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September 25-26, 2017 Chicago, USA

Keynote Forum

Day 1

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MYCOLOGY & MUSHROOMS

September 25-26, 2017 Chicago, USA



Yury O Chernoff

Georgia Institute of Technology, USA

Fungal models for amyloids and prions

Statement of the Problem: Prions are alternatively folded self-perpetuating protein isoforms involved in a variety of biological and pathological processes. Most prions are based on self-assembled protein aggregates (amyloids). In humans, amyloids and prions are associated with important diseases, such as Alzheimer, Parkinson and Huntington diseases, and transmissible spongiform encephalopathies. In yeast and other fungi, prions are protein-based non-Mendelian elements that control heritable traits.

Methodology & Theoretical Orientation: Due to relative simplicity of cultivation procedures and availability of convenient phenotypic assays, fungi provide a great opportunity for deciphering the general mechanisms of the formation and propagation of amyloids and prions.

Findings: Yeast and fungal prions influence a variety of physiological functions. Prion formation and loss are modulated by environmental and physiological conditions. *De novo* formation of an yeast prion can be induced by a transient overproduction of a prion-forming protein. The process of prion formation includes generation of the intermediate aggregated structures, associated with cytoskeletal networks and quality control compartments. Propagation of yeast prions is controlled by the same cytosolic Hsp104/70/40 chaperone machinery that is involved in protection of yeast cells against proteotoxic stress. Chaperones fragment prion polymers thus providing oligomeric seeds for new rounds of prion propagation. Ribosomeassociated chaperones antagonize prion formation and interfere with the ability of cytosolic chaperones to promote prion propagation. Chaperone and cytoskeletal machineries mediate effects of environmental stresses on prions.

Conclusion & Significance: The impact of prions on fungal biology is still underestimated. An 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. Many components of this machinery possess homologs or functional counterparts in higher eukaryotes, thus making yeast prions an excellent model for deciphering the general mechanisms of amyloid/prion formation and propagation in norm and pathology.

Biography

Yury O Chernoff is an Expert in Yeast Genetics and Molecular Biology. His major areas of research include protein biosynthesis, folding, aggregation, protein-based epigenetic inheritance, and yeast models for amyloid and prion disorders. He has demonstrated that self-perpetuating protein isoforms (prions) can be induced by transient protein overproduction and discovered the crucial role of chaperones in prion propagation. His research has also established evolutionary conservation of prion-forming properties, led to development of a yeast system for studying cross-species prion transmission, helped to establish yeast assays for aggregation and toxicity of mammalian aggregating proteins, and contributed to studying the involvement of cytoskeletal networks and protein quality control pathways in prion and amyloid phenomena. He is the Founding Editor-in-Chief of the international journal *Prion*, published by Taylor and Francis, Inc. In 2015, he has been elected a Fellow of the American Association for the Advancement of Science (AAAS).

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Isak Pretorius

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Conducting wine symphonics with the aid of synthetic yeast genomics

perfectly balanced wine can be said to create a symphony in the mouth. To achieve the sublime, both in wine and music, $\mathbf A$ requires imagination and skilled orchestration of artistic craftmanship. For wine, inventiveness starts in the vineyard. Similar to a composer of music, the grapegrower produces grapes through a multitude of specifications to achieve a quality result. Different Vitis vinifera grape varieties allow the creation of wine of different genres. Akin to a conductor of music, the winemaker decides what genre to create and considers resources required to realize the grape's potential. A primary consideration is the yeast: inoculate the grape juice or leave it 'wild'; which specific or combined Saccharomyces strain(s) should be used; or proceed with a non-Saccharomyces species? Whilst the various Saccharomyces and non-Saccharomyces yeasts perform their role during fermentation, the performance is not over until the 'fat lady' (S. cerevisiae) has sung (i.e. the grape sugar has been fermented to specified dryness and alcoholic fermentation is complete). Is the wine harmonious or discordant? Will the consumer demand an encore and make a repeat purchase? Understanding consumer needs lets winemakers orchestrate different symphonies (i.e. wine styles) using single- or multi-species ferments. Some consumers will choose the sounds of a philharmonic orchestra comprising a great range of diverse instrumentalists (as is the case with wine created from spontaneous fermentation); some will prefer to listen to a smaller ensemble (analogous to wine produced by a selected group of non-Saccharomyces and Saccharomyces yeast); and others will favour the well-known and reliable superstar soprano (i.e. S. cerevisiae). But what if a digital music synthesizer-such as a synthetic yeast-becomes available that can produce any music genre with the purest of sounds by the touch of a few buttons? Will synthesizers spoil the character of the music and lead to the loss of the much-lauded romantic mystique? Or will music synthesizers support composers and conductors to create novel compositions and even higher quality performances that will thrill audiences? This article explores these and other relevant questions in the context of winemaking and the role that yeast and its genomics play in the betterment of wine quality.

Biography

Isak Pretorius is working as the Deputy Vice Chancellor and Vice President (Research) at Macquarie University in Sydney. He is internationally recognized as a pioneer in synthetic yeast genomics and wine biotechnology, and the translation of research outcomes to industry. He has published more than 200 peer-reviewed research papers and book chapters (current Scopus H-index of 47) and presented at more than 600 conferences (many as Invited Keynote Speaker) and research seminars. He has won many research grants (more than \$90 million) and awards, and filed six patents. Over the past three decades, he has supervised or co-supervised 33 PhD students and 56 MSc students. Currently, he leads the Australian team as part of the international Synthetic Yeast Genome (Yeast 2.0) project.

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Xianming Chen

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Biology, genetics, functional genomics, evolution, and epidemics caused by the stripe rust pathogen

Puccinia striiformis, an obligate biotrophic parasite, causes stripe rust of wheat, barley, and many grasses. Stripe rust of wheat is important worldwide and can cause yield losses up to 4.5 million tones plus millions of dollars spent on chemical control in the United States. The basidiomycete fungus has been recently demonstrated, under controlled conditions, to have a heteroecious macrocyclic life cycle consisting of five spore stages with uredinial, telial, and basidial stages on cereals and grasses, and pycnial and aecial stages on Berberis and Mahonia species. However, the role of alternate hosts for sexual reproduction of the fungus under the natural conditions in the United States is limited due to the enclosed telia that are covered by host epidermis, lack of dormancy, and degradation of teliospores in the winter, in addition to the dry weather conditions when teliospores are able to germinate and the mismatching phenology of barberry plants. As a suicidal factor, telial formation reduces the production of urediniospores, and thus reduces the aggressiveness and fitness of the pathogen. Mapping populations have been developed through sexual reproduction on barberry and used to construct a consensus map of the fungus and for mapping virulence loci using simple sequence repeat (SSR), single-nucleotide polymorphism (SNP), and genotyping by sequencing (GBS) markers. Molecular markers also have been used to determine the genetic structure of the pathogen population and evolutionary mechanisms. Mutation and somatic recombination have been determined as major mechanisms for the pathogen to produce new races and genotypes, and host selection plays an important role in shifting the population. As auxiliary hosts, grasses have been found to harbor more diverse populations. The secretomics of the stripe rust pathogen is studied to identify virulence effectors and determine mechanisms of the pathogen-host interactions for developing more efficient strategies for control of stripe rust.

Biography

Xianming Chen has his expertise in plant pathogenic fungi, especially the stripe rust pathogen of cereal crops. His research focuses on stripe rust of wheat and barley. He and his colleagues have conducted basic and applied research to develop better methods for control of stripe rust. His research areas include plant resistance (genetics, molecular mapping and cloning of resistance genes, and resistance mechanisms); biology, genome and functional genomics, races and population structures of stripe rust pathogens; and epidemiology and control of diseases (developing resistant germplasm, disease monitoring and forecasting, and integrated control).

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Mycology & Mushrooms

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Shiping Tian

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Biosynthesis and regulating mechanisms of patulin in Fungi

Statement of the Problem: Contamination of food and feed by fungal secondary metabolites known as mycotoxins is a global health issue. Patulin is one of important mycotoxins, and produced by several species belonging to *Penicillium, Aspergillus, Paecilomyces, Byssochlamys.* Among them, *Penicillium expansum* infects a wide range of fruits and vegetables, and is the main producer of patulin. Long-term exposure to patulin may cause serious health issues in humans, because patulin can induce immunological, neurological and gastrointestinal diseases. Level of patulin in food has been limited in many countries worldwide. However, the molecular mechanisms of biosynthesis and regulation of patulin are still unclear. Here, we identified the gene cluster of patulin in *P. expansum*, and characterized functions of patulin genes.

Methodology & Theoretical Orientation: Whole genome sequencing was performed for patulin producer *P. expansum* and non-patulin producer *Penicillium italicum*. Bioinformatic analysis was used to identify patulin gene cluster. Knockout analysis and subcellular localization were used to characterize gene function.

Findings: Whole genome sequences of *P. expansum* (33.52 Mb) and *P. italicum* (28.99 Mb) were obtained. A total of 71 backbone genes and 55 gene clusters related to secondary metabolism were predicted in *P. expansum*. Further, we identified a cluster of 15 genes responsible for the biosynthesis of patulin. Patulin gene clusters within more than 10 *P. expansum* related fungal species were compared and gene loss in some non-patulin producing species was identified. The importance of all the genes in patulin cluster is ascertained by gene knockout analysis. Deletion of the majority of genes completely blocked patulin production. Among them, PePatL may act as a pathway specific transcription factor, and play essential role in patulin biosynthesis. Moreover, LaeA, a global regulator, was also involved in the regulation of patulin regulation. In addition, patulin production did not contribute to the pathogenicity of *P. expansum*.

Conclusion & Significance: Our findings indicate previously unknown roles of genes in the patulin cluster and cast insight into the molecular mechanism in biosynthesis and regulation of this important mycotoxin

Biography

Shiping Tian has her expertise in postharvest biology and technology in fruits. Her research fields mainly focus on Molecular mechanism of fruit ripening, senescence and quality maintenance; pathogenicity and mycotoxin biosynthetic pathway of fungal pathogens and regulating mechanisms; induced resistance of fruit against postharvest fungal pathogens. She has published more than 150 papers in international journals such as *Genome Biology, Plant Journal, Molecular and Cellular Proteomics, Molecular Plant and Microbe Interactions.* She also acts as an Associate Editor of an international journal *Postharvest Biology and Technology.*

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Mycology & Mushrooms

September 25-26, 2017 Chicago, USA



Balbina J Plotkin

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Mycobiome and interkingdom interactions

Mamalian hosts contain a diverse mycobiome. Colonization sites on the oral and genital mucosa are shared by *Candida albicans, Staphylococcus aureus* and herpes simplex virus (HSV-1, and HSV-2); however, their interactions are poorly understood. To test whether viral entry into cells results in the differential display of receptors shared between HSV, *C. albicans* and/or *S. aureus*, HeLa229 cells were infected with HSV-1 (KOS) gL86 or HSV-2 (KOS) 333gJ- then exposed to *S. aureus* (ATCC 25923) and/or *C. albicans* (30 min; 370 C; n=16). Adherence of *C. albicans* yeast cells and *S. aureus* to HSV-1 infected HeLa cells varied over time. The level of C. albicans adherence to HSV-1 infected cells was enhanced as compared to controls. Adherence was maximized at 90 min. (191% of control) and 180 min. 146% of control. Interestingly, between 105 and 150 minutes there was inhibition of adherence that ranged from 92% to 97% of control. In contrast, adherence of *S. aureus* was inhibited. The HSV-mediated inhibition occurred over the initial 120 minutes. Inhibition ranged from a low of 77% of adherence to uninfected homologous controls at 45-60 minutes to restoration of adherence to control levels at 120-165 minutes before decreasing to 92% of control at 180 minutes. Our model suggests that the HSV-1 antagonist interaction with *S. aureus* as well as its enhancing interaction with *C. albicans* is a dynamic time-dependent interaction which may correlate with rate of receptor turnover or unmasking as it correlates with the HSV-1 entry process.

Biography

Balbina J Plotkin has received her PhD from the University of Tennessee. She is a Professor in the Department of Microbiology and Immunology at Midwestern University. Her field of expertise, in which she has published more than 50 papers in peer reviewed journals, is that of identification and characterization of interkingdom quorum signaling compounds and their role in biofilm formation and antimicrobial resistance. In addition, she and her colleagues have developed a novel methodology for studying the initial steps in the interactions of microbiome members across the animalis, fungi, and eubacteria kingdoms with herpes simplex virus (HSV-1 and HSV-2)

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Keynote Forum

Day 2

Mycology & Mushrooms

September 25-26, 2017 Chicago, USA



Mark A Weaver

Agriculture Research Service, USA

Preventing mycotoxin contamination of corn through biological control and transgenic insect protection

Corn is a global food and feed staple, totaling over 1 billion metric tons annually and the crop in the United States alone Was valued at over \$50 billion US dollars. This commodity can be infected with fungal plant pathogens in storage or while growing in the field. Such fungal contamination is a serious threat because some fungi may contaminate the grain with mycotoxins. The mycotoxin of greatest concern in corn production is aflatoxin, a secondary metabolite of some strains of *Aspergillus flavus* and other *Aspergillus spp*. Fumonisin, produced by *Fusarium verticillioides*, is another mycotoxin that is important in certain environments. These secondary metabolites may lead to the grain being rejected and add expense to grain processing and marketing. A number of field studies, particularly in the Southern U.S., have validated the use of biocontrol fungi to prevent aflatoxin contamination. For example, a three-year, fourteen site experiments demonstrated a \$200 per hectare increase in net returns by using a product for the biocontrol of aflatoxin. Other studies have examined the transgenic insect protection, such as Bt corn, to prevent fumonisin contamination, by reducing damage from Lepidopteran insects and subsequent opportunistic fungal infections. More recently, improved transgenic corn hybrids have greater than 90% reduction in earworm (*Helicoverpa zea*) damage and a 60% reduction in fumonisin compared to isogenic hybrids without insect protection. The threat of mycotoxin contamination is highly variable and difficult to predict, but it may be possible to use biological control with transgenic insect protection to provide broad and robust protection from mycotoxin contamination in corn.

Biography

Mark A Weaver has published research papers on cover crops, microbial herbicide metabolism in soils and wetlands, and biological control of weeds. His work includes development of biocontrol strains of *Aspergillus flavus* and the post-release tracking of biocontrol agents. Presently he is developing molecular tools for landscape-scale monitoring of *A. flavus*.

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MYCOLOGY & MUSHROOMS

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Presenting Author: Wan Abd Al Qadr Imad Wan-Mohtar

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Upstream and downstream processing of Ganoderma lucidum mycelial extract: A road to natural remedies?

fumankind has experimented with various sources and techniques to counter global health issues that include drug L resistance and newly-developed types of infections. In 2010, approximately 15 million people died from contagious infections, despite the readily-available extensive synthetic prescribed drug combinations in the market. Extra effort must be dedicated to the development of non-synthetic, natural-based remedies, particularly from medicinal mushrooms. To date, a safely established mushroom called Ganoderma lucidum shows the potential to be one of the best natural-based medicinal therapies combatting global health issues. This study describes the efficient production of the underutilised mycelium of G. lucidum and in vitro testing of potential therapeutic effects obtained from the sulphated glucan derived from such mycelial cultures. For G. lucidum, most of the reported positive bioactivities are obtained from the fruiting bodies and not from their mycelial cultures. Such cultures represent a much faster way to produce glucan from G. lucidum compared to extraction from the flesh. If G. lucidum derived materials, having multifunctional effects are to be used to combat global health issues, they will need to be produced in bulk, quickly, cheaply and to a consistent quality. A mycelial cultivation called repeated-batch fermentation (RBF) has been done in a bioreactor solving the typical long cultivation time and generated efficient productivities. An elegant sulfation technique was applied to the extracted glucan, thus enhancing the water-solubility and therapeutic responses via multiple aseptic in vitro assays: antimicrobial, antifungal, anti-proliferative and immunomodulatory. The reported upstream process of G. lucidum via RBF has successfully improved the glucan production with a shorter cultivation time. The downstream process has indicated the benchmarks in battling global health issues, introducing a novel "quad-functional" approach of this bioreactor-derived material. These two processes may lead to a natural remedy, thus overcoming the problem of using singularfunction synthetic drugs in health industries.

Biography

Brian McNeil B.Sc. (1st Class Hons in Applied Microbiology, Strathclyde 1980), Ph.D. funded by Carnegie Trust in Fermentation Technology 1984. Lecturer in Department of Bioscience 1989-1997, Senior Lecturer 1997-2003, Reader 2003, Professor of Microbiology 2005-date, Assistant Head of Institute 2009-2012 b.mcneil@strath.ac.uk

Wan Abd Al Qadr Imad Wan-Mohtar is a Senior Lecturer and Young Scientist in Institute of Biological Sciences, Faculty of Science, and University of Malaya, Malaysia. He is graduated from Strathclyde Institute of Pharmacy and Biomedical Sciences, Glasgow under the supervision of fungal fermentation expert Prof Brian McNeil and Prof Linda Harvey. His field of interest is on extended liquid fermentation and microbiology of mushrooms which rooted from BSc in Microbiology (Oyster mushrooms), MSc in Food Biotechnology (Local Basidiomycetes) and PhD in Fermentation Technology (*Ganoderma lucidum*). He has his expertise in mushroom liquid cultivation in order to boost the supply of the natural therapeutic compound thus improving health and wellbeing through *G. lucidum*. His optimisation of extended batch fermentation and sulphated glucan from *G. lucidum* mycelium creates potential pathways for replacing the singular-function synthetic drugs via quad-functional sulphated glucan. He has built this idea after years of experience in research, evaluation, teaching and administration both in laboratories and educational institutions.

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Mycology & Mushrooms

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Savitha Janakiraman

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Comparative study on whole genome sequences of *Aspergillus terreus* (soil fungus) and *Diaporthe ampelina* (endophytic fungus) with reference to lovastatin production

Lovastatin is a competitive inhibitor of the enzyme hydroxymethyl glutaryl coenzyme A reductase (HMGR) in cholesterol biosynthetic pathway and hence used in the treatment of hyperlipidemia. In a previous study, we report a tropical soil isolate, *Aspergillus terreus* (KM017963), which produces ample amount of lovastatin than its counterpart, which are endophytic in origin. Bioinformatic analysis of whole genome sequence of *A. terreus* (AH007774.1), a soil isolate revealed the presence of gene cluster responsible for lovastatin production, whereas, endophytic fungi including a species of *A. terreus* showed no homology with the lovastatin gene cluster. The molecular study was also carried out targeting PCR amplification of the two important genes, *lovE* (a regulatory gene) and *lovF* (transcriptional regulatory factor) in genomic and c-DNA of soil and endophytic fungi. Expression of the two genes was successful in *A. terreus* (KM017963), whereas the same was not achieved in endophytic fungi. To further validate our above findings, in the present study, the whole genome sequencing of *A. terreus* and a selected endophytic fungus, *Diaporthe ampelina* (Phomopsis) was performed. Lovastatin gene cluster, when aligned on the consensus sequence of both genomes, the entire lovastatin gene cluster was detected in a single scaffold (1.16) of *A. terreus* genome. On the contrary, there was a complete absence of lovastatin gene cluster in the genome of *D. ampelina* (an endophyte). The probable reasons for the absence of lovastatin gene cluster in endophytic fungi will be discussed.

Biography

Savitha Janakiraman has received her PhD degree in Botany, Madras University and postdoctoral research in University of Hull, England under the Jawaharlal Nehru (UK) fellowship. Currently, she is working as Professor in Bangalore University, Department of Microbiology. She is the Chairman of Board of Examination (BOE) and Member of Board of syllabus and Academic Council of Bangalore University. She has published several research papers and has several research projects offered by Government funding agencies. Her interest of research is on Industrial Microbiology and Environmental Microbiology.

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