutical Biology and Biotechnology (Heinrich-Heine University of Duesseldorf, Germany), in 2015, under the supervision of Professor Dr. Peter Proksch. Currently, he is a postdoctoral researcher at the same institution. His research interest is focused on the isolation and identification of new bioactive secondary metabolites from marine invertebrates and microorganisms.

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## **Scientific Tracks & Abstracts** **(Day 2)**





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## Imaging yeast cell wall architecture and studying the effect of antifungal drug Terbinafine at the single cell level by Raman microscopy

Hemanth Nag Noothalapati Venkata  
Shimane University, Japan

Fungal cell wall is a dynamic organelle that plays a vital role, particularly in cellular growth, elongation and division. Any modification or disruption of the wall leads to lysis and cell death, hence serving an excellent target for anti-fungal drugs. Chemically, the cell wall architecture in fungi is complex comprising mainly polysaccharides (glucan, mannan and chitin) and a small proportion of glycoproteins. Traditionally, electron microscopy and biochemical extraction methods were employed while recently immunocytochemical analysis is used to understand its structure. The former lacks chemical specificity requiring genetically modified cells to study different structures in detail while the later involves development of fluorescent monoclonal antibodies specific to glycosidic linkages among cell wall polysaccharides. Hence we aim to develop a label-free method based on confocal Raman microscopy to visualize distribution of various polysaccharide components of fungal cell and spore wall. Fission yeast *Schizosaccharomyces pombe* is used as a model to demonstrate our method. First, space-resolved Raman spectra from lipid droplets, cytoplasm and cell wall were obtained to identify marker bands for individual components followed by imaging. Then, by employing multivariate curve resolution (MCR) analysis, we successfully separated Raman spectra of several pure bio-macromolecular components. We then studied pharmacokinetics and pharmacodynamics of antifungal drug terbinafine at the single cell level in yeast model. We believe that our method will help in understanding the complex fungal spore wall architecture and eventually lead to advancements in drug discovery and development in the future.

### Biography

Hemanth Nag Noothalapati Venkata has completed his PhD from National Chiao Tung University, Taiwan. During his PhD, he studied spatio-temporal relationship between proteome and lipid droplet in single fission yeast cells in vivo by Raman microscopy. He then developed methods to study single cell biochemistry utilizing carbon isotopes during his Post doctorate at Ultimate Spectroscopy and Imaging Laboratory, NCTU. Later he moved to Shimane University, Japan as an Assistant Professor and has been actively working on medical and biological applications of Raman microspectroscopy.

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## Preparation of ion exchangers based on prepared bacterial cellulose for removal of $\text{Cu}^{++}$ , $\text{Zn}^{++}$ , $\text{Hg}^{++}$ from wastewater

Sohair Farag, H M Ibrahim, A Amr, M S Asker and A El-Shafae  
National Research Center, Egypt

Herein we prepared BC as ion exchanger to be used in pollution prevention via preparation of bacterial cellulose using Egyptian bacteria isolated in our laboratory from rotten apple, Preparation of ion exchanger based on prepared BC and functionalized by succinic anhydride and then measure adsorption of heavy metal cation from waste water and desorption cycles for reusability.

### Biography

Sohair Farag has her expertise in applied chemistry and technology of carbohydrate, polymer, pretreatment and finishing of cellulosic based textile-pollution prevention and preparation and applications of nanoparticles. Her open and contextual evaluation model based on responsive constructivists creates new pathways for improving carbohydrate chemistry and technology. She has built this model after years of experience in research, evaluation, teaching and administration in university.

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## Potential of CO<sub>2</sub> elimination and valued byproducts production by marine microalge isolated from Southern Taiwan

**Hsin-Ta Hsueh**

National Cheng Kung University, Taiwan

The increasing trend of atmospheric CO<sub>2</sub> concentration is still significant in the world. Therefore, CO<sub>2</sub> elimination by photosynthetic microorganisms, one of green technology in this issue, is worthy to be developed. In this regard, two microalgae species was isolated from seawater nearby power plant in Southern Taiwan and compared their potential on CO<sub>2</sub> elimination and nitrogen affinity in advance. The higher one potential species on CO<sub>2</sub> elimination was used as candidate to see the valued byproducts content under nitrogen deprivation. The results show the maximal growth rate is over 4 d<sup>-1</sup> and the nitrogen affinity constant is only 0.03 mM. In addition, the carbohydrate content is over 70% and productivity is about 0.7 g/L/d. This information reveals the species isolated in this study can be used as one of applied microbiology for CO<sub>2</sub> elimination and bioethanol precursor production.

### Biography

Hsin-Ta Hsueh has completed his PhD and Postdoctoral studies from National Cheng Kung University, Taiwan. He is the Assistant Research Fellow of Sustainable Environment Research Laboratories, National Cheng Kung University. He has published more than 30 journal papers in the field of air pollution control by biological, chemical/physical technologies.

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## Redox conditions modulates functions of Epstein-Barr nuclear antigen 1 protein

Gyanendra Singh<sup>1</sup> and Ashok Aiyar<sup>2</sup><sup>1</sup>National Institute of Occupational Health, India<sup>2</sup>LSU Health Sciences Center, USA

Epstein-Barr virus (EBV) infects around 95% of human population and its causal association with B-cell lymphomas in children from Sub-Saharan African countries has been established by various epidemiological and molecular studies. Epstein-Barr nuclear antigen 1 (EBNA1), an EBV protein is required for immortalization and transformation of B-cells and results in wide spectrum of diseases that range from infectious mononucleosis to malignancies such as Hodgkin's lymphoma, non-Hodgkin's lymphoma, AIDS related immunoblastic lymphomas, gastric carcinoma, post-transplant lymphomas etc. It is known that transcription activation requires a domain of EBNA1 that binds AT-rich DNA and a second domain termed unique region 1 (UR1) that is conserved in the EBNA1 orthologs of other EBV-like gammaherpesviruses. We have shown in earlier studies that EBNA1's ability to activate transcription is zinc dependent and the two conserved cysteines within UR1 domain are absolutely required for zinc coordination and also respond to the change in the redox microenvironment. We have used bimolecular fluorescence complementation and co-immunoprecipitation techniques to demonstrate that zinc is essential for EBNA1 to transactivate. In addition to zinc regulation, the two critical cysteines within conserved UR1 region are also subject to redox regulation. Oxidative stress conditions are known to cause cysteine oxidation and results in reduced EBNA1's ability to transactivate. We wanted to know whether by over expression of redox proteins such as apurinic/aprimidinic endonuclease redox effector factor-1 (APE1/Ref-1) modulates EBNA1's ability to transactivate and counteracts the effect of oxidative stress on EBNA1. Our results identify a novel mechanism by which redox regulators modulates EBNA1's ability to transactivate and counteracts the effect of oxidative stress on EBNA1.

### Biography

Gyanendra Singh has earned his PhD from Central Drug Research Institute and moved to USA for pursuing research in areas of microbiology and molecular biology at LSU Health Sciences Center, New Orleans, LA and K-State University, Manhattan, KS. He is an expert in molecular biology, microbiology and virology that can be seen from his publications (>26) appeared in *Journal of Virology*, *PLoS One*, *PLoS Pathogens* and *Journal of Biological Chemistry*. Currently he is a Scientist in National Institute of Occupational Health and is also serving as an Editor-In- Chief of the *Journal of Metabolomics and Systems Biology* as well as Associate Editor of *Universal Journal of Biotechnology & Bioinformatics*. He has been in the Editorial Board Member of reputed journals.

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## Isolation and characterization of thermophilic *Streptomyces sp.* with potential production of actinokinase

**Hanan Moawia Ibrahim**

Ministry of Higher Education &amp; Scientific Research, Sudan

The study aimed to produce a potent fibrinolytic enzyme actinokinase from local isolate in batch fermentation, culture of identified thermophilic *Streptomyces* spp. grown on glucose yeast extract peptone medium pH of 8.0. The hemolytic activity of the crude enzyme and time spend for complete lysis was tested using blood agar media and test tubes containing clotted blood. The in vivo clot lysis of the crude enzyme was found to be faster (20 minutes) compared to the other commercial fibrinolytic enzyme (90 minutes). The enzyme was stable at a broad range of pH ranging from 5 to 9. The thrombolytic potential of this particular isolate indicated that it could extract a promising actinokinase with potent activity.

### Biography

Hanan Moawia Ibrahim has completed her PhD from UKM (Malaysia) at School of Bioscience and Biotechnology. She is the Deputy Director of Central Laboratory, Sudan. She has published more than 20 papers in reputed journals and has been serving as an Editorial Board Member of repute for the followings international peer-reviewed journals: Asian Journal of Biological Sciences, Asian Journal of Biochemistry, Asian Journal of Biotechnology, Research Journal of Microbiology and Pakistan Journal of Biological Science.

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## The importance of biodiversity on the functional performance of wastewater treatment plants

**Deborah Patsch**

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Microbial communities perform functions that provide crucial services to ecosystems and human society in wastewater. They detoxify pollutants and consume environmental nutrients, thus mitigating the potentially deleterious effects of these chemicals on ecosystems and human health. However the role of community composition and biodiversity to perform these functions has not been clearly understood. We are therefore addressing a critical and unresolved ecological question: When are community composition and biodiversity important for the provision of a particular ecosystem function and when are they not? We hypothesize that community composition and biodiversity are more important for rare ecosystem functions than for common ecosystem functions. If an ecosystem function is rare, then differences or changes in community composition could have profound effects on the biotransformation rate of that function. In contrast, if an ecosystem function is common, then differences or changes in community composition are unlikely to have an effect on that function. We addressed this knowledge gap with an extensive study, measuring the kinetics of 95 different ecosystem functions for 35 different wastewater treatment plant communities. We then correlated their performance with their taxonomic and functional biodiversity levels, which were determined through metagenomic and metatranscriptomic approaches.

### Biography

Deborah Patsch has completed her Bachelors in Molecular Biology at the University of Graz, Austria and completed her Master's studies at Southern Illinois University of Carbondale, USA. She is currently pursuing PhD as a Marie Curie Fellow at ETH Zurich and Eawag where she focuses her research on microbial ecology related topics.

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