PULSUS
WWW.PULSUS.COM

Volume.1, Issue.2

Journal of Microbiology and Biotechnology Reports

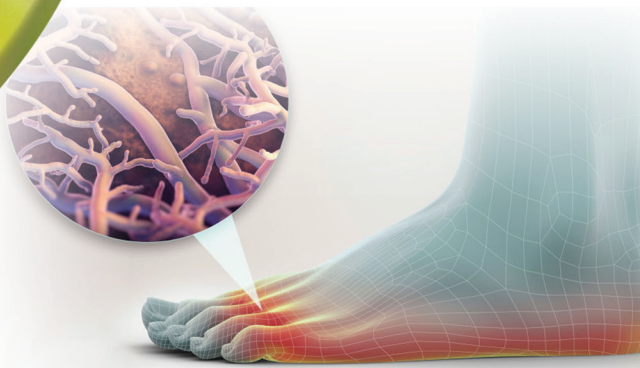
Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 | Atlanta, Georgia, USA

PULSUS
WWW.PULSUS.COM

Pulsus Group: 40 Bloomsbury Way, Lower Ground Floor, London, United Kingdom, WC1A 2SE, USA/ Canada Toll Free: +1-800-982-0387, UK Toll Free: +0-800-088-5419



Scientific Program

Fungal Infections 2017

November 16	
Hall-Majestic I	
09:00-10:00	**Registrations**
Opening Ceremony @ 10:00-10:25	
Keynote Forum	
10:25-11:05	**Title: Molecular actions of heme, an important molecule impacting fungal virulence and drug resistance**
	Li Zhang, The University of Texas at Dallas, USA
11:05-11:45	**Title: Fungal prions, stress and cellular memory**
	Yury Chernoff, Georgia Institute of Technology, USA
Panel Discussion	
Coffee Break 11:45-12:00	
12:00-12:40	**Title: Electrochemical biosensors for rapid diagnosis of fungal infections in agriculture**
	Ramaraja Ramasamy, The University of Georgia, USA
12:40-13:20	**Title: Complexes of potentially pathogenic microscopic fungi in anthropogenic polluted soils**
	Maria Korneykova, INEP KSC, Russia
Panel Discussion	
Lunch Break 13:20-14:20	
Session I: Fungal Biotechnology and Pharmaceutical Mycology | Fungal Diseases: Detection, Diagnosis and Preventions | Fungal Diversity and Ecology	
Session Chair: Yury Chernoff, Georgia Institute of Technology, USA **Session Co-chair: Li Zhang,** The University of Texas at Dallas, USA	
Session Introduction	
14:20-14:55	**Title: Genomics, transcriptomics, proteomics, and biochemistry of white-rot basidiomycete *Trametes hirsuta* 072**
	Andrey R. Pavlov, Fidelity Systems, Inc., USA
14:55-15:30	**Title:High-throughput screening to identify regulators of meiosis-specific gene expression in *Saccharomyces cerevisiae***
	Yona Kassir, Technion-Israel Institute of Technology, Israel
15:30-16:05	**Title: Prion-like properties of a yeast G protein receptor involved in regulation of mating**
	Tatiana Chernova, Emory University, USA
Pannel Discussion @ 16:05-16:15	
Coffee Break 16:15-16:30	
Posters Session and Networking	
Poster Judge: Li Zhang, The University of Texas at Dallas, USA	
P 01	**Title: Variation of anti-fungal saponin concentration in *Apostichopus japonicus***
	Akira Yano, Iwate Biotechnology Research Center, Japan
P 02	**Title: Yeast assay for amyloid aggregation in proteopathies**
	Zachery Deckner and Pavithra Chandramowlishwaran, Georgia Institute of Technology, USA
P 03	**Title: Physiological regulation of heritable protein aggregation**
	Rebecca Howie, Georgia Institute of Technology, USA
P 04	**Title: Aggregate formation by prionogenic proteins in yeast**
	Anastasiya Grizel, St. Petersburg State University, Russia
P 05	**Title: Short-length DNA marker for the determination of malayan box turtle (*Cuora amboinensis*) materials in food chain and traditional chinese medicines**
	Asing, University of Malaya, Malaysia

November 17

Hall-Majestic I

Keynote Forum

10:00-10:40	**Title: Methods for characterizing fungal communities in the human microbiome**
	Kyle Bittinger, Children's Hospital of Philadelphia, USA
10:40-11:20	**Title: Candida-associated gastric ulcer until yesterday, today, and from tomorrow**
	Kenji Sasaki, Midtown Medicare Clinic, Japan

Panel Discussion

Coffee Break 11:20-11:40

Session: Medical and Clinical Mycology | Fungal Infectious Diseases | Current Trends, Innovations and Future Prospects in Mycology | Fungal Biotechnology and Pharmaceutical Mycology

Session Chair: Li Zhang, The University of Texas at Dallas, USA
Session Co-chair: Kyle Bittinger, Children's Hospital of Philadelphia, USA

Session Introduction

11:40-12:15	**Title: A comparative study on the growth of *Aspergillus* species on formulated culture media from food crop wastes and sabouraud dextrose agar**
	Janet Uchechukwu Itelima, University of Jos, Nigeria
12:15-12:50	**Title: Genome shuffling of mangrove endophytic *Aspergillus luchuensis* MERV10 for improving the cholesterol-lowering agent lovastatin under solid state fermentation**
	Hind AlZahrani, KAU University, Saudi Arabia

Young Researchers Forum

YRF Judge: Li Zhang, The University of Texas at Dallas, USA
YRF Judge: Kyle Bittinger, Children's Hospital of Philadelphia, USA

12:50-13:20	**Title: Heme promotes transcriptional and demethylase activities of Gis1, a member of the histonendemethylase JMJD2/KDM4 family**
	Tianyuan Wang, The University of Texas at Dallas, USA

Panel Discussion

Lunch Break 13:20-14:20

14:20-14:50	**Title: The hnRNP-like yeast termination factor Nab3 can employ heterologous low complexity domains in place of its essential low complexity domain**
	Travis Loya, Emory University, USA
14:50-15:20	**Title: Characterizing protein interactions promoting heme regulation of the JMJC domaincontaining protein Gis1 in yeast**
	Purna Chaitanya Konduri, The University of Texas at Dallas, USA
15:20-15:50	**Title: Bioremediation potential of fungi isolated from uranium mine in Brazil**
	Ednei Coelho, University of São Paulo, Brazil

Panel Discussion @ 15:50-16:00

Coffee Break 16:00-16:20

Awards and Closing Ceremony

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infection

November 16-17, 2017 Atlanta, Georgia, USA

Keynote Forum

Day 1

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Li Zhang

The University of Texas at Dallas, USA

Molecular actions of heme, an important molecule impacting fungal virulence and drug resistance

Statement of the Problem: Heme, iron protoporphyrin IX, is a crucial metallonutrient and a major source of iron for living organisms ranging from bacteria to humans. In humans, 95% of functional iron is in the form of heme. Heme is a central molecule in oxygen metabolism and utilization. It serves as a prosthetic group or cofactor for many proteins and enzymes involved in oxygen utilization and metabolism. The utilization of heme as an iron source strongly impacts the virulence of most pathogenic bacteria and some pathogenic fungi. For example, *Candida albicans* secrets a hemolytic factor and uses heme and hemoglobin as an iron source. *Cryptococcus neoformans* can subsist on solely heme- and hemoglobin-sourced iron. Further, *Histoplasma capsulatum* can only utilize iron in the form of heme. Consequently, disrupting heme uptake may be a viable approach to inhibit fungal infection. Additionally, understanding how heme acts to control various cellular processes should provide novel insights into how pathogenic fungi can be suppressed. Particularly, our lab has extensively investigated the molecular mechanisms underlying heme regulation of two yeast regulators, the heme activator protein Hap1 and the important regulator of nutrient sensing and signaling, Gis1. Heme directly controls the transcriptional activity of Hap1, while it controls the transcriptional and demethylase activities of Gis1. I will describe our latest studies to design heme-sequestering agents and to study the molecular mechanism by which heme controls Gis1 activity.

Biography

Li Zhang has completed her PhD from UCLA and postdoctoral studies from MIT department of Biology. She is the Cecil H and Ida Green Distinguished Chair in Systems Biology Science at the University of Texas at Dallas. Her laboratory has worked on studying heme signaling and function for 20+ years. She has published many original research articles and a book entitled heme biology: The secret life of heme in regulating diverse biological processes on this subject. Her recent representative publications include heme, an essential nutrient from dietary proteins, critically impacts diverse physiological and pathological processes, published in nutrients, and a holistic view of cancer bioenergetics: Mitochondrial function and respiration play fundamental roles in the development and progression of diverse tumors, published in the journal *Clinical and Translational Medicine.*

li.zhang@utdallas.edu

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Yury O Chernoff

Georgia Institute of Technology, USA

Fungal prions, stress and cellular memory

Prions are alternatively folded self-perpetuating protein isoforms involved in a variety of biological and pathological processes, and typically based on self-assembled protein aggregates (amyloids). In humans, amyloids and prions are associated with important diseases, such as Alzheimer, Parkinson or Huntington diseases, and transmissible spongiform encephalopathies. In yeast and other fungi, prions are protein-based non-Mendelian elements controlling heritable traits. Due to relative simplicity of cultivation procedures and availability of convenient phenotypic assays, fungi provide a great opportunity for deciphering both mechanisms of prion formation or propagation and biological impact of prions. Fungal prions influence a variety of physiological functions. By using a yeast model, it has been shown that prion formation and loss are modulated by environmental and physiological conditions. *De novo* formation of a yeast prion can be induced by a transient overproduction of a prion-forming protein. Protein quality control machinery of the cell plays a key role in the processes of prion formation and propagation in yeast. Propagation of yeast prions is controlled by the same cytosolic chaperone machinery (Hsp104/70/40) that is involved in protection of cells against proteotoxic stresses. Chaperones fragment prion polymers, generating oligomeric seeds for new rounds of prion propagation. Ribosome-associated chaperones antagonize prion formation and interfere with the ability of cytosolic chaperones to promote prion propagation. Chaperone balance and cytoskeletal networks mediate effects of environmental stresses on prions. Heat stress induces metastable prions, persisting for a number of cell generations after stress and thus maintaining a cellular memory of stress.

Biography

Yury O Chernoff has completed his PhD from St. Petersburg State University (Russia) in 1985, and performed Postdoctoral studies at Okayama University (Japan) and University of Illinois (Chicago, USA). He is a Professor and the Center Director at Georgia Institute of Technology (Atlanta, USA), supervises a lab at St. Petersburg State University (Russia), is a founding Editor-in-Chief of the journal *Prion* (Taylor & Francis, Inc.), and has been elected a Fellow of the American Association for the Advancement of Science (AAAS). He has published about 100 papers (h-index 41). His expertise is in protein biosynthesis, misfolding, amyloids/*prions* and protein-based inheritance.

yury.chernoff@biology.gatech.edu

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Ramaraja Ramasamy

The University of Georgia, USA

Electrochemical biosensors for rapid diagnosis of fungal infections in agriculture

Economic losses to agriculture due to pest and pathogen infections are estimated at $40 billion annually and the economic losses to the health care industry due to food borne illnesses are estimated at $15 billion in the US alone. Early detection of pest or pathogen infection in agricultural crops and reliable detection of harmful pathogens in food are important to minimize agricultural productivity loss, ensure food safety, improve food quality and minimize food related public health issues. There is a pressing need to develop rapid, highly selective and sensitive detection technologies for early identification of plant and human pathogens. While a variety of molecular methods are currently being used for this purpose, an inexpensive, high selective, rapid method for the detection of pathogens is highly desired. Electrochemistry biosensors offer unique advantages to this application. Electrochemical sensors have been widely explored for medical and environmental sensing applications, but not as much for food and agricultural applications. An electrochemical biosensor uses a highly selective bio-recognition element such as enzymes, antibody, aptamer or virus and is capable of detecting biding events with ultra-low detection limits. This presentation will focus on some of the recent developments in our lab in the development of electrochemical biosensors for detection of crop diseases and fungal plant pathogens.

Biography

Ramaraja Ramasamy is currently working as Adjunct Professor in The University of Georgia, USA. His primary focus is on electrochemical energy conversion, but focus areas also include biosensors and bio-nanomaterials. His research is highly interdisciplinary and overlaps with Material Science, Biochemistry, Microbiology, Biotechnology and Analytical Chemistry.

rama@uga.edu

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Maria Korneykova

Russian Academy of Sciences, Russia

Complexes of potentially pathogenic microscopic fungi in anthropogenic polluted soils

This study was undertaken to investigate the species diversity and structure of potentially pathogenic (opportunistic) fungal complexes in podzolic soils polluted by fluorine, heavy metals (Cu, Ni, Co), oil products (diesel fuel, gas condensate, mazut). Lists of potentially pathogenic fungi isolated from soils are made specifically for north-western part of Russia (Kola Peninsula). The majority of studied fungi species belong to the following genera: *Penicillium, Aspergillus, Mucor, Lecanicillium* and *Phoma. Penicillium miczynskii* was identified as the most stable type of fungus with respect to all studied types of oil products. *Mucor hiemalis* was identified as the most sensitive type. An increase of 15% portion of potentially pathogenic fungi as compared to the background soil in zones of aluminum and copper-nickel plants was revealed. The results indicate an increase of 20–25% of potentially pathogenic fungi in pollution of soil with oil products. The structure of fungal complexes was observed to have changed in the polluted soils and the species number and frequency of occurrence of potentially pathogenic fungi were also increased. Strains of fungi isolated from contaminated soil show a greater degree of pathogenicity (based on protease, amylase, hemolytic activity) compared to strains isolated from pure soil.

Biography

Maria Korneykova is a Mycologist, has completed her PhD from Komarov Botanical Institute Russian Academy of Sciences, Saint Petersburg. She is the Acting Head of Laboratory of Microoorganisms Ecology of Institute of the Industrial Ecology Problems of the North of Kola Science Centre of Russian Academy of Sciences. She has published more than 15 papers in reputed journals. She has 15 years of experience in ecology of fungi, air mycology, soil mycology, opportunistic fungi and their effect on human health.

korneykova.maria@mail.ru

Notes:

Fungal Infections 2017

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infection

November 16-17, 2017 Atlanta, Georgia, USA

Scientific Tracks & Abstracts

Day 1

Sessions

Day 1 November 16, 2017

Fungal Biotechnology and Pharmaceutical Mycology | Fungal Diseases: Detection, Diagnosis and Preventions | Fungal Diversity and Ecology

Session Chair
Yury Chernoff
Georgia Institute of Technology, USA

Session Co-chair
Li Zhang
The University of Texas at Dallas, USA

Session Introduction

Title: **Genomics, transcriptomics, proteomics, and biochemistry of white-rot basidiomycete *Trametes hirsuta* 072**

Andrey R. Pavlov, Fidelity Systems, Inc., USA

Title: **High-throughput screening to identify regulators of meiosis-specific gene expression in *Saccharomyces cerevisiae***

Yona Kassir, Technion-Israel Institute of Technology, Israel

Title: **Prion-like properties of a yeast G protein receptor involved in regulation of mating**

Tatiana Chernova, Emory University, USA

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Genomics, transcriptomics, proteomics, and biochemistry of white-rot basidiomycete *Trametes hirsuta 072*

Andrey R Pavlov[1], Tatiana V Tyazhelova[1], Konstantin V Moiseenko[1], Daria V Vasina[1], Olga V Mosunova[1], Tatiana V Fedorova[1], Lilya G Maloshenok[1], Elena O Landesman[1], Sergei A Bruskin[3], Nadezhda V Psurtseva[4], Alexei I Slesarev[2], Sergei A Kozyavkin[2] and **Olga V Koroleva[1]**

[1]A N Bach Institute of Biochemistry Russian Academy of Sciences, Russia
[2]Fidelity Systems, Inc., USA
[3]N I Vavilov Institute of General Genetics Russian Academy of Sciences, Russia
[4]Komarov Botanical Institute, Russia

Wood-rotting fungi are organisms with the highest natural capacity to degrade lignocellulose substrates, which is enabled by complex systems of extracellular enzymes, whose expression and secretion depend on the nature of the environment. We sequenced and assembled the complete genome of the white rot saprotrophic fungus *Trametes hirsuta 072* (Basidiomycota, Polyporales) providing a framework for studies of gene transcription, translation, and secretion of essential fungal proteins. The genome sequence is assembled in 13 chromosomes and a circular mitochondrion, and it is partially annotated. Our transcriptomic and proteomic studies are focused primarily on ligninolytic oxidases and enzymes providing degradation of cellulose and hemicellulose. Our results identified seven laccase genes containing exons and introns, including the respective promoter regions. We found 18 ligninolytic peroxidase genes encoding nine putative lignin peroxidases, seven putative short manganese peroxidases, and two putative versatile peroxidases. The expression of the genes at various conditions of the fungal growth was studied on the transcriptomic and proteomic levels. Only a few genes encoding ligninolytic, cellulolytic, and hemicellulolitic enzymes were expressed in large quantities providing specific response of the fungus to the particular conditions of growth.

Biography

Andrey R Pavlov is currently working as a Research Scientist in Fidelity Systems, Inc., Gaithersburg, Maryland, USA.

ppav2002@yahoo.com

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

High-throughput screening to identify regulators of meiosis-specific gene expression in *Saccharomyces cerevisiae*

Yona Kassir
Technion-Israel Institute of Technology, Israel

Transcriptional regulation is a key mechanism that controls the fate and response of cells to diverse signals. Therefore, the identification of the signal transduction pathways as well as the DNA-binding proteins, which mediate these signals, is a crucial step in elucidating how cell fate is regulated, and how can we perturb it. In the talk, I will discuss bioinformatics and functional high-throughput genomic approaches. Our model system is the budding yeast *Saccharomyces cerevisiae*, and the *IME1* gene that encodes the master regulator of meiosis. High throughput technology, based on fluorescent reporters (R-SGA), allows the screening of an array of all viable yeast gene deletion mutants. This protocol promoted the identification of too many potential transcription factors, and signal transduction factors. The main problem we faced was to discriminate between false and true regulators. Bioinformatic analysis identified potential cis-regulatory sequences with perfect homology to known transcription factors (TF). However, these consensuses and their corresponding TFs were found to be nonfunctional in the R-SGA analysis. Moreover, many TFS were shown to bind to a non-perfect site. The most rewarding approach was to examine a TF only if its known upstream regulators were also found in the screen. Specific examples will be given. In conclusion, our results support the view that although bioinformatic analysis can provide a useful guide, functional assays are required for accurate identification of TF-binding site interactions in complex promoters.

Biography

Yona Kassir is currently working as a Professor Emeritus at Technion-Israel Institute of Technology, Israel.

ykassir@tx.technion.ac.il

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Prion-like properties of a yeast g protein receptor involved in regulation of mating

Tatiana Chernova[1], Aysha Rashid[1], Sindhu Subramanian[1], Yury Chernoff[2] and **Keith D Wilkinson[1]**
[1]Emory University School of Medicine, USA
[2]Georgia Institute of Technology, USA

G-protein-coupled receptors (GPCRs) are integral membrane proteins that initiate responses to extracellular stimuli by mediating ligand-dependent activation of cognate heterotrimeric G proteins. Ste18 is a gamma-subunit of a G-protein receptor that is conserved in evolution and plays a key role in a variety of cellular processes, including pheromone-signaling pathway that is crucial for the yeast mating. We demonstrate that Ste18 possess prion-like properties. Upon overproduction, Ste18 forms detergent-resistant amyloid-like aggregates and promotes formation of [*PSI*$^+$], a prion isoform of Sup35/eRF3. Ste18 mutants, defective in anchoring to plasma membrane, are not able to form detergent-resistant aggregates or induce [*PSI*$^+$] prion, while a mutant, deficient in signal transduction but not in membrane anchoring, is able to do so. These data show that prion-like properties of Ste18 depend on its association with a membrane and resemble our previous results for another protein, Lsb2 (see Chernova et al., 2017 *Cell Reports* 18: 751-761), whose prion properties depend on association with a peripheral actin cytoskeleton. Our findings emphasize the significance of a specific intracellular location for prion formation. Ste18 is short-lived, ubiquitinated, and degraded by a proteasome. Levels of Ste18 protein are increased when proteasome function is impaired, suggesting that Ste18 may form aggregates in response to proteotoxic stress when proteasome is malfunctioning Potential involvement of prion-like aggregation in regulation of G-protein dependent signaling and yeast mating will be discussed in the light of our data and recent developments, suggesting the role of protein aggregation in diseases and in regulation of some biological processes.

Biography

Tatiana Chernova received her PhD in Microbiology from Institute of Agricultural Microbiology, Academy of Agricultural Sciences, Pushkin, St. Petersburg, Russia in 1986, and performed postdoctoral studies at University of Illinois (Chicago, USA) and Winship Cancer Center, Emory University School of Medicine (Atlanta, USA). She is an Assistant Professor at Department of Biochemistry, Emory University School of Medicine (Atlanta, USA). She has published 27 peer-reviewed papers, that are cited 2050 times, with typically more 100 citations per year in the last 10 years. Her expertise is in protein postranslational modifications (including ubiquitination), misfolding and degradation, yeast prions and glycobiology.

tcherno@emory.edu

Notes:

Fungal Infections 2017

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infection

November 16-17, 2017 Atlanta, Georgia, USA

Poster Presentations

Day1

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Variation of anti-fungal saponin concentration in *Apostichopus japonicus*

Akira Yano
Iwate Biotechnology Research Center, Japan

Apostichopus japonicus is an edible sea cucumber inhabits the coastal waters of Japan. The sea cucumber has been eaten over thousands of years. In China, dried sea cucumbers are expensive but popular medicinal foods. In Japan, slice of raw sea cucumber is usually eaten with soy sauce and vinegar. Japanese researcher, Dr. Shigetoshi Shimada, found the anti-fungal saponin, holotoxins, from *A. japonicus* in 1969. He developed the drug for athlete's foot by sea cucumber extract. Recently, we tried to use *A. japonicus* as a functional food for oral care of eldery, and reported the *A. japonicus* jelly could reduce the oral Candida of elderly in the care-house1. *A. japonicus* processed foods will be valuable for prevention of oral candidiasis. However, we found the large individual differences of saponin concentration of sea cucumbers. It is necessary for establishment of the system for quality control of *A. japonicus* functional foods. First of all we surveyed the saponin of *A. japonicus* at the various places. We also analyzed saponins of *A. japonicus* at the same place throughout a year. We revealed that *A. japonicus* from the northern part of Japan tended to be higher concentration of saponins, and saponin contents were markedly decreased in Apr., Aug. and Nov. It has to select the proper districts and season of *A. japonicus* for producing anti-fungal functional foods. It was also described as *Stichopus japonicus*.

Biography

Akira Yano has completed his PhD from University of Tokyo and postdoctoral studies from National Institute of Advanced Industrial Science and Technology. Then he worked at the National Institute of Infectious Diseases and National Institute of Public Health as Government Researcher. In 2006, he moved in Iwate Biotechnology Research Center, and became the Manager of the Department of Bioresouce Sciences in 2015. He has studied on local bioresources, especially of functional foods for healthy life.

akiray@ibrc.or.jp

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Yeast assay for amyloid aggregation in proteopathies

Zachery Deckner, Pavithra Chandramowlishwaran, Meng Sun, Denis Kiktev and **Yury O Chernoff**
Georgia Institute of Technology, USA

Amyloid proteins (including transmissible amyloids, prions) cause heritable, sporadic and infectious diseases in humans. Formation of the amyloid fibril is postulated to occur through a two-step process. First, the normal soluble protein is converted into small aggregates or nuclei of the prion isoform of that protein by a process called nucleation. Second, these nuclei seed the conversion of protein molecules containing the same or similar amino acid sequence thereby sequestering them into long fibrils. A similar molecular mechanism is employed by yeast prions, which are not homologous to known mammalian amyloid and prion proteins by sequence, and control heritable traits. We have developed a yeast-based assay that allows us to study the initial nucleation mechanism of any mammalian amyloidogenic protein. Here, we show that chimeric proteins composed of Sup35 fragments, including prion-forming domain and fused to aggregation-prone regions of mammalian prion protein (PrP), human amyloid beta (associated with Alzheimer's disease), human α-synuclein (associated with Parkinson's disease), human amylin (associated with type II diabetes), or the M-region of tumor suppressor protein 53 (associated with many forms of cancer), nucleate new Sup35 prions even in the absence of of the Rnq1 prion or any other pre-existing nuclei. Our data indicate that prion/amyloid properties of mammalian amyloidogenic proteins that are detected in yeast and mammalian (or *in vitro*) systems are controlled by the same sequence elements.

Biography

Zachery Deckner has completed his BS in Biology from GCSU and is currently a PhD student at Georgia Tech. He is working on identifying and studying new amyloidogenic proteins implicated in various proteopathies. He has mentored undergraduuate students and wants to take up a teaching career after his graduation.

zdeckner3@gatech.edu

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Physiological regulation of heritable protein aggregation

Rebecca L Howie, Lina Manuela Jay-Garcia, Margaret Murphy and **Yury O Chernoff**
Georgia Institute of Techology, USA

Ordered protein aggregates (amyloids) and their transmissible forms (prions) are associated with a variety of neurodegenerative disorders, which can be studied using yeast as a model. In yeast and other fungi, prions control heritable traits. Prion formation and loss are modulated by environmental and physiological conditions, including nutrient limitation and heat stress. Our data show that propagation of yeast prions is controlled by the same cytosolic chaperones that are responsible for the protection of yeast cells against proteotoxic stress. Yeast prions are adjusted to physiological levels of chaperone proteins and hijack the cellular stress defense machinery for their own propagation. Chaperones of the ribosome associated complex, which are involved in proper folding of a nascent polypeptide, antagonize initial prion formation. During stress, the decrease in overall translational activity is accompanied by a relocation of the ribosome associated chaperones into the cytosol, resulting in the impairment of a prion-like propagation of misfolded proteins. Cellular asymmetric segregation apparatus, controlling the asymmetry of mitotic division, influences maintenance and properties of self-perpetuating protein aggregates both during recovery from stress and in the process of replicative aging. Overall, this intimate relationship with the protein quality control machinery of the cell plays a key role in the processes of prion formation and propagation in yeast.

Biography

Rebecca L Howie is pursuing a PhD at Georgia Tech in the School of Biological Sciences, with a focus on protein misfolding. Before becoming a full-time graduate student, she worked at the CDC as part of the National Antimicrobial Resistance Surveillance Team in the Enteric Diseases Laboratory Branch for over six years, studying antimicrobial resistance in foodborne pathogens. Prior to her work at CDC, she worked in anti-bioterrorism as a contractor in the Asymmetric Threat Protection Division at Tyndall AFB, FL.

rhowie3@gatech.edu

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Aggregate formation by prionogenic proteins in yeast

Anastasia V Grizel[1], Aleksandr A Rubel[1] and **Yury O Chernoff[1,2]**
[1]St. Petersburg State University, Russia
[2]Georgia Institute of Technology, USA

Cross-beta protein polymers (amyloids) cause diseases in mammals and control heritable traits in yeast. Initial amyloid formation is poorly understood. Amyloid (prion) form of the *Saccharomyces cerevisiae* protein Sup35 ([*PSI*$^+$]) is induced by overproduction of the Sup35 prion domain (PrD) either in the presence of the prion isoform of another protein (for example, Rnq1), or when Sup35 PrD is attached to another amyloidogenic protein, e. g. human Abeta peptide. This is accompanied by generation of various types of protein aggregates, among them filamentous structures representing intermediates of prion formation. We studied if filaments could be formed by Sup35 PrDs from other yeast species, or by chimeric constructs including both Abeta peptide and a fluorophore. Divergent Sup35 PrDs from various yeast species, or a chimeric protein composed of *S. cerevisiae* Sup35 PrD and human Abeta were tagged with fluorophores and expressed in the *S. cerevisiae* cells, either containing ([*PIN*$^+$]) or lacking ([*pin*$^-$]) the Rnq1 prion. Sup35 PrDs from various yeast species differed from each other by morphology of aggregates formed in the [*PIN*$^+$] cells. Some divergent proteins produced almost no filaments, although this did not necessarily correlate with the evolutionary distance. The Sup35 PrD-Abeta-CFP construct rapidly and efficiently formed dot-like aggregates in the [*pin*$^-$] cells. However, this aggregation did not result in [*PSI*$^+$] induction, indicating that either prion formation or immobilization of full size sup35 into a prion is inhibited by the attachment of fluorophore to the C-terminus of Abeta. Supported by SPbSU grant 1.50.1038.2014, RFBR 15-04-06650 and RSF 14-50-00069.

Biography

Anastasia V Grizel has received her PhD in Biophysics from Lomonosov Moscow State University in 2012, and performed postdoctoral studies at St. Petersburg State University. She currently is a Research Scientist at St. Petersburg State University (Russia). Her area of research includes genetic, cytological and structural analysis of protein aggregation, primarily in the yeast model. She has published six papers in scientific journals.

avgrizel@gmail.com

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Short-length DNA marker for the determination of Malayan box turtle (*Cuora amboinensis*) materials in food chain and traditional Chinese medicines

Asing and **Md Eaqub Ali**
University of Malaya, Malaysia

Malayan box turtle (*Cuora amboinensis*) (MBT) is a protected species and prohibited in Muslim foods and medicines. Despite having medicinal values, turtles are reservoirs of heavy metals and potential carriers of health-threatening microbes and allergens. To monitor turtle traffcking, there is a need of a convenient and reliable method for the quantitative tracing of turtle materials in food chain and medicines. Several polymerase chain reaction (PCR) assays have been proposed for the detection of MBT species under various routes but they are based on long-length targets which break down under the state of decomposition, making them unsuitable for the forensic and archaeological detection in food chain, medicines and other potential routes. To overcome this research gap, for the first time, we developed and validated a short length DNA marker for the qualitative and quantitative detection of MBT tissues by Conventional PCR, PCR-RFLP and SYBR green real-time PCR systems. It combined a 120 bp-site of the MBT mitochondrial cytochrome b gene and a 141bp-site of 18S rRNA gene as the universal marker for the eukaryotes. The assay specificity was checked against 20 different species and biomarker stability was tested under various food processing conditions, including boiling, autoclaving and micro oven heating under pure, admixed and commercial food matrices. The limit of detection (LOD) of the conventional PCR and PCR-RFLP assays was 0.0001 ng MBT DNA under pure state and 0.01% (w/w) MBT meat under admixed and commercial matrices. In contrast, the LOD of the SYBR green duplex PCR system was 0.00001 ng DNA and 0.001% (w/w) MBT meat under mixed matrices. PCR amplified target was further validated by sequencing and restriction digestion with *Bfa*1 endonuclease and distinctive fingerprints (72, 43 and 5 bp) were obtained. The MBT target was further quantified by a duplex SYBR green real time PCR system consisting of MBT target and internal positive control, wherein the melting curve clearly reflected two distinctive peaks at 74.63±0.22°C and 81.40±0.31°C for the MBT and eukaryotic targets, respectively, under pure, admixed and commercial matrices. The quantification limit (ng) was 0.00001for pure meat, 0.0030±0.00001 for binary mixtures, 0.0021±0.00008 for meatball, 0.0042±0.0037 burger and 0.0013±0.00006 frankfurter products. The analysis of 150 reference meat samples reflected 98.19 to 166.57 % target recovery, 92.23-98.15 % PCR efficiency and 0.001% LOD under various matrices. A total of 183 commercial meat products were screened but no turtle contamination was found. Finally, 153 and 120 TCM samples were surveyed by PCR-RFLP and SYBR Green PCR and 40% and 23% of them were found to be MBT-positive (0.00157 to 0.0612 ng/µL), respectively. These authentications provided better security, firstly, through short-length biomarker target which offer extraordinary stability and sensitivity and secondly, through molecular fingerprints which authenticated the post-amplified target by restriction digestion. Thus, the novel assay demonstrated sufficient merit for use in any forensic and/or archaeological authentication of MBT, even under a state of decomposition.

Biography

Asing is a graduate student at University of Malaya, Malaysia and he is working under the supervision of Dr Md Eaqub Ali.

asing95bio@yahoo.com

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infection

November 16-17, 2017 Atlanta, Georgia, USA

Keynote Forum

Day 2

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Kyle Bittinger

University of Pennsylvania, USA

Methods for characterizing fungal communities in the human microbiome

Fungi play an integral role in the human microbiota, the sum total of all microorganisms occupying the human body. When investigating the microbiota with high-throughput DNA sequencing approaches, fungi require the application of specialized methods to be characterized accurately. Here, we review some of the pitfalls and traps to avoid when analyzing combined communities of bacteria and fungi, and present methods for improving accuracy. We show how the methods can be applied to yield insight on the role of fungi in health and disease. Finally, we discuss the application of whole-genome shotgun metagenomic DNA sequencing to combined communities of bacteria and fungi.

Biography

Kyle Bittinger has completed his PhD in Physical Chemistry from MIT, and started his investigations on the human microbiome at the University of Pennsylvania in 2009. He helped to develop the widely used QIIME software for analysis of DNA sequence data. As part of the NIH Human Microbiome Project, his work focused on the role of diet in shaping the gut microbiota in health and disease. He directs the bioinformatics group at the CHOP Microbiome Center, part of the joint PennCHOP microbiome program.

kylebittinger@gmail.com

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Kenji Sasaki

Midtown Medicare Clinic, Japan

Candida-associated gastric ulcer until yesterday, today, and from tomorrow in quest of the etiology

Candida-associated gastric ulcer, though formerly thought to affect only debilitated persons, has been reported to occur in apparently healthy individuals. Though had been reported to demonstrate nothing but nonspecific endoscopic features, the disease occasionally exhibits an apparently typical finding designated a candidarium. The natural history of the disease had been unknown and the fungus had been reported to be no longer detected once the ulcers were healed and no recurrence of the disease had been described. However, the ulcer is shown to not only occur but also recur in a different site with a different shape in a non-diabetic, *Helicobacter pylori*-negative patient without antecedent ulcers, who has not been given non-steroidal anti-inflammatory drugs (NSAIDs), antibiotics, or antineoplastic agents, which implies that, contrary to the prevailing opinion, *Candida* is no innocuous bystander but an etiologic perpetrator. Immune deficiency has recently been reported in relation to candidiasis, which is considered to explain the cause of intractable or recurrent Candida-associated gastric ulcer. In the oropharyngeal field, *Candida albicans* has recently been shown to secrete a hitherto unknown cytolytic peptide pore-forming toxin (PFT), candidalysin, into a pocket in the epithelium which penetrates into and to activate mitogen-activated protein kinase (MAPK)/MAPK phosphatase 1 (MPK1)/c-Fos pathway, triggering release of damage as well as immune cytokines. While the PFT, exerting an effect even on the adjacent cells, directly injures the tissue with damage cytokines, immune counterpart activates polymorphonuclear leukocytes (PMN) to eventually terminate inflammation, which results in restoring the fungus to the commensal state or eradicating it. Since it cannot be negated that such a phenomenon occurs in the gastric mucosa, a theoretically strong possibility has come up that the so called Candida-associated gastric ulcer is actually Candida-induced ulcer. Therefore, the disease should be reinvestigated in the light of the recent immunological, microbiological, and molecular biological findings.

Biography

Kenji Sasaki has received his MD and, as an Immunologist, PhD from Tohoku University School of Medicine in 1973 and 1977, respectively. He is trained at Miyagi Cancer Center. He is a Board Certified Fellow and Preceptor of the Japan Gastroenterological Endoscopy Society, Board Certified Gastroenterologist of the Japanese Society of Gastroenterology, Board Certified Member of the Japanese Society of Internal Medicine and Editorial Board Member of CRIM. He has published several papers on gastroenterology in international journals and served as a reviewer for *JMM, JPP* and *J Gastrointest Dig Syst.*

kydosarnymai@aria.ocn.ne.jp

Notes:

Fungal Infections 2017

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infection

November 16-17, 2017 Atlanta, Georgia, USA

Scientific Tracks & Abstracts

Day 2

Sessions

Day 2 November 17, 2017

Medical and Clinical Mycology | Fungal Infectious Diseases | Current Trends, Innovations and Future Prospects in Mycology | Fungal Biotechnology and Pharmaceutical Mycology

Session Chair
Li Zhang
The University of Texas at Dallas, USA

Session Co-chair
Kyle Bittinger
Children's Hospital of Philadelphia, USA

Session Introduction

Title: **A comparative study on the growth of *Aspergillus species* on formulated culture media from food crop wastes and sabouraud dextrose agar**

Janet Uchechukwu Itelima, University of Jos, Nigeria

Title: **Genome shuffling of mangrove endophytic *Aspergillus luchuensis* MERV10 for improving the cholesterol-lowering agent lovastatin under solid state fermentation**

Hind AlZahrani, KAU University, Saudi Arabia

Young Researchers Forum

Title: **Heme promotes transcriptional and demethylase activities of Gis1, a member of the histonendemethylase JMJD2/KDM4 family**

Tianyuan Wang, The University of Texas at Dallas, USA

Title: **The hnRNP-like yeast termination factor Nab3 can employ heterologous low complexity domains in place of its essential low complexity domain**

Travis Loya, Emory University, USA

Title: **Characterizing protein interactions promoting heme regulation of the JMJC domaincontaining protein Gis1 in yeast**

Purna Chaitanya Konduri, The University of Texas at Dallas, USA

Title: **Bioremediation potential of fungi isolated from uranium mine in Brazil**

Ednei Coelho, University of São Paulo, Brazil

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

A comparative study on the growth of *Aspergillus* species on formulated culture media from food crop wastes and sabouraud dextrose agar

Janet Uchechukwu Itelima
University of Jos, Nigeria

In developing countries where conventional media used for the isolation and growth of microorganisms are very expensive and sometimes inaccessible to researchers, there is a growing interest regarding the utilization of agro-waste materials and other organic wastes for the formulation media used for cultivating microorganisms. A comparative study was carried out to test the suitability of formulated culture media from food crop waste materials (yam, sweet potato and potato peels) and that of a conventional medium for cultivating *Aspergillus* species isolated from different foodstuffs. Three formulated media which included Yam Glucose Agar (YPGA), Sweet Potato Peels Glucose Agar (SPPGA) and Potato Peels Glucose Agar (PPGA) were prepared and used in comparison with Sabouraud Dextrose Agar (SDA) which is a conventional culture medium. One gram of each of the foodstuffs was disinfected using 1% Sodium hypochlorite solution (1% NaOCl) for one minute, followed by three successive rinses in sterile distilled water after which they were coarsely crushed and plated directly unto sterilized Sabouraud Dextrose Agar (SDA). To inhibit bacteria growth, antibiotic drug (gentamicin) in solution, was added to the media. The *Aspergillus* species isolated from foodstuffs which included *Aspergillus niger*, *Aspergillus flavus Aspergillus tamari* and *Aspergillus fumigatus* were aseptically inoculated in duplicate into the three different formulated culture media including SDA which served as a control. The cultures were incubated at room temperature (25ºC) for five days. The diameter of the fungal isolates on both the control medium and formulated media was measured in mutual perpendicular direction to ascertain the redial growth, starting from the second day to the fifth day of incubation. The four species of *Aspergillus* species isolated from different food stuffs grew profusely on the different formulated media with the exception of YPGA which yielded poor radial growth of the fugal isolates. Although the percentage radial growth of each of the organism on SPPGA and PPGA did not differ significantly ($p>0.05$) from each other, *A. niger* and *A. fumigatus* yielded maximum percentage radial growth of (100%) each on SPPGA and PPGA, while *A. flavus* and *A. tamari* yielded (100%) each only on SPPGA. Fugal growth on YPGA gave lowest percentage radial growth of 50.7, 50.2, 48.6 and 43.5% for *A. niger*, *A. fumigatus*, *A. flavus* and *A. tamari* respectively. All the species of Apergillus yielded 100% radial growth on the control (SDA). As the formulated media, especially (SPPGA and PPGA) compared favourably with the conventional medium (SDA) in the terms of the radial growth exhibited by the different species of *Apergillus*, it is therefore a clear indication that they could be good alternative culture media for the cultivation of these fungal isolates.

Biography

Janet Uchechukwu Itelima has her expertise in Applied Microbiology and passion in research related to Applied Microbiology, Biotechnology, and Plant Science, lecturing, and community services. She has obtained her PhD and she is currently an Associate Professor of Applied Microbiology. She is an Academic Staff of the Department of Plant Science and Technology, Faculty of Natural Sciences University of Jos, Nigeria. She has published 35 papers both nationally and internationally. She has also written two books. She is deeply involved in motivating students on how to obtain academic excellence. She has attended workshops and conferences both nationally and internationally, where she presented papers, chaired sessions and served in advisory committee.

janetitelima@yahoo.com

Notes:

Annual Congress on
Mycology and Fungal Infections
November 16-17, 2017 Atlanta, Georgia, USA

Genome shuffling of mangrove endophytic *Aspergillus luchuensis* MERV10 for improving the cholesterol-lowering agent lovastatin under solid state fermentation

Hind A A Al-Zahrani, Mervat Morsy Abbas Ahmed El-Gendy and Ahmed Mohamed Ahmed El-BondLly
University of Jeddah, Saudi Arabia

In the screening of marine mangrove derived fungi for lovastatin productivity, endophvtic 4s/›ergi//us *luchuensis* MERV10 exhibited the highest lovastatin productivitv (9.5 mg/Eds) in solid state fermentation (SSF) using rice bran. *Aspergillus luchuensis* MERV10 was used as the parental strain in which to induce genetic variability aker application of different mixtures as well as doses of mutagens followed by three successive rounds of genome shuffling. Four potent mutants, UN6, UN28, NEll, and NE23, with lovastatin productivity equal to 2.0-, 2.11-, 4 .95-, and 2.11-fold higher than the parental strain, respectively, were applied for three rounds of genome shuffling as the initial mutants. Four hereditarily stable recombinants (F3/3, F3/7, F3/9, and F3/13) were obtained with lovastatin productivity equal to TO.8, 5 7.0, 49.7, and 11.0 m@gds, respectively. Recombinant strain F3/7 yielded 57.0 mg/gels of lovastatin, which is 6-fold and 2.85-fr›ld higher, respectively, than the initial parental strain and the highest mutants UN28 and NE23. It was therefore selected for the optimization of lovastatin production through improvement of SSF parameters. Lovastatin procluctivity was increased! 32-fold through strain improvement method included mutations and three successive rounds of genome shuffling followed by optimizing SSF factors.

Biography

Hind AA Al-Zahrani is currently working as a Research Scientist at University of Jeddah, Saudi Arabia.

hend.alzahrani.1@gmail.com

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infection

November 16-17, 2017 Atlanta, Georgia, USA

Young Researchers Forum

Day 2

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Heme promotes transcriptional and demethylase activities of Gis1, a member of the histonendemethylase JMJD2/KDM4 family

Tianyuan Wang
The University of Texas, USA

The yeast Gis1 protein is a transcriptional regulator belonging to the JMJD2/KDM4 subfamily of demethylases that contain a JmjC domain, which are highly conserved from yeast to humans. They have important functions in histone methylation, cellular signaling, and tumorigenesis. Besides serving as a cofactor in many proteins, heme is known to directly regulate the activities of many proteins ranging from transcriptional regulators to potassium channels. This study reports a novel mechanism of heme regulation of Gis1 transcriptional and histone demethylase activities. We found that two Gis1 modules, the JmjN+JmjC domain and ZnF, can bind to heme specifically *in vitro*. *In vivo* functional analysis showed that the ZnF, not the JmjN+JmjC domain, promotes heme activation of transcriptional activity. Likewise, measurements of the demethylase activity of purified Gis1 proteins showed that full-length Gis1 and the JmjN+JmjC domain both possess demethylase activity. However, heme potentiates the demethylase activity of full-length Gis1, but not that of the JmjN+JmjC domain, which can confer heme activation of transcriptional activity in an unrelated protein. These results demonstrate that Gis1 represents a novel class of multi-functional heme sensing and signaling proteins, and that heme binding to ZnF stimulates Gis1 demethylase and transcriptional activities.

Biography

Tianyuan Wang is a PhD student in Department of Biological Sciences at the University of Texas at Dallas, under the guidance of Dr. Li Zhang. The Zhang lab is interested in investigating the molecular mechanisms underlying heme signaling in eukaryotic cells. She is currently focusing on the study of heme regulation on yeast transcriptional factor Gis1, which is highly homologous to the mammalian JmjC domain-containing KDM4B protein. Her research interests also include heme regulation of KDM4 subfamily demethylase activity and heme availability in lung cancer initiation and tumorigenicity. Prior to joining graduate school at the University of Texas at Dallas, she has obtained her Bachelor's degree in Biological Sciences at China Agricultural University, where she worked as a Research Assistant and was invoved in the project proteomic analysis of Arabidopsis response to environmental stress.

Tianyuan.Wang@utdallas.edu

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

The hnRNP-like yeast termination factor Nab3 can employ heterologous low complexity domains in place of its essential low complexity domain

Travis Loya
Emory University, USA

Many RNA-binding proteins possess domains with biased amino acid content. A common property of these low complexity domains (LCDs) is that they assemble into an ordered amyloid form, juxtaposing RNA recognition motifs in a subcellular compartment in which RNA metabolism is focused. Yeast Nab3 is one such protein that contains RNA-binding domains and a low complexity, glutamine/proline-rich, prion-like domain that can self-assemble. Nab3 also contains a region of structural homology to human hnRNP-C that resembles a leucine zipper which can oligomerize. We determined that the LCD and the human hnRNP-C homology domain of Nab3 are experimentally separable, as cells are viable with either segment, but not when both are missing. In exploiting the lethality of deleting these regions of Nab3, we tested if heterologous prion-like domains known to assemble into amyloid can substitute for the native sequence. These results suggest there are different cross-functional classes of amyloid-forming LCDs and that appending merely any assembly-competent LCD to Nab3 does not restore function or rescue viability. As LCD's are known to be mediators of RNA granule formation *in vivo*, we are also exploring the subcellular localization of wild-type and mutant Nab3's in response to sugar deprivation. Wild-type Nab3 localizes to granules during sugar deprivation, while LCD mutants show a loss of localization, showing this to be an LCD-mediated process. Analysis of Nab3 has provided insights into the diversity of LCD mediated interactions as well as a means of dissecting their function in the cell.

Biography

Travis Loya is a third year graduate student in the Biochemistry, Cell, and Developmental Biology program in the Laney graduate school at Emory University. He has participated in multiple short reviews for F1000 as well as published five manuscripts and one review article during his time in the lab of Dr. Danny Reines. He plans to graduate in 2018 and move on to an academic post-doctoral position continuing to explore the emerging field of low complexity domain containing proteins and their roles in biology.

tloya2@emory.edu

Notes:

Annual Congress on
Mycology and Fungal Infections
November 16-17, 2017 Atlanta, Georgia, USA

Characterizing protein interactions promoting heme regulation of the JMJC domaincontaining protein Gis1 in yeast

Purna Chaitanya Konduri
University of Texas, USA

Heme plays versatile and fascinating regulatory roles for fundamental biological processes. Heme serves as a signaling molecule for oxygen levels in yeast as heme function is entwined with molecular oxygen levels. Heme and oxygen regulate the expression of many genes in eukaryotes by modulating activity of regulatory proteins. In yeast, Gis1 is a DNA-binding transcriptional regulator belonging to the JMJD2/KDM4 subfamily of demethylases. It is highly homologous to the mammalian JmjC domain-containing protein JMJD2B, which plays an important role in histone demethylation, oxygen regulation, and hormonal signaling. Notably, recent experiments in our lab showed that heme regulates Gis1 transcriptional and demethylase activities. Biochemical studies indicate that heme binds directly to Gis1 (JmjN+JmjC domain, ZnF) and JMJD2B proteins. This study aims to dissect the molecular interactions promoting heme regulation of Gis1 activity by characterizing Gis1-interacting proteins. Our Affinity Purification Mass Spectrometry (AP-MS) studies indicate that Gis1 interacts with different sets of proteins under conditions of hypoxia, low heme, and high heme. Together, our results show that Gis1 represents a novel class of transcriptional regulators, with multiple interacting partners playing a role in mediating heme signaling.

Biography

Purna Chaitanya Konduri has completed her BE in Biotechnology from PES Institute of Technology, Bangalore, India in 2008 and MS in Molecular and Cell Biology from UT Dallas in 2014. She is currently pursuing her PhD in Molecular and Cell Biology at UT Dallas in Dr. Li Zhang's Lab. She is working on understanding the mechanism underlying heme regulation of transcription factors in yeast. Specifically, she works on characterizing protein interactions involved in heme regulation of JMJC-domain containing transcription factor Gis1. She has co-authored in a journal article accepted in Nucleic Acids Research and also in a book chaper.

pxk121430@utdallas.edu

Notes:

Annual Congress on
Mycology and Fungal Infections
November 16-17, 2017 Atlanta, Georgia, USA

E-babe- bioremediation potential of fungi isolated from uranium mine in Brazil

Ednei Coelho
University of São Paulo, Brazil

The Osamu Utsumi was one of the most important uranium (U) mine in Brazil and since its activities had ceased in 1995 the decommissioning process has been considered a important environmental challenge. The aim of this study was to identify and evaluate the bioremediation potential of fungal species recovered from soil, water and sediment samples collected from uranium mine. A total of 65 fungi were isolated and molecularly identified using ITS region (rDNA). *Penicillium* was the most prevalent genus isolated (53%). The characterization of the samples showed that the U concentration was high in all substrates (soil: 58 to 268 mg/kg; water: 4.46 to 1.05 mg/L; sediment: 283 to 488 mg/kg). The pH of the water samples was 3.2 and the water activity (Aa) of the soil samples was 0.98. Fourteen fungal isolates showed the U minimum inhibitory concentration (MIC) of 2000 mg/L, while 51 isolates were able to grow up to the maximum concentration tested (2000 mg/L). The uranium tolerance index showed that *Talaromyces amestolkiae* was the most tolerant species. However, *Trichoderma koningiopsis* demostrated the best U biosorption capacity, removing 5.8 mg of uranium per gram of live biomass. Our finds indicate that fungi isolated from U-contaminated sites presents great metal tolerance and high bioaccumulation capacity, which makes them potential candidates for bioremediation.

Biography

Ednei Coelho has completed his Master's degree in Microbiology at the University of São Paulo (USP), has experience in Microbiology, with emphasis on Mycology, mycotoxins, gamma radiation and electron beam, physical-chemical food analysis, HPL/CLAE analysis. Currently holds a PhD in Microbiology at the Institute of Biomedical Sciences of the University of São Paulo (ICB-USP), where he works with isolation and identification of fungi in a contaminated uranium mine, which will later be used in bioremediation.

ednei@usp.br

Notes:

Fungal Infections 2017

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infection

November 16-17, 2017 Atlanta, Georgia, USA

e-Posters

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Draft genome sequence of 11 clinical and environmental Colombian isolates of genus *Aspergillus*

Gomez OM[1,2], Freyle C G[2,3], Tamayo D P[2,3], Rua A L[2,3], McEwen J G[2,4] and **Hernandez O[2,3]**
[1]Universidad de Antioquia, Colombia
[2]Corporación Para Investigaciones Biológicas, Colombia
[3]Universidad de Antioquia, Colombia
[4]Universidad de Antioquia, Colombia

Background: The genus *Aspergillus* is a group of opportunistic fungi that cause infections, with high morbi-mortality in immunosuppressed patients. Approximately 350 species have been described in this genus, classified in 4 subgenus and 20 sections. In Colombia, *Aspergillus fumigatus* is the most frequent species in these infections. However, in the last years an increase in the incidence of other species has been observed. This added to an increase in the quantity and diversity of *Aspergillus* isolates in hospital environments.

Aims: Characterize the phenotype and genotype of clinical and environmental Colombian isolates of *Aspergillus spp.*

Methods: We collected 11 Colombian isolates of *Aspergillus*: 4 from diferents clinical samples, six from hospital environments and 1 from extra-hospital environments. The isolates were identified according to their macro and microscopic characteristics. Genomic DNA for sequencing was prepared from mycelium culture using phenol/chloroform extraction. Library preparation and 150-bp paired-end sequencing was performed using the Illumina HiSeq 2500 platform. The reads was de novo assembled using SPAdes 3.10 pipeline. The draft genome assembly quality was analyzed by QUAST. Augustus v3.0.1 and GlimmerHMM were used for gene prediction. Inference by sequence homology was performed with OrthoFinder v2.0.9. IQtreev1.4.4 software was used for phylogenetic reconstruction by ML.

Results: In this study, four of the eleven isolates classified phenotypically were re-classified correctly after genome analysis. We obtained whole genome sequence of 4 clinical and 7 environmental isolates, including 3 novel genome sequences of the genus *Aspergillus* not reported in the databases: *A. tritici (Clinical), A. tamari* (hospital environment) and *A. amoenus* (extra-hospitalenvironment).

Conclusion: The results of this study provide useful data for the genomic comparison between clinical and environmental isolates of *Aspergillus*. Valuable information that can be used to understand the evolutionary relationships, determine the diversity and level of production of enzymes and secondary metabolites, predict the pathogenicity and response of this opportunistic fungus to antifungal agents.

Biography

Gomez OM is currently working as Faculty at Universidad de Antioquia, Colombia.

oscargomez24@hotmail.com

Notes:

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

The rise and the fall of irradiation treatment for ringworm during the first half of the 20th century: A comprehensive historical perspective

Shifra Shvarts
Ben Gurion University, Israel

Throughout the course of human history, ringworm has always been considered as a difficulty to treat disease that carried a stigma, said to be a disease of the poor and the uneducated. The spread of the industrial revolution which prompted countless people to migrate from the farms to the cities; crowded living conditions, poor hygiene and a high incidence of contagious diseases in the cities led to the spread of ringworm on a massive scale, particularly among children. Ringworm had often led to social ostracism that was very detrimental to the life of the child and his family. Traditional treatment entailed manually plucking out hair from the roots to, a painful process that caused mental trauma to children. The invention of the X-ray machine and the discovery that exposure to low doses of X-rays triggers hair loss transformed irradiation into the preferred treatment strategy for ringworm and it was quickly adopted by the medical community as a humane and most advanced treatment protocol for children with ringworm. Irradiation for ringworm from the outset of the 20th century until 1960 was the standard treatment for the disease in all western countries. This work examines the rise of irradiation treatment for ringworm and profiles the mass ringworm irradiation campaigns (over 200,000 children) conducted in Eastern Europe, Serbia, Morocco, Israel and the United States in the first half of the 20th century. The work focuses on historical, social and health aspects of various groups treated with irradiation for ringworm, how they coped with the social stigmas associated with the disease and its treatment, as well as the impact of treatment over time on the lives of the irradiated children.

Biography

Shifra Shvarts is a Professor for the history of Medicine and Health Sciences, Ben Gurion University and The Gertner Institute of Epidemiology and Health Policy Research, Sheba Medical Center, Israel, Since 2005, she has concentrated her research on the ways various countries in the world, including Israel, has grappled with latent negative health risks and other ramifications of irradiation in childhood as a treatment regime for ringworm, and subsequent social aspects of this treatment that has arisen, reflected in legislation of a compensation for ringworm victims law by Israel and debate elsewhere over how best to inform former patients and monitor them.

shvarts@bgu.ac.il

Notes:

Fungal Infections 2017

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infection

November 16-17, 2017 Atlanta, Georgia, USA

Accepted Abstracts

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Review of species distribution and susceptibility of invasive isolates of *Candida spp* as evaluated using the previous and recently revised clinical breakpoints and method dependent epidemiological cut of values

A Serda Kantarcioğlu
Istanbul University, Turkey

Invasive *Candida* infections often cause high morbidity and mortality especially in the critically ill or immunosuppressive patients. Although *Candida albicans* was the most frequently isolated species as the causative agent of *Candida* infections, geographical differences and changes over time in the species distribution and the susceptibility to antifungals were reported in several surveillance programs. Some variations have been shown to occur among institutions, localities, or countries. It is significant to determine the species distribution and antifungal resistance in large medical centers. We reviewed the species distribution and antifungal susceptibility data of 1371 invasive *Candida* strains isolated in a large university hospital mycology laboratory over 16 years. Susceptibility tests against amphotericin B and azoles were routinely performed using Clinical and Laboratory Standards Institute guidelines from 1998 to 2012 and using Etest from 2012 to 2014. The Sensititre YeastOne colorimetric method was used to test *Candida* echinocandin susceptibility between 2012 and 2014. All test results were routinely reported to clinicians. In this retrospective analysis, resistance or non-wild type phenotypes to systemic antifungals were determined by the previous and recently revised CLSI breakpoints (BPs) and by method dependent species-specific epidemiological cutoff values respectively. The new epidemiological BPs provided by CLSI changed the percentage of resistant *C. albicans*, *C. parapsilosis* and particularly *C. tropicalis* isolates to fluconazole.

mycologist1@yahoo.com

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Diversity of *Aspergillus* species associated with groundnut *(Arachis hypogaea L.)* in eastern Ethiopia as revealed by InDels and their potential for aflatoxin production

Abdi Mohammed[1], Alemayehu Chala[2], Mashilla Dejene[1], Chemeda Fininsa[1], Chris Ojiewo[3], Amare Ayalew[4], David A Hoisington[5], Victor S Sobolev[6] and **Renee S Arias[6]**

[1]Haramaya University, Ethiopia
[2]Hawassa University, Ethiopia
[3]ICRISAT, Ethiopia
[4]African Union Commission, Ethiopia
[5]University of Georgia, USA
[6]Peanut Research Laboratory, USA

Aspergillus species cause aflatoxin contamination, which becomes a health threat in agricultural products and leads to commodity rejection by domestic and international markets. Hence, it is necessary to discriminate diversity and aflatoxin producing species in the eastern Ethiopia. Therefore, the current study was undertaken to elucidate the genetic diversity of *Aspergillus* isolates through InDel (Insertion and Deletions of sequences) markers and evaluate *in vitro* aflatoxin production abilities of the isolates using YES (Yeast Extract Sucrose) medium. A total of 276 isolates were used for genetic diversity fingerprinting of DNA using 23 InDel markers based on aflatoxin biosynthesis gene cluster. Cluster analysis was analyzed by NJ (neighbor joining) and by PCoA (Principal Coordinate Analysis). The *Aspergillus* isolates studied in the current work grouped into three clusters. In addition, 269 isolates were tested for aflatoxin production using UPLC (Ultra Performance Liquid Chromatography). Aflatoxigenic isolates had a maximum of 247 µg mL-1 aflatoxin B1 and 139 µg mL^{-1} aflatoxin G_1. This study provides insight into the genetic biodiversity of aflatoxin biosynthesis gene cluster of *Aspergillus* in relation to *in vitro* aflatoxin production of isolates in the country. The prevalence of aflatoxigenic isolates was much higher (93% of the tested isolates) than the non-aflatoxigenic.

abdi.mohammed22@yahoo.com

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Invasive mucormycosis in chronic granulomatous disease

Abdulnasir Al-Otaibi[1], Dayel Al-Shahrani[2], Eman Al-Idrissi[2], and **Hail Al-Abdely[3]**
[1]University of Toronto, Canada
[2]King Fahad Medical City, Saudi Arabia
[3]King Faisal Specialist Hospitals and Research Centre, Saudi Arabia

*Mucor*mycosis is an uncommon fungal infection caused by members of the order *Mucorales*. Populations at risk for this potentially life-threatening infection include hematopoietic stem-cell transplant (HSCT) recipients, patients with hematological malignancies, diabetes mellitus, ketoacidosis, burns, trauma, premature neonates, and patients receiving iron chelation. *Rhizopus* is the most commonly identified species, followed by *Mucor* spp. Common patterns of mucormycosis are cutaneous, gastrointestinal, rhinocerebral, and pulmonary. Amphotericin B is the antifungal drug of choice for treatment of mucormycosis. Combination polyene-caspofungin treatment was found to be associated with improved survival in patients with rhino-orbital-cerebral mucormycosis, compared to polyene monotherapy. Surgery is an important adjunctive therapy and was shown to decrease mortality in patients with mucormycosis. We described rare presentations of pulmonary mucormycosis caused by *Rhizopus* spp. in 2 patients with CGD; with chest wall and spinal involvement in a child, and cardiovascular involvement in an adult patient. Case 1: A 2-year-old girl presented with pneumonia and pleural effusion that failed to respond to prolonged courses of broad spectrum antibiotics and pleural drainage. Examination revealed a febrile, malnourished child with enlarged liver and spleen. Chest examination showed a firm mass extending from the axial to the posterior aspect of the right chest wall. CT scan showed consolidation involving right lower lobe, middle lobe, and posterior segment of the right upper lobe with pleural effusion. A right chest wall mass with intraspinal extension was also noted. Cultures of tissue obtained from surgical biopsy of the chest wall mass grew *Rhizopus* spp. She was subsequently diagnosed to have CGD based on oxidative burst test result. Treatment with liposomal amphotericin B was initiated at a dose of 5 mg/kg/day then increased to 7 mg/kg/day. Caspofungin and interferon γ (IFN-γ) were added to treatment. She underwent surgical debulking of the chest wall mass and near-total pneumonectomy. She was then referred to a specialized center for HSCT.

abdulnasir.al-otaibi@sickkids.ca

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Detection and diagnosis of wood decay fungi in wooden heritage using different image techniques

Alfieri, Paula Vanesa and **Correa M Veronica**
LEMIT, Argentina

This study was based on the current deteriorated status of wood slats from locomotive turntable of Provincial Railway Station La Plata. Wood specie of the slats was determined by conventional methods being *Schinopsis sp*. while fungal species was determined morphological being *Phellinus chaquensis* (white-rot fungus). Determination of the fungus and its *in-vitro* cultural features were based on Iaconis and Wright and Robledo and Urcelay. Fungal degradation wants be measured by non-destructive methods: area occupied by mycelium and basidiomata were observed by x-ray radiography and computer tomography (CT) and quantified by image analysis with Image J software. Greyscales of the images obtain indicated density changes, being black scale the less dense and white scale the densest. To establish the microstructural wood deterioration (cell wall), scanning electron and optical microscopy (SEM and OM) images were analyzed. It was concluded that deterioration analysis by images is a non-destructive alternative methodology, which allows to measure structural condition of material. This is essential in heritage conservation because it allows defining correctly the deteriorated status useful to planning a conservation strategy, avoiding the asset loss.

paulaalfieri@gmail.com

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Do climate changes affect the fruiting timing of wild mushroom populations in Israel?

Dalia Lewinsohn Dalpitriot
University of Haifa International School, Israel

Despite the semi-arid climate of Israel the mushrooms mycobiota is quite varied and has been studied over the years. We found both early and late fruiting in many wild mushroom species in the 2015 mushroom season, that displayed unusual temperatures and rain. Distribution in some cases, several species fruited twice on that year. Similar findings were also reported by researchers from Norway, England, France, Germany and other countries. Is this phenomenon related to global warming changes? Our findings cannot answer this question. We conclude that due to the abnormal weather we could detect a fluctuation in the timing of mushroom appearance, which could be the result of global changes. In order to investigate the causes of these observations, we suggest examining and combining previous herbarium mushroom fruiting records and meteorological information.

dalpitriot@gmail.com

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Ergotism and the ergot fungus in Ethiopia

Dawit Abate
Addis Ababa University, Ethiopia

Ergotism is a current human health problem on the Ethiopian highlands. A few outbreaks of ergotism in the country have been documented in the last few decades. The problem continues to date and a multi-purpose research was undertaken. Field studies showed that the problem is prevalent on highlands between 2,300- 3,000 m above sea level and where barley and wild oats (*Avena abyssinica*) are grown as major crops. It was found that *A. abyssinica* is the only cereal host for the Ethiopian ergot fungus. Based on molecular mycological studies, the fungus is characterized as a pathovar of *Claviceps purpurea*. Both gangrenous and convulsive ergotism are apparent in affected village communities with symptoms typical of ergotism. It was noted that extensive invasion by the fungus and development of the sclerotia on wild oats in farmers' fields and the consequent outbreak of ergotism in Ethiopia is unpredictable in time and space. Farmers, unfortunately, are not aware of the source and cause of the problem. Chemical analysis of ergot sclerotium showed that a cocktail of 16 toxic ergot alkaloids including ergocornine, ergocryptine, ergometrine, ergosine and lysergic acid derivatives are contained in the sclerotium. From studies based on affected communities, it was apparent that ingestion of the sclerotium from ergot infested oats is the cause of the problem. Prevention and control of ergot toxicosis requires a deeper understanding of environmental variables and a systematic ecological study.

dawitabate0@gmail.com

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Genetic diversity of *Aspergillus flavus* and occurrence of aflatoxin contamination in stored maize across three agro-ecological zones in Kenya

Grace W Gachara[1], Anthony K Nyamache[1], Jagger Harvey[2], Gbemenou Joselin Benoit Gnonlonfin[2] and **James Wainaina[2]**
[1]Kenyatta University, Kenya
[2]Biosciences Eastern and Central Africa-International Livestock Research Institute, Kenya

Aflatoxin contamination at post-harvest poses a serious challenge in achieving millennium development goals on food security especially in the developing world. In Kenya, major outbreaks of aflatoxicoses have been attributed to poor post-harvest storage practices. In this study, we conducted a cross-sectional survey within three Agro-ecological zones in Kenya, to determine occurrence and distribution of total aflatoxin in stored maize and the aflatoxigenicity potential of *Aspergillus flavus* in stored maize. The counties selected were; Kitui, Nakuru and Kitale (in Trans-Nzoia County). Sampling sites were selected based on previous aflatoxicoses outbreaks (Kitui) and major maize production areas (Nakuru and Kitale) where little information exists on the occurrence of aflatoxin contamination. A total of one hundred and thirty (130) kernel maize samples were random collected during the period between June and August 2012. Moisture content was determined using the standard oven method and *Aspergillus flavus* was isolated by direct plating technique. Genetic diversity of the isolates was determined by PCR and Single Sequence Repeats (SSR) micro satellites analysis. Positive strains were induced to produce B1 aflatoxins on Yeast Extract Sucrose Agar (YESA) and quantified using competitive ELISA technique. The results indicated mean moisture content of maize ranged between 6% and 34%, although this was found not to be significantly different ($p=0.23>0.05$). However, total aflatoxin contamination of postharvest stored maize samples between sites was significantly different ($p=0.000$, <0.05); with the highest contamination in Kitale at a mean of (9.68 µg/kg). *A. flavus* was isolated in 70% (N= 91) of the maize samples collected at postharvest. *A. flavus* isolates with the highest aflatoxigenicity potential were from Nakuru County with mean aflatoxin level at 239.7 µg/kg. Genetic distance based on Neighbor Joining (NJ) clustered the *A. flavus* isolates into five main clusters. Principal coordinate Analysis (PCA) analysis showed five distinct clusters with both axes explaining 60.17% of the variance. This study showed widespread distribution of aflatoxin contamination and a highly toxigenic *A. flavus* in stored maize in three major agro ecological zones in Kenya. These results suggest a potential health risk of aflatoxin outbreaks within these areas, thus call for more investigations.

kikogash@gmail.com

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Biodiversity investigation and potential of fungal endophytes of peppermint and their extract effect on chickpea rot pathogens

Kanika Chowdhary[1], Nutan Kaushik[2] and **Satyawati Sharma[1]**
[1]Centre for Rural Development and Technology, India
[2]TERI Institute, India

India is the highest producer of *Cicer arietinum* (Chickpea), however the crop is highly susceptible to plant fungal diseases i.e. *Sclerotinia sclerotiorum*, *Botrytis cinerea, Fusarium oxysporum and Rhizoctonia solani*. For a sustainable and environment friendly alternative, anti-plant pathogenic efficacy of fungal endophytes were investigated. Endophytic fungal agglomerate of Indian medicinal plant, *Mentha piperita* was investigated for biodiversity, bio control potential towards chickpea rot causing phytopathogens and their metabolite profiling. 63 pure fungal isolates were recovered from medicinal plant sampled in different seasons from distinct regions of India. Endophytic fungi were identified by ITS-rDNA sequence process. PCA divulged seasonal variability with exclusive presence of *Colletotrichum sp., Diaporthe phaseolorum, Alternaria sp., Hypocrea sp. and Rhizopus oryzae* in second sampling season. Shannon diversity index (H') was found to be highest in leaf (1.253) from Mukteshwar. Menhinick's index discern that stem tissues from Mukteshwar have maximum species richness (Dmn=1.75). Best antifungal activity was exhibited by extracts of Acremonium sp. (MPM-2.1) with < 1mg/ml IC50 value towards phytopathogens. GC-MS chromatography of potent biocontrol fungus Acremonium sp. (MPHSS-2.1) confirmed presence of antifungal compounds 1-heptacosanol and 1-nonadecane.

kanikatokasiit@gmail.com

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Biofilm induction in mucormycosis-causing fungi and the synergistic antifungal activity of Amphotericin B and thyme oil

Karaleen Anderson, Olga Ruiz Kopp and Mariel Hatch
Utah Valley University, USA

Fungal infections caused by opportunistic pathogens have gained clinical importance in the last decade, with a significant increase in infections due to the *Zygomycetes, Mucor, Rhizopus and Absidia*. These serious and sometimes fatal infections are often associated with biofilm formation. The formation of biofilm often increases resistance to antifungal agents when compared to free living colonies. This study investigates both the biofilm formation and the antifungal susceptibility of two species known to cause mucormycosis infections namely: *Rhizopus oryzae* and *Absidia corymbifera*. Upon successful biofilm formation, the synergistic effects between thyme oil and amphotericin B were tested. Results indicate that both *R. oryzae* and *A. corymbifera* are able to form biofilms under specific conditions and that these biofilms were significantly inhibited by Thyme oil. The MIC_{50} of thyme oil on *Absidia corymbifera* and *Rhizopus oryzae* was 0.0005 µL/mL and 0.0001 µL/mL respectively. Results also indicate a strong synergistic relationship between Amphotericin B and Thyme oil when used in combination against fungal biofilms.

koppol@uvu.edu

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Investigating the effect of arbuscular mycorrhizal fungi (Glomus etonicatum) and air pollutants on growth parameters of maize (Zea mays L.)

Mobina Jamali[1] and **Naser Alimohamadloo**[2]
[1]Ministry of education, Iran
[2]Islamic Azad University, Iran

To investigate the effect of Glomus etonicatum and air pollutants and acidic rain on growth parameters of maize plants (Zea mays L.), a completely randomized experiment with ten replications was conducted from February 2016 to April 2017. Experimental treatments included four categories containing the plants treated by mycorrhiza fungus irrigation by acidic rains and control water with (PH=7), and witnessing plants irrigation by acidic rain and control water. Results from analysis of variance revealed that the effect of mycorrhizal inoculation on chlorophyll, protein and carotenoid content of leaves, plant height, leaf dry wt, leaf fresh wt, root fresh wt, fruit number and leaf number and surface, were significant ($p<0.05$). Mycorrhizal inoculation enhanced all parameters significantly in comparison to the witnessing plants and the highest value for these traits obtained by the plants inoculated with mycorrhiza irrigation by control water and the least obtained in witnessing plants irrigation by acidic rain water. Furthermore, the research revealed that the amount of these parameters in plants inoculated with mycorrhiza irrigation by acidic rain, is significantly more than witnessing plants irrigation by control water. In general, inoculation by mycorrhizal fungi in addition to enhancing growth parameters can enhance the photosynthesis and production of oxygen in maize even under acidic rain circumstances and air polluted environments, compared to non-mycorrhizal plants in regular circumstances.

jamalimobina@yahoo.com

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Pulmonary zygomycosis among HIV/AIDS subjects with respiratory symptoms in Calabar, Nigeria

Ofonime M Ogba, Lydia N Abia-Bassey and **James Epoke**
University of Calabar, Nigeria

Introduction: Zygomycosis is a rare infection but the incidence is on the rise as a result of increased use of chemotherapy and steroids among immunosuppressed patients. It is an invasive angiotropic infection with fungi of the *Mucorales* order, which includes Mucor species, *Rhizopus* species, *Rhizomucor* species, and multiple others. The second most common form of the infection is pulmonary.

Materials & Methods: HIV-positive subjects with respiratory symptoms were enrolled for the study. Subjects selection was based on HIV screening and the ability to produce sputum. A structured questionnaire was administered to all the subjects after obtaining their informed consent for demographic data. Ethical approval was obtained from the ethical research committee, UCTH, Calabar, Nigeria. Blood samples were obtained for CD4 count determination to ascertain the immune status of the patients. Sputum samples produced early in the morning were obtained twice from the subjects and subjected to macroscopy, microscopy and culture. The immune status of the subjects was assessed by CD4 count levels. Identification to the species complex level was performed by macroscopic and microscopic morphology.

Results: *Rhyzopus arrhyzus* 50.0% and *Litchthenia* species 50% were the only *Mucorales* encountered among subjects in this study. 3.0% pulmonary zygomycosis prevalence was recorded in the study. Subjects with *Rhizopus arrhyzus* infection presented hemoptysis and cough while those with Absidia infection presented with variable symptoms including; cough, chest pain, sinusitis and fever. The mean CD4 counts of subjects with and without zygomycosis were 123.0±136.2 351.3±254.3 respectively. There was a statistically significant effect of zygomycosis on the CD4 counts of subjects (t=2.18, p=0.02).

Conclusion: This study reveals that pulmonary zygomycosi is a health problem among HIV/AIDS patients in our locality. The immune status may have been influenced by the infection.

olawumioyebanji@gmail.com

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Glomus fasciculatum fungi as a bio-convertor and bio-activator of inorganic and organic P in dual symbiosis

Rafia Azmat
University of Karachi, Pakistan

This article describes mechanism of Phosphorus supply from the soil into plants under VAM fungal inoculation. It was already established that VAM fungi symbiosis helps in uptake of nutrients especially P which is not easily accessible under ordinary condition of soil. For this investigation, *Conocarpus erectus L* species and Glomus fasciculatum was identified and selected in four experimental set up including i) control (E_1), ii) VAM inoculated (E_2), iii) VAM and excess of CO_2 (E_3) and iv) VAM and drought (E_4). All Plants except E_3) were cultivated under natural condition and watered alternative day whereas E4 was watered after regular interval of 4 days. Analysis of soil and plant's P were carried out after 12 months. Phosphorus in plants were analysed in roots, stem, and leaves separately and correlated with soil remaining phosphorus. Results showed that soil P was less in four experimental set up when compared with P of standard soil. It was found that P accumulation in plants was varied in all four experimental conditions based on VAM symbiosis. It was found that the roots of E_2 and E_3 plants showed highest P accumulation as compared to E1 and E4 which were linked with absence of VAM and drought conditions. P translocation into E4 plants showed that movement of P based on availability of water condition due to which it was less in leaves too over E_1, E_2 and E_3 plants. Experimental facts and nonstop growth of plants recommended that VAM fungi act as a bio-converter and bio-activator of soil nutrients especially of Phosphorus, and their hypal interaction absorb soil nutrients and convert inorganic P to organic one for plant development. Continuous growth of one year old conocarpus plant support the proposed idea that phosphorus cycle exists during VAM inoculations which strengthen the plant and activate photobiological activity that helps in increasing photosynthetic rate and stimulate all biological processes of plant including H+ co-transporter couple with inorganic phosphorus and its ultimate supply to plants.

rafiasaeed200@yahoo.com

PULSUS
WWW.PULSUS.COM

Annual Congress on

Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

Primary cutaneous mucormycosis in a patient with burn wounds due to *Lichtheimia ramosa*

Kaur R[1], Bala K[2] and **Ahuja R B[3]**
[1]Lady Hardinge Medical College, India
[2]AIIMS, India
[3]MAMC, India

Mucormycosis is usually an invasive mycotic disease caused by fungi in the class mucormycetes. Here, we report a case of cutaneous mucormycosis due to *Lichtheimia ramosa* in a 20-year-old female patient with burn injuries. She was admitted to the hospital with accidental flame burns covering 60% total burn surface area. After 15 days of admission to hospital, the burn wound showed features of fungal infection. Culture showed white cottony growth belonging to the *Mucorales* order. Morphological identification confirmed it as *L. ramosa*. She was managed surgically and medically with the help of amphotericin B. Patient survived due to prompt diagnosis and appropriate medical and surgical treatment. Early diagnosis is critical in prevention of morbidity and mortality associated with the disease. Fungal infection in burn wounds can be difficult to diagnose and manage.

drkaur@hotmail.com

Annual Congress on

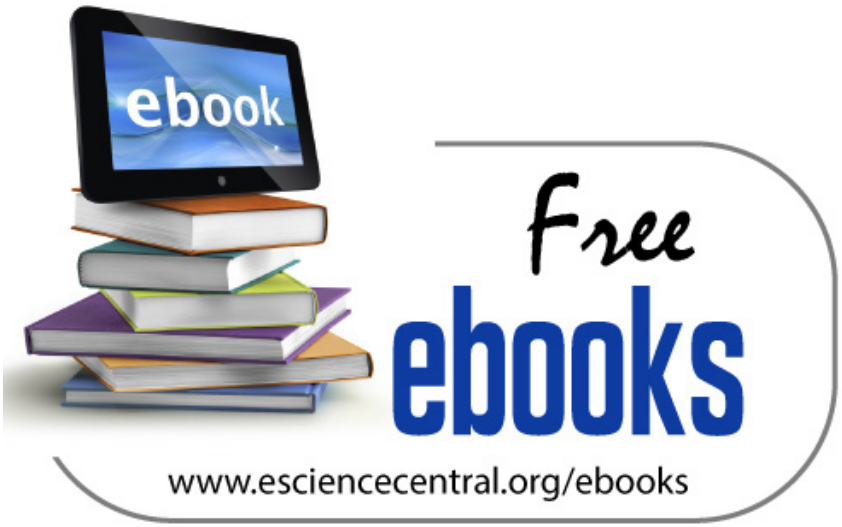
Mycology and Fungal Infections

November 16-17, 2017 Atlanta, Georgia, USA

INDEX

Upcoming Conferences

International Conference on **Vascular Biology, Medicine & surgeons meeting** **Dec 04-05, 2017 | Dallas, USA** *vascular.cmesociety.com*
International Heart Conference **Dec 04-05, 2017 | Dallas, USA** *heart.cmesociety.com*
Nursing and Healthcare Congress **Dec 08-09, 2017 , Dallas, USA** *nursing.cmesociety.com*



eBooks

Free 'Open Access' eBooks is an initiative of International Publisher established in the year 2012 with the sole aim of sharing the scientific knowledge and information globally in all the emerging areas of Life Sciences, Health Sciences, Engineering & Technology, Social Sciences and Business Management. For more info please visit https://www.esciencecentral.org/ebooks/

Fungal Infections 2017