UNIVERSITY OF SCIENCE
VIETNAM NATIONAL UNIVERSITY
HO CHI MINH CITY

ABSTRACT BOOK

MOH-VN
2018

The 1st International Conference on MICROBIOLOGY AND ONE HEALTH

moh-vn.com

SEPTEMBER
19 - 22

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- Bacillus cereus
- Norovirus GI & GII

Bioterrorism
- Brucella
- Ebola
- Vibrio cholerae
- TG, typhus group
- Clostridium botulinum neurotoxin (A, B,E,F)

Clinical (RUO)
- Influenza (A/B/RSV)
- MERS-Corona Virus

MOH-VN 2020

coming in 2020

University of Science, VNU-HCM

227 Nguyen Van Cu, Dist.5, Ho Chi Minh city, Viet Nam

www.hcmus.edu.vn

Welcome Message

Dear Friends and Colleagues,

It is our great pleasure to welcome you to The 1st International Conference on Microbiology and One health (MOH-VN), which is held from September 19 to 22, 2018 in Ho Chi Minh City, Vietnam.

The MOH-VN 2018 covers a diverse range of microbiological activities and topics, which aims at bringing together Leading academic scientists, Researchers, Medical doctors and Scholars to provide an international forum for face-to-face discussion on topics of microbiology, particularly on Microbiology and One Health. This event offers an opportunity to build and expand scientific network to promote international collaboration.

The Scientific Program includes 45 oral presentations and 29 poster presentations in 6 different topics on various aspects of microbiology. It is also our honor to have 3 plenary lecturers who are leading in microbiological research. The Conference highlights the following topics:

1. Pathogenesis and infection
2. Drug discovery
3. Antimicrobial resistance, diagnostics and treatment
4. Zoonosis, One Health and environmental microbiology
5. Vaccine development
6. Bioinformatics and microbiome

The conference will offer the excellent opportunity for the interaction between the scientific community and the microbiological-related industry partners to provide a platform for exchanging ideas and innovative applications in various issues of this rapidly changing area.

Lastly, we hope you will enjoy the contents of the conference and have valuable and unforgettable time through our program in the most lively city in Vietnam.

See you again at the next MOH-VN 2020 in Vietnam.

Sincerely yours,

Prof. Tran Linh Thuoc

Prof. Guy Thwaites

Prof. Dang Duc Anh

Committee

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Date	Time	Program	
DAY 1 Sep. 19 (Wed)	13:00 -	Registration (Hall I)	
	13:00 – 17:00	Pre-conference event: Scientific writing and opportunities for postgraduate studies (Hall I)	
	17:30 – 21:00	Welcome dinner	
DAY 2 Sep. 20 (Thu)	8:00 – 9:00	Registration	
	9:00 – 9:30	Opening ceremony (Hall I)	
	9:30 – 10:10	Outside photography and coffee break	
	10:10 – 11:10	**Plenary lecture 1**	
	11:30 – 13:00	Lunch	
	13:00 – 14:30	**Division 1, Session 1** **Pathogenesis and Infections** (Hall I)	**Division 2, Session 1** **Drug discovery** (Room I.23)
	14:30 – 15:15	Coffee break and **poster session**	
	15:15 – 17:00	**Division 1, Session 2** **Pathogenesis and Infections** (Hall I)	**Division 2, Session 2** **Drug discovery** (Room I.23)
	17:30 – 21:00	**GALA DINNER**	
DAY 3 Sep. 21 (Fri)	8:30 – 10:00	**Division 3, Session 1** **Antimicrobial resistance, diagnostics and treatment** (Hall I)	**Division 4, Session 1** **Zoonosis and One Health** (Room I.23)
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	10:30 – 11:30	**Division 3, Session 2** **Antimicrobial resistance, diagnostics and treatment** (Hall I)	**Division 4, Session 2** **Zoonosis and One Health** (Room I.23)
	11:30 – 13:00	Lunch	
	13:00 – 14:50	**Division 5** **Vaccine development** (Hall I)	**Division 6** **Bioinformatics and Microbiome** (Room I.23)
	14:50 – 15:30	Coffee break	
	15:30 – 17:10	**Plenary lecture 2 and 3** (Hall I)	
	17:10 – 17:30	**Poster award and closing ceremony** (Hall I)	
DAY 4 Sep. 22	8:00 – 17:00	Tour to Mekong Delta	

Detailed program

DATE 1: SEPTEMBER 19, 2018 (PRE-CONFERENCE)	
13:00 – 17:00	Pre-conference event: Scientific writing and opportunities for postgraduate studies (Hall I)
17:30 – 21:00	Dinner for invited guests of the conference MOH-VN

DATE 2: SEPTEMBER 20, 2018		
8:00 – 9:00	Registration	
9:00 – 9:30	Opening ceremony	
9:30 – 10:10	Outside photography and coffee break	
	Chairs: Prof. Dang Duc Anh (National Institute of Hygiene and Epidemiology, Vietnam) **Prof. Michael Otto** (National Institute of Health, USA)	
10:10 – 11:10	***Plenary lecture 1***: Bad bugs and bad drugs – antimicrobial resistance in Southeast Asia	**Guy Thwaites**, Oxford University Clinical Research Unit, VIETNAM
11:30 – 13:00	Lunch	

Division 1: Pathogenesis and Infections		
13:00 – 14:30	Division 1, Session 1. **Chairs: Prof. Dang Duc Anh** (National Institute of Hygiene and Epidemiology, Vietnam) **Prof. Thomas Bock** (Robert Koch-Institute, Germany)	
13:00 – 13:25	Hepatitis E Virus: A new emerging public health burden	**Thomas Bock**, Division of viral gastroenteritis and hepatitis pathogens and enteroviruses, Robert Koch-Institute, GERMANY
13:25 – 13:50	Avian Influenza H5N1 characterization in Vietnam	**Le Thi Quynh Mai**, National Institute of Hygiene and Epidemiology, VIETNAM
13:50 – 14:10	Development of diagnostic kits for the early rapid detection of arboviral diseases	**Chom-Kyu Chong**, GenBody Inc., KOREA
14:10 – 14:30	Clinical characteristics and virology of Hand, Foot and Mouth Disease in Southern Vietnam	**Hoang Minh Tu Van**, Oxford University Clinical Research Unit, VIETNAM
14:30 – 15:15	Coffee break and **poster session**	

15:15 – 17:00	Division 1, Session 2. **Chairs: Prof. Le Thi Quynh Mai** (National Institute of Hygiene and Epidemiology, Vietnam) **Prof. Won Hee Jung** (Chung-Ang University, Korea)	
15:15 – 15:40	Two cases report: anemia aplasia with Parvovirus infection in renal transplant recipients	**Thanh Thanh Suzanne MCB**, University of Medicine and Pharmacy at Ho Chi Minh City, VIETNAM
15:40 – 16:05	Whole Genome DNA Sequence Analysis of *Salmonella enterica* isolated from the caecum/fecal material of (live) swine and chicken in the Southeast region of Vietnam	**Moon YF Tay,** Nanyang Technological University Food Technology Centre (NAFTEC), Nanyang Technological University (NTU), SINGAPORE
16:05 – 16:30	Effect of Zinc and nano-curcumin on the development of antibiotic resistance in *Staphylococcus aureus*	**Nguyen Thi Thu Hoai**, International University, VNU-HCM, VIETNAM
16:30 – 16:55	Understanding the Mechanism of Action of the Anti-Dandruff Agent Zinc Pyrithione against Malassezia restricta	**Won Hee Jung**, Department of systems biotechnology, Chung-Ang University, KOREA

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13:00 – 13:25	Strategies Focused on Overcoming Bacterial Resistance: Design and Discovery of New Anti-infective Agents	**Josef Jampilek**, Department of Pharmaceutical Chemistry, Faculty of Pharmacy, Comenius University in Bratislava, SLOVAKIA
13:25 – 13:50	Efflux pump inhibitors approach to combat multi-drug resistant bacteria	**Thai Khac Minh**, Department of Medicinal Chemistry, Faculty of Pharmacy, University of Medicine and Pharmacy at Ho Chi Minh City, VIETNAM
13:50 – 14:10	Antifungal Activity of Some Hydrosols from Aromatic Plants against Candida	**Luong Thi My Ngan**, University of Science, VNU-HCM, VIETNAM
14:10 – 14:30	Screening of sponge-derived bacteria for antibiotic producing isolates	**Pham Thi Mien**, Institute of oceanography, Nha Trang, VIETNAM
14:30 – 15:15	Coffee break and **poster session**	

15:15 – 17:00	Division 2, Session 2. **Chairs: Prof. Thai Khac Minh** (University of Medicine and Pharmacy at Ho Chi Minh City, VIETNAM) **Prof. Rachel Ee** (National University of Singapore, SINGAPORE)	
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15:40 – 16:05	Fungal Production of Biopharmaceutical Enzymes	**Vijai Kumar Gupta**, Tallinn University of Technology, ESTONIA
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DATE 3: SEPTEMBER 21, 2018		
Division 3: Antimicrobial resistance, diagnostics and treatment		
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8:55 – 9:20	Antibiotic Resistance Challenge in Vietnam - Situation and Solutions	**Pham Hung Van**, Hochiminh City Society of Clinical Microbiology, VIETNAM
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9:40 – 10:00	Overexpression of OXA β-lactamases in carbapenem resistant *Acinetobacter baumannii* strains isolated in Southern Vietnam	**Nguyen Tuan Anh**, University of Medicine and Pharmacy, Ho Chi Minh City, VIETNAM
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10:30 – 11:30	Division 3, Session 2. **Chairs: Dr. MD. Pham Hung Van** (Hochiminh City Society of Clinical Microbiology, Vietnam) **Prof. Diep An Binh** (University of California, San Francisco, USA)	
10:30 – 10:50	Influence of host stresses and antibiotic resistance on cell length distribution, cell envelope ultrastructure and accumulation of lipid inclusions in clinical *M. tuberculosis* isolates	**Vijay Srinivasan**, Oxford University Clinical Research Unit, VIETNAM
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8:50 – 9:10	A multidisciplinary approach to understand the transmission of zoonotic antimicrobial resistant bacteria in Vietnam	**Ngo Thi Hoa**, Zoonosis group, Oxford University Clinical Research Unit, VIETNAM
9:10 – 9:25	Occurrences and Quantitative Microbial Risk Assessment of Antibiotic Resistant bacteria in Tropical, Urban Water Bodies	**Le Thai Hoang**, International University, VNU-HCM, VIETNAM
9:25 – 9:45	Rapid Molecular Diagnosis of Infectious Diseases using a Portable LabChip-based Real-time PCR	**Sung-Woo Kim**, Ph.D., CEO. MiCo BioMed Co., Ltd., Seoul, Korea
9:45 – 10:00	AMR research in food animals	**Vo Thi Tra An**, Faculty of Animal Science and Veterinary Medicine, Nong Lam University, Nong Lam University, VIETNAM
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10:30 – 11:30	**Division 4, Session 2.** **Chairs: Prof. Timothy Barkham & Prof. Ngo Thi Hoa**	
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11:00 – 11:15	Detection of *Legionella* spp. in water and air samples by culturing methods from air conditioning systems in Ho Chi Minh City, Viet Nam	**Nguyen Ai Le,** Faculty of Environment, University of Science, Vietnam National University – Ho Chi Minh City, VIETNAM
11:15 – 11:30	The importance for the Development of a One Health curriculum for Universities in Vietnam	**Pham Duc Phuc**, Vietnam One Health University Network (VOHUN), VIETNAM

Division 5: Vaccine development		
13:00 – 14:50	**Chairs: Prof. Diep An Binh** (University of California, San Francisco, USA) **Prof. Kristian Mueller** (Bielfeld University, GERMANY)	
13:00 – 13:30	Active and Passive Immunization to Prevent Severe Invasive Diseases Caused by *Staphylococcus aureus*	**Diep An Binh**, University of California, San Francisco, USA
13:30 – 13:50	Synopsis of APP in Vietnam swine industry and optimization of antigen mass production in laboratory conditions	**Dinh Xuan Phat**, Nong Lam University Ho Chi Minh City, VIETNAM
13:50 – 14:20	Engineering and Production of recombinant Adeno-Associated Virus (rAAV): potential for cancer therapy and vaccine development	**Kristian Mueller**, Department of Cellular and Molecular Biotechnology, Bielfeld University, GERMANY
14:20 – 14:40	Development of the system to display recombinant proteins on the surface of vegetative *Bacillus subtilis* cells and its potential applications in vaccine delivery vectors	**Nguyen Duc Hoang**, Head of Department of Microbiology, University of Science, VNU-HCM, VIETNAM

	Division 6: Bioinformatics and Microbiome	
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13:00 – 13:25	Genomic insights into a foodborne outbreak of Group B *Streptococcus*	**Swaine Chen**, Senior research scientist, Infectious diseases group, Genome institute of Singapore, SINGAPORE
13:25 – 13:40	Propidium monoazide (PMA) sample pretreatment impacts the abundance of rare populations in high-throughput sequencing analysis of CF lung mycobiome and bacteriome	**Nguyen Do Ngoc Linh**, Phan Chau Trinh University, VIETNAM
13:40 – 13:55	Metagenomics for Diagnosis of Sterile Site Infection: Balancing Automation with Expert Interpretation	**Catherine Anscombe**, Oxford University Clinical Research Unit, VIETNAM
13:55 – 14:10	Understanding diarrhea recovery from a microbiome perspective	**Tran Tuan Anh**, Oxford University Clinical Research Unit, VIETNAM
14:10 – 14:35	Genomics of *Cryptococcus neoformans*	**Philip Ashton**, Lead Bioinformatician, Oxford University Clinical Research Unit, UK
14:35 – 14:50	Virulent factors and pan-genome analysis of the clinical multidrug-resistant Acinetobacter baumannii strains in a Vietnam Hospital	**Nguyen Si Tuan**, Head of Department of Clinical Microbiology, Thongnhat Dongnai General Hospital, VIETNAM
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16:20 – 17:10	***Plenary lecture 3***: Probiotic *Bacillus* eliminates pathogen colonization by blocking quorum-sensing signaling	**Michael Otto**, Chief of the Pathogen Molecular Genetics Section, National Institute of Allergy and Infectious Diseases, NIH, USA
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DATE 4: SEPTEMBER 22, 2018	
8:00 – 17:00	**One-day tour to the Mekong Delta**

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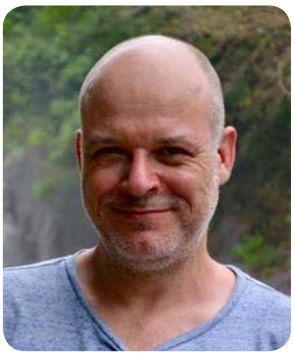

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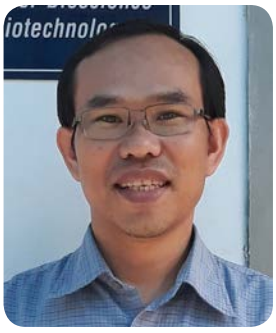

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PLENARY SESSION

O-01

Bad bugs and bad drugs - antimicrobial resistance in Southeast Asia

Guy Thwaites

Director, Oxford University Clinical Research Unit, a Wellcome Trust Africa Asia Programme

Abstract

Over the last 80 years drugs that kill bacteria, viruses, fungi and parasites – or 'antimicrobials' – have caused unparalleled improvements in human health. Around fifty years ago, it seemed as though antimicrobial drugs would lead to a world free from infectious diseases. In 1967 the Surgeon General of the United States of America famously quipped that, "The time has come to close the book on infectious diseases. We have basically wiped out infection in the United States."

The reasons why this statement has been proven wrong are numerous and complex. The emergence of novel infectious diseases, like HIV, provides one explanation; but we have also squandered many of our key weapons in the battle against infections and antimicrobial drugs, in particular. Infectious diseases, from tuberculosis to malaria, and more recently HIV, have evolved genetically determined mechanisms that allow them to resist killing by antimicrobial drugs. This is called antimicrobial resistance, or 'AMR'. In large measure, the creation and spread of AMR infectious diseases has been caused and accelerated by the misuse of antimicrobials. Controlling the spread and consequences of AMR infections is now one of greatest challenges to global health.

In this lecture, I will describe the work of the Oxford University Clinical Research Unit (OUCRU) in Ho Chi Minh City to tackle AMR infections in Southeast Asia. OUCRU has been working in the region for more than 25 years and has witnessed the steady rise of AMR across all its major infectious diseases. I will tell the story of these changes, how they have affected the health of those in the region, and how we, with many others, are trying to control AMR and the devastating effects it can have on individuals and communities.

Biography

Guy Thwaites is an academic infectious diseases physician and clinical microbiologist. He has been Director of the Oxford University Clinical Research Unit/Wellcome Programme in Vietnam since October 2013. He is responsible for the scientific strategy of the programme, with its major research themes of emerging viral infections, dengue, brain infections, tuberculosis, malaria, enteric infections, antimicrobial drug resistance and care of the critically ill. His personal research interests focus on severe bacterial infections, including meningitis and Staphylococcus aureus bloodstream infection, and tuberculosis. He has a longstanding research interest in the diagnosis, treatment and pathophysiology of tuberculous meningitis. Much of his research has been centred on large, pragmatic, randomized controlled trials which have addressed questions of key clinical importance, but have also provided the framework for providing unique insights into disease pathogenesis, antimicrobial pharmacology, and host and bacterial genetics.

Presenting author details

Full name: Guy Thwaites
Research profile: https://www.ndm.ox.ac.uk/principal-investigators/researcher/guy-thwaites

O-44

Probiotics for Prevention of Infectious Diseases and Cancers

Hideyuki Shibata

Yakult Central Institute, Tokyo, Japan

Abstract

Human gut is colonized by a huge number of bacteria, and this complex microbial community is called gut microbiota. It has been revealed that the gut microbiota is in close interaction with the development of the immune system. Also, the composition of the gut microbiota is known to be varied between healthy and diseased individuals. Although the cause-and-effect relationship between the microbiota dysbiosis and the manifestation of diseases remains to be established, the well-balanced gut microbiota is supposed to be critical to maintain human health. The human gut microbiota is stably controlled in healthy settings, but some factors such as imbalanced diets, severe stress, infections, medications, and surgery may affect the balance of the gut microbiota. The use of probiotics is being identified as a promising way to prevent the microbiota dysbiosis and to restore homeostatic balance. There has been considerable research on probiotics to see their beneficial functions to maintain human health. We have been accumulating clinical evidences on *Lactobacillus casei* Shirota (LcS), one of the most studied probiotics over the years. LcS is known to reduce symptoms of gastrointestinal disorders, to have a tendency to suppress an incidence of upper respiratory tract infection in the elderly, to suppress enteric infections in people with the immature or vulnerable immune system, and to prevent a recurrence of bladder cancer and colorectal cancer. Our epidemiological study also revealed that an incidence of breast cancer is reduced by long-term regular consumption of fermented milk containing LcS together with isoflavone from adolescence. This session aims to introduce some recent human studies assessing the benefit of LcS on our health and to describe the underlying mechanisms of these actions via the restoration of the gut microbiota and the immune modulation.

Biography

Graduated from the Faculty of Agricultural Chemistry, Kobe University and joined Yakult Central Institute in 1991. Received a Ph.D. degree at Kobe University in 2000. Worked at National Cancer Center Research Institute in Tokyo from 2000 to 2002. Joined Yakult U.S.A. Inc., California, in 2009 and assigned to be a vice president in 2012. Returned to Yakult Central Institute in 2015 and now serving as an associate chief researcher & manager for international science management section at research management center, Yakult Central Institute.

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O-45

Probiotic *Bacillus* eliminates pathogen colonization by blocking quorum-sensing signaling

Michael Otto

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Abstract

Probiotic nutrition is frequently claimed to improve human health. In particular, live probiotic bacteria obtained with food are believed to reduce pathogen colonization and thus, susceptibility to infection. However, the underlying mechanisms remain poorly understood. Here, we report that the consumption of probiotic *Bacillus* bacteria comprehensively abolishes colonization with the dangerous pathogen, *Staphylococcus aureus*. We discovered that the widespread fengycin class of *Bacillus* lipopeptides achieves colonization resistance by inhibiting the *S. aureus* Agr quorum-sensing signaling system. Our study presents a detailed molecular mechanism underlining the importance of probiotic nutrition in reducing infectious disease. Notably, we provide human evidence supporting the biological significance of probiotic bacterial interference and show for the first time that such interference can be achieved by blocking a pathogen's signaling system. Furthermore, our findings suggest a probiotic-based method for *S. aureus* decolonization and new ways to fight *S. aureus* infections.

Biography

Dr. Otto completed his PhD in 1999 at the age of 32 years at the University of Tubingen, Germany. He became a principal investigator at the National Institute of Allergy and Infectious Diseases (NIAID), U.S. National Institutes of Health (NIH) in 2001. He is currently chief of the Pathogen Molecular Genetics Section in the Laboratory of Bacteriology at NIAID. He has published more than 200 papers in reputed journals and has been serving as an editorial advisory board member of PLoS Pathogens, Infection and Immunity, and the Journal of Bacteriology, among others.

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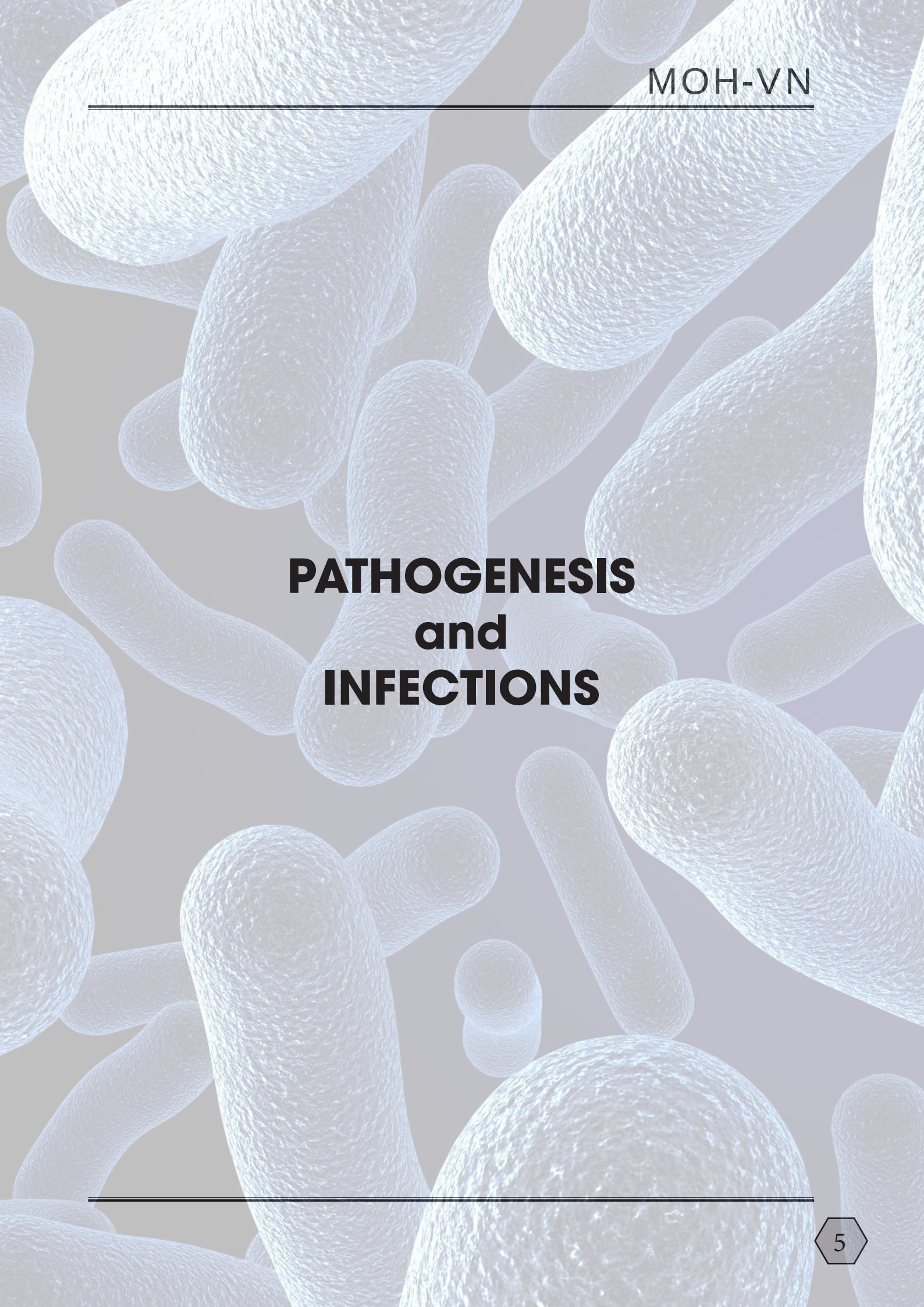

PATHOGENESIS and INFECTIONS

O-02

Hepatitis E Virus: A new emerging public health burden

Thomas Bock

Robert Koch Institute, Germany

Abstract

Hepatitis E virus (HEV) infection is a leading cause of acute hepatitis worldwide while an estimated one-third of the world's population has been infected by HEV. However, HEV infection is a largely underestimated public health problem not only in Europe affecting, e.g., an estimated 400,000 humans in Germany every year.

Although HEV infections usually take a clinically asymptomatic course, a considerable number of patients develop severe hepatitis that can progress to fulminant hepatic failure. HEV infection is mainly self-limiting but can lead to chronicity in immunocompromised patients. Moreover, a variety of extrahepatic symptoms can develop. There is no EMA-approved vaccine against HEV available and antiviral treatment options are very limited.

Chronic Hepatitis E is defined by the persistence of HEV genomes (RNA) and/or anti-HEV IgM for more than 3 months. Chronic infections are reported from immunocompromised patients. The molecular mechanisms of the pathogenesis of HEV infection leading to different clinical outcomes are poorly understood. It is believed that both viral and host factors contribute to the wide spectrum of clinical manifestations of HEV. Clinical observations suggest that the course of hepatitis E, including chronification, may differ between HEV variants. For patients with chronic HEV infection, treatment with ribavirin has been shown to effectively clear HEV. However, antiviral resistance mutations can occur in the HEV genome.

To combat HEV infection our research aims (i) to better understand the epidemiology and disease burden of HEV infections, (ii) to explore strategies to prevent human HEV infections (e.g. by ensuring food and water safety and by reducing HEV infections by blood products), (iii) to define clinical courses and understand the pathophysiology of HEV infections in distinct patient groups and (iv) to explore novel antiviral intervention strategies which will be tested in animal models and finally in a clinical proof-of-concept trial.

Biography

Thomas Bock has completed his PhD at the University of Heidelberg. He is the head and director of the Division Viral Gastroenteritis and Hepatitis Pathogens and Enteroviruses at the Robert Koch Institute, Berlin, Germany, the national Public Health Institue, and Professor at the University of Tuebingen, Institute of Tropical Medicine, Germany. He has published more than 140 papers in peer-reviewed journals and has been serving as an editorial board member of repute.

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O-03

Avian Influenza H5N1 characterization in Vietnam

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Abstract

Highly pathogenic avian influenza (HPAI) A/H5N1 viruses continue to circulate in poultry in many countries, causing disease and economic loss, and remaining a threat to human health. Vietnam has been one of the more severely affected countries with H5N1 (CFR of 49.6%).

Mutation and reassortment of highly pathogenic avian influenza A(H5N1) viruses at the animal–human interface remains a major concern for emergence of viruses with pandemic potential. To understand the relationship of H5N1 viruses circulating in poultryand those isolated from humans, comprehensive phylogenetic and molecular analyses of viruses collected from both hosts inVietnam between 2003 and 2010 were performed. We examined the temporal and spatial distribution of human cases relative to H5N1 poultry outbreaks and characterized the genetic lineages and amino acid substitutions in each gene segment identified inhumans relative to closely related viruses from avian hosts. Six hemagglutinin clades and 8 genotypes were identified in humans, all of which were initially identified in poultry. Several amino acid mutations throughout the genomes of viruses isolated from humanswere identified, indicating the potential for poultry viruses infecting humans to rapidly acquire molecular markers associated with mammalian adaptation and antiviral resistance. Human Avian Influenza H5N1 was not reported in Vietnam since 2011, however, the H5 viruses are circulating in poultry population still. Then, a new H5H6 was confirmed – that is caused of reassortment event, this one was first reported in 2014 and continue to circulate up to date.

Biography

A/Prof Mai has been Vice Director of the National Institute of Hygiene and Epidemiology (NIHE), and is also Director of National Influenza Center, Vietnam. Dr Mai obtained her medical doctor degree from the Military Academy of Medicine, Viet Nam in 1989 and her PhD in Virology from NIHE in 2000. Dr Mai has been working at NIHE since 1990, her work especially focuses on viral emerging infectious diseases SARS (2003), seasonal and avian influenza A/H5N1 (2004 up to date), Dengue fever and Zika. Dr Mai's group was the first to confirm that the pathogenic avian influenza A (H5N1) caused human infections in Viet Nam. In recent five years, Dr Mai has continually conducted the research in corporation with NIC team, focus on influenza evolution, reassortant in genome of seasonal and animal influenza virus that may lead to potential pandemic in the future, effectiveness of vaccine in community. Dr Maihas been a PI or has participated as senior researcher of national and international projects. She contributed as author and co-author of total 89 international publications in related fields including *Nature* (2005, 2006), *New England Journal of Medicine* (2009), *Science* (2014), *the Lancet* (2017).

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O-04

Development of diagnostic kits for the early rapid detection of arboviral diseases

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Abstract

Dengue virus (DENV), zika virus (ZIKV), chikungunya virus (CHIKV), and yellow fever virus (YFV) share many common clinical features, making it difficult to distinguish between them. However, the treatments for the diseases caused by these viruses are substantially different. Therefore, early diagnosis is the key for successful clinical management and control of epidemics. At GenBody Inc., we aim to develop sensitive and specific assays for the diagnosis of DENV, ZIKV, CHIKV, and YFV infection. A DENV IgG/IgM Ab rapid diagnostic test (RDT) was developed, wherein dengue viruses were cultured in animal cells and were used as antigens to retain the native viral coat protein. Monoclonal antibodies (mAbs) were then developed against domain I of envelope glycoprotein (EDI). A clinical evaluation proved that the new RDT is more effective in detecting anti-dengue antibodies than two major commercial tests. A highly accurate dengue NS1 rapid test was developed using anti-DENV NS1 mAbs generated against the DENV NS1 protein with high affinity. Clinical evaluation shows that the test detects 4 dengue serotypes with improved diagnostic performance. The RDT kit for detecting IgG/IgM antibodies against ZIKV was developed using monoclonal antibodies to the envelope (E) and non-structural protein 1 (NS1) of ZIKV. These proteins were produced using baculovirus expression vector with Sf9 cells. To develop and evaluate CHIKV-specific IgM detection test, baculoviruses carrying E1 envelope protein genes of CHIKV were generated. The sero-reactivity of recombinant CHIKV E proteins were determined using residual blood, collected from CHIKV-confirmed patients. The CHIK IgM test was strongly reactive toward anti-CHIKV IgM and showed almost no cross-reactivity with anti-Dengue and flavivirus antibodies. We also developed a highly accurate YFV NS1 rapid test using two mouse monoclonal antibodies against native YFV NS1. The detection limits of the IC test were ≥0.16 × 10^1 PFU/ml and 0.8 ng/ml. No cross reactivity was shown with other flaviviruses such as DENV and ZIKV as well as with an alphavirus such as CHIKV and MAYV.

The 4 RDTs developed in this study were very sensitive and highly specific. Upon validation, these RDTs would serve as a method of choice for point-of-care diagnosis and large-scale surveys of viral infection under clinical or field conditions in endemic areas worldwide.

Biography

Chong Chom-Kyu earned his PhD in Chemistry from Chungbuk National University in 2000. Prior to founding Genbody Inc. in 2012, he had more than 10 years working on the development of IVD kits at various companies, including Asan Pharmaceutical Co. Ltd. and SK Bioland Co. Ltd. He was also an Assistant Professor at Biochemistry Department, Chungbuk National University from 2009 to 2011. In the last 10 years, Dr. Chong co-authored over 30 publications in peer-reviewed journals and several patents.

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O-05

Clinical characteristics and virology of Hand, Foot and Mouth Disease in Southern Vietnam

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Abstract

Hand, foot and mouth disease (HFMD) has been associated with large outbreaks among young children, including severe illness and fatality, in the Asia-Pacific Region since 1997. Severe illness is most often associated with enterovirus A71 (EV-A71). Vietnam experienced a large sustained outbreak of almost 200.000 hospitalised cases and over 200 deaths in 2011-12, the large majority occurring in southern Vietnam.

A prospective study was conducted in three referral hospitals: Children's Hospital 1, Children's Hospital 2 and Hospital for Tropical Diseases. Patients were enrolled from all severity. Between July 2013 and July 2015, 1547 children were enrolled. Four serotypes of EV-A71, Coxsackie virus (CV) A6, A10 and A16 were responsible for 1005/1327 (75.7%) of diagnosed cases. We found an unexpected dominance of EV-A71 among both in and outpatients, and a strong association with severe illness. CV-A6 and A10 emerged in Vietnam during our study period and replaced CV-A16. CV-A10 was associated with different clinical and laboratory characteristics.

Our analysis revealed the persistence of EV-A71 subgenogroup B5 in Vietnam from 2013 to 2015 without any major outbreak notification despite the observed high level of genetic diversity of EV-A71. The relative genetic diversity of subgenogroup B5 increased sharply in 2012, leading to subgenogroup switch from C4 to B5 and then remained stable from 2013 to 2015. Subgenogroup B5 were dominantly circulated in Vietnam during the study time and might import to Vietnam from two independent sources. Results from this study, covering demography, clinical features and virology, provides a full view of HFMD in Southern Vietnam and therefore may have great impact for disease management and control.

Biography

Hoang Minh Tu Van earned her Bachelor of Medicine from the University of Medicine and Pharmacy – Ho Chi Minh City in 2007 and worked as a General Practitioner for one year before taking the Master of Medicine (Infection and Immunity) course in University of Sydney – Australia. Back to Vietnam, she worked as both a clinician and researcher in Children's Hospital 2 for six years. Van has completed her PhD thesis with Oxford University, entitle " Clinical characteristics, virology and host genetic markers of Hand, Foot and Mouth Disease in Southern Vietnam" and now she is a post-doc researcher in Oxford Clinical Research Unit, Vietnam.

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O-06

Two cases report: anemia aplasia with Parvovirus infection in renal transplant recipients

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• *University of Medicine and Pharmacy at Hồ Chí Minh city*
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Abstract

Anemia is a frequent problem in renal transplant recipients, the most frequent cause being erythropoietin, allograft failure, iron deficiency, hemolytic anemia, immunosuppressants and virus infection. Parvovirus B19 can cause persistent viremia and erythropoietin resistant erythroid aplasia in immunosuppressed patients. Two cases has Parvovirus B19 infection. Two men patients with a renal transplant at 36 and 41 years of age. A triple immunosuppressive treatment with prednisolone, tacrolimus and mycophenolate mofetil was then initiated. They were development of anemia (Hb 5- 6 g/dL) during the postransplant period, after transplant 3 - 4 months, but it was not consistent with acute rejection. Anemia assessments by decreased erythrocytes and erythroid aplasia on bone marrow aspiration. Blood parvovirus B19 PCR level was found to be $1.91.10^9$ and $5.2.10^{10}$ IU/mL. Immunosuppressive drug doses were down and IVIG treatment was instituted for 3-5 days. After this treatment, the hemoglobin level increased from 6.5 to 12 mg/dl in first patient and 5 to 13 mg/dL in the second patients at the 2nd month, respectively. In conclusion, when anemia develops in renal transplant recipients in the absence of rejection and hemolysis, parvovirus infection should be considered.

Biography

Suzanne Monivong Cheanh Beaupha (Thanh Thanh) has completed her Dr at the age of 24 years from University of Medicine and Pharmacy at Hồ Chí Minh city. I has completed PhD at the age of 51 years, she is a lecture as Hematology in University of Medicine and Pharmacy at Hồ Chí Minh city , and she is a vice director of Hematology Department in Chợ Rẫy hospital in HCM city . She has published more than 20 papers in journals of Medicine in Viet Nam

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O-07

Whole Genome DNA Sequence Analysis of *Salmonella enterica* isolated from the fecal material of swine and chicken in the Southeast region of Vietnam

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[2]University of Science, VNU-HCM, Vietnam [3]Food and Agriculture Organization Regional Office for Asia and the Pacific, Thailand

Abstract

Antimicrobial usage in agricultural animal production contributes to the development and spread of antimicrobial resistant pathogens in both animals and humans, posing a significant threat to public health. In Vietnam, 70% of the antimicrobials that are used in animals are antibiotics. However, no data on antibiotic use in agriculture are available and little is known on the genetic diversity and antimicrobial resistance (AMR) profile of non-typhoidal *Salmonella enterica* (NTS) from animals, which can be spread from animals to humans through food chain and direct contact with animals shedding *Salmonella*. This study aimed to compare the genetic diversity and AMR profiles of NTS that were isolated from the fecal material of swine and chicken in the Southeast region of Vietnam. A total of 76 cecal *Salmonella enterica* isolates from chicken (n=29) and swine (n=47) were selected for the study. All isolates were tested for phenotypic antibiotic resistance to 10 drugs from 6 classes and were also subjected to whole genome sequencing. The AMR genes, serovar types, replicon sequences, genome and plasmid sequence types of these isolates were identified in their assembled genomes by ResFinder, SeqSero, PlasmidFinder and Multi-Locus Sequence Typing. The most common phenotypic resistances for both chicken and swine were beta-lactam and tetracycline. On the contrary, resistance to fluoroquinolone and colistin were more common in chicken isolates whereas resistance to aminoglycoside and phenicol were more common in swine isolates. All isolates had at least one resistance gene, and the maximum number of resistance genes seen is twenty-two and they were found in one Kentucky (ST198) chicken isolate. Enteritidis of ST11 (n=12) was the most common serovar in chicken whereas Typhimurium of ST34 (n=27) was the most common serovar in swine. Our study reflects distinct epidemiology of NTS colonization and AMR in chicken and swine in the the Southeast region of Vietnam and demonstrates the value of using whole genome sequencing in understanding the genetic diversity of NTS at a greater resolution.

Disclaimer: The analysis is still ongoing and preliminary findings are reported here.

Biography

Moon Tay is currently working as a Research Fellow in NTU Food Technology Centre (NAFTEC), under Prof Jorgen Schlundt. She received her Bachelor of Science (Hons.) Degree in Biological Sciences from NTU in 2009 and her Ph.D in Integrated Biology and Medicine from Duke-NUS Medical School in 2015. Prior to joining NAFTEC, Moon worked as Research Fellow in Prof Mary Chan's multidisciplinary research group that aims to develop new antimicrobial polymers, which are less likely to evoke resistance as compared to antibiotics and yet, can effectively kill bacteria and with low toxicity to mammalian cells. Moon's current research is focused on using next generation sequencing to detect emergence and spread of antimicrobial resistance genes across the food chain and evaluating the potential of next generation sequencing in improving food safety through a lab-based One Health approach.

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O-08

Effect of Zinc and nano-curcumin on the development of antibiotic resistance in *Staphylococcus aureus*

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Abstract

Combating the threat of antibiotic resistance has been the major focus of medical research recently due to the widespread of multidrug resistance and scarcity of newly introduced antimicrobials. This study aimed to investigate the effectiveness of Zn^{2+} and nano-curcumin in delaying antibiotic resistance development in *Staphylococcus aureus*. To do this, *S. aureus* ATCC®29213 was exposed to sub-inhibitory concentrations of flouroquinolones either ciproflocaxin, levofloxacin or ofloxacin in the presence of either Zn^{2+} or nano-curcumin. Minimal inhibitory concentrations (MICs) of each antibiotics were measured each day in 14 days of antibiotic exposure and expression of *recA* gene, an important gene in antimicrobial resistance development, was monitored using reverse transcription real-time quantitative PCR (RT-qPCR). Results showed that the addition of Zn^{2+} (400 µM) into fluoroquinolone antibiotics was helpful in reducing the rate and magnitude of antibiotic resistance development. Nano-curcumin (8 µg/mL), however, showed no significant effect on the resistance development process. Furthermore, in the presence of Zn^{2+} but not Nano-curcumin, the expression of *recA* was repressed by up to 15-fold compared to the control. In summary, our study strongly supports the combination therapy, Zinc and antibiotics, for effective treatment of *S. aureus* infections.

Biography

Hoai Nguyen has completed her PhD at the age of 27 from Greifswald University and postdoctoral studies from Catholic University of Louvain. She founded and leads Medical Microbiology group at International University since 2011. She has published more than 10 papers in reputed journals and more than 20 on others. She also serves as reviewer of many journals.

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O-09

Understanding the Mechanism of Action of the Anti-Dandruff Agent Zinc Pyrithione against *Malassezia restricta*

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Abstract

Dandruff is known to be associated with *Malassezia restricta*, which is the most frequently isolated fungus from human skin. To treat the disease, zinc pyrithione (ZPT) has been used as an anti-dandruff ingredient in various anti-dandruff shampoos. There have been several studies that have investigated the mechanism of ZPT; however, they mainly used a non-pathogenic model yeast *Saccharomyces cerevisiae* and a different *Malassezia* species *M. globosa* whose contribution to dandruff is known to be minimal. The aim of the current study was to understand how ZPT inhibits the growth of *M. restricta*. We analyzed the intracellular metal contents of ZPT-treated *M. restricta* cells. The transcriptome profile of the ZPT-treated cells was also compared with that of untreated cells. The transcriptome changes caused by the ZPT treatment were confirmed by expression analysis of the proteins and by assessing the enzymatic activities. Our data show that the ZPT treatment dramatically increased the intracellular zinc levels along with a small increase of the intracellular copper content in *M. restricta*. This result was different from what was shown in the study using *S. cerevisiae*. However, similar to what was found in a previous study, our transcriptome analysis showed that ZPT inhibits Fe-S cluster synthesis in *M. restricta*. Apart from the above findings, we observed that ZPT treatment causes a significant reduction in the expression of lipases whose activities are believed to contribute to the survival and virulence of *M. restricta* on human skin. Overall, the results of our study suggest that at least three inhibitory mechanisms may be associated with the action of ZPT against *M. restricta*: i) an increase in the intracellular zinc levels, ii) the inhibition of the Fe-S cluster synthesis, and iii) a decrease in lipase expression.

Biography

Dr. Won Hee Jung is currently a professor in the Department of Systems Biotechnology at Chung-Ang University, South Korea. His current research focuses on molecular and genetic analysis of regulatory mechanisms of iron and zinc uptake systems in the human fungal pathogen *Cryptococcus neoformans*. He has also recently started to work on the human cutaneous fungal pathogen *Malassezia*, which causes various skin diseases including seborrheic dermatitis, dandruff and atopic dermatitis. Dr. Jung obtained his PhD degree from University of Manchester (UMIST), U.K., where he worked
on the cAMP signaling pathway in another human fungal pathogen, *Candida albicans*.

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DRUG DISCOVERY

O-10

Strategies Focused on Overcoming Bacterial Resistance: Design and Discovery of New Anti-infective Agents

Josef Jampilek

Department of Pharmaceutical Chemistry, Faculty of Pharmacy, Comenius University in Bratislava, Slovakia

Abstract

The development of the resistance to used anti-infectives and the development of cross-resistant or multidrug-resistant strains are global problems. Scaffolds of (aza)naphthalenes and their simple one-ring analogues can be considered as privileged structures. These scaffolds can be easily and rapidly functionalized, which provides a possibility of a great number of targeted modifications as well as modification/optimization of physicochemical properties. This contribution is focused especially on the investigation of ring-substituted hydroxy(aza)naphthalenes and their one-ring analogues bearing amide and/or carbamate moieties that demonstrated promising effects against a number of human pathogens. Structure-activity relationships and the supposed mechanism of action are discussed. In addition, attention is paid to agents decreasing bacterial resistance, i.e. to agents that do not have sufficient intrinsic bacteriostatic or bactericidal activity, but in combination with clinically used antimicrobial drugs are able to restore the effect of these drugs or demonstrate synergistic antimicrobial properties together with the drugs.

This study was supported by sanofi-aventis Pharma Slovakia.

Biography

Josef Jampilek completed his Ph.D. degree in Medicinal Chemistry at the Faculty of Pharmacy of the Charles University (Czech Republic) in 2004. In 2004-2011, he worked in expert and managerial posts in the R&D Division of the pharmaceutical company Zentiva (Czech Republic). Prof. Jampilek deepened his professional knowledge at the Medicinal Chemistry Institute of the Heidelberg University (Germany) and at multiple specialized courses. In 2009, he became an Associate Professor of Medicinal Chemistry at the Faculty of Pharmacy of the University of Veterinary and Pharmaceutical Sciences Brno (Czech Republic). In 2017, he became a Full Professor of Medicinal Chemistry at the Faculty of Pharmacy of the Comenius University (Slovakia). He is an author/co-author of more than 30 patents/patent applications, more than 170 peer-reviewed scientific publications, 7 university textbooks, 20 chapters in monographs, and many invited lectures at international conferences and workshops. He also received several awards for his scientific results, e.g., from Aventis, Elsevier, Willey and Sanofi. The research interests of Prof. Jampilek include design, synthesis, and structure-activity relationships of heterocyclic compounds as anti-infectious and antiproliferative agents as well as photosynthesis inhibitors. He is also interested in ADME and drug bioavailability.

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O-11

Efflux pump inhibitors approach to combat multi-drug resistant bacteria

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Abstract

Antimicrobial drug resistance occurs when bacteria undergo certain modifications to eliminate the effectiveness of drugs, chemicals or other agents designed to cure infections. To date, the burden of resistance has still remained one of the most major clinical concerns as it renders prolonged and complicated treatments thereby increasing the medical costs with lengthier hospital stays. Of complex causes for bacterial resistance, there has been increasing evidence which proved the significant role of efflux pumps in antibiotic resistance. Coadministration of efflux pump inhibitors (EPIs) with antibiotics has been considered one of the promising ways not only to improve the efficacy but also to extend the clinical utility of existing antibiotics. This presentation begins with outlining current knowledge about bacterial efflux pumps and drug designs applied in identification of their modulating compounds. Following, the application of in silico approaches in search of novel and potent Staphylococcus aureus NorA efflux pump inhibitors were presented.

Acknowledgements: This research is funded by Vietnam National Foundation for Science and Technology Development (NAFOSTED) under grant number 106-YS.05-2015.31 to Khac-Minh Thai and 108.05-2017.12 to Minh-Tri Le.

Biography

Dr Khac-Minh Thai graduated in Pharmacy in 2000 from the University of Medicine and Pharmacy at Ho Chi Minh City, Vietnam and earned the Master's degree in Pharmacy in 2004 with Prof. Hyun-Ju Park from College of Pharmacy, Sungkyunkwan University, Korea. He got his PhD degree in 2008 under the guidance of Prof. Dr. Gerhard F. Ecker at Department of Medicinal Chemistry, University of Vienna, Austria. Currently, Dr Thai serves as Associate Professor at Department of Medicinal Chemistry, Faculty of Pharmacy, University of Medicine and Pharmacy at Ho Chi Minh City, Vietnam. He was a visiting professor at University of Franche-Comté (UFC), Medical and Pharmaceutical Sciences, Besanson, France on Apr-May 2016. His researching work in recent years is application of pharmacoinformatics including both ligand-based approach and structure-based approaches to provide the in silico models for classification and prediction of toxicological and bioactive compounds. He is a member of the Editorial Board of BioMed Research International, MedPharmRes and published 25 peer-reviewed papers, 3 book chapters, 53 vietnamese articles, >40 conference contributions and 9 invited lectures.

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O-12

Antifungal Activity of Some Hydrosols from Aromatic Plants against *Candida albicans*

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Abstract

The need for new therapies to combat drug-resistant pathogens is one of major public health concerns. *Candida albicans* is common yeast that infects in humans and the fourth most hospital acquired infection worldwide. Essential oil is on top of the hydrosol layer during steam distillation and widely known for its antimicrobial property. However, less information is reported on the activity of the hydrosol. In the present study, nine hydrosols were obtained by steam distillation of nine aromatic plants in South Vietnam, namely, *Acorus calamus, Coriandrum sativum*, *Ocimum basilicum*, *Litsea cubeba*, *Melaleuca alternifolia*, *Cymbopogon nardus*, *C. citratus*, *Citrus hystrix*, and *C. sinensis*, and anti-yeast activity of these hydrosols was evaluated against the growth of *C. albicans*. The results indicated that the hydrosol from *L. cubeba* exhibited the highest anti-yeast activity (MIC = 10%, MYC = 25%), followed by those from *C. nardus*, *C. citratus,* and *O. basilicum*. The remaining hydrosols showed low or no activity against *C. albicans*. GC-MS data show that the main essential oil constituents of the hydrosol of *L. cubela* were neral (32.92%) and geranial (27.12%).

Key words: antifungal, aromatic plant, *Candida albicans*, hydrosol, *Litsea cubeba*, steam distillation

Biography

She received Ph. Degree in Agricultural Biotechnology, Seoul National University, in February, 2013 under the supervision of Prof. Young-Joon Ahn. During PhD. student period, she carried out studies about antiviral and antimicrobial activities of plant extracts or compounds against human rhinovirus and gastrointestinal bacteria including *Helicobacter pylori*. After graduating, she has been working as a lecturer at Faculty of Biology and Biotechnology, University of Science, Vietnam National University Ho Chi Minh City. Her work currently focuses on antimicrobial activities of plant and fungi preparations against harmful fungi and bacteria such as *Candida albicans, Salmonella* Typhimurium, *Staphylococcus aureus*, *Klebsiella pneumonia*, *Pseudomonas aeruginosa* and *Helicobacter pylori*.

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O-13

Screening of sponge-derived bacteria for antibiotic producing isolates

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Abstract

Bacterial associated with invertebrates were considered as a good source for biological active compound exploitation. However, this kind of research was very limited in our land. In this study, sponge-derived bacteria were isolated, extracted and tested for bacterial inhibition, the strong active strains were identified by 16SRNA analysis. The results showed that there were 8/25 bacterial strains with antibacterial activity. We reported here for the first time strain HM4 isolated from Vietnamese sponge, was most closed to the well-known actinomyces *Streptomyces graminearus*. This HM4 strain was strongly inhibited to *Bacillus subtilis* ATCC6633 and *Escherichia coli* O157. The strain HM2 inhibited to *B. subtilis* and *E. coli* while strain HM15 showed active against *B. subtilis* and *Serria marcescens* PDL100 causing white spot fatal disease in reef building coral *Acropora palmate*. They were identified as *Bacillus siamensis* and *B. subtilis* respectively. Indeed, the sponge-derived bacteria were able to inhibit both Gram-negative and Gram-positive indicator bacteria. Also, they varied in colonies characteristics, shapes, sizes, and antibiotic susceptibility types. Therefore, they were concerned as completely different potential strains. We suggested that classification research of those remain potential strains should be added for further developing of other biologically active substances.

Key words: Sponge-derived bacteria, *Streptomyces* sp., *Bacillus* sp., Antimicrobial activity

Biography

Pham Thi Mien has completed her PhD at GEOMAR Kiel Germany in Marine Microbiology Department in 2014. She is working at Institute of Oceanography in Nha Trang Viet Nam. She is interesting in marine microbials for bioactive compounds. Also try to connect microbials with other marine invertebrates for understanding of their role and function in host and those relationships.

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O-14

Synthetic Peptide-Based Antimicrobials & Their Delivery: Prospects & Challenges

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Abstract

The dramatic increase in antibiotic-resistant infections has created a pressing need for new and more efficacious antibiotics. An area that has garnered renewed interest is the development of antimicrobial peptides (AMPs) and proteins. AMPs are a distinctive class of potent, broad-spectrum antibiotics produced by the body's innate immune system and act as the first line of defense against disease-causing microbes. By using natural AMPs as templates, our team has developed synthetic AMPs effective against a variety of microorganisms, including drug-resistant clinical isolates of Mycobacterium tuberculosis and Pseudomonas bacteria. Because AMPs are small, expensive to produce and labile in biological systems, our team also systematically evaluated various physically crosslinked hydrogel systems with strong electrostatic interactions with cationic peptides for effective loading and controlled drug release. Several developmental prospects and challenges will be highlighted in order for this unique class of therapeutics to emerge as integral tools for combating drug resistant infections.

Biography

Dr Rachel P. L. Ee completed a PhD in Pharmaceutics at the College of Pharmacy, University of Illinois at Chicago. After her postdoctoral fellowship in the industry, Dr Ee returned to her alma mater as a faculty in the Department of Pharmacy, National University of Singapore (NUS). She is currently the Deputy Head (Research) as well as the Director of the new Pharmaceutical Science Programme in NUS. Her research is focused on the design and development of novel biotherapeutics and hydrogel formulations for the delivery of drugs, genes and cells. She received the Deutscher Akademischer Austausch Dienst (DAAD) Research Exchange Fellowship and UCLA-Banco Santander W30: Women Leaders in University Administration Program Award as recognition of her research and administrative excellence in 2014.

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O-15

Fungal Production of Biopharmaceutical Enzymes

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Abstract

Fungal biomolecules provide key biosynthetic tools and platform chemicals to produce many important drugs and pharmaceutical products. As these biomolecules are currently produced in small quantities, many companies seek to develop fungal biotechnology to enhance low-cost production of target biomolecules. Additionally, fungal metabolic system is a fundamentally controlled process and the regulations of metabolism are exceptionally receptive to physicochemical stimuli that happen because of environmental and cellular conditions. We mine the potential of native fungal candidates to produce pharmaceutically-relevant enzymes, especially carbonyl reductases (CR) and lipase (LP) as key pharma enzyme and, by improving production processes, aims to increase fungal product yields. CR are used in the preparation of beta-lactam antibiotics which are intermediates in the production of penicillins and cephalosporins. LP from fungi has been used to synthesize lovastatin, a drug that lowers serum cholesterol levels. Also, the production of 2-arylpropanoic acid derivatives is primarily accomplished through the catalysis by LP.

Thus, it is necessary to understand metabolic mechanism of the novel fungal biomolecules synthesis. Our strategy is to develop an efficient and low-cost process that enhances production of pharmaceutically-relevant, broth-based fermentation products from fungi.

Biography

Dr. Vijai Kumar Gupta is the Senior Research Scientist, Microbial Biotechnology at ERA Chair of Green Chemistry, Tallinn University of Technology (TUT), Tallinn, Estonia. Before joining TUT, he worked as Senior Researcher for good few years at MGBG group at Department of Biochemistry, National University of Ireland Galway, Ireland. He is one of the leading experts in the area of- *Microbial Biotechnology and Applied Mycology.* He has received a many national and international awards and the fellow of societies of international repute including Linnaean Society; Mycological Society of India; and Indian Mycological Association. He is the editor of few well reputed journals including, *PLOS One, BMC Microbiology, BMC Fungal Biology and Biotechnology, Microbial Cell Factories, Scientific Reports* and *Microbiome* and edited 27 books, for internationally reputed publishers like *Elsevier press, Wiley-Blackwell, Frontiers, Taylor and Francis, Springer-Nature, CABI and De Gruyter.* Also, he has 91 papers in his hands in internationally reputed journal and developed 02 IPs in the area very efficient and low-cost methodology for producing enzymes.

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O-16

Development of local antibiotic delivery system from fibrin gel to prevent bacterial biofilm graft infection

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Abstract

Prosthetic vascular graft infection is one of the most serious complications after vascular surgery. Fibrin gel (FG) has many useful characteristics as biocompatibility, biodegradation, adhesion and haemostasis for development of local antibiotic delivery system. In this study, human plasma was collected from peripheral blood that was used to create fibrin gel by supplement ion Ca^{2+}. Fibrin gel containing antibiotic was then evaluated in some characteristics such as surface structure, biodegradation, delivery antibiotic, cytotoxicity and prevention of bacterial biofilm *in vitro*. The results showed that fibrin gel was excellent material for extended delivery of antibiotic. Most importantly, fibrin gel containing antibiotic were not toxic for human fibroblast cells *in vitro* and inhibited growth of bacterial biofilm *in vitro*. This research as the first step for development of antibiotic delivery system for effective treatments for graft infection.

Biography

Vu has completed his Master of Microorganism at the age of 25 years from University of Science, Vietnam National University and has attended Animal Physiology Major PhD program at the University of Science, Vietnam National University Ho Chi Minh City. He is deputy head of Department of Physiology and Animal Biotechnology and researcher at Laboratory of Tissue engineering and Biomedical materials (TEBM). He has published more than 10 papers in *international journals*.

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O-17

Oral vaccines produced by molecular display technology

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Abstract

Candidiasis is one of serious and major infectious disease caused by the virulent fungus *Candida albicans* or other *Candida* species. Pharmacotherapy of candidiasis often involves the administration of antifungal drugs such as amphotericin B, micafungin and caspofungin. Unfortunately, several mutants of *Candida* with reduced susceptibility to these drugs have emerged [1]. As well as a pharmacotherapy, a vaccination against Candidiasis is an important strategy in efforts to prevent infection of *Candida species*.

In recent, we have developed molecular display technology using microbial cells. This technology uses genetically engineered microorganisms to produce foreign proteins on their surface [2]. The use of cell surface display system to prepare target proteins is well established for use with the yeast *Saccharomyces cerevisiae*. It has been applied to wide variety of fields, for example, bioremediation, whole cell biocatalysts, biosensors, screening of ligand peptides for receptors and so on. We present that the antigens displayed on yeast cell generated by using this molecular display technology offer a novel type of oral vaccine against candidiasis, conveniently. The enolase 1 protein (Eno1p) from *C. albicans* was selected as the model antigenic protein to be displayed on the surfaces of *S. cerevisiae* cells [3].

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[3] Shibasaki S & Ueda M (2016) *Methods Mol Biol.* **1404**: 497-509.

Biography

Seiji Shibasaki has completed his PhD at the age of 27 years in Kyoto University in Japan. He studied biochemistry and biotechnology as Associate Professor at Kobe City College of Technology in Japan and as visiting researcher at Royal Institute of Technology in Sweden. At present, he has been an Associate Professor of Hyogo University of Health Sciences since 2007. In 2018, he delivered lectures on bioprocesses and biomaterials at Turku University of Applied Sciences in Finland as a visiting professor. He has published more than 50 papers related in molecular biotechnology in reputed journals.

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ANTIMICROBIAL RESISTANCE, DIAGNOSTICS and TREATMENT

O-18

The problem of antibiotic-resistant and antibiotic-tolerant pathogenic bacteria

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Abstract

When Alexander Fleming discovered penicillin by chance in 1928, he speculated already that penicillin-resistant bacteria may come up. Now, in 2018, antibiotic-resistant bacteria are a major problem worldwide. In Germany, about 8000 patients die each year, because the pathogenic bacterium causing the infection is resistant against all known antibiotics and in the US about 90 000 people do not survive the infection. Besides antibiotic-resistant bacteria also antibiotic tolerant bacteria have been described. These type bacteria have been detected in 1944 by chance and were designated as persister cells. Later, it was shown that these cells stop growth because of the absence of any metabolic activity. Besides dealing with these two types of bacteria, I will report on several methods how can try to kill these bacteria.

Biography

Wolfgang has completed his PhD at the age of 26 years from the Johannes-Gutenberg University followed by postdoctoral studies at the University of Konstanz. He is Professor of Genetics and Gene Technology at the University of Bayreuth and retired since October 2013. He has published about 150 papers in reputed journals and has been serving as an editorial board member of FEMS Microbiology Letters and still serves as an editorial board member of the Journal Cell Stress and Chaperones and of the Journal of Biotechnology.

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O-19

Antibiotic Resistance Challenge in Vietnam - Situation and Solutions

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Abstract

Doctors today are hard to select the effective antibiotic regimen for treatment of bacterial infections caused by hospital-acquired bacteria because these agents are among the ESKAPE pathogens: ***E.*** *faecium* resistant to vancomycin has been increasingly recognized from clinical isolates, methicillin-resistant ***S.*** *aureus* (MRSA) in most of the hospitals is usually more than 70%, ***K.*** *pneumoniae* and other Enterobacteriaceae producing ESBL have been reported no less than 50% in large hospitals, more than 80% of ***A.*** *baumannii* are extremely drug resistance (XDR), more than 30% of ***P.*** *aeruginosa* are multi-drug resistance (MDR), and more and more carbapenem-resistant *Enterobacteriaceae* have been recognized in the clinical isolates. It is not easy dealing with these pathogens because *E. faecium* resistant to vancomycin are virtually untreatable by other antibiotics, *MRSA* are resistant to all beta-lactam and vancomycin failure rate is over 80% if the MIC over 1.5mcg/ml, *K. pneumoniae* and *E. coli* producing ESBL are resistant to all cephalosporins, *A. baumannii* XDR are only sensitive to colistin and tigecycline, but both antibiotics are not effective with monotherapy, *P. aeruginosa* MDR are the challenge in selecting antibiotics treatment because the quick development of carbapenem group 2 resistance, and finally it is almost the end of choice of antibiotic treatment for carbapenem-resistant Enterobacteriaceae. Solutions for this situation should include: (1) The competent authorities of the state must strictly and seriously control the quality of antibiotics and strictly control the use of antibiotics in humans and in livestock; (2) The hospital must effectively monitor the use of antibiotics in the hospital; (3) Clinical microbiology lab must be able to detect the above-mentioned resistance to help physicians to adjust the antibiotic treatment in a reasonable way; (4) Clinicians must be able to identify emerging resistance when reading antibiotic susceptibility results to avoid the use of resistant antibiotics as well as to adjust the antibiotics treatment to achieve pKpD effects.

Biography

Dr. Pham Hung Van has completed his Medical Doctor in 1978 and his Philosophy Doctor of Epidemiology and Microbiology in 1995 from the University of Medicine and Pharmacy in Ho Chi Minh City. He was the Lecturer of this university from 1978 to 2013. He is the Principal Investigator of ANSORP from 1998, President of the Vietnam Association of Medical Molecular Biology from 2007, President of HCMC Society of Clinical Microbiology from 2013, and Prevost of Phan Chau Trinh University from 2017. His studies have focused on the surveillance of the major bacterial pathogens and the methods to detect the micro-organism pathogens from clinical samples. He has written 3 books published by the Medical Publisher (Nha Xuat Ban Y Hoc) 31 international papers (15 first author, 15 co-author), 52 national papers (23 first authors, 27 co-authors).

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O-20

14-drug microtitre plate assay for quantitative drug susceptibility testing of *Mycobacterium tuberculosis*

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Abstract

The global emergence of multidrug resistance (MDR) tuberculosis (TB) cases has demanded an accurate, simple and rapid drug susceptibility testing (DST) method for drug resistance (DR) identification. Microtitre DST, a new culture-based assay, is designed to have many remarkable advantages compared to the other DST methods currently in use. This assay is a semi-automated system with a 96-well microtitre plate containing a range of concentrations of 14 drugs used for TB treatment, including first-second line and 2 new compounds. MIC (minimum inhibitory concentration) measurements are determined at day 14 post incubation. The Vizion Digital system is harnessed for automated reading, using a software, called the Automated Mycobacterial Growth Detection Algorithm (AMyDA). The assay was evaluated to be consistent and accurate through external quality assessment *Mycobacterium tuberculosis* (Mtb) strains in previous literatures. Here we applied microtitre DST and AMyDA software on Mtb clinical strains to investigate their correlations with Mgit DST and determine how they could be deployed in diagnostic workflow.

The MICs of 194 Mtb clinical strains tested by microtitre DST were compared with categorical results (sensitivity or resistance) from Mgit. The results showed that the overall categorical agreement with Mgit was 95.8% (95%, 93% and 99.5% for ethambutol, isoniazid and rifampicin, respectively). We also assessed the using of the AMyDA software for MIC recording. Out of 2002 MIC values of 156 clinical isolates inferred by both manual and automatic readings at day 14, the overall proportion of consensus MICs was 87%. The discrepancy results are mainly due to the insufficient growth of Mtb at day 14, which made plates unreadable by the software.

Our results further confirmed the accuracy and consistency of microtitre DST assay to be used as a new and helpful diagnostic tool. The AMyDa software could be used in combination with manual reading to infer the consensus MICs and to detect the significant difference in plate interpretation, particularly with plates being difficult to interpret. Together these new tools can be applied in TB diagnosis to determine MICs of all antiTB drugs and to optimise DR treatment.

Biography

Ms Hoang Ngoc Nhung graduated from University of Science, Viet Nam National University Ho Chi Minh City in 2006. She also obtained the Master degree of Microbiology here in 2013. She has been working in Oxford University Clinical Research Unit since 2013 as a senior research assistant in Tuberculosis group. Her research interest is drug resistance of *Mycobacterium Tuberculosis*.

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O-21

Overexpression of OXA β-lactamases in carbapenem resistant *Acinetobacter baumannii* strains isolated in Southern Vietnam

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Abstract

Antibiotic resistance is one of the most important challenges to health care sector worldwide. In particular, multidrug resistant bacteria causing nosocomial infections such as *Acinetobacter baumannii* raise great concerns. Previous studies in Vietnam were mostly focused on clinical epidemiology and determination of antibiotic resistant bacteria ratio. Investigations on mechanisms of action through resistant genes activities or molecular epidemiology of endemic resistant bacteria attracted much less attention. This study aims at clarifying the mechanism of action of imipenem resistance through *bla*OXA genes expression in some *A. baumannii* clinical strains isolated from three hospitals in Southern Vietnam. Determination of the relationship between *bla*OXA genes expression level and imipenem resistance showed that induced strains bearing *bla*OXA-51 gene expressed weak and unchanged *bla*OXA gene. However, strains carrying "*bla*OXA-51, IS*Aba1*_*bla*OXA-23" and "*bla*OXA-51, IS*Aba3*_blaOXA-58" highly expressed *bla*OXA genes under imipenem induction. The IS*Aba3* insertion sequence was identified in all strains harboring *bla*OXA-58, but only one strain possessing IS*Aba3* upstream of *bla*OXA-58 gene exhibited an upregulation of *bla*OXA-58 gene when induced. The IS*Aba3* insertion sequence was intact, uninterrupted by other insertion sequences as reported by previous studies. This study provided new insights into the mechanism of imipenem resistance, an essential antibiotic used for the treatment of multidrug resistant *A. baumannii*. Data collected in this study contributed to the understanding of multidrug resistance characteristics of clinical *A. baumannii* strains isolated in Vietnam.

Biography

Nguyen Tuan Anh has just completed his PhD from University of Science, Vietnam National University Ho Chi Minh City. His studies focus on the detection, quantification, genotyping and drug resistance mechanisms of bacteria and virus from different clinical samples. Now he is teaching at the University of Medicine and Pharmacy at Ho Chi Minh city and head of molecular diagnostic group at University Medical Center.

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O-22

Influence of host stresses and antibiotic resistance on cell length distribution, cell envelope ultrastructure and accumulation of lipid inclusions in clinical *M. tuberculosis* isolates

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Abstract

Tuberculosis (TB) is a major public health problem in developing countries; antibiotic tolerance and resistance further complicates this problem. *Mycobacterium tuberculosis* (*M.tb*), the causative agent of TB, can tolerate host stresses and antibiotics; hence, prolonged antimicrobial treatment is required to cure the infection. Factors which may contribute to *M.tb* survival under stress conditions are the unique cellular adaptations of the bacilli. These include cell length heterogeneity, multi-layered cell envelope and accumulation of lipid inclusions, and these have been implicated in differential susceptibility to antibiotics. However, there is limited understanding of these cellular adaptations in clinical *M.tb* isolates, and how host stresses influence these adaptations. We investigated the influence of host stresses and antibiotic resistance on the cell length distribution in a large set of clinical *M.tb* isolates (n = 158), from pulmonary TB patients in Vietnam. This revealed that host stresses and rifampicin resistance significantly increased the cell length distribution of clinical *M.tb* isolates. We selected few clinical *M.tb* isolates (n = 8) from this study and further analyzed the influence of host stresses on the cellular ultrastructure of the bacilli. Ultrastructural analysis of *M.tb* isolates revealed cell envelope modifications and accumulation of lipid inclusions in sputum, under oxidative stress and iron deficiency. Currently we are investigating the level of antibiotic tolerance in clinical *M.tb* isolates and its implications for treatment progression and emergence of antibiotic resistance.

Biography

Dr. Vijay Srinivasan has done his PhD (2014) from the Indian Institute of Science, Bangalore, India. He has been working as a post-doctoral researcher at the University of Oxford from 2015. He has been studying the cell biology, host stress and antibiotic tolerance of clinical *Mycobacterium tuberculosis* isolates at the Oxford university clinical research unit, Ho Chi Minh city, Vietnam. He has published nine peer reviewed publications in international journals on cellular adaptations, population heterogeneity and antibiotic tolerance of mycobacterial species.

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O-23

Effect of two alternative methods of pooling sputum prior to testing with Xpert MTB/RIF

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Abstract

Pooling sputum specimens is one potential strategy for reducing the cost of using Xpert MTB/RIF for the diagnosis of pulmonary tuberculosis. We sought to compare the sensitivity of two alternative method of pooling. Patients being assessed for TB, whose initial sputum was Xpert MTB positive, were recruited and their sputum specimens were pooled for analysis with sputum specimens that were Xpert MTB negative. Two alternative pooling strategies were employed: one in which the concentration of sample reagent (buffer) was maintained at 2:1 (standard), in accordance with the manufacturer's instructions, and another in which the concentration of sample reagent was reduced to 1:1. We tested 101 Xpert MTB positive sputum specimens. Among these, 96% of valid test results (95% confidence interval 89% to 99%) were positive using the "standard buffer method". Using the "reduced buffer pooling" method 94% of valid test results (95% CI 87% to 98%) were positive. McNemar's test for the difference in paired proportions was not significant (P=0.56). We have confirmed that pooling sputum specimens is a valid method of reducing the cost of testing sputum using Xpert for detecting pulmonary tuberculosis. Two alternative pooling strategies yielded similar results.

Biography

Dr. Phuong NTB have been worked as bacteriologist for 20 years. She have conducted molecular epidemiologic, drug resistant, and human susceptibility and diagnostic studies for infectious diseases (*Tuberculosis, Aspergillus*, MRSA/MSSA, ESBL producing bacteria…)..She also conduct other technical activities assigned by the project management committee and provide documents, templates, guidance, SOP, and other project support to the Lab team during the project implementation. She have technical and management experience in research design and implementation, data collection, analysis and triangulation for non-profit organizations.

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O-24

Genomic analysis reveals the re-emergence of a nosocomial outbreak caused by multidrug resistant *Klebsiella pneumoniae*

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Abstract

Multidrug resistant (MDR) *K. pneumoniae* is listed among the most urgent public health threats due to its virulence and insusceptibility to a wide range of antimicrobials. Infection with this pathogen frequently leads to fatal outcomes, especially in low-income hospital settings. Patan Hospital is a 450-bed government hospital located within the Kathmandu Valley, Nepal. The hospital has previously witnessed multiple outbreaks caused by MDR *K. pneumoniae* in the neonatal intensive care unit (NICU). Particularly, a carbapenemase producing sequence type (ST) 15 *K. pneumoniae* clone was responsible for an outbreak with mortality rate up to 75% in 2012. Recently in 2015, this same NICU suffered again from an MDR *K. pneumoniae* outbreak. In this study, using whole genome sequencing (WGS) and state-of-the-art analytic approaches, we aimed to define the nature of this recent outbreak. We found that the 2015 outbreak in Patan Hospital was caused by the same MDR ST15 *K. pneumoniae* reported in 2012. Albeit genetically similar, these recent strains were susceptible to carbapenems due to deletion of the *bla*NDM-1 cassette. Using Bayesian phylogenetic inference, we determined the outbreak strain was introduced to Patan Hospital in late 2010 and subsequently caused major outbreaks in NICU in 2012 and again in 2015. This clone acquired four different plasmids encoding resistance to numerous therapeutic antimicrobials, and this may underlie its successful propagation and associated high mortality. This study demonstrates the viability of applying WGS in nosocomial outbreak investigation. Insights provided through this study are invaluable in tailoring infection control strategies as well as raising public awareness.

Biography

She received a Master of Science in Microbiology in 2015 from the University of Science, National University of HCMC, Viet Nam. During her research, she had an opportunity to learn bioinformatics skills. Particularly, her degree was investigating the genetic characteristics and molecular evolution of *Shigella sonnei*. She has been working as a research assistant in bioinformatics in Enteric Infection Group for 3 years. Now, she is focusing on analysis of *Klebsiella pneumoniae* genomes to continue chasing her passion in this interesting science. These help her to gain a profound understanding on how bacteria could evolve to become resistant to a wide range of antibiotimicrobials.

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ZOONOSIS and ONE HEALTH

O-25

Streptococcus agalactiae appears to be primarily a foodborne infection, associated with aquaculture, in parts of Southeast Asia

Timothy Barkham

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Abstract

In Singapore in 2015 *Streptococcus agalactiae* (GBS) serotype III, Sequence Type (ST) 283 caused the first reported foodborne outbreak of invasive GBS; it was acquired from farmed fish. Cases included meningitis and septic arthritis amongst young adults with few co-morbidities. Previously, ST283 had only been reported from humans in Hong Kong and one fish in Thailand. We investigated the extent of ST283. We reviewed the literature. Whole genome sequencing was used to assess the phylogeny of ST283 found in human and/or animal collections. The ST283 clone accounted for 20-70% of all invasive human GBS in countries in SE Asia between 2000 and 2017, but only four reports were found outside Asia. GBS bacteraemia rates in Thailand and Lao PDR were triple those in the UK; the excess was ST283. All 62 (100%) GBS from fourteen fish farms in Malaysia and Vietnam were ST283. ST283 was found in a diseased frog in China. Serotype III GBS causing die offs in fish farms in Thailand between 2003-2006, and Brazil in 2016, are suspected to be ST283, but it is absent from other animal reports, globally.

Biography

Dr Barkham studied medicine and then specialised as a Microbiologist at St. Thomas' Hospital in London. He then worked at the Hammersmith Hospitals for two years before moving to Singapore in 1999. He enjoys clinical infectious diseases, epidemiology and outbreak investigation. He has a 20% teaching appointment at the National University of Singapore. He has developed diagnostic assays that are marketed in Singapore and elsewhere in Asia.

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O-26

A multidisciplinary approach to understand the transmission of zoonotic antimicrobial resistant bacteria in Vietnam

Ngo Thi Hoa

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Abstract

The rapid development of antimicrobial resistant (AMR) bacteria questions our current control measures for the infectious disease field. Antimicrobial usage (AMU) in agriculture is the important contributing factor to the current AMR development, the global public health threat. The research findings of the current microbiological and epidemiological studies revealed the common usage of several classes of clinically critical important antibiotics in community for both human and animal populations. This contributes to the high prevalene of AMR bacteria in associated environments. The findings in the whole genome sequence studies implied the bi-direction sharing of AMR bacteria between animals and humans. Understanding of community members on an appropriateness of AMU and AMR development is limited, which impacts their practices. However they are awared of the potential impact on public health. These findings indicated that managing AMU in Vietnam will require feasible holistic approaches which would impact the whole society to change the current situation.

Biography

Ngo T. Hoa completed her PhD training at Royal Holloway, University of Londona and spent three years at Yale University as postdoc fellow, funded by Wellcome Trust. She joined Oxford University Clinical Research Unit, HCMC, Vietnam in 2005. She has led the Zoonoses group since 2013. She has published more than 60 papers in internaional peer reviewed journals.

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O-27

Occurrences and Quantitative Microbial Risk Assessment of Antibiotic Resistant bacteria in Tropical, Urban Water Bodies

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Abstract

Quantitative microbial risk assessment was performed to estimate the risk of gastrointestinal infections and illnesses caused by antibiotic resistant bacteria through recreational activities (e.g. kayaking, sailing, dragon- boating) in tropical, urban water bodies in Singapore. Antibiotic resistance prevalence of waterborne pathogens including *Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella spp., E. coli, and Enterococcus spp.* in various water bodies were quantified using specific selective medium supplemented with commonly prescribed antibiotics in Singapore, including meropenem, ceftazidime, sulfanomide, trimethoprim, amikacin and ciprofloxacin. At least 20 isolates per samples were picked for AST susceptibility test in Vitek system to confirm the level of antibiotic multidrug resistance, and followed by PCR to detect the corresponding antibiotic resistance determinants. At least 15 samples from different locations and time points for each bacteria were used to fit suitable distribution models. Probability of infection and illness caused by these antibiotic resistant bacteria were predicted using the Crystal Ball simulation tool and burden of disease was calculated in DALYS.

Biography

Dr Le Thai Hoang is a lecturer at the Department of Environmental Engineering and International University, Vietnam National University, Ho Chi Minh City. He received his PhD degree in Biological Engineering from the Chonbuk National University in South Korea in 2012. His research interest and specialisation are in the area of Environmental Biotechnology, Water quality, Antibiotic resistance, Infectious pathogen and Quantitative microbial risk assessment (QMRA). Prior to joining HCMIU, he spent 4 years as a postdoc research fellow at National University of Singapore from 2013 to 2016, and worked on some projects in the Environment and Water Industry program with PUB to develop the molecular microbiology techniques characterize and quantify antibiotic resistance (i.e., bacteria and genes) from various water sources including reservoirs, catchments, canals, Wastewater / NEWater / Drinking water treatment plants and marine water. He published more than 20 papers and patents reporting his discoveries in the research field of Environmental Biotechnology.

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O-28

Rapid Molecular Diagnosis of Infectious Diseases using a Portable LabChip-based Real-time PCR

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Abstract

We developed and commercialized innovative two systems for rapid and efficient nucleic acid extraction and quatitative amplification qPCR system. It takes 5-30 minutes for DNA/RNA extraction from 1-16 lysed samples using Veri-Q Prep M16 sample prep instrument. For the rapid amplication and quantification of of the extracted DNA/RNA, we generated a disposable plastic microfluidic Lab-on-a-Chip (LabChip)-based real-time PCR system. It takes a about 10-20 min for 45 cycles of real-time PCR for DNA or 30 min for reverse transciption and 45 cycles of real-time PCR (RT-qPCR) for RNA using our Veri-Q PCR316 system. It is a portable (4kg), 4 color system (4-plex), can be operated by touch screen (stand-alone) and by car-battery. It also has a function of data-trasferring from PCR machine to PC through android-based smart phone system. We recently developed 35 different types of highly dangerous pathogen kits for real-time PCR optimized for our LabChip-based real-time PCR. Our kits showed high sensitivity ranging from 1-70 copies/reaction. Korea Center for Disease Control and Prevention (KCDC) is using our qPCR kits for Emergency Cares for the country. They eqipped them in the mobile labs for rapid detection of bio-terroristic pathogens during the Pyung Chang Winter Olympic Games in 2018. We are moving forward to the devlopment of rapid accurate handheld or wearable point-of-care test (POCT) system to detect and monitor various infectious diseases.

Biography

Sung-Woo Kim is currently a CEO of Mico Nanobiosys. He received a BA at Korea University and MA in Seoul National University in Seoul, Korea. After his Ph.D. at Columbia University in 1994, he was trained as post-doc at Harvard Medical School for 3 year. Then he worked for Harvard Medical School as a faculty member from 1996 to 2006. He found a molecular diagnostic company, NanoBioSys Inc. in 2009 and worked as a CEO. Now he is working for Mico Nanobiosys, MiCo Group. He led his group to generate a rapid real-time PCR system using a disposable plastic LabChip first time. This invention is patented over 17 countries. He produced more than 90 patents related to rapid molecular diagnosis field over 9 years. Based on these achievements, he received several big governmental R&D grants from Korean NIH, Commercialization Ministry, Agriculture Ministry, and Science-Technology Ministry. He exceptionally received big governmental grants and excellency awards for R&D and management. He was also selected as an invited speaker to introduce its application for Point-of-Care Testing (POCT) at Biological Weapon Convention (BWC), UN, Geneva, Switzerland (2013.8.14).

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O-29

Antimicrobial resistance research in food animal in Vietnam

Vo Thi Tra An

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Abstract

The impact of AMR on our life is real and very important. Let's have a look at the estimated figure that O'Neill has reported. At present, AMR cause death to 700,000 cases per year, more than haft that traffic accident made. In about the next 30 years, the death caused by AMR may increase more than 10 fold at meet the figure of 10 million, even higher than death due to cancer. Research on AMR will contribute to the understanding of the mechanism that the bacteria develop and transfer their resistance, the prevalence and level of resistance among bacterial population and the association between the use of antibiotics and resistance and so on. This review has been made from the data of 33 articles within 10 years. Majority of articles published susceptibility results of pathogens from the sick animals. The rest was about bacteria from the healthy animal, carcass, meat, milk and the environment. The research was conducted mainly in South and North of Vietnam where the animal farms and veterinary institutes were allocated. The research relating to AMR in Vietnam contributed to the change in the legislation as well as the practice of antibiotic use in animal husbandry.

Biography

Vo Thi Tra An has completed her Ph.D. at the age of 33 years from Utrecht University and appointed the title Associate Professor at the age of 40. She is the Head of Veterinary Biosciences Department in FACVM, Nong Lam University. She has published 60 papers in local and international journals. She has been granted for several projects relating to AMR by international organizations. She is now a lecturer in Nong Lam University and has been serving as an editorial board member of Journal of Agriculture and Development.

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O-30

Mapping out socio-economic drivers of antimicrobial usage in poultry farms in Vietnam: A combined participatory epidemiology and Q-sort approach

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Abstract

In Mekong Delta region of Vietnam, antimicrobials are widely used by poultry farmers but little is known about socio-economic drivers that influence the way farmers give antimicrobials to their flock. This study aims to identify socio-economic drivers related to farmers' attitude of antimicrobial usage (AMU) using a combination of participatory epidemiology (PE) and Q-sort approach. 26 focus group interviews (FGD) were conducted on 125 farmers (chicken and duck) and 73 farmers' advisors, including veterinarians, vet-shop owners, and commune animal health workers (CAHWs) in 5 districts of Dong Thap province (Mekong Delta). Through interviews, 46 statements relevant to AMU including antimicrobials' perceived reliability, practice, costs and impact on flock health were created. Those statements were then processed using Q-sorting using a structured sub-group of famers (n=28) and farmers' advisors (n=26). Four and three discourses were selected in the farmer group and farmers' advisor group respectively, representing 50-55% of the total explained variance. These discourses contained different attitudes of AMU among farmers. One consensus point among the farmer group is the perception that antimicrobials are more expensive than biosecurity methods. Consensus points among members of the farmers' advisor group members were: (1) high-quality drugs have a relatively higher price than poor-quality counterparts; and (2) controlling disease using antimicrobials is more costly than using other biosecurity methods. The methodology applied allowed to obtain meaningful insights into perceptions of the different stakeholders involved in antimicrobial prescription and usage in poultry farming. This knowledge can contribute improvement to success of intervention strategies aimed at curbing indiscriminate use of antimicrobials in the region.

Biography

Dr. Bao's interests include infectious diseases and veterinary public health. In July 2017 he was awarded a Doctorate in Science (PhD) by the National Veterinary School of Toulouse (France). His PhD studies focused on how Vietnamese farmers could be better involved in the surveillance and control of Foot-and-Mouth Disease at the local level. He is currently a lecturer at the Faculty of Animal Science and Veterinary Medicine within Nong Lam University (Ho Chi Minh City). He has published 7 papers in international journals.

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O-31

Whole genome sequencing reveals limited contribution of non-intensive chicken farming to extended-spectrum beta-lactamase producing *Escherichia coli* colonization in humans in southern Vietnam

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Abstract

Overuse of antimicrobials in agriculture in Asia has been reported, but the risk of acquisition of extended-spectrum beta-lactamase (ESBLs) in humans through non-intensive chicken farming still remains unclear. We collected faecal samples from 204 randomly selected farmers and their chickens, and from 306 community-based individuals who did not raise poultry in Vietnam. Whole genome sequencing was employed to examine genomic relatedness of ESBL-Ec colonizing chickens and humans in Vietnam. The prevalence of ESBL-Ec colonization was 20.0% in chicken farms, 31.1% in chicken farmers, 49.5% in rural individuals and 38.3% in urban individuals. Multivariable analysis showed that colonization with ESBL-Ec in humans was associated with human usage of antimicrobial drugs (OR=2.52, 95%CI=1.08–5.87). Whole-genome sequencing revealed that CTX-M genes were the most predominant ESBL genes, found in 468/486 (96.2%) of ESBL-Ec isolates. However, the distribution of CTX-M genes across chicken and human isolates was different. CTX-M-55 was identified as the most common ESBL-encoding gene in chicken isolates (72.1% versus 12.9% in human isolates, p<0.001), whilst CTX-M-27 was more prevalent in human isolates (44.2% versus 7.0% in chicken isolates; p<0.001). On 16/204 farms (6.9%; 95%CI=3.4–10.3%) ESBL-Ec were detected phenotypically in both the farmers and their chickens. On 3/204 farms (1.5%; 95%CI=0–3.1%), ESBL genes of ESBL-Ec isolated from the farmers and their chickens were identical. However, we detected identical sequence types of ESBL-Ec between chicken and farmer isolates in only one farm. Isolates also revealed 1 pairwise SNP distance based on core gene alignment, indicating potential sharing of ESBL-Ec between the chickens and farmer on that farm. The findings suggest that non-intensive chicken farming is not a major source of ESBL-Ec colonization in humans and human antimicrobial drug usage appears to be an important driver of ESBL-Ec colonization in humans in Vietnam.

Biography

Dr. Nguyen Vinh Trung is a researcher at the Oxford University Clinical Research Unit in Ho Chi Minh City, Vietnam. His research interests include epidemiology of zoonotic pathogens and dynamics of antimicrobial resistance in bacterial populations

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O-32

Detection of *Legionella* spp. in water and air samples by culturing methods from air conditioning systems in Ho Chi Minh City, Viet Nam

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Abstract

Legionella spp., facultative intracellular Gram negative, may cause acute respiratory infection in humans referred to as legionellosis. But there is a lack of information about the present and concentration of these bacteria in environmental sources. Thus, this study was designed to detection and numeration of L*egionella* by culturing methods at 18 sites (hospitals, official buildings, universities) in Ho Chi Minh City, Viet Nam. Fifty four water and air samples were collected from condensed water of the air conditioning system and surrounding air over 3 months period. After pre-treatment by acid and heat, the samples were analyzed for the presence of *Legionella* spp. by culturing onto buffered charcoal yeast extract (BCYE) agar. The results showed that the *Legionella* concentrations in the water samples ranged 0-200 CFU/ml. Besides, *Legionella* concentrations were higher in the buildings that has center air conditioning systems than the one with individual air conditioning systems. However, in the air samples, these values ranged 0-27,5 CFU/ml. Interestingly, there were a relationship of the *Legionella* concentrations in these two environments. Thus, the results of this study emphasized that the water from the air conditioning systems in various building may serve as a reservoir for *Legionella* spp. .

Key words: Legionella spp., air conditioning systems, buffered charcoal yeast extract (BCYE) agar.

Biography

Dr Nguyen Ai Le is a lecturer at the Faculty of Environment, University of Science, Vietnam National University – Ho Chi Minh City, Viet Nam. She has completed her PhD since 2013 from Division of Sustainable Energy and Environmental Engineering, Graduate School of Engineering, Osaka University, Japan. Her research interest and specialisation are in the area of Environmental Microbiology, Bio-remediation, Biological Wastewater-Waste Treatment, Bio-energy.

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O-33

The importance for the Development of a One Health curriculum for Universities in Vietnam

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Abstract

Emerging pandemic threats such as highly pathogenic avian influenza, SARS, Ebola, Middle Eastern Respiratory Syndrome, Zika, coupled with other complex global challenges such as climate change, urbanization, food safety and antimicrobial resistance (AMR), have fueled the One Health (OH) movement in recent times. As such, a large number of academic institutions, with support from the public sector, have adopted this collaborative approach to prevent or prepare for the next high consequence event. However, the speed of operationalization of such a transformative process has varied and has necessitated the need for illustrative regional “success stories.”

With support from the US Agency for International Development (USAID) Emerging Pandemic Threats program, the Southeast Asia One Health University Network (SEAOHUN) has promoted OH capacity-building based on a common, regional set of core knowledge, skills, attitudes and behaviors relevant to building successful OH professionals. These "OH Core Competencies" were designed by SEAOHUN faculty in partnership with University of Minnesota, Tufts University and Training Resources Group, Inc., and they have served as the basis for designing a robust framework for OH educational platforms for university training as well as career development programs.

OH curriculum for students is one of the most important conditions to build a new generation with strong knowledge, ability to respond with emerging and re-emerging diseases. In Vietnam, the medical, public health and veterinary training program are gradually improved along with the development of science and technology. OH approach has been partly incorporated into their curriculum in different subjects. However, this curriculum has not met the needs of OH core competencies. Therefore, Vietnam needs building new subjects or strengthening the integration of OH modules into existing subjects. In recent years, we were implemented different activities for building the training program bases on OH approach, included review current curriculum, create framework, develop training materials, test the teaching tools and apply to the training programs. A total of 20 universities belong Vietnam One Health University (VOHUN) were reviewed all current training programs, based on 7 OH core competency modules, 8 OH technical modules. Utilizing this competency-based framework, VOHUN has created a portfolio of educational OH modules to more effectively teach these competencies to undergraduate and postgraduate students. This presentation will focus on key outcomes and achievements of VOHUN in transforming public health, veterinary and other health institutions and curricula across Vietnam.

Biography

Pham-Duc PHUC holds a Medical Degree from Hanoi Medical University (1995) and a Master in International Health from the University of Copenhagen (2003). He got his PhD degree (2011) from the University of Basel - Swiss Tropical and Public Health Institute. Dr Phuc has been involved in many research projects on health risks related to water and sanitation, especially infectious diseases. Early 2012, he has joined Hanoi University of Public Health, Vietnam as a researcher where he conducts research in collaboration with staff and students. He has been developing and participating in different initiatives with national and international donors to generate funding for research and training on health risks assessment in water, environmental sanitation and food safety. He is a leader of the Center for Public Health and Ecosystem Research; and he also is coordinating the Vietnam One Health University Network since 2012.

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VACCINE DEVELOPMENT

O-34

Active and Passive Immunization to Prevent Severe Invasive Diseases Caused by *Staphylococcus aureus*

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Abstract

Staphylococcus aureus causes bacteremia, pneumonia, and septic shock that are associated with mortality rates of 10%, 30% and 55%, despite appropriate antimicrobial therapy. Using relevant rabbit infection models, we have shown that specific staphylococcal toxins played critical roles in disease pathogenesis. We further showed that active immunization with toxoids or passive immunization with specific anti-toxin antibodies reduced mortality in animal efficacy studies. Adjunctive therapy with anti-toxin antibodies, either alone or in combination with anti-staphylococcal antibiotics, improved animal survival outcomes. These active and passive immunization approaches are currently being evaluated in human efficacy studies (Phase I/IIA). In this lecture, I will offer my insights on how we are translating basic science discoveries to the development of novel vaccine and immunotherapeutics to combat a major infectious disease problem.

Biography

Dr. Diep received his BA (2000) and PhD (2005) from UC Berkeley and his postdoctoral training (2008) from UCSF. He is currently an Associate Professor at UCSF. Dr. Diep has long-standing research interests in the clinical and molecular epidemiology and pathogenesis of multi-drug resistant infections (55+ publications, >7000 citations). His group was among the first to characterize widespread disease epidemics caused by the community-associated MRSA clone USA300. He directed NIH R01-sponsored development of rabbit models that demonstrated mechanisms by which staphylococcal toxins cause lethal pneumonia. In his recent translational work, Dr. Diep and industry colleagues showed that active immunization with toxoids and passive immunization with specific anti-toxin antibodies reduced mortality and prevented major morbidity in preclinical efficacy studies.

Disclosures: Dr. Diep was funded by United States National Institutes of Health (NIH), Food and Drug Administration (FDA), Department of Defense DARPA, Biomedical Advanced Research and Development Authority CARB-X, and various industry partners, including Achaogen, Arsanis, AstraZeneca/MedImmune, Genentech, Integrated Biotherapeutics, Merck/Cubist and Pfizer.

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O-35

Synopsis of APP in Vietnam swine industry and optimization of antigen mass production in laboratory conditions

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Abstract

Actinobacillus pleuropneumoniae (APP) is one of the pathogenic bacteria causing severe swine disease in Vietnam as well as other pig-raising countries in the world. APP can be found as the major causative agent of an outbreak of respiratory disease in a farm or it can be an opportunistic pathogen after immunosuppressive infection in pigs such as the disease of PRRSV, PCV2, CSFV or Mycoplasma hyopneumoniae. Currently, APP is controlled by using antibiotics and some imported vaccines. Besides the studies of vaccine efficacy and antibiotic resistance of the bacteria, one study was aimed to produce antigen mass of APP for vaccine development in laboratory condition. Three liquid medium (Brain Heart Infusion - BHI broth, Muller Hinton - MHI broth and Tryptone Yeast Extract - TYE broth) was used to evaluate the growth ability of APP in the condition of supplementing with 10 µg of nicotinaminde adenine dinucleotide per ml of media. Resultant optimal media was used to determine its growth curve and mean generation time (MGT). To generate inactivated whole-cell antigen, the APP suspension was treated with different formaldehyde concentration (0%, 0.05%, 0.1%, 0.2% and 0.4%). Results indicated that BHI medium was the best for growing APP, in which, the lag phase was 2 hours and the time to enter exponential phase was 2-6 hours, and the stationary phase lasted for 18 hours before death phase. The mean generation time (MGT) is about 27 to 28 minutes. The minimum formaldehyde concentration and time to kill all the APP cells was 0.1 % for 2 hours of incubation. This presentation will include different aspect of APP in Vietnam such as prevalence, vaccine use, antibiotic use, antibiotic resistance, clinical signs and research result of antigen mass production.

Biography

Dr. Phat is presently a lecturer and a researcher at Nong Lam University Ho Chi Minh City, Vietnam (formerly named University of Agriculture and Forestry). With the experiences about molecular techniques and viral biology obtained during his doctoral and postdoctoral programs in the University of Nebraska - Lincoln (NE, USA), he is now also serving as a consultant for clinical/molecular diagnosis of veterinary diseases, vaccine application in practical condition of animal farms and doing research for vaccine development. He has 14 peer-reviewed papers published.

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O-36

Engineering and Production of recombinant Adeno-Associated Virus (rAAV): potential for cancer therapy and vaccine development

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Abstract

Recombinant versions of Adeno-associated virus emerged as the premier choice for gene therapy due to beneficial characteristics of transduction, immunogenicity and safety. So far, two drugs based on wild-type AAV serotypes 1 and 2 (Glybera, Luxturna) have been approved as replacement therapy for monogenetic diseases. Unfortunately, current production strategies are inefficient and/or difficult to scale and available wild-type tropisms might not allow for the targeting of desired cell types.

We analyzed and rationally engineered the rAAV capsid for targeting, purification and detection and the rAAV genome for easy modification and rapid prototyping. The use of our constructs is demonstrated with a tumor-cell specific suicide gene therapy also named virus directed enzyme prodrug therapy (VDEPT).

Specifically, we used a DARPin N-terminally fused to the capsid protein or peptides fused in a capsid loop structure to target epidermal growth factor receptor (EGFR) overexpressing cells. Specificity was demonstrated with a set of cells expressing a range of EGFR densities. As gene of interest a fluorescent protein enabled microscopy and flow cytometry, and thymidine kinase or cytosin deaminase were used to activate prodrugs. In addition, we evaluated HEK293 suspension culture conditions for rAAV production in a fermenter and tested the stable integration of helper genes. Viral particles were purified by ultracentrifugation and analyzed by qPCR, electron microscopy and atomic force microscopy. rAAV may also serve as scaffold for vaccination.

Biography

Kristian Müller is a professor of cellular and molecular biotechnology at Bielefeld University, Germany. He was an assistant professor and group leader at the University of Freiburg and the University of Potsdam. Prior to his independent career, he worked as a postdoctoral scientist at the University of California at Berkeley, and he received his Ph.D. from the University of Zurich and his Diploma in Biochemistry from the University of Hannover. Within the realm of protein engineering and synthetic biology he performs basic research and develops technology, which he utilizes to drive innovations such as cancer biotherapeutics.

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O-37

Development of the system to display recombinant proteins on the surface of vegetative *Bacillus subtilis* cells and its potential applications in vaccine delivery vectors

Nguyen Duc Hoang

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Abstract

Since *Bacillus subtilis* does not produce any endotoxins such as lipopolysaccharides, it confers a significant advantage for use in humans and animals. Here, I present the establishment of the system to immobilize covalently recombinant proteins on the surface of B. subtilis vegetative cells. I will also show the proofs to demonstrate functions of sorting sequences and sortases of *B. subtilis*, which could be applied to anchor a target protein on the surface. Finally, I will show some data concerning the use of *B. subtilis* as potential delivery vectors.

Biography

Dr. Nguyen Duc Hoang graduated at the University of Science, Vietnam National University Ho Chi Minh City in 1998 and obtained his master degree in 2003. During his master course, he spent one year for 'International Post-Graduate University Course in Microbiology' at ICBiotech of Osaka University and Kyoto University (10/2000 – 9/2001) and worked on yeast Saccharomyces cerevisiae. After that, he moved to the University of Bayreuth (9/2003-7/2006), Germany and obtained his Ph.D. at the department of genetics for the work on B. subtilis "Construction of plasmid-based expression and secretion vectors and study of the immobilization of proteins on the surface of B. subtilis cells". As the consequence, the first commercial expression plasmids, pHT series, for B. subtilis was generated and the project of using controllable stabilizing elements combined with promoters to enhance protein expression level has been developed. In 11/2006 he moved to Max Planck Institute for molecular physiology to work as postdocs in the area of biochemistry/ chemical biology and cell biology and started several molecular biological projects in chemistry-based research group relating to cancer studies. He has worked for the University of Science since 6/2011. He is currently the director of Center for Bioscience and Biotechnology and Head of Department of Microbiology. His research group focuses on gene expression in B. subtilis in the deferent locations, in the cytoplasm, on the surface, and as secretion into the culture medium, and applications of this technology for production of recombinant proteins, vaccine delivery vectors, …

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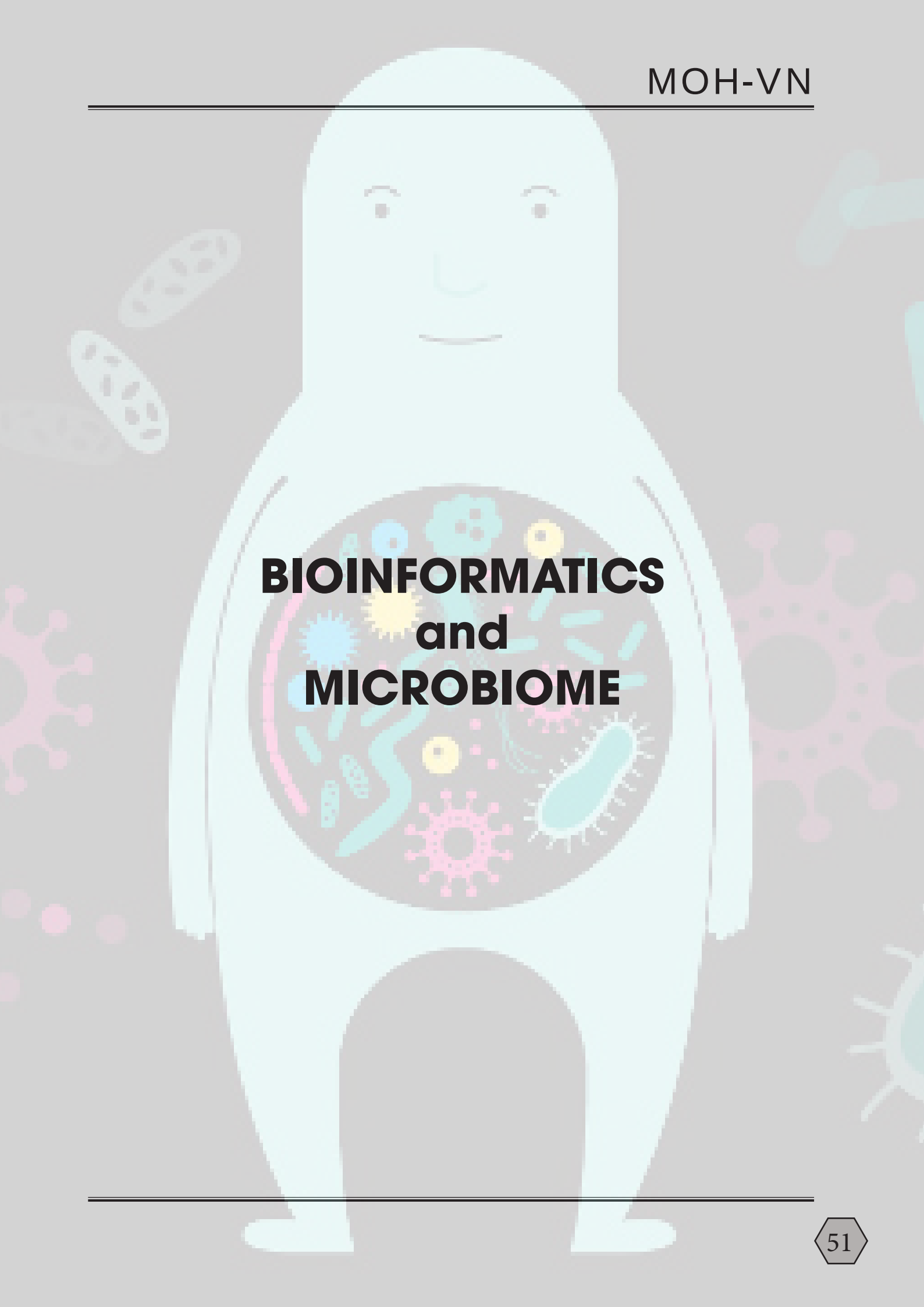

BIOINFORMATICS and MICROBIOME

O-38

Genomic insights into a foodborne outbreak of Group B *Streptococcus*

Swaine Chen

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Abstract

In 2015, an unprecedented outbreak of invasive Group B Streptococcal infection occurred in Singapore. Initial epidemiology linked infections to the consumption of raw fish. The causative bacteria was a serotype III, ST283 strain of GBS. Whole genome sequencing was performed on human and fish ST283 isolates from Singapore, Thailand and Hong Kong. Genomic analysis of over 200 ST283 strains sampled from 1998-2015 showed that the 2015 outbreak was caused by a single strain of ST283 GBS. We identified that the same strain of ST283 has been causing infections in Singapore since 2011. A Bayesian analysis predicted that ST283 emerged in 1994 (95% confidence interval 1991-1997). We used bacterial genomics to establish a definitive link between raw fish consumption and invasive GBS disease. Our work, combined with previously published studies, indicates that ST283 has been in Southeast Asia for nearly 20 years and raises the hypothesis that many of these infections have been foodborne, an unprecedented route of infection for GBS. I will also discuss lessons learned with respect to the use of whole genome sequencing for outbreak investigations.

Biography

Dr Swaine Chen is a Senior Research Scientist in Infectious Diseases at the Genome Institute of Singapore and an Assistant Professor of Medicine at the National University of Singapore. His work combines his training in medicine, biology, chemistry, and mathematics to understand how and why bacteria are able to cause infections in humans. This understanding, in turn, may enable us to detect and treat infectious diseases more effectively and more quickly in the future. Another major aspect of his work is using DNA sequencing to detect and understand outbreaks of infectious diseases, especially those that are unexpected, like the Group B Streptococcus outbreak associated with yu sheng fish in 2015 in Singapore. He completed his M.D./Ph.D. at Stanford University in Developmental Biology, followed by a postdoc at Washington University School of Medicine in St. Louis. He has published 48 peer reviewed manuscripts.

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O-39

Propidium monoazide (PMA) sample pretreatment impacts the abundance of rare populations in high-throughput sequencing analysis of CF lung mycobiome and bacteriome

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Abstract

Introduction

Thanks to the development of next generation sequencing (NGS), recent studies have shown that the lung of patients with cystic fibrosis is a complex poly-microbial flora, also called the CF lung microbiome, which includes not only bacteria but also fungi (yeast and filamentous fungi), and viruses and phages. Dysbiosis (loss of the abundance and the diversity) of the lung microbiome has been associated with the patient's decreased lung function and poor clinical status. Indeed, NGS is a technique that may introduce biases on numerous methodological steps. One of the most important biases is that this technique could not differentiate among the living microorganisms, the dead or damaged cells, and the extracellular DNA. Our study aimed to determine whether a sample pretreatment with propidium monoazide (PMA) in NGS, which can target selectively the DNA of viable cells, could reflect more closely the clinical status of patients.

Methods

We compared NGS data of bacteriome and mycobiome of 15 sputum samples from 5 CF patients that were characterized using the Ion Torrent technique with and without prior PMA treatment of the DNA-extracts.

Results

PMA pretreatment had no significant effect on the entire and abundant bacterial community (genera expressed as operational taxonomic unit with a relative abundance of ≥1%) but caused a significant difference in the rare biosphere community (< 1%) when analysing the alpha biodiversity Simpson index (p=0.029). Similarly, regarding beta diversity (non-metric Bray-Curtis dissimilarity analysis), the rare phylotypes also differed more dramatically than the total and abundant ones. Regarding the mycobiome data, there was no difference between PMA-treated and untreated samples.

Conclusion

PMA pretreatment seems to change the relative abundance of bacteria, especially in the rare populations, but not fungi. Given such a cumbersome protocol (PMA pretreatment coupled with NGS), we discuss its potential interest within the follow-up of CF patients. As only few studies suggested the use of this protocol in the characterization of the bacteriome may be clinically relevant, further studies using PMA pretreatment are warranted to improve our “omic” knowledge.

Biography

NGUYEN Do Ngoc Linh graduated from Hanoi medical school in 2011. Then she completed her Master in Microbiology at Paris XII University then her PhD at the age of 30 years at Pasteur Institute of Lille. She has published 4 papers in international journals. Her field of interest is medical microbiology, human microbiome and metagenomics analysis. Actually she is the head of academic affairs and scientific research of Phan Chau Trinh University in Quang Nam. Her career path is to contribute to the medical education and scientific research, especially in the “omic” field.

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O-40

Metagenomics for Diagnosis of Sterile Site Infection: Balancing Automation with Expert Interpretation

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Oxford University Clinical Research Unit, HCMC

Abstract

Background: A quick literature search will demonstrate the increasing popularity of metagenomic sequencing methods to diagnose patients when other methods have failed. However there is growing interest in using metagenomic methods more routinely. At OUCRU, Vietnam, we are investigating its use in central nervous system (CNS) infections and in patients with fever of unknown aetiology. In order to examine this data effectively we have developed an analysis pipeline which is rapid, requires low RAM.

Methods: The pipeline takes raw reads from Illumina sequencing, removes host reads and classifies the remaining samples using CLARK in light mode. After classification, a prediction of genome coverage is made for each organisms identified based on number of reads and the genome size of the corresponding organism. If a threshold (default 0.1%) is met the reference for that taxon ID is downloaded and sample reads mapped. Outputs include mapping statistics such as genome coverage and number of reads mapped. A report on the frequency at which taxon IDs are found across the run is automatically generated, allowing users to consider the possibility of contamination.

Results: The pipeline was used to analyze sequencing results from 23 CSF samples collected from patients presenting with CNS infection in Vietnam. After pipeline completion, the number of reference mapping results was 104. The results were then edited for clinical significance by a microbiologist. Results identified pathogens in 17 samples, 8 *Streptococcus suis*, 4 enteroviruses, two cases of mumps and one *S. pneumoniae*, Japanese encephalitis and Varicella-zoster virus (VZV). In addition, Hepatitis B was identified in 5 cases, but was not considered a cause of CNS disease, but merely reflective of the high incidence of Hepatitis B in Vietnam. Genome coverage of these pathogens varied from 0.83% to 81.33%. All findings were confirmed with specific PCR, with Ct values ranging from 27 to 40.

Biography

Dr Anscombe completed her BSc (Hons) in Biology at the Univerity of York (UK) in 2009, majoring in cellular and molecular biology. She then went on to train as a Clinical Scientist (Microbiology) for the NHS, during which time she completed a MSc in Clinical Microbiology at Queen Mary University London. During this time she specialised in improving diagnosis of infectious diseases using molecular methods. Subsequently, she undertook a PhD investigating the use of highly sensitive methods for diagnosis of infectious diseases using next generation sequencing, which was completed at Public Health England and awarded by Queen Mary University London. Her first postdocotoral position was as a clinical scientist in the Enteric Virus Unit at Public Health England, where she contributed to improving molecular assays, and devloped molecular methods for the UK Polio Surviellnce project. Since September 2016 Dr Anscombe has work as a postdoctoral researcher in the Emerging Group at OUCRU. Here her work focusses on devleoping bioinformatic analysis pipelines to detect pathogens in sterile sites using metagenomic sequencing methods. Her research aims to improve our understanding of the aetiology of infectious diseases, particularly life threatening diseases such as sepsis and central nervous system infections.

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O-41

Understanding diarrhea recovery from a microbiome perspective

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[7] The Department of Medicine, University of Cambridge, Cambridge, United Kingdom

Abstract

Diarrheal diseases inflict substantial mortality and morbidity in young children worldwide. The human gut microbiota has proved to be essential in understanding our health and diseases, but its structure and dynamic under the impact of diarrhea remains unexplored. In this study, we set out to characterize the gut microbiota succession over the duration of diarrhea. We included over 200 stool samples from 90 Vietnamese children with diarrhea, which were sampled longitudinally (day 1, 7, and 15). Total DNA from the stool samples were extracted and subjected to 16S rRNA gene profiling using Illumina sequencing. We found that the gut microbiota structure was significantly different between the early and recovery phases of diarrhea. Particularly, the acute phase was dominated by *Streptococcus* and *Escherichia*, while other gut commensals such as *Bacteroides*, *Eubacterium*, *Lachnospiraceae*, and *Clostridium* were significantly depleted. During 15 days of study, the gut microbiota recovered to resemble those of the healthy gut, and this occurred concurrently with gradual elevation of alpha diversity. Using a combination of statistical tests and machine learning approaches, we showed that *Acidaminococcus sp., Butyricicoccus pullicaecorum,* and *Bifidobacterium bifidum* exhibited negative associations with diarrheal duration in this patient group. This indicates that these species may act as potential probiotic candidates for accelerating diarrhea recovery rate and restoration of the healthy gut microbiota. Overall, this study enhances our understanding on the dynamic of the gut microbiota under the perturbation of infectious diarrhea.

Biography

TRAN Tuan-Anh is a graduate from the Erasmus Joint Master Program on Molecular Nano- and Biophotonics. He has conducted research for five years and published several scientific papers in bioinformatics. He is currently interested in applying machine learning to computational chemistry and biology.

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O-42

Genomics of *Cryptococcus neoformans*

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Oxford University Clinical Research Unit, Ho Chi Minh City, Vietnam

Abstract

C. neoformans var. *grubii* (*C. neoformans*) is an environmentally acquired pathogen causing 181 000 HIV-associated deaths each year. We used whole genome sequencing (WGS) to characterise 699 isolates, primarily *C. neoformans* from HIV-infected patients, from 5 countries in Asia and Africa. We found that 91% of our clinical isolates belonged to one of three highly clonal sub-clades of VNIa, which we have termed VNIa-4, VNIa-5 and VNIa-93. Parsimony analysis revealed frequent, long distance transmissions of *C. neoformans*; international transmissions took place on 13% of VNIa-4 branches, and intercontinental transmissions on 7% of VNIa-93 branches. The median length of within sub-clade internal branches was 3-6 SNPs, while terminal branches were 44.5-77.5 SNPs. The short median internal branches were partly driven by the large number (12-15% of internal branches) of polytomies in the within-sub-clade trees. To simultaneously explain our observation of no apparent molecular clock, short internal branches and frequent polytomies we hypothesise that *C. neoformans* VNIa spends much of its time in the environment in a quiescent state, while, when it is sampled, it has almost always undergone an extended period of growth. Infections with VNIa-93 were associated with a significantly reduced risk of death by 10 weeks compared with infections with VNIa-4 (Hazard Ratio = 0.45, p = 0.003). We detected a recombination in the mitochondrial sequence of VNIa-5, suggesting that mitochondria could be involved in the propensity of this sub-clade to infect HIV-uninfected patients. These data highlight the insight into the biology and epidemiology of pathogenic fungi which can be gained from WGS data.

Biography

Philip completed his BSc in Applied Biology at Cardiff University in 2008. He subsequently undertook a PhD at Public Health England on the genomics, proteomics and transcriptomics of *Clostridium botulinum*. He spent 2012-2016 working as a bioinformatician at Public Health England, focusing on the genomics of gastrointestinal bacterial pathogens, in particular *Salmonella*, but also VTEC O157 and *Shigella flexneri*. While there he was part of the team who implemented WGS for routine typing of *Salmonella*. From July 2016 to December 2017 he worked on the genomics of *Cryptococcus neoformans,* a fungal infection typically affecting those with HIV/AIDS at the Oxford University Clinical Research Unit (OUCRU) in Ho Chi Minh City. Since March 2018 he has been the Lead Bioinformatician at OUCRU, working on a variety of bacterial infections, with a focus on *Mycobacterium tuberculosis.* He has published more than 30 papers on infectious disease genomics, including in Nature Biotechnology, Lancet Infectious Diseases and Genome Medicine.

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O-43

Virulent factors and pan-genome analysis of the clinical multidrug-resistant *Acinetobacter baumannii* strains in a Vietnam Hospital

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[1]Department of Biotechnology, Faculty of Chemical Engineering, Ho Chi Minh City University of Technology, HCM National University.

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Abstract

Acinetobacter baumannii, an emerging infectious agent in humans, is a major cause of hospital-acquired infections worldwide due to its impressive propensity to rapidly acquire resistance elements to a wide range of antimicrobial agents. We sought to explore the genomic properties, phylogenetic relationships, and comparative genomics of this pathogen. For this purpose, *A. baumannii* strain DMS06670 was isolated from a sputum specimen obtained from a male patient with hospital-acquired pneumonia. Assembly of whole-genome shotgun sequences of strain DMS06669 and DMS06670 yielded an estimated genome size of 4.2Mb and 3.8 Mb. In this manner, the identification of potential antibiotic resistance genes was conducted, and we predicted that the probability of *A. baumannii* DMS06669 (our strain in previous study) and DMS06670 as a human pathogen is 85.8% and 85.3%, with 632 and 622 pathogenic families, respectively. Additionally, the clusters of orthologous groups (COGs) analysis in protein sequence of *A. baumannii* strain DMS06669 and DMS06670 was compared with the other four genomes showed that the orthologous protein clusters responsible for multi-drug exist inside highly antimicrobial resistant strains. Phylogenetic analysis revealed that, based on the average nucleotide identity value, *A. baumannii* DMS06670 is a sister group to the LAC-4 and BJAB0715 strains of *A. baumannii* while *A. baumannii* strain DMS06669 is a sister group to strains ATCC_17978, D1279779, ZW85-1, ab031, and SDF. Lastly, comparative analysis of twenty-three available genomes of *A. baumanii* strains revealed a pan-genome consisting of 15,883 genes. Our findings provide insight into the molecular mechanisms leading to antibiotic resistance in *A. baumannii*.

Keywords: Acinetobacter baumannii, pan-genome analysis, antibacterial agents, comparative whole-genome analysis

Biography

Si-Tuan has started working at Thongnhat Dongnai General Hospital from 2010. He has been the Head of Department of Clinical Microbiology - Thongnhat Dongnai General Hospital since 2014. He graduated with the master program in Molecular Biology of Microbiology from University Sud XI. After that, he graduated with a specialized in medical microbiology from the University of Medicine in Ho Chi Minh City in 2011. From 2013 to now, he is a PhD student specializing in microbiology at the National University of Ho Chi Minh City. He is currently a fourth-year medical student at the School of Medicine, Tan Tao University. Si-Tuan has published 7 scientific papers in specialized journals in Viet Nam and 2 scientific papers in ISI journals about *Acinetobacter baumannii*. He is the specialist in multidrug-resistant *Acinetobacter baumannii* field.

My research interests are centered on the clinical microbiology and molecular biology. I am generally interested in the antimicrobial resistance, pathogenesis and infection, bioinformatics and microbiome, nosocomial infectous diseases. More recently, I have become increasingly interested in bacterial genome. In particular, I focus on the evolution of drug resistance genes, the function of disease proteins, and the new drug resistance genes.

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POSTER

P-01

Characterization of E-type colicin produced by *Shigella* sp.

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Abstract

Shigellae are intracellular Gram-negative pathogens that cause a wide range of illnesses, from mild abdominal discomfort to death. The major cause could be the contamination of *Shigella* in fresh and processed food. The development of natural food preservatives with the use of bacteriocins produced by bacteria instead of chemical preservatives in food products has dramatically increased in recent years. The most extensively studied Gram-negative bacteriocins are colicins. There are only a few reports on the characterization of bacteriocin from *S. sonnei* and *S. flexneri* in Vietnam. The study aimed at determination of the colicin type of *S. sonnei* and *S. flexneri* strains isolated from Vietnamese patients with diarrhea and to characterize its properties. Detection and classification of colicin genes (colicin E1 to E9) were performed by PCR and confirmed by sequencing. Among 37 strains of *Shigella* isolated from Vietnamese patients, *S. flexneri* was the most prevalent species (78.4%), followed *by S. sonnei* (24.5%). Eleven *Shigella* strains epidemiologically related showed the colicinotype. Most frequently colicino genotype E5 were found (18.5%), E8 (16.2%), and E9 (5.40%). Colicinotype E5 was predominant in Nha Trang where E8 and E9 commonly found in Hue. Notably, E-type colicins (E5, E8, E9) were produced by majority of *S. sonnei.* By DNA sequencing, the PCR product obtained from bacteriocinogenic *S. sonnei* and *S. flexneri* showed 99% identity to complete sequence of E-type colicins. Our study has provided genetic characterization of colicinogenic genes from *Shigella* strains. It is to our knowledge; the first report of Vietnamese patients with diarrhea that *S. flexneri* and *S. sonnei* isolated from them contained different E-type colicins. The study information may provide with potential exists for application of bacteriocins as effective inhibitive agents against other important Gram-positive pathogens to enhance product safety by inserting genes from bacteriocins from Gram-negative bacteria into fermentative Gram-positive bacteria.

Biography

I am curently a reseacher at National Institute of Hygiene and Epidemiology and have been studied my microbiology doctorate in Vietnam Academy of Science and Technology. I received a Master of Science from Hanoi University of Science and Technology with a concentration in molecular epidemiology. I also completed my university degree in microbiology at Hanoi Open University. I have worked in bacteriology since the begining of my career and has recieve some awards for my work. I was awarded several extramural grants prior to working at NIHE, including Excellent achivement in preventative work of acute diarrhea in pandemic 2007 given by Ministry of Health and First prize in youth creative research technique organized by Ministry of Health.

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P-02

Anti-*Helicobacter pylori* Activity of Essential Oil from *Hyptis suaveolens* (L.) Poit

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[2]Thu Dau Mot University, Binh Duong

Abstract

The *Helicobacter pylori* infection is highly associated with a number of gastroduodenal diseases in humans. More than 70% of people in Vietnam were reported to have infection caused by *H. pylori*. Utilization of plant essential oils as a therapeutic alternative to conventional antibiotics is an appealing strategy for prevention and treatment of the infection. *Hyptis suaveolens* (L.) Poit has been used in folk Vietnamese medicine for treatment of abdominal pain. The present study assessed the antibacterial activity of *H. suaveolens* essential oil against *H. pylori* growth *in vitro* and inhibition of *H. pylori* colonization in mouse stomach. The results exhibited that the essential oil was highly active against the tested *H. pylori* ATCC 43504 strain with MIC value of 0.625 mg/ml, and resulted in a decrease in the numbers of bacteria (89.65%) colonizing in the stomach tissues of mice compared with those in mice without treatment.

Key words: antibacterial activity, essential oil, *Helicobacter pylori*, *Hyptis suaveolens*

Biography

He received Ph. Degree in Agricultural Biotechnology, Seoul National University, in February, 2013 under the supervision of Prof. Young-Joon Ahn. During PhD. student period, he carried out researches on repellence and toxicity of plant essential oils and their compounds against harmful insects. After graduating, he has been working as a lecturer at Faculty of Biology and Biotechnology, University of Science, Vietnam National University Ho Chi Minh City. His work currently focuses on antimicrobial and anti-insect activities of extracts and essential oils from plants in natural environment and tissue cultures.

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P-03

Regulation of gene expression in *E.coli* by interaction of RHAU peptide and G-quadruplex

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[3]Laboratory of Biophysic, PAP-SPMS, Nanyang Technological University, Singapore

Abstract

DNA and RNA G-quadruplexes are G-rich sequences which are four-stranded structures formed by stacking multiple G-tetrads (Figure 1). The formation of G-quadruplex structure involves in regulating many biological processes such as replication, transcription, translation and telomere elongation. Therefore, the existence of G-quadruplexes in the genome is considered to be a new molecular target for cancer therapeutics. Investigation and development of small molecules, proteins and peptides which can selectively recognize and bind different structures of G-quadruplexes at high affinity that can be applied as a valuable and versatile tool to study the G-quadruplex formation and regulation of gene expression in bacteria or living cells.

DNA and RNA G-quadruplexes are G-rich sequences which are four-stranded structures formed by stacking multiple G-tetrads (Figure 1). The formation of G-quadruplex structure involves in regulating many biological processes such as replication, transcription, translation and telomere elongation. Therefore, the existence of G-quadruplexes in the genome is considered to be a new molecular target for cancer therapeutics. Investigation and development of small molecules, proteins and peptides which can selectively recognize and bind different structures of G-quadruplexes at high affinity that can be applied as a valuable and versatile tool to study the G-quadruplex formation and regulation of gene expression in bacteria or living cells.

Biography

Dr. Dang Thanh Dung, has spent for 4 years as the position of Fellow Research at Nanyang Technological University, Singapore. He has experience in DNA and RNA G-quadruplex and biological functions of G-quadruplexes and proteins interaction. Before that, he has spent a period at Max Planck Institute, Germany, working on fluorescent protein engineering. In 2008-2012, He started as a Ph.D. student in chemical biology at Biomedical Engineering Department, Eindhoven University of Technology in Eindhoven, The Netherlands. The PhD's project focused on "Supramolecular induced protein dimerization", the main goal of this project was to use cucurbit[8]uril to reversibly control protein dimerization and activation. He has been the first author paper on the renowned international journals such as *Angewandte Chemie International Edition* (IF around 11.7) and *Chemical Science* **(IF around 9.1). Overall, he has experience in molecular biology, protein & DNA engineering, chemical biology and cell biology.**
Currently, Dr. Dang is a head of the research group in Chemical Biology at the Center for Bioscience and Biotechnology, University of Sciences, National University-HCMC, Vietnam **and a head of the research group at** Laboratory of Gene Technology & Applied Biotechnology, Faculty of Biotechnology, Ho Chi Minh City Open University, Vietnam.

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P-04

Clinical cases discussions of infectious diseases

S Gokhale

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Abstract

The infectious diseases are the most prevalent causes of morbidity and mortality. Prompt clinical diagnosis supported by laboratory investigations to establish etiology is imperative for proper management. A series of cases on infectious diseases will be presented. This interactive session will consists of clinical presentation, selection of investigations, reports and interpretation of investigations leading to diagnosis and treatment. The presentation will progress with the interaction, interjection and polling by the participants at all stages. This will provide opportunity for the participants to air their views, thoughts and experiences leading to enrichment. This activity over a period of about 60 minutes will enhance the clinical skills, selection and interpretation of laboratory investigations and treatment of patients. This presentation is aimed to benefit the clinicians, infectious diseases specialists, public health specialists, microbiologists, travel medicine specialists.

Biography

Dr Shishir Gokhale is Professor and Head, Department of Microbiology at the Manipal College of Medical Sciences, Pokhara, Nepal. He has over 3 decades of experience in diagnostic microbiology and infectious diseases, undergraduate and post graduate medical education. He has been invited speaker at numerous academic fora, has presented and published his research in numerous conferences and journals. He is The American Society for Microbiology's Country Ambassador for Nepal.

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P-05

Prevalence, antibiotic resistance and medical herbal susceptibility of *Salmonella* spp. from infected quail livestock

Doan, Thi Ngoc Thanh

Tien Giang University, Viet Nam

Abstract

This study was conducted to determine the prevalence, antibiotic resistance and medical herbal susceptibility pattern of *Salmonella* species from quail livestock with Salmonellosis symptoms in Tien Giang province using conventional biochemical tests, serology and Kirby-Bauer disk diffusion method. Of the 186 samples (quail, manure and eggs) examined, 61 were contaminated with *Salmonella* given a prevalence of 32.8%. The isolates were found in 48 out of 146 quail internal organ samples, in 11 out of 30 abnormal eggs and in 2 out of 10 manure samples. The serotype *S.*Gallinarum which is considered the main pathogen causing the disease was the highest prevalence (44.2%). The antibiotic resistance results showed that the isolates highly resisted against amoxicillin (83.6%), ampicillin (85.2%) and erythromycin (63.9%). In contrast, some antibiotics still have effect on *Salmonella* such as tetracyclin (3.3% isolates showed resistance), enrofloxacin (8.2%) and colistin (9.8%). Significantly, prevalence of isolates resisted three or more tested antibiotics was 72.1%. The results of testing antibiotic activity of essential oils from 4 medical herbs showed that most of isolates are susceptible to *Ocimum basilicum* oil (93.3% of the isolates showed inhibition zone diameters ≥ 20 mm) and to *Eucalyptus globulus* Labill oil (40.0%). This result is potential for adding some herbal oils as additives, replacing of antibiotic, into quail feed to prevent Salmonellosis.

Biography

Doan, Thi Ngọc Thanh has completed her PhD at the age of 31 years from Konkuk University in Biotechnology. She is the vice dean of Agriculture and Food Technology Falculty, Tien Giang University. She is working on plant and animal pathogen, applied microbiology, gene manipulation and protein application.

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P-06

Assessing the feasibility of using *Bacillus subtilis* as a vaccine display system for Betanodavirus in European sea bass

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Center for Bioscience and Biotechnology, University of Science, Vietnam National University, Ho Chi Minh City, 70000, Vietnam

Abstract

Over the past three decades, Betanodavirus, the causative agent of viral encephalopathy and retinopathy (VER) disease, has become a serious problem in marine finfish aquaculture, particularly European sea bass (*Dicentrarchus labrax*) in the Mediterranean. The most sensible way of controlling this disease is to apply effective biosecurity and to vaccinate the fish. The use of *Bacillus subtilis* as a vehicle for antigen delivery is a relatively new approach in human vaccinology and has been shown to have a significant adjuvant effect when used to display model antigens such as H5N1, tetanus toxin, ovalbumin (OVA) or HIV gagp24. A great deal is already known about the genetics of the bacterium, and it is relatively straightforward to genetically manipulate the bacterium and integrate stable constructs into its chromosome. Foreign antigens have been expressed on the surface of *B. subtilis,* both as vegetative cells and spores, and both have been used as delivery vectors for vaccines with antigens displayed on their surface. A *B. subtilis* display system was used here to anchor the full coat protein (CP) of betanodavirus genotype RGNNV onto the surface of vegetative *B. subtilis* cells. We have confirmed that the proteins were correctly displayed on the surface of the bacterium using ELISA, western blotting, confocal microscopy and proteomic analysis of the bacterial ShaveOME, a technique that analyses the proteins displayed on the surface of the bacterium. The latter showed significant coverage of many bacterial surface proteins together with the CP peptides of Betanodavirus, and strong staining of the bacterium was obtained with monoclonal and polyclonal antibodies against the virus by confocal microscopy; both techniques confirmed the display of the Betanodavirus CP on the surface of the *B. subtilis*. Vaccination trials are currently being undertaken in which European seabass have been vaccinated with the inactivated *B. subtilis* and efficacy is being examined by experimental infection.

Biography

Truong Thi Tinh Tuom is a researcher at Center for Bioscience and Biotechnology. She is also a PhD student at University of Science, Vietnam National University, Ho Chi Minh City since 2016. Her major is a Microbiology and she has experience in expression and purification of protein, isolate bacteria from nature and antibiotic sensitivity test for bacteria.

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P-07

Phage therapy against bacterial pathogens of striped catfish in the Mekong Delta, Vietnam

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Abstract

Striped catfish (*Pangasianodon hypophthalmus*) farming in the Mekong Delta Vietnam (MKDVN) importantly contributes to national aquaculture export. Currently, the most common diseases are hemorrhagic septicemia caused by *Aeromonas hydrophila* and white spots in the internal organs caused by *Edwardsiella ictaluri*. Inadequate control due to antibiotics resistance of these pathogenic bacteria has led to the output reduction, export loss, community health and environment risks. In this study, phage therapy was initially investigated its possibility to treat the bacteria *in vitro*. Main methods are micriobiological method and phage assay. Seven phages specific to *A. hydrophila* with short latent period (about 25 to 45 minutes) and/or high burst size (about 31 to 94) were isolated and selected. Three phages specific to *Edw. ictaluri* with short latent period of 55 minutes and high burst size of about 90 – 120 were isolated and selected. Inactivation of the bacteria by single phage was evaluated. Some phages attaching different bacterial receptors were then subjected to phage cocktails to control the bacteria. Strategies in the phage cocktails to control *A. hydrophila* and *Edw. ictaluri* were shown to apply in the prospective control of these bacteria *in vivo*.

Biography

Hoang Anh Hoang obtained his PhD in Biological and Environmental Engineering from Tokyo Institute of Technology (Japan) in 2014. He has worked at Department of Biotechnology, Ho Chi Minh City University of Technology (HCMUT) since 2014. His research group focuses on science and engineering of phages and solid organic waste treatment. The group now has collaboration with scientists in Vietnam, Japan, UK, etc. to investigate and apply proper solutions for food safety and environment in Vietnam. He has been a PI of seven research projects funded by various national and international agents.

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P-08

Studies of common antibiotic resistance-associated genes of *Acinetobacter baumannii*

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Abstract

Pneumonia is a serious infectious disease that affects people of all ages, especially, in children under 5, it is one of most common leading causes of death. In many cases, pathogenic agents are bacteria, thus, the patients can be cured by using suitable antibiotics. However, antibiotic resistance is promptly increasing, posing great challenges for treatments. In 2017, the World Health Organization (WHO) announced the list of the twelve most dangerous bacteria, ranking *Acinetobacter baumannii,* a pathogen causing pneumonia*,* at the first place. In Vietnam, infections by multi antibiotic resistance strains of *A. Baumannii* is alarming. It is important to note that, timely identification of resistance-associated genes could assist in prediction of prescribed drug efficacy, hence improve treatment outcomes. In this study, the presence of 4 beta-lactamase encoding genes including OXA-23, OXA-51, VIM, and IMP was determined simultaneously by multiplex PCR, either directly with sputum samples or with purified DNA, giving results within 3-4 hours instead of 2 days compared to the culture method. Within 58 samples positive with *A. baumannii* collected from the hospital, OXA-51 fragment was dominant (81%), whereas, VIM fragment was only identified in one sample (DNA and sputum samples) (1,7%). The antibiograms indicated for 19 samples were used to find correlation between genotype and resistance phenotype. For further studies, beta-lactam gene fragments will be analyzed to find correlations between nucleotide sequences and antibiotic resistance to investigate resistance mechanism.

Biography

Mr. Ta passed the entrance university exam with the score 24/30, and became a student of Biology Faculty of Ha Noi University of Science. He started laboratory practice as a member in a research group from the Faculty of Environmental Sciences that collected air samples in the hospital and determined pneumonia pathogens's presence using microbiological and molecular biology methods. In late 2017, he joined the project to study antibiotic resistance in Acinetobacter baumannii led by Dr. Yen Pham in VNU Key Laboratory of Enzyme and Protein Technology, collaborating with National Lung Hospital. He has been examining resistance-associated genes using PCR/sequencing and preparing data for manuscript writing.

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P-09

E-BABE- Prevalence and antibiotic resistance pattern of Vibrio spp. isolated from aquaculture and environment in Tien Giang province

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Abstract

This study is to survey the prevalence and antibiotic resistance pattern of *Vibrio* spp. isolated from the aquaculture and its environment in Tien Giang, Viet Nam. 501 samples including 311 water and 190 aquaculture samples were collected and analyzed. The results showed 161 water and 82 aquaculture samples infected with 8 Vibrio species in which *V. parahaemolyticus*, *V. mimicus*, *V. alginolyticus* were abundant. There were 96,7% of Vibrio strains resisting to at least one antibiotic, 18,1% of the strains expressing multiple antibiotic resistance. In particular, one *V. parahaemolyticus* strain resisted to 6 kinds of examined drugs (Imipenem, Cefotaxim, Cefepime, Ceftazidime, Amikacin và Ampicillin).

Biography

He was head of Micro lab., director of branch of Sac Ky Hai Dang company and then become Eurofins Sac Ky Hai Dang Co., Lt, from 2010 to 2017. He has completed his Master degree at VNUHCM – University of Science, Viet Nam in 2015. From 2017, he is vice director of Viet Tin Analysis Testing Company Limited.

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P-10

Effect of Vietnam *Helicobacter pylori* clinical strains on activity of NF-kB pathway

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Abstract

Helicobacter pylori (H. pylori), a Gram-negative bacterium, colonizes in the gastric mucosa of at least half of the world's population. Chronic *H. pylori* infection might lead to gastritis, peptic ulceration, gastric cancer (GC). Recent studies have reported that *H. pylori* infection activates NF-κB pathway in infected gastric epithelial cells and significantly increases the risk of developing gastric ulcer disease and GC. NF-κB pathway has been demonstrated to play a key role in regulating the immune response to infection and dysregulation of NF-κB has been linked to cancer. Additionally, it is shown that the impact of *H. pylori* on infected cells is associated with bacterial virulence that is diverse among geographical regions as well as populations. Therefore, we aimed to investigate the effect of *H. pylori* strains from Vietnamese subjects on the activity of NF-κB transcription factor and expression of its target genes in this study. Our results might contribute to the understanding of the virulence of Vietnam *H. pylori* strains in inflammation-induced carcinogenesis.

Biography

Pham Thi Hong Dao was born in Dong Nai, Vietnam in 1993. She received the B.Sc., and M.Sc. degrees from University of Science, Vietnam National University Ho Chi Minh City, in 2015, and 2018. Since then, she has been researcher in Department of Genetics, University of Science. Her main area of research interest is association between *Helicobacter pylori* infection and gastric cancer, especially inflammation and genetic stability.

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P-11

Adeno-associated virus capsid protein expression in *Escherichia coli* and assembly *in vitro*

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Abstract

The use of recombinant adeno-associated virus (rAAV) for research and clinical applications has significantly increased in recent years with approvals of rAAV gene therapy products by the European Medicines Agency and FDA. However, current methods to produce rAAV utilize cultured mammalian or insect cells are costly, time-consuming and laborious. Here, we introduce a cost and time saving strategy that bases on *in vitro* production. Viral proteins were expressed in *Escherichia coli* which is known as a robust cell factory for heterologous protein production. An assembly protocol was successfully established *in vitro* to generate virus-like particles (VLPs) that contain only VP3 proteins. Hybrid VLPs composing VP1 and VP3 were also formed. These results open a toolbox for using AAV VLPs not only as a carrier in gene therapy but also as a display scaffold for immunization.

Biography

DINH TO LE is a PhD student at Department of Cellular and Molecular Biotechnology, Faculty of Technology, Bielefeld University, Germany. He was a teaching assistant and researcher at Department of Molecular and Enviromental Biotechnology, Faculty of Biology and Biotechnology, University of Science Ho Chi Minh City, Vietnam. He received his MSc in Microbiology from University of Science Ho Chi Minh City, Vietnam.

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P-12

Immunogenicity evaluating of a B-cell Epitope predicted from influenza virus A/H5N1 NA antigen

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[1]*Pasteur institute Ho Chi Minh city*
[2]*University of Science, VNU-HCM*

Abstract

Previously, using bioinformatic tools, we have succesfully predicted conserved B cell epitopes NaBc, a peptide of 21 aminoacids on conserved domains of NA antigen from H5N1 influenza A virus. To increase the immunogenicity of this B cell epitope, protein molecule containing three sequences of epitope has been synthetized as the recombinant using genetic manipulating techniques with Escherichia coli as host cell. The immunogenicity of the recombinant protein (GST-(NaBc)3) was examined by immunization in mice. Using neuraminidase inhibition (NAI) method, the results show that recombinant protein GST-(NaBc)3 antisera at dilution ¼ could inhibit 25% of the NA enzymatic activity of influenza virus A/Vietnam/CD293/2013(H1N1). While the trade vaccine antisera could inhibit 31,44% of the NA enzymatic activity of influenza virus A/Vietnam/CD293/2013(H1N1) at the same dilution).

Biography

Tran Thi Hong Kim has completed her PhD at the age of 34 years from VNUHCM University of Science, Viet Nam. She had been a lecturer for 9 years at University of Science VNUHCM. From 2015 up to now, she work as a researcher in Respiratory Viruses Laboratory/National Influenza Centre (NIC), Microbiology and Immunology Department in Pasteur Institute Ho Chi Minh City, Vietnam.

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P-13

Rapid detection of streptomycin in milk by DNA aptamer-gold nanoparticle

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[1] NTT Hitech Institute, Nguyen Tat Thanh University
[2] Institute of Tropical Biology, Vietnam Academy of Science and Technology

Abstract

Streptomycin is one of common antibiotics belongto aminoglycoside group that are widely used for treatment of gram-negative infectious diseases in fodder animals. However, incorrect and uncontrolled application of streptomycin could result in the presence of residues of this drug in foodstuffs and causes serious side effects on human. Therefore, it is very important to develop a rapid, simple and specific method to detect streptomycin in food products. In this study, a rapid method based on a streptomycin-specific aptamer and gold nanoparticle was developed for detection of streptomycin. In the presence of streptomycin, the competitive binding of the target and the DNA aptamer decreases the stability of gold nanoparticle in NaCl solution, triggers the aggregation, and exhibits visible color change of gold nanoparticle solution. This change can be seen by naked eye or UV-vis. Through UV-vis spectroscopic quantitative analysis, streptomycin can be detected at the concentration of 250 nM .The presence of other aminoglycoside antibiotics shows neglectable disturbance. The results indicated the selected aptamer and method are specific to streptomycin and rapid detection of the target can be achieved both in the standard solution and in milk sample. This results showed the established method may have enormous potential utility for practical streptomycin in food products in the future.

Keywords: aptamer, detection, streptomycin, gold nanoparticle.

Biography

Nguyen Hoang Dung has completed his PhD at the age of 30 years from Inha University. He is Deputy director of Microbiogy Department, Institute of tropical biology, VAST. He has published more than 25 papers in reputed journals. Dr. Dung are now working in screening and isolation of bioactive compounds for natural resources (plants, microorganism) for cosmetic applications. He has much experience of animal cell culture, fermentation and bioactive compounds isolation by chromatography (HPLC, GC), spectroscopic (LC-MC, NMR and FT-IR) methods.

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P-14

Screening of the bioactivities of artificially-cultivated *Cordyceps pseudomilitaris* DL0015 in Vietnam

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Abstract

Cordyceps pseudomilitaris DL0015 is known as an entomopathogenic fungus with many precious bioactivities. In Viet Nam, this fungus have been discoveried naturally in the Langbiang mountain, Hoang Lien and Muong Phang national parks. In this study, we obtained one ethanol extract (EtOH) by ethanol extraction and four fractional extracts including petroleum ether (PE), ethyl acetate (EA), butanol (BuOH), and water (W) by liquid-liquid extraction. In addition, intracellular polysaccharide (IPS), and exo polysaccharide (EPS) crudes were also extracted from the post-extracted biomass residue and the cultured broth, respectively. *In vitro* bioactivities of 7 extracts were then assessed by using antibacterial, antifungal and anti-inflammatory assays. The results showed that the EA extract inhibited against the growth of *Escherichia coli, Pseudomonas aeruginosa, Salmonella typhimurium, Enterococcus faecalis, Staphylococcus aureus,* and Methicillin-resistant *Staphylococcus aureus*-MRSA at 200 mg/mL. Interestingly, its inhibition of gram-positive bacteria was better than gram-negative bacteria. Meanwhile, the EtOH, PE and BuOH extracts strongly exhibited anti-inflammatory capacity through inhibiting albumin denaturation with IC_{50} values of 129,27 µg/mL, 90,76 µg/mL and 99 µg/mL, respectively. In contrast, most of these extracts did not inhibit the growth of eight pathogenic fungi like *Candida albicans*, *Microsporum gypseum*, *Trichophyton rubrum*, *Trichophyton mentagrophytes*, *Aspergillus niger*, *Aspergilus fumigatus*, *Penicillium* sp., and *Fusarium* sp. To sum up, we suggest that the artificially-cultivated *C. pseudomilitaris* DL0015 should be used as a future potential medicinal fungus in Vietnam.

Keywords: Cordyceps pseudomilitaris, antibacterial activity, antifungal activity, anti-inflammatory activity

Biography

My name's Xuyen. I graduated in Biology Pedagogy at Can Tho University in 1996 and received Master degree in Microbiology at University of Science - VNU-HCM in 2006. Now, I am a PhD student in Microbiology at University of Science - VNU-HCM.
I have been being a lecturer at Van Lang University for more 15 years . From 2008 to present, I have been the author and co-author of several papers published in prestigious academic journals. At present, my special research is on Cordyceps fungi including studies on biological characteristics, active substances, biological activity, etc.

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P-15

Development of an Antigen Diagnostic Kit for Yellow Fever Virus Detection Using Monoclonal Antibodies against Non-Structural Protein

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Abstract

The early diagnosis of Yellow Fever virus (YFV) infection is important for successful clinical management and epidemiological control. The non-structural protein 1 (NS1) of flavivirus, a highly conserved and secreted glycoprotein, is abundant in the serum of flavivirus-infected patients and is a useful early diagnostic marker. We developed a highly accurate YFV NS1 rapid test using two mouse monoclonal antibodies (MAbs) that recognize distinct epitopes of the NS1 protein of YFV as capture and detection antibodies. The YFV NS1 rapid test displayed exclusive specificity to YFV without cross-reaction with other flaviviruses such as DENV and ZIKV as well as with alphaviruses such as CHIKV and MAYV. Additionally, the high specificity was indicated in no false positive in normal (0/150) and DENV-infected (0/10) serum specimens. The detection limit of the test was as low as 0.1^6 X 10^1 plaque-forming units (PFU)/ml of YFV-infected culture supernatant. In monkey infected with YFV, the NS1 protein was readily detected in tissue samples. The sensitivity of the YFV NS1 rapid test was significantly higher than that of commercialized antibody pairs in tissue samples from YFV-infected monkeys. This newly developed YFV NS1 test with high sensitivity and specificity could be used as an efficient method for the early diagnosis of YFV infection in animals or humans.

Biography

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P-16

Primary study on bacteriocin synthesized from the strain *Lactobacillus plantarum* UL485 isolated from Chao of Hue province in Vietnam

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Abstract

The early diagnosis of Yellow Fever virus (YFV) infection is important for successful clinical management and epidemiological control. The non-structural protein 1 (NS1) of flavivirus, a highly conserved and secreted glycoprotein, is abundant in the serum of flavivirus-infected patients and is a useful early diagnostic marker. We developed a highly accurate YFV NS1 rapid test using two mouse monoclonal antibodies (MAbs) that recognize distinct epitopes of the NS1 protein of YFV as capture and detection antibodies. The YFV NS1 rapid test displayed exclusive specificity to YFV without cross-reaction with other flaviviruses such as DENV and ZIKV as well as with alphaviruses such as CHIKV and MAYV. Additionally, the high specificity was indicated in no false positive in normal (0/150) and DENV-infected (0/10) serum specimens. The detection limit of the test was as low as 0.1^6 X 10^1 plaque-forming units (PFU)/ml of YFV-infected culture supernatant. In monkey infected with YFV, the NS1 protein was readily detected in tissue samples. The sensitivity of the YFV NS1 rapid test was significantly higher than that of commercialized antibody pairs in tissue samples from YFV-infected monkeys. This newly developed YFV NS1 test with high sensitivity and specificity could be used as an efficient method for the early diagnosis of YFV infection in animals or humans.

Biography

After finishing my Ph.D at the Royal Holloway College of University of London with the thesis titled “The Use of Bacterial Spores as Mucosal Vaccines”, I returned to the Laboratory of Enzyme-Protein, Institute of Microbiology and and Biotechnology atVNU in Hanoi. Since then I have been continuing my research as a senior researcher in microbiology, biochemistry and molecular biology. I have published more than 30 papers, 10 of which are in international journals, and the rest are in Vietnam’s specialized journals of biology.

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P-17

Myosin class V proteins play important roles in dimorphism of the human pathogenic fungus *Mucor circinelloides*

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[2] *Hanoi National University of Education, 136 Xuan Thuy, Cau Giay, Hanoi*

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Abstract

Mucormycosis has emerged as a second most common filamentous fungal infection in human caused by species belonging to order Mucorales, especially in immunocompromised patients, with a high mortality ratio. Our understanding of its virulence determinants is limited, leading to the lacking of efficient therapies. Dimorphism is one of the phenotypic characteristics that can be used as a marker for virulence screening. *Mucor circinelloides*, a dimorphic fungus, has become an attractive model for studies on carotenogenesis, RNAi mechanism and mucormycosis. Our previous study identified Mcmyo5 protein belonging to Myosin class V which plays an important role in *Mucor* pathogenesis. We found three proteins with high similarities of amino acid sequences compared to Mcmyo5, suggested that they could be putative Myosin class V members in the *Mucor* genome. In this report, using RNAi plasmids to silence the target genes, we demonstrated the involvement of these genes in the morphogenesis of the fungus *M. circinelloides*. The silenced strains affecting the candidate genes exhibit strong reduction of growth rate, vegetative sporulation compared to the controlled strain. In addition, the mycelia of those silenced strains present the yeast-like grow, instead of normal filamentous hyphae, suggesting the virulence of those strains also were significant reduced.

Biography

Trung Trieu is a postdoctoral research fellow in the Prof. Tamas Dalmay's lab at the School of Biological Sciences, University of East Anglia, United Kingdom. He is interested in RNA biology in fungi and human. More specifically, his work focused on the RNAi mechanism, functional genomics, and mucormycosis in filamentous fungus *Mucor circinelloides*. In addition, he has worked on biological functions of the Y RNA-derived small RNA in human cancerous and non-cancerous cells.

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P-18

Antimicrobial Resistance Of *Salmonella enterica* recovered from native *Ayam Kampung* Chickens (*Gallus Domesticus*) and other environmental sources in Selangor, Peninsular Malaysia

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Abstract

In recent years, the emergence of antimicrobial resistance among *Salmonella* strains has become a major public health threat worldwide. Many studies exploring the prevalence and antimicrobial resistance of *Salmonella* from poultry and poultry related products have been described. In Malaysia, several large foodborne disease outbreaks involving human fatalities has been linked to eating chickens contaminated with *Salmonella*. The current study was designed to investigate the antibiogram profiles of *Salmonella* among local chicken flocks in Selangor, Peninsular Malaysia. From November 2016 to February 2018, a total of nineteen village chicken flocks were visited in Selangor. From these flocks, a total of 598 samples were collected comprising cloacal swabs (*n=403*), eggs (*n=36*), pooled poultry drinking water samples (*n=95*), pooled poultry feeds (*n= 32*) and pooled flies samples (*n=32*). A total of 30 isolates were recovered from these samples comprising cloacal swabs (*n = 12*), feed (*n=5*), flies (*n=5*) and water (*n=8*). The estimated prevalence at individual bird level is 2.98% (12/403, 95% CI: 1.7 - 5.1). However, all the eggs (inner content and shell surface) screened were negative for the organism. The detection rates of the organism were 8.4% (8/95), 15.6% (5/32) and 15.6% (5/32) for pooled poultry water, feed and flies respectively. The antibiotic resistance profiles of the isolates demonstrated varying level of resistance against tetracycline, nalidixic acid, ampicillin and chloramphenicol. Whereas, all the isolates tested were susceptible to gentamicin, norfloxacin, cefotaxime and ciprofloxacin. Of the 30 isolates, 20 (66.7%) demonstrated resistance to one or more antimicrobial agent. Out of the 20, 10 (50%) were multidrug resistant (MDR) to two or more antimicrobial agents. The results of this study highlighted the presence and perpetuation of *Salmonella* among Ayam kampung in the study area albeit at a lower detection as compared to that reported for commercial chickens.

Biography

Saleh Mohammed Jajere, DVM (Nigeria) PgDipLSHTM (LHSTM) MSc (RVC, London) has completed his doctor of veterinary medicine (DVM) from university of Maiduguri, Nigeria (2002 to 2008) and has graduated with distinctions in ten courses. He then secured a one-year commonwealth shared scholarship to study MSc degree in veterinary epidemiology in Royal veterinary college, university of London from 2010 to 2011. He currently works with university of Maiduguri, Nigeria and he his in third year of PhD research degree in veterinary epidemiology, Fakulti Veterinar, Universiti Putra Malaysia. He is working on the prevalence, associated risk factors, antimicrobial resistance and molecular characterization by multilocus sequence typing (MLST) of Salmonella enterica from local chickens in the central and southern Peninsular Malaysia. He has published more than 20 papers with few published in reputable journals and has been reviewing manuscript from other authors in some reputable journals.

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Antibiotic resistance of *Staphylococci* and *Pseudomonas aeruginosa* isolates from patients with a corneal ulcer at the Eye Hopital Ho Chi Minh City, 2015

Phan Thi Phuong Trang, Nguyen Thi Kim Khanh, Truong Thi Tinh Tuom, Huynh Thi Kim Phuong, Nguyen Duc Hoang

University of Science, Vietnam National University, Ho Chi Minh City, 70000, Vietnam

Abstract

Staphylococci and *Pseudomonas aeruginosa* are 2 bacteria that cause corneal ulcers and have high rates of antibiotic resistance. In this study, we collected 2228 specimens from patients who diagnosed the corneal ulcer at the HCMC Eye Hospital from 1/2015 to 9/2015. These samples were rapidly tested to assessment of pathogenic bacteria or fungi. The next, the bacteria samples were enriched in the BHI medium. Isolated and evaluated of antibiotic resistance of infectious specimens with two bacterial strains. In the 890 samples which contained bacteria, had 621 (70%) samples of Staphylococci and 119 (13%) samples of *P. aeruginosa*. Staphylococci were multi-resistance up to 47% while *P. aeruginosa* was 32%. Staphylococci resisted to common antibiotics such as Cefotaxime, Cefoxitin, Azithromycin and *P. aeruginosa* resisted to Amoxicillin, Cefotaxime, Imipenem. Specially, 7% of Staphylococci were resisted to 6 antibiotics out of a total of 7 tested antibiotics and 6 samples secret ESBL (broad-spectrum beta-lactamase antibiotic). Bacteria which secret ESBL will become to bacteria with a wide range of antibiotics, including prophylactic antibiotics (cephalosporin). The results of this study will provide the resistant bacterial knowledge for doctor to select the appropriate antibiotics for the treatment of corneal ulcers.

Biography

Huynh Thi Kim Phuong has completed her Master last year. Her subject is a Microbiology. She is working as researcher at Center for Bioscience and Biotechnology, University of Science, Vietnam National University, Ho Chi Minh City. She has been working here for over 4 years with the following cloning, development of vector expression for *Bacillus subtilis,* identify bacteria and fungi by 16S RNA ribosome.

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P-20

Identifying the constraints and/or opportunities in a One Health surveillance system for antibiotic resistance in Vietnam

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Abstract

Antibiotic resistance (ABR) is a global concern requiring international and inter-sectoral collaboration to tackle the threat to the health of our human and animal populations and the environment [1]. The One Health approach principles recognises the interconnectedness of the health of people to the health of the environment and animals [2]. Antibiotics are used widely across the human, animal, environment domains and each are considered to contribute to the emergence of antimicrobial resistance [3].

A One Health Surveillance System for ABR has been strongly advocated for by the international community [4]. The Vietnamese government recognised the multifaceted risk ABR poses to public health and the country's sustainable development. In 2013, the inter-ministerial strategy to combat ABR, developed by the government, includes prioritising a surveillance system for ABR and targets food-producing animals, retailed food, community and hospital settings [5]. However, the implementation of policies requiring inter-sectoral collaboration can be challenging [6].

Using a One Health approach, this project aims to: (1) assess the technical and logistical capacity of the surveillance system to respond to antibiotic resistance found within the pork value chain in Vietnam; (2) identify potential intervention options for strengthening cross-sectoral surveillance for antibiotic resistance.

Using a qualitative research methodology, the author will conduct semi-structured interviews with key informants working within the animal and public health sectors to qualitatively study and understand the capacity of the surveillance system to respond within a One Health framework in Vietnam.

The information obtained will be compared to a retrospective analysis of reported investigations of *non-typhoidal Salmonella* foodborne infection outbreaks in Vietnam since 2013. This analysis aims to establish any implementation gaps in a One Health ABR surveillance system in Vietnam and identify potential intervention options.

Biography

Marisa Mitchell is currently completing a Master of Health Security (Agrosecurity) at The University of Sydney. She has completed a Bachelor of Science (Health Science) with Curtin University, Certificate IV Marketing and Certificate IV Public Relations with North Sydney Tafe. She has worked within the public health sector in health promotion, public policy and communications, contributing to Australian not-for-profits organisations and International non-government organisations.

As part of a Health Security Internship, Marisa completed a joint internship with the Food and Agriculture Organization of the United Nations and the Charles Perkins Centre, The University of Sydney where her research project focused on the One Health Approach to Antimicrobial resistance. Marisa is working with the International Livestock Research Institute as a research assistant under the Australian Volunteer Program, funded by the Australian Government.

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P-21

Development of immunochromatographic lateral flow strip tests for rapid detection of *Escherichia coli* O157

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[2]National Institute of Hygiene and Epidemiology, Hanoi
[3]Hung Yen University of Technology and Education

Abstract

Escherichia coli (*E. coli*) is commonly found in the lower intestinet of humans and warm-blooded animals. It is a major cause of diarrhea in children, accounting for 20 to 40% of the causes of diarrhea. *E. coli O157* is one of its serotypes, and a main foodborne pathogen causing severe disease in humans worldwide. Recently, shiga toxin-producing *E.coli O157* are also significant threats to public health. Hence, the development of quick tests for detection of *E.coli O157* has become crucial for timely treatment as well as prevention of potential oubreaks caused by this bacterium. This study aimed to develop immunochromatographic lateral flow strip tests for rapid detection of *E. coli O157* bacteria. The conjugate of gold nanoparticles – anti *E.coli* O157 antibodies was optimized, and tested in conjunction with the immunochromographic assay. The optimal conditions of antibody-gold nanoparticles conjugation were found with the antibody concentration of 0.5 µg/mL, pH 7.0, and 90 min in incubation at 37°C. Furthermore, the limit of dection of the strips for *E.coli* O157 was found at 10^2 cfu/mL. Primary results showed that the immunochromatographic lateral flow strip tests were successfully developed for rapid detection of *E.coli* O157 with a high sensitivity and selectivity.

Keywords: lateral flow strip, *E. coli* 157, immunochromographic assay, rapid test

Acknowledgements: This research was supported by the bilateral project between Italy and Vietnam, coded NĐT.05.ITA/15.

Biography

Huy received a PhD at Hanoi University of Science and Technology (HUST), Vietnam, in 2012. Currently, he is a senior researcher of the Center for Bio-medical Research, National Institute of Hygiene and Epidemiology (NIHE), Hanoi; an expert of electron microscopy; and responsible for the Nanobiomedicine Group. He also takes a role as Vice-Editor in Chief of the Vietnam Journal of Preventive Medicine (Vietnam Association of Preventive Medicine); part-time lecturer of several universities. He is a co-founder of Nano Energy & Nano-Biomedical Research Group (NEB Group, http://neb-researchgroup.vn), member of Vietnam Young Academy - VYA{http://vietnamyoungacademy.org} (chair for the term of 2017). In 2017, he was selected as a member of Global Young Academy - GYA {https://globalyoungacademy.net}. He has more than 60 articles published in peer-reviewed journals, editor of one book, and co-author of 6 chapters. His current research interests are bionanomaterials, biosensors/biochips, biological ultrastructures, and technology solutions for environmental treatments.

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Development of a set of PCR-based techniques for detecting pathogens causing bacterial meningitis

Assoc. Prof. Dr. Ngo Viet Quynh Tram, MD

Hue University of Medicine and Pharmacy, Vietnam

Abstract

Bacterial meningitis is an acute central nervous infection with high mortality or permanent neurological sequelae if remained undiagnosis. However, traditional diagnostic methods for bacterial meningitis pose challenge in prompt and precise identification of causative agents. The present study aims to set up in-house PCR assays for diagnosis of six pathogens causing the disease including *H. influenzae type b, S. pneumoniae, N. meningitidis, S. suis serotype 2, E. coli* and *S. aureus.* The in-house PCR assays for detecting six above-mentioned bacteria were optimized after specific pairs of primers and probes collected from the reliable literature resources and then were performed for 116 cerebrospinal fluid (CSF) samples from patients with suspected meningitis in Hue Hospitals, Vietnam. As a result, for detecting six mentioned above bacteria, we created a multiplex real-time PCR for *S. suis serotype 2, H. influenzae* type b and *N. meningitidis,* three monoplex real-time PCRs for *E. coli, S. aureus* and *S. pneumoniae.* Application of the in-house PCRs for 116 CSF samples, the results indicated that 48 (39.7%) cases were positive with *S. suis serotype 2* while 41 (35.3%) cases were identified by culture; one case was positive with *H. influenzae* type b whereas no case was detected by culture; 4 cases were positive with *E. coli* versus 2 cases were identified by culture; pneumococcal meningitis were 19 (16.4%) cases, an increase of two-fold compared to culture result. Meningitis with *S. aureus* and *N. meningitidis* were not observed in any CSF samples in this study. In conclusion, this study was developed a set of real-time PCR assays for the sensitive and specific detecting of six mentioned above meningitis etiological agents, a rapid tool for routine diagnosis of bacterial meningitis.

Biography

Dr. Ngo Viet Quynh Tram is a Medical Doctor, a Senior Research Scientist and an Associate Professor in Department of Microbiology and the Institute of Biomedical Research and Biotechnology belong at Hue University of Medicine and Pharmacy, Vietnam. Her researchs focus on tradional and molecular techniques for detecting bacteria/virus causing infected diseases as well as the characteristics of drug resistance and resistant encoding genes of bacteria strains isolated from the patients. The results may enable to detect and treat infectious diseases more effectively and more quickly. Another aspect of her work is the characteristic of molecular epidemiology of *M. tuberculosis*, *A. baumanni, S. suis* and *Enterovirus* A71 to understand outbreaks of these infectious diseases in Central Vietnam. She completed her M.D. at Hue University of Medicine and Pharmacy and Ph.D. at Sassari University, Italy in Molecular and Clinical Microbiology. She has published 50 articals in national journals and 7 articals in internal journals.

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P-23

Marine-Derived Fungi with Antimicrobial and Anti Cancer Activities Isolated from West Sumatran Marine Sponge *Haliclona fascigera*

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Abstract

Marine sponges are well known to be the host for a large community of microorganisms, which comprise a significant percentage (up to 50-60%) of the biomass of the sponge host. The role of these diverse microbes in sponge biology varies from source of nutrition to mutualistic symbiosis with the sponge. Symbiotic marine microorganism in sponge was assumed to be the original producers of the potential of biologically active metabolite and structurally unique compounds. This research is focused on the discovery, isolation and structure determination of biologically active natural products from marine sponge-derived fungi. The Antimicrobial and cytotoxicity bioactivities of isolated fungi were determined using Agar diffusion method against some pathogenic microbial and MTT assay, respectively. In this study, we have isolated 25 fungi from marine sponge *H. fascigera*. There were 8 isolates of the fungi that considered active to Staphylococcus aureus and 1 isolate active to Candida albicans. In Brine Shrimps Lethality Test result, all fungal extracts were cytotoxic because of their LC50 < 1000 ppm, and ranging from 1 to 335 ppm. While sixteen extracts (80%) were toxic (LC50 < 100 ppm) and further tested its cytotoxic activity against HeLa, Widr, T47D and Vero cell lines. This study concluded that marine-derived fungi of marine sponge *H. fascigera* can be developed as a new source of antibiotic and anticancer compounds.

Biography

Dian Handayani has completed her PhD at the age of 30 years from Wuerzburg University, Gemany in 1998. She is a lecturer of Pharmacy Department, Faculty of Pharmacy, Andalas University, Padang West Sumatera, Indonesia. She has published more than 15 papers in reputed journals. Her researchs focuses on bioactiv compounds from marine invertebrates and currently she is researching microorganisms derived from marine invertebrates and mangroves, such as fungi and bacteria. One of her targeted finding is the discovery of new antibiotics and anticancer compounds that are produced by various marine invertebrates derived fungi from West Sumatera, Indonesia.

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P-24

Evolutionary phylodynamics of porcine epidemic diarrhea viruses (PEDVs) circulating in Vietnam

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Abstract

Porcine Epidemic Diarrhea (PED) is a highly contagious swine disease caused by PED virus (PEDV), a member of *Coronaviridae* family. To investigate the recent distribution of the PEDV strains in Vietnam, the full-length of the spike (S) gene of the 40 PEDV strains collected from endemic outbreaks during 2013-2016 were analyzed. Phylogenetic analysis of the complete S gene sequences revealed that most of the Vietnamese PEDV strains were clustered into G2b group. In contrast, there are some strains collected in 2014 (in Quang Tri province), and in 2015-2016 seasons (HUA-PED176 and HUA-PED254 strains collected in the Southern) were clustered into the G1b group. The nucleotide (nt) and deduced amino acid (aa) analyses based on the complete S gene sequences showed that the Vietnamese PEDV strains were closely related to each other, sharing at nt and aa levels of 93.2-99.9% and 92.6-99.9%, respectively. N-glycosylation pattern and mutations in antigenic region were observed in Vietnamese PEDV strains. In general, the recent circulating of the Vietnamese PEDV strains belonged to the two different virulent lineages, the G2b- and G1b-PEDV, in which the G2b-PEDV as a major agent of recent PED outbreaks in whole country. This study provides up-to-date information on the viral circulating, genetic distribution, as well as evident for effective PEDV vaccine in Vietnam.

Biography

Van Thai Than is currently working at Faculty of Biotechnology & Environmental Sciences, Nguyen Tat Thanh University. His most interested fields are included viral epidemiology and evolution, viral immunology, gene expression, viral sub-unit vaccines.

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P-25

Investigating antibacterial activity from the extract of *Aspergillus terreus* - RTN3 strain isolated from *Alpinia chinensis* Rosc

Vo Thi Ngoc My

Nguyen Tat Thanh University

Abstract

Endophytic fungi and plants are closely related to each other in an efficient ecosystem. In this close relationship, fungi can use the nutrients from plants to survive, while bringing many beneficial substances to plants in return. These substances generating from fungi such as metabolic products that have biological activity as growth hormones and antibiotics that help protect plants from disease-causing microorganisms. Strain of *A. terreus* - RTN3 isolated from *Alpinia chinensis* Rosc has the potential to produce metabolites effecting against *S. aureus* MRSA. In this research, we cultivated and extracted the compounds from medium inhibiting the growth of *S. aureus* MRSA, then identified the number of antibacterial compounds in the crude extracts by thin-layer chromatography and diffusion method. The extract contained three active compounds with antibacterial activity. From 1.7 g crude extracts obtained by the column chromatography, 3 fractions 6, 7, 8 containing antimicrobial-activity substances were obtained with the masses of 53 mg, 151 mg and 520 mg respectively. The MIC values for the extract were determined as 64 µg/ml, 16 µg/ml, 32 µg/ml and 32 µg/ml with respect to fraction 6, 7 and 8. This study has demonstrated that in optimal culture conditions, *A. terreus*-RTN3 produces metabolic responses to *S. aureus* MRSA.

Biography

Vo Thi Ngoc My completed her doctorate at the age of 33 from the University of Science HCM city. She is currently the head of the department and scientific research unit at the pharmacy falcuty located at Nguyen Tat Thanh University. Her major is microbiology and botany and she has conducted several researches on endophytic fungi in recent five years.

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P-26

Antioxidant and antimicrobial activites on clinical urinary infectious strains of asteraceae medicinal plants

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Abstract

Many reports showed that *Escherichia coli*, *Klebsiella pneumoniae* were the leading cause in urinary infectious. Asteraceae species usually contain a large amount of essential oils, polyphenols, flavonoid compounds, which are often studied for antimicrobial and antioxidant activities. Thus, the applications of these extracts in treating infectious diseases need a assessment on pathogenenic bacteria strains isolated from clinical. In the study, we carried out screening the antimicrobial and antioxidant activities of ethanol extracts and essential oils from 9 species of Asteraceae on 30 urinary clinical strains causing urinary tract infection, collected from District 2 Hospital, Ho Chi Minh city, Vietnam. Plant crude extracts were obtained by cold soaking with 96% ethanol for 24 hours and the essential oils were extracted by steam distillation. Agar diffusion method was used for initial evaluation of antimicrobial properties of crude extracts and essential oils. Minimum inhibitory concentrations of activity extracts were determined by agar dilution method. Antioxidant capacity were assesesed by DPPH (1,1-diphenyl-2-picrylhydrazyl) radical scavenging assay. Crude extracts from *Taraxacum officinale, Chrysanthemum morifolium*, *Ageratum conyzoides, Tagetes erecta* and essential oils from *Ageratum conyzoides, Helianthus annuus, Artemisia vulgaris* had the antimicrobial activity on tested micro-organisms. Ethyl acetate fraction from *Ageratum conyzoides* showed the most potent effect on urinary clinical strains (*E. coli* and *K. pneumoniae)* with MIC at 1.25 mg/ml and 12.5 mg/ml, respectively. The results of the DPPH test showed that *Tagetes erecta* extract had the lowest IC_{50} (17.280 µg/ml) and 2.5 times higher than vitamin C (7.321 µg/ml). The ethyl acetate fraction from *Ageratum conyzoides* had the strongest antimicrobial activity on urinary clinical strains (*E. coli* and *K. pneumoniae*). The crude extract from *Tagetes erecta* flowers had a high potential for antioxidant capacity. Further studies on their activity and pharmaceutic is advocated to apply for a healthcare serum to prevent recurrent UIT.

Biography

Phan Canh Trinh graduated Bachelor of Pharmacy in 2015 and Bachelor of Information Technology at 2018. He is a lecturer and researcher in microorganism and their secondary metabolites at University of Medicine and Pharmacy at Ho Chi Minh city.

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P-27

Improvement of antibacterial efficacy using antibiotic encapsulated silica containing redox nanoparticles

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Abstract

Althought versatile antibiotics have been investigated, there is still an urgent need for the development of efficient treatments for infectious diseases, and prevention of bacterial resistance. During infection, pathogenic microorganisms cause inflammatory response and induce generation of reactive oxygen species (ROS) leading to tissue damage and serious organ failure. In addition, the increase of ROS is reported as the mechanism of drug resistance in bacteria. We have recently developed silica-containing redox nanoparticle (siRNP) as a drug delivery system, which possesses high drug absorption characteristics of silica moieties in addition to antioxidant properties of nitroxide radical to scavenge ROS. In this study, an antibiotics cephalothin was encapsulated into siRNP (Cephalothin@siRNP), and antibacterial activity was investigated using possitive-Gram bacteria (*Staphylococcus aureus*) and negative-Gram bacteria (*Escherichia coli*). The size of siRNP was several tens of nanometers (50-60 nm) and slightly increased after drug encapsulation. Drug solubility was significantly improved by internalizing into the core of siRNP. In an antibacterial assay, although the difference of inhibitory zone in *S. aureus* and *E. coli* cultured plates was not observed by treatment with cephalothin and cephalothin@siRNP, regrowth of *E. coli* colonies in the inhibitory zone was found in cephalothin treated plate. Interestingly, this re-growth was significantly reduced in plate with cephalothin@siRNP, as shown in the Figure. This result suggested that the activity of cephalothin is prolonged using siRNP, which may also suppress the resistance. Further investigation will be carried out to understand the mechanism and to develop an effective antibiotic therapy for treatment of infectious diseases.

Biography

Vong Binh Long has completed his PhD in 2015 from University of Tsukuba, Japan and postdoctoral fellow 2 years later at same University. He is currently working at Department of Biochemistry, Univeristy of Science Ho Chi Minh city. He has published more than 15 papers in reputed journals, and his research activities focus on the development of innovative biomaterials for biomedical applications such as nanomedicine for treatment of oxidative stress-induced diseases including infection diseases.

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P-28

Viral pathogens associated with acute respiratory infections among Myanmar children in Yongonduring 2014-2015

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Abstract

Background: It is estimated that about 1.9 million children die from acute respiratory infection (ARI) every year, ranking as the second leading cause of children death. A wide range of pathogens are responsible for ARI. In children, viral pathogens like rhinovirus (HRV), respiratory syncyntial virus (RSV) and Influenza virus are the main causes of ARI. The spread of new emerging respiratory virusesas SARS-CoV, MERS-CoV and recently re-emerging of HEV-D68 had huge impact on global health and economy.However, the epidemiology and impact of respiratory viruses in tropical and developing countries are still limited.

Aim and Method: To investigate the epidemiology, clinical and molecular characteristic of respiratory viruses on pediatric hospitalized ARI in Myanmar, ahospital-based prospective surveillance was conducted from January 2014to August 2015 collected demographic, clinical data and nasopharyngeal swab from children under 5 year of age admitted to Yongon Hospital with ARI symptom. Respiratory viruses was screened by multiplex PCR assay and genotyped by sequencing.

Result: Among enrolled of 400 pediatric hospitalized ARI case, 262 (66%) positive for any virus detected with 10% were co-infection. HRV, RSV, and Influenza A virus were three common viruses at 129 (32.4%); 72(18%); and 35 (8.8%), respectively. Children ARI hospitalized with any respiratory viruses detected were younger but have more frequency of wheeze (40.1% versus 26.1%) and difficulty breathing (69.8% vs 58%). Children infected with RSV were younger than RSV negative group but significant severe with more frequency of wheeze (65.4 vs 31.2%); difficulty breathing (84.6% vs 63.5%); check-wall indrawing (67.3% vs 33.9%) and diagnosis severe LRTI (67.3% vs 39.7%). Almost of RSV-A were ON1 genotype while RSV-B were BA genotype. However, the demographic and clinical characteristic between RSV- A and B were not significant different. Using the specific primers for Picornavirus genus at 5'-UTRhave detected 177 (45%) samples. Sequencing have genotyped 151 (85%) of HRVthat classified at 54(32%) HRV-A; 6(3.9%) HRV-B and 91 (53%) HRV-C while17 (9.6%) HEV that classified at 1 (0.6%) HEV-A/B; 10 (6.4%) HEV-C and all of 6(3.9%) HEV-D were D68 species. Children ARI hospitalized with HRV-A genotype were younger but have more frequency of co-infection with other viruses (29% vs 13%) and longer duration of illness in day (3 vs 2) compare with HRV-C genotype group. However the clinical severity between two group HRV-A and -C were not significant different.

Conclusion: Respiratory viruses is main viral pathogen of ARI hospitalized among Myanmar children. The study findings have important implications for monitoring, surveillance and health policy for preventive medicine in Myanmar.

P-29

Isolation of *Agrobacterium rhizogenes* with hairy root induction on Periwinkle (*Catharanthus roseus* L. G. Don)

Nguyen Nhu Nhut[1,2]*, Bui Van Le[1]

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[2]*Giatuong Ltd. Co., Binhduong branch*

Abstract

Introduction: Periwinkle (*Catharanthus roseus* L. G. Don) is capable of biosynthesis of valuable alkaloid compounds used in the specific treatment of cancer diseases. Unfortunately, the content of these compounds is very low in the plants. Because of its ability to grow rapidly and genetic stability, hairy root culture is considered to be a potential technique for production of the alkaloids from Periwinkle. Hairy roots are formed from transgenic cells from *Agrobacterium rhizogenes*, a bacterium presents widely in the soil. In this study, we isolated *A. rhizogenes* as a tool for transgenic studies and initially applied in the exploitation of Periwinkle hairy roots for alkaloid biosynthesis.

Materials:

- Soil samples from rhizosphere.

- *In vivo* legume plants.

- *In vivo* and *in vitro* Vin002, VIN005, VIN072 and VIN077 Periwinkle cultivars.

Methods:

- *A. rhizogenes* isolated by using MG-Te selected medium and identified by morphology, biochemical tests, *in vivo* pathology, present of Ri plasmid, and 16S RNA gene sequencing.

- Hairy roots induced by directly *A. rhizogenes* infection on tissues.

- Total alkaloid extracted by percolation method.

Results: From 235 samples of rhizophere soil of some Vietnamese crops, thirteen strains of *A. rhizogenes* with three types of colonies were able to induce forming hairy roots on legume plants and four Periwinkle varieties (VIN002, VIN002, VIN072, VIN072 and VIN077) isolated. Most conditions to produce hairy roots on four Periwinkle were different from each other. In suitable conditions, the rates of samples forming hairy roots varied in Periwinkle cultivars. The hairy roots obtained from the different cultivars of Periwinkle requested different conditions for growth on agar media. In conditions wasn't suitable, the hairy root lines developed into callus, bud, wood... With 30 investigated hairy root lines from each Periwinkle cultivar, 12 months hairy root cultures could lost *rol* genes. A randomly study on 20 different hairy roots lines from each cultivar showed that most of the lines had a significant higher total alkaloid content than the *in vivo* non-transgenic roots, especially, the hairy root lines from VIN005 and VIN072 Periwinkle.

Conclusion: The results obtained in addition to the contribution of indigenous *A. rhizogenes* collection as a tool for later hairy root studies, too initially showed potential for alkaloid production from the Periwinkle hairy roots.

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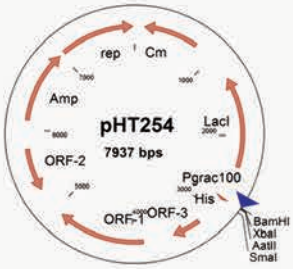
CENTER OF BIOSCIENCE AND BIOTECHNOLOGY

Experimental research

Expression system

Strong expression systems allowing protein production up to 42% in *Bacillus subtilis*

A promoter library allowing fine-tune protein expression in *B. subtilis*

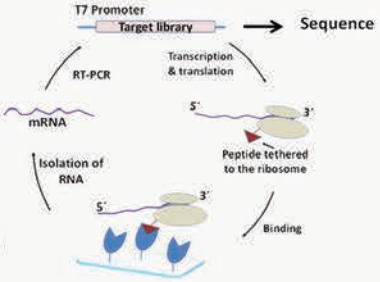


A typical expression vector

Ribosome display

Screening for peptide/protein binding to target proteins

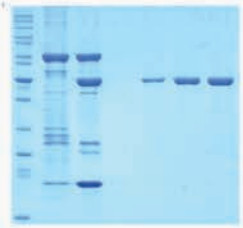
Screening for nanobodies binding to specific target



Recombinant protein

Development of bacterial recombinant strains that can express recombiant proteins

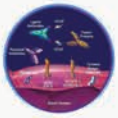
Expression of recombinant proteins in cytoplasm, on the surface and culture medium



Production of recombiant proteins for basic study and trials

Infectious disease and vaccine

Development of vaccine delivery vector based on alive bacteria and of vaccine based on protein



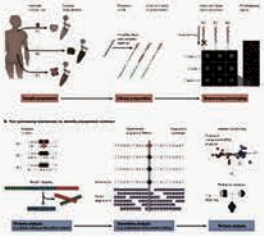
Development of "microbiorobot" using B. subtilis genetics tool box for vaccince and cancer treatment

Bioinformatics research

Genomics

Comparative bacterial genomic analysis

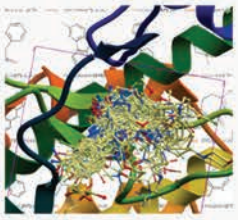
NGS analysis



Virtual Screening

Antibody against *Listeria monocytogenes*

Nanobody



Data mining & Database Analysis

Microarray data

Gene expression

Keywords:

- Expression system
- Recombinant protein
- Recombinant antibody
- Infectious disease
- Vacine development
- Microbiorobot
- Bioinformatics
- Industrial microbiology

REFERENCE (Selected papers)

1. Nguyen *et al.* (2011) Analysis and application of *Bacillus subtilis* sortases to anchor recombinant proteins on the cell wall, AMB Express **1**: 22.
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3. Nguyen *et al.* (2013) Proline Primed Helix Length as a Modulator of the Nuclear Receptor-Coactivator Interaction. *JACS* **135**: 4364-4371.
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