JOINT EVENT

6th World Congress and Expo on **Applied Microbiology**

&

8th Edition of International Conference on

Antibiotics, Antimicrobials & Resistance

&

12th International Conference on **Allergy & Immunology**

October 21-22, 2019 Rome, Italy

Scientific Tracks & Abstracts

Day 1

Day-1

SESSIONS

Discovery of Antibiotics | Antibiotic Therapy | Antimicrobial Resistance | Medical Use of Antibiotics Antibiotic Resistance and Prevention | Interaction and Side-effects of Antibiotics | Antimicrobial Peptides Antibiotics Overuse and Resistance Environmental Microbiology (Soil Microbiology & Water Microbiology) Industrial Microbiology, Microbial Biotechnology & Future Bioindustries | Aquatic and Marine Microbiology

Chair: **Hiroshi Ohrui,** Yokohama University of Pharmacy, Japan

SESSION INTRODUCTION

Title: **From ecology to bacterial resistance to antibiotics-Impact of chemical stress and role of efflux pumps**
Dijoux-Franca Marie-Genevieve, Université Claude Bernard Lyon 1, France

Title: **Novel Sortase A inhibitors to counteract gram-positive bacterial biofilms**
Maria Valeria Raimondi, University of Palermo , Italy

Title: **Retail chicken carcasses as a reservoir of antimicrobial- resistant *Escherichia coli***
Nahla Omer Eltai, Biomedical Research Centre-Qatar University, Qatar

Title: **Hospital-acquired infections in Ukraine**
Yulian Konechnyi, Danylo Halytsky Lviv National Medical University, Ukraine

Title: **Inhibition of *Streptococcus* biofilm formation and its degradation by *Streptomyces* α 1,3-glucanases**
Mamoru Wakayama, Ritsumeikan University, Japan

Title: **Identification of bioaerosols from environmental samples in the AIST, Tsukuba, Japan**
Panyapon Pumkaeo, Gifu University, Japan

Title: **Lysogens in the natural microbial communities of the warm Red Sea**
Ruba Abdulrahman Ashy, King Abdullah University of Science and Technology, Saudi Arabia

Title: **Plantaricin plays a role for post-fermented tea**
Yolani Syaputri, Gifu University, Japan

Title: **I've got you under my skin: A case of toxic epidermal necrolysis-like cutaneous manifestation of systemic lupus erythematosus**
Estherly Grace M Gonzales, Bicol Medical Center, Philippines

Title: **Immune response in *leishmaniasis* in regard to vaccine development**
Ali Khamesipour, University of Medical Sciences (TUMS), Iran

Title: **Rhodesian Human African *Trypanosomiasis* (rHAT) in Kafue national park, Zambia**
David Squarre, National Parks and Wildlife, Zambia

6th World Congress and Expo on **Applied Microbiology**
&
8th Edition of International Conference on **Antibiotics, Antimicrobials & Resistance**
&
12th International Conference on **Allergy & Immunology**
October 21-22, 2019 Rome, Italy

From ecology to bacterial resistance to antibiotics-Impact of chemical stress and role of efflux pumps

Dijoux-Franca Marie-Genevieve, N H Pham, L N Nguyen, O T K Nguyen, S Michalet and **S Nazaret**
Université Claude Bernard Lyon 1, France

The resistance of bacteria to antibiotics has been declared by the WHO as a major public health issue since 2014. Indeed, the list of bacteria capable of resisting almost all available antibiotic molecules is growing. For a long time this problem has been linked to the misuse of antibiotics and has been limited to the hospital environment. More recently, it has integrated human activities (industrial environments, etc.) and agricultural environments. Thus the role of the environment as a source but also in the transmission of antibiotic resistance raises many questions. In the fight of the antibiotic resistance spread, it is currently impossible to limit vision simply to the aspect of human or animal health. Indeed, all ecosystems are linked (human, animal, environment). It is therefore essential to analyze the situation in a global "One Health" context integrating the issue of antimicrobial resistance in all these ecosystems. It is therefore essential to increase the field of knowledge on the environmental factors that could be involved in the phenomenon of antibiotic resistance and its dispersion. There are particularly favorable environments for the dispersal of multidrug resistance, such as all areas of strong human activity (mining areas ...) and farms. It is recognized that in these areas pollution by organic waste, metallic trace elements, are all factors triggering adaptation mechanisms developed by microorganisms. But what about the role of plants and their metabolites in this environment?. In this context of antimicrobial resistance plants metabolites can be considered according to different aspects. Present in the soil, they can be considered in the same way as other environmental factors that can impact the structure of soil bacterial communities. Isolated, these metabolites can have antimicrobial activities in the search for new antibiotics. And finally, others can act on the resistance mechanisms in these particular environments.

Biography

Dijoux-Franca Marie-Geneviève has completed her PhD in Chemistry of Natural Compounds at Champagne-Ardenne University and Postdoctoral studies from NIH-Fort Detrick, Frederick MD, USA. She works as a Professor of Botanical Pharmacy and Phytochemistry at University Lyon 1. She has published more than 63 papers dealing with natural compounds and their impacts on biological systems. Since 2006, she joined the Laboratory of Microbial Ecology. Her research scope is the role of natural compounds in environmental multiresistance, their impact on efflux pumps and their potent activities as MDR reversion.

Notes:

6th World Congress and Expo on **Applied Microbiology**
&
8th Edition of International Conference on **Antibiotics, Antimicrobials & Resistance**
&
12th International Conference on **Allergy & Immunology**
October 21-22, 2019 Rome, Italy

Novel Sortase A inhibitors to counteract gram-positive bacterial biofilms

Maria Valeria Raimondi[1], Roberta Listro[2], Maria Grazia Cusimano[1], Mery La Franca[1], Teresa Faddetta[1], Giuseppe Gallo[1], Domenico Schillaci[1], Simona Collina[2], Ainars Leonchiks[3] and **Giampaolo Barone[1]**
[1]University of Palermo, Italy
[2]University of Pavia, Italy
[3]APP Latvian Biomedical Research and Study Centre, Latvija

Sortase A (SrtA) is a membrane enzyme responsible for the covalent anchoring of surface proteins on the cell wall of Gram-positive bacteria. Nowadays it is considered an interesting target for the development of new anti-infective drugs which aim to interfere with important Gram-positive virulence mechanisms. Along the years, we studied the anti-staphylococcal and anti-biofilm activity of some natural and synthetic polyhalogenated pyrrolic compounds, called pyrrolomycins. Some of them were active on Gram-positive pathogens at a μg/mL range of concentration (1.5-0.045 μg/mL) and showed a biofilm inhibition in the range of 50-80%. In light of these encouraging results, herein we present our efforts in the design and synthesis of novel pyrrolomycins. To dispose of sufficient amount for the in-depth *in vitro* investigation, we developed an efficient and easy-to-use microwave synthetic methodology. All compounds showed a good inhibitory activity toward SrtA, in accordance with the molecular modelling studies, having IC_{50} values ranging from 130 to 300 μM comparable to berberine hydrochloride, our reference compound. Particularly, the pentabromo-derivative exhibited the highest capability to interfere with biofilm formation of *S. aureus* with an IC_{50} of 3.4 nM. This compound was also effective in altering *S. aureus* murein hydrolase activity, responsible for degradation, turnover, and maturation of bacterial peptidoglycan and involved in the initial stages of *S. aureus* biofilm formation.

Biography

Maria Valeria Raimondi has completed her PhD in Pharmaceutical Science at the University of Palermo, Italy and Post-graduated Master in Drug Design and Development at University of Pavia, Italy. She has worked as a Visiting Scientist in Medicinal Chemistry at University of Hamburg-Fakultät MIN-Fachbereich Chemie-Organische Chemie. She works as an Assistant Professor in Medicinal Chemistry at University of Palermo, Italy. She is a Lab Chief for Laboratory of Synthesis of Heterocyclic Compounds with Potential Biological Activity at University of Palermo, Italy, Department of Biological, Chemical and Pharmaceutical Sciences and Technologies. She has published more than 40 papers in international peer-reviewed journals.

Notes:

6th World Congress and Expo on **Applied Microbiology**
&
8th Edition of International Conference on **Antibiotics, Antimicrobials & Resistance**
&
12th International Conference on **Allergy & Immunology**
October 21-22, 2019 Rome, Italy

Retail chicken carcasses as a reservoir of antimicrobial-resistant *Escherichia coli*

Nahla Omer Eltai, Hadi Yassine, Tahra El- Obied, Sara Al hadidi Asma Al Thani and **Walid Alali**
Biomedical Research Centre-Qatar University, Qatar

Antibiotic resistance is one of the major public health challenges in both developed and developing countries. The development and spread of resistant bacteria have been linked to the misuse of antibiotics in human and animal populations. Moreover, the spread of resistance has been associated with the consumption of food contaminated with pathogenic and non-pathogenic resistant bacteria. There is limited information of antibiotic resistance contamination of raw chicken meat in Qatar. The objective of this study was to determine the prevalence of antibiotic resistance among local and imported chicken whole carcasses in Qatar. A total of 270 chicken carcasses locally-produced (chilled) and imported (chilled and frozen) were obtained from three different hypermarket stores in Qatar. A total of 216 Escherichia coli (E. coli) were isolated and subjected to antibiotic susceptibility testing using disc diffusion method. Furthermore, extended-spectrum β-lactamase (ESBL) production was determined via double disc synergetic test. In addition, isolates harboring colistin resistant was determined using multiplex-PCR and DNA sequencing. Nearly 89% (192/216) of the isolates were resistant to at least one of the 18 antibiotics. In general, isolates from local and imported chicken carcasses showed relatively higher resistance to sulfamethoxazole (62%), tetracycline (59.7%), ampicillin and trimethoprim (52.3%), ciprofloxacin (47.7%), cephalothin, colistin (31.9%) and gentamicin (15.7%). On the other hand, less resistance was recorded against amoxicillin/clavulanic acid (6%), cefuroxime (6.9%), ceftriaxone (5.1%), nitrofurantoin (4.2%) and piperacillin/tazobactam (4.2%), cefepime (2.3%), meropenem (1.4%), ertapenem (0.9%), fosfomycin (1.8%), and amikacin (0.9%). Nine isolates (4.2%) were ESBL producers. Furthermore, 63.4% (137/216) were multidrug resistant (MDR). The percentage of MDR, ESBL producers, and colistin-resistant isolates were significantly higher among local chilled isolates compared to imported chilled and frozen chicken samples. Our findings indicate high antibiotic resistant prevalence in chicken carcasses in Qatar, including ESBL, MDR and colistin resistance. Such resistant E. coli could potentially spread to humans through consumption of chicken meat. Development and implementation of a stewardship program to control and monitor the use of antibiotics in animal production locally and introduce testing of imported chicken for antibiotic resistance are needed in Qatar.

Biography

Nahla Omer Eltai has completed her PhD at Humboldt University, Berlin, Germany; Postdoctoral studies from University of the West of England, U K She is a Research Associate at Biomedical Research Centre, Qatar University, Qatar. She has published more than seven papers in the field of antibiotic resistance in reputed journals. Her research interests are multidisciplinary with emphasis on molecular diagnostic approaches, antimicrobial susceptibility and resistance, test of new natural antimicrobial agents. She is adopting the one health system approach by studding antimicrobial resistance in agriculture, environment and human.

Notes:

6th World Congress and Expo on **Applied Microbiology**
&
8th Edition of International Conference on **Antibiotics, Antimicrobials & Resistance**
&
12th International Conference on **Allergy & Immunology**
October 21-22, 2019 Rome, Italy

Hospital-acquired infections in Ukraine

Yulian Konechnyi, Andrij Albokrinov and **Olena Korniychuk**
Danylo Halytsky Lviv National Medical University, Ukraine

Introduction: According to WHO, approximately 15.0% of all hospitalized patients suffer from Hospital-Acquired Infection (HAIs). Data from USA and Europe show 1,3% to 2,03% cases of HAIs in hospitalized patients. In Ukraine -5-7.000 proven cases of HAIs and 500.000 unregistered cases per year. One of the methods to prevent HAIs is control strategy in Intensive care unit (ICU), where last-line antibiotics are currently used.

Objective: To define spectrum of microbial flora and antimicrobial sensitivity of HAIs in some ICU in Lviv city, Ukraine.

Methods: It was investigated 124 clinical materials from 60 patients at the public hospitals in Lviv during July 2018 - May 2019. Were isolated 144 strains of pathogenes. HAIs was defined as infection that appeared in patient later than 48 hours after hospital admission. Causative bacterial strains were isolated and identified using bacteriological method (Mueller Hinton Agar, Blood Agar, Saburo Agar, selective & differential media CHROMID*VRE, CHROMID*MRSA SMART, CHROMID*Candida etc. (Biomerieux)) and biochemical tests MIKRO-LA-TEST NEFERMtest24, CANDIDAtest21, STAPHYtest24 etc. (ErbaLacema). Antibiotic sensitivity test was done according to Kirby-Bauer technique.

Results: HAIs structure was as follows: *Staphylpcoccus lentus* (17.7%), *Eschrichia coli* (20.2%), *Klebsiella pneumoniae* (9,7%), *Pseudomonas aeruginosa* (24.2%), *Streptococcus spp*. (2.4%), *MRSA* (3,2%), *Candida albicans* (8.1%). There were several types of HAIs which are rarely founded, such as *Staph.simulans, Staphylococcus gallinarum*, *Staphylococcus haemolyticus Staphylococcus lugdunensis, Aerococcus viridans*, *Pragia fontium, Aeromonas ichthiosmia, Raoultella terrigena, Burkholderia pseudomallei, Macrococcus caseolyticus, Pseudomonas oryzihabitans, Pseudomonas putida, Candida dubliniensis, Candida membranifaciens, Candida glabrata*. Anti-microbial sensitivity assessment showed that more than 90.0 % pathogens were multidrug resistance (MDR). 75% of strains were atypical strains (T-index ≥ 0,25).

Conclusion: In the era of antibiotics HAIs are still uncontrollable. Most cases of HAIs in Ukraine are not recognized as epidemics. More than 90.0 % pathogens are MDR and most of them are atypical strains. Diagnostic capabilities show a number of rare species of microorganisms that cause nosocomial infections. It is important to use this fact when one attempts to design prevention or control strategy to reduce HAIs either at WHO level, or at the level of local health care unit.

Acknowledgement: We thank directors of the hospitals and ICU teams.

Ethical Committee: 25/06/2018 № 6.

Biography

Yulian Konechnyi is doing his PhD in microbiology at Danylo Halytsky Lviv National Medical University, Ukraine. He has completed his MD and have specialization in internal medicine. He has worked as lecturer at the department of microbioly in microbiology, virusology and immunology topics, at Danylo Halytsky Lviv National Medical University, Ukraine. He has published 10 different papers.

6th World Congress and Expo on **Applied Microbiology**
&
8th Edition of International Conference on **Antibiotics, Antimicrobials & Resistance**
&
12th International Conference on **Allergy & Immunology**
October 21-22, 2019 Rome, Italy

Inhibition of *Streptococcus* biofilm formation and its degradation by *Streptomyces* α 1,3-glucanases

Mamoru Wakayama, Panti Niphawan, Cherdvorapong Vipavee and **Yosuke Toyotake**
Ritsumeikan University, Japan

Streptomyces thermodiastaticus HF3-3 from soil was screened as an α-1,3-glucanase producing strain. The strain HF3-3 showed the highest α-1,3-glucanase activity in culturing it by using α-1,3-glucan as a sole carbon source. It produces two types of α-1,3-glucanases namely AglST1 and AglST2, which were homogenously purified by column chromatography: DEAE-cellufine A500 and HiTrap QHP-GE. SDS- PAGE showed the approximate molecular weight 62 and 91 kDa for AglST1 and AglST2, respectively. AglST1 and AglST2 specifically acted on α-1,3-glucan. They exhibited the same optimum of pH 5.5. Their optimum temperatures were slightly different, which were 65 °C and 60 °C for AglST1 and AglST2, respectively. The other characteristics including pH stability, the effect of NaCl, the effect of ion metals, and the effect of toothpaste ingredients (NaF, SDS, BTC) had been studied. The results indicated AglST1 and AglST2 were insensitive toward various substances. Notably, the outstanding properties of AglSTS from *S. thermodiastaticus* HF3-3 were thermostable which would be worth in applications. From amino acid sequence analysis, AglST would be classified as a new subfamily of glycoside hydrolase 87, since its sequence has high homologous with mycodextranase, and shows low identity with the known sequences of α-1,3-glucanase. The recombinant α-1,3-glucanases, designated as rAglST1 and rAglST2, were successfully expressed in *E. coli* with showing the most properties same as the wild-type enzyme. rAglSTs could retarded the formation and degraded the fully formed biofilm effectively. In conclusion, α-1,3-glucanases from *S. thermodiastaticus* HF3-3 have been characterized and could be used practically in the application of dental care.

Biography

Mamoru Wakayama has his expertise in enzymology and fermentation technology. He has consistently been studying the enzymes involved in amino acid metabolisms as well as the enzymes responsible for degradation of non-digestible poly saccharides such as chitin and alpha-1,3-glucan.

Notes:

6th World Congress and Expo on **Applied Microbiology**
&
8th Edition of International Conference on **Antibiotics, Antimicrobials & Resistance**
&
12th International Conference on **Allergy & Immunology**
October 21-22, 2019 Rome, Italy

Identification of bioaerosols from environmental samples in the AIST, Tsukuba, Japan

Panyapon Pumkaeo, Wenhao Lu, Youki Endou, Tomohiro Mizuno, Junko Takahashi and **Hitoshi Iwahashi**
Gifu University, Japan

The bioaerosols are the atmosphere particles, mists or dust of μm range, associated with metabolically active or inactive viable particles. They contain living organism's included microorganisms such as viruses, bacteria, and fungi also plant material as well as pollen. Next Generation Sequencing (NGS) is a novel method of DNA sequencing that quickly and efficiently read the underlying sequence of an organism by means of massively parallel sequencing. The aim of this study is identifying organisms which contained in environmental samples by using NGS. This study monitored the environmental sample (bioaerosols) from November 2013 to January 2015 for 50 days using air samples were collected at AIST, Tsukuba, Japan. Samples were bio-analyzed using a next-generation sequencing method. In this study, we used two NGS platform, GS FLX+ (Roche 454 sequencing) and Illumina Misep. The sample was detected plants, eukaryotes and bacteria. The sample was divided into two subgroup subgroups according to the size of its bioaerosols, large subgroup contains bioaerosols whose diameter is bigger than 3.3μm, and small subgroup contains those smaller than 3.3μm.The most abundant bacteria in several samples were of the Actinobacteria (class), Alphaproteobacteria, Bacilli and Clostridia. For the animal detection using internal transcribed spacer 1, only uncultured fungi were detected in more than half of the hits, with a high number of Cladosporium sp. in the samples. For the plant identification, the ITS1 information only matched fungal species. However, targeting of the rbcL region revealed diverse plant information, such as *Medicago papillosa*. In conclusion, traces of bacteria, fungi, and plants could be detected in the bioaerosols, but not of animals using those primers.

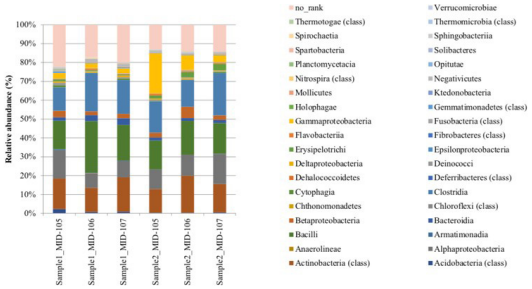

Fig. 1. Identification of bacterial 16S rDNA sequences in bioaerosols at the class level. Sample1: large-sized dust sample; Sample2: small-sized dust sample; MID-107: collection period from November 29, 2013 to December 14, 2013; MID-106: collection period from December 15, 2013 to December 26, 2013; and MID-105: collection period from December 26, 2013 to January 16, 2014.

Recent Publications

1. Choi, Jae-Hoon, Ayaka Kikuchi, Panyapon Pumkaeo, Hirofumi Hirai, Shinji Tokuyama and Hirokazu Kawagishi (2016) Bioconversion of AHX to AOH by resting cells of Burkholderia contaminans CH-1. Bioscience, Biotechnology and Biochemistry 80 (10):2045-2050.
2. Panyapon Pumkaeo. 2018. "Identification of Bacteria from bioaerosl at AIST, Tsukuba, Japan." Proceedings of International Symposium on Animal Production and Consevation for Sustainable Development 2018 UGSAS-GU & BWEL Joint Poster Session on Agricultureal and Basin Water Environmental Sciences 2018:P18.

Biography

Panyapon Pumkaeo has completed his Bachelor's degree from the Department of Microbiology, Faculty of Science, Kasetsart University, Bangkok, Thailand. Currently, he is pursuing his PhD at United Graduate School of Agricultural Science (UGSAS) in Gifu University, Japan. His research is about "Bioaerosol." He would like to analyze the bioaerosol sample that collected in the atmosphere by using the Next Generation Sequencing (NGS) to know the information of organism present in aerosol where they come from which impact in environment, to avoid bio-invasion. Also, he would like to apply the result from NGS data for developing the primers too easy for identifying the organism in Bioaerosol.

Notes:

6th World Congress and Expo on **Applied Microbiology**
&
8th Edition of International Conference on **Antibiotics, Antimicrobials & Resistance**
&
12th International Conference on **Allergy & Immunology**
October 21-22, 2019 Rome, Italy

Lysogens in the natural microbial communities of the warm Red Sea

Ruba Abdulrahman Ashy, Curtis Suttle and **Susana Agusti**
King Abdullah University of Science and Technology, Saudi Arabia

Viruses are the most abundant microorganisms in marine environments. Viral infections can be either lytic (virulent) or lysogenic (temperate phage) within the host cell. The Red Sea is a narrow oligotrophic basin classified as the warmest water temperatures, which may affect the dynamics of microbial community. Studies on lysogenic bacteria in the Red Sea remain unexplored. The aim of this study was to quantify viral dynamics in the Red Sea and to investigate the occurrence of lysogenic bacteria based on a temporal study. Over two years, we quantified fortnightly environmental parameters and virus and bacterial abundances in a coastal station of the Red Sea. During the second year, monthly seawater samples were examined for prophage induction by mitomycin C. Water temperatures were high, from 25.4 to 31.93 °C and total viral and bacterial abundances ranged from 1.51 to 8.56 × 106 and from 1.94 to 3.16 x 105 cells mL-1, respectively. The burst size was calculated as 13.81. We determined that 12.24 % ±4.82 (SE) of the treated bacteria were lysogenized with the highest percentage of 55.8% observed in January 2018 when bacterial abundances were low. Second small proportions were identified in July and September, which potentially related to the stressful conditions to phages with no induction, was observed in the spring time where bacterial abundances were at the highest. Our results confirm that lysogenized cells were favoured when bacterial populations were low; however, there was no clear relationship between lysogeny and seasonal changes in the Red Sea environmental conditions, as the stressful summer did not induce high lysogeny neither lytic infection.

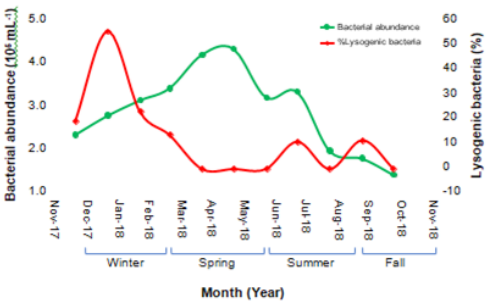

Figure: Percentages of lysogenic bacteria (red line and diamonds) and monthly mean (±SE) bacterial abundance (green line and dots) quantified in the natural microbial communities of the coastal Red Sea during the second year of the study (December 2017 to October 2018).

Biography

Ruba Abdulrahman Ashy is pursuing her PhD in Environmental Science and Engineering Department, Red Sea Research Center at King Abdullah University of Science and Technology, Thuwal, Saudi Arabia. She worked as a teacher assistant of Microbiology Science from 2009 at King Abdulaziz University, SA. Her PhD research interest is in environmental microbiology and virology. Her main aim focuses on determining the potential viability of lysogenic bacteria or infectious viruses and their survival in certain environmental areas by the development and the evaluation of virus detection methods. This research will explore the factors behind the spread of viral infections in different environmental areas including the Red Sea.

6th World Congress and Expo on **Applied Microbiology**
&
8th Edition of International Conference on **Antibiotics, Antimicrobials & Resistance**
&
12th International Conference on **Allergy & Immunology**
October 21-22, 2019 Rome, Italy

Plantaricin plays a role for post-fermented tea

Yolani Syaputri[1], **Masanori Horie**[2] and **Hitoshi Iwahashi**[1]
[1]Gifu University, Japan
[2]Health Research Institute, AIST, Japan

Post-fermented tea samples, before fermentation, primary and secondary fermentation process from each company were collected and studied. Klebsiella *pneumoniae subsp. ozaenae, Pseudomonas glareae, Klebsiella variicola*, and Pseudomonas aeruginosa were observed in tea leaf before fermentation. Furthermore, in primary and secondary fermentation *Lactobacillus plantarum* became one of the major lactic acid bacteria species can survive in these processes. The results showed that *plnA, plnEF*, and *plnNJK* existed in primary and secondary fermentation. Two potentials *L. plantarum* were isolated from post-fermented tea samples, *L. plantarum* IYO1501 and *L. plantarum* IYO1511. plnA and plnEF were encoded on plasmid of *L. plantarum* IYO1501 and *L. plantarum* IYO1511. Whereas, plnNJK was encoded on *L. plantarum* IYO1511 chromosome. Schematic representation of *plnA, plnEF*, and plnNJK gene cluster in *L. plantarum* showed different schematics gene cluster. The cluster structure of plantaricin encoding region was not shown yet around plantaricin gene region before. plnA on *L. plantarum* IYO1501 showed 96% homology of GenBank. The results showed clearly that *L. plantarum* IYO1501 and *L. plantarum* IYO1511 produced plantaricin on plasmid and on chromosome and play an important role for the success of the product.

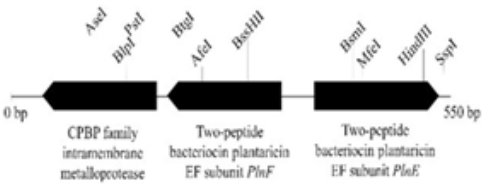

Figure: plnEF, Gene cluster L. plantarum IYO1501 on plasmid

Recent Publications

1. Strong Antimicrobial of Lactic Acid Bacteria and Species Identification of Virgin Coconut Oil Products in Padang West Sumatera, Indonesia (2017). International Journal on Advance Science, Engineering and Information Technology (IJASEIT)
2. Isolation and Characterization of *Lactobacillus spp*. From Virgin Coconut Oil, West Sumatra. 2018. International Symposium on Animal Production and Conservation for Sustainable Development
3. Probiotic Research in Several Products of Virgin Coconut Oil from Padang, Indonesia. 2018. Journal of Physic

Biography

Yolani Syaputri is pursuing her PhD at Gifu University. She has worked in the area of especially food fermentation, lactic acid bacteria, and bacteriocins. Currently, she is developing fermented tea from Gifu, Japan. She is interested to find a potential lactic acid bacterium which is isolated from many samples. She focused on identification bacteriocin gene or structural gene, immunity protein and secretion gene to get the genetic information and develop them to make a good product.

6th World Congress and Expo on **Applied Microbiology**
&
8th Edition of International Conference on **Antibiotics, Antimicrobials & Resistance**
&
12th International Conference on **Allergy & Immunology**
October 21-22, 2019 Rome, Italy

I've got you under my skin: A case of toxic epidermal necrolysis-like cutaneous manifestation of systemic lupus erythematosus

Estherly Grace M Gonzales, Kristy Pinoy-Villamayor and **Richard John Pelo**
Bicol Medical Center, Philippines

Introduction: Systemic Lupus Erythematosus has several presentation and cutaneous lesion is the second most frequent presentation of SLE. Toxic Epidermal Necrolysis-like cutaneous lupus erythematosus was considered as a rare variant of Acute Cutaneous Lupus Erythematosus with different presentation with the classical drug-induced TEN. Differentiating the two entity will be useful in the management and determining the outcome of the patient.

Objectives: : In this report, we present a rare presentation of a newly diagnosed case of Systemic Lupus Erythematosus presenting with Toxic Epidermal Necrolysis-Like skin lesions. Specifically, to present the clinical manifestations, approach to management and correlate it with previous case reports.

Case: A 37 years old female who presented with 6 years history of multiple joint pains, alopecia, photosensitivity, and intermittent undocumented fever. She was admitted due to appearance of TEN-like skin lesions. This case was diagnosed with SLE based on SLICC Criteria: hematologic, mucocutaneous and autoimmune criteria. TEN- like cutaneous lupus erythematosus was considered by using Naranjo and Hartwig scoring system. Patient was managed with steroids and hydroxychloroquine wherein lesions resolved.

Conclusion: This case highlighted that TEN is not always due to drug reaction hence, may be attributed to other disease. This concluded that TEN like cutaneous lupus erythematousus does exist and it is a rare manifestation of SLE. Early recognition, proper physical examination, and diagnostic procedure should be done in a prompt manner to aid in the diagnosis and treatment.

Biography

Estherly Grace M. Gonzales has completed her pre medical degree of Bachelor of Science in Nursing at the age 20 from Universidade de Sta. Isabel as cum laude and had her medical degree at the age of 26 years from Far Eastern University- Dr. Nicanor Reyes Medical Foundation. She is currently on resident training in the Department of Internal Medicine in Bicol Medical Center, a premier hospital of Bicol Region in the Philippines.

6th World Congress and Expo on **Applied Microbiology**
&
8th Edition of International Conference on **Antibiotics, Antimicrobials & Resistance**
&
12th International Conference on **Allergy & Immunology**
October 21-22, 2019 Rome, Italy

Immune response in *leishmaniasis* in regard to vaccine development

Ali Khamesipour
University of Medical Sciences (TUMS), Iran

Leishmaniasis is a parasitic neglected disease reported from over 100 countries. The available tools to control the disease control are not fully effective. The only tool to control a disease like leishmaniasis is development of effective vaccines. There is almost no vaccine available against any infectious disease caused by intracellular parasites in which cellular immune response is responsible for protection. In murine model of leishmaniasis, the type of immune response which generated govern the outcome of the disease; in resistant strains of mice Th1 type response is generated and a lesion similar to human CL develops, the lesion heals spontaneously and upon healing the animals are protected against further lesion development, in contrary the same infection in susceptible BALB/c mice induces Th2 response which accompanies a severe systemic disease and eventually every infected mouse succumbed to the disease. Although in murine model of leishmaniasis, generation of Th1 response induces cure and protection against further infection, but generation Th1 or Th2 is not the whole story. The surrogate marker(s) of protection in human intracellular infections such as leishmaniasis is not well known. In human leishmaniasis, cure and protection accompany with induction of strong immune response which is shown *in vivo* by leishmanin skin test and *in vitro*, by a high level of IFN-γ, low level of IL-5 and IL-10 which is an indication of induction of Th1 response. A Th2 response is seen in visceral leishmaniasis, and non-healing cutaneous leishmaniasis (CL) refractory to treatment. Protection in CL caused by *Leishmania major*, is mediated by the expansion of antigen specific IFN-γ producing CD4+ and CD8+ T cells. Memory T cell population is responsible for Leishmania-induced IFN-γ production. Effector memory T cells are responsible for protection against Leishmania infection.

Recent Publications

1. Elikaee S, Mohebali M, Rezaei S, Eslami H, Khamesipour A, Keshavarz H, Eshraghian MR. Development of a new live attenuated *Leishmania major* p27 gene knockout: Safety and immunogenicity evaluation in BALB/c mice. Cell Immunol. 2018 Oct;332:24-31.
2. Nateghi Rostami M, Seyyedan Jasbi E, Khamesipour A, Miramin Mohammadi A, Plasma levels of tumor necrosis factor-alpha (TNF-α), TNF-α soluble receptor type 1 (sTNFR I) and IL-22 in human leishmaniasis. Trop Biomed 2015 Sep;32(3):478-84.
3. Hosseini-Vasoukolaei N, Mahmoudi AR, Khamesipour A Yaghoobi-Ershadi MR, Kamhawi Sh, Valenzuela JG, Arandian MH, Mirhendi H, Emami Sh, Saeidi Z, Idali F, Jafari R, Jeddi-Tehrani M, Akhavan AA. Seasonal and Physiological Variations of Phlebotomus papatasi Salivary Gland Antigens in Central Iran. J. of Arthropod-Borne Dis. 2015. 27;10(1):39-49.
4. Khamesipour A. Therapeutic vaccines for leishmaniasis. Expert Opin Biol Ther. 2014 Jul 31:1-9.
5. Davoudi N, Khamesipour A Mahboudi F, McMaster WR. A dual drug sensitive L. major induces protection without lesion in C57BL/6 mice. PLoS Negl Trop Dis. 2014 May 29;8(5):e2785.
6. Khamesipour A. The Need to Teach Vaccine Safety to Basic Scientists and Public Health Officials. Current Drug Safety, 2015;10(1):76-9.

Biography

Ali Khamesipour, PhD is a Professor in Center for Research and Training in Skin Diseases and Leprosy, TUMS, Tehran, Iran. He is a Chair, Iranian National Leishmaniasis Network and was a Visiting Professorin the Department of Community Medicine, the Federal University of Piauí, Brazil, 2018 to April. He completed his Post-doc 8/1992 - 8/1993, UCI, Irvine, College of Medicine, Department of Pathology, Irvine, USA and PhD in Department of Medical Microbiology and Immunology, School of Medicine, SIU, USA 1992. He published about 183 papers in reputed journals. His research interest is Search for surrogate marker(s) of cure and protection in leishmaniasis and vaccine development.

Notes:

6th World Congress and Expo on **Applied Microbiology**
&
8th Edition of International Conference on **Antibiotics, Antimicrobials & Resistance**
&
12th International Conference on **Allergy & Immunology**
October 21-22, 2019 Rome, Italy

Rhodesian human African *Trypanosomiasis* (rHAT) in Kafue national park, Zambia

David Squarre[1], **Chihiro Sugimoto**[2], **Boniface Namangala**[1], **Kyoko Hayashida**[2] and **Junya Yamagishi**[2]
[1]National Parks and Wildlife in Zambia, Zambia
[2]Hokkaido University, Japan

Statement of the Problem: The World Health Organization (WHO) describes Human African Trypanosomiasis (HAT) as a neglected tropical disease affecting mostly the poor communities in sub Saharan Africa. The disease is caused by a multi host haemo-flagellate protozoan parasite of genus Trypanosoma and is transmitted by infected tsetse fly (Glosinna spp). The Kafue National Park (KNP), located in Central Zambia was considered devoid of the parasite due to lack of compelling data on presence, abundance and diversity of the circulating parasites especially in wildlife populations and the risk to public health has not been elucidated. The lack of true information on trypanosome diversity and its expression in wildlife reservoir population renders the current control of the disease sub optimal.

Methodology & Theoretical Orientation: Case studies of a 46 years old male resident of KNP and cross sectional study to screen wildlife reservoir of the KNP for rHAT was employed. Blood samples from both affected patients and wildlife reservoirs were assessed using a combination of molecular methods such as LAMP, ITS-PCR, SRA-PCR and the results were validated by Mini-Ion Sequencing.

Findings: The study demonstrated the presence of rHAT in human and wildlife populations of KNP. Further characterization of the parasites reveal the diversity of trypanosomes in KNP.

Conclusion & Significance: The outcomes of this study reaffirms the presence of rHAT in KNP and further declares that KNP is a genuine neglected and re-emerging foci of rHAT. The first step to control this neglected disease is the recognition of its presence and its perceived risk. Based on results contained here, it is recommended that the already fixed and accessible health facility be strengthened with capacity to diagnose and treat rHAT within and around the KNP. Based on this data the risk of rHAT infection to the public can be correctly estimated and appropriate intervention instituted.

Recent Publications

1. Masahiro Kajihara, Bernard M. Hang'ombe, Katendi Changula, Hayato Harima, Mao Isono, Kosuke Okuya, Reiko Yoshida, Akina Mori-Kajihara, Yoshiki Eto, Yasuko Orba, Hirohito Ogawa, Yongjin Qiu, Hirofumi Sawa, Edgar Simulundu, Daniel Mwizabi, Musso Munyeme, David Squarre, Victor Mukonka, Aaron S Mweene, Ayato Takada: Marburgvirus in Egyptian Fruit Bats, Zambia. Emerging Infectious Diseases 05/2019; 25(8)., DOI:10.3201/eid2508.190268

2. David Squarre, Ilunga Kabongo, Musso Munyeme, Chisoni Mumba, Wizaso Mwasinga, Lottie Hachaambwa, Chihiro Sugimoto, Boniface Namangala: Human African Trypanosomiasis in the Kafue National Park, Zambia. PLoS Neglected Tropical Diseases 05/2016; 10(5):e0004567., DOI:10.1371/journal.pntd.0004567

3. David Squarre, John Yabe, Chisoni Mumba, Maxwel Mwase, Katendi Changula, Wizaso Mwasinga, Musso Munyeme: Toxaemia secondary to pyloric foreign body obstruction in two African lion (Panther leo) cubs.

Asian Pacific Journal of Tropical Biomedicine 08/2015; 5(9)., DOI:10.1016/j.apjtb.2015.07.010

4. M Mwase, C Mumba, D Square, S Kawarai, H Madarame: Cutaneous Squamous Cell Carcinoma presenting as a Wound with Discharging Sinus Tracts in a Wild African Lion (Panthera leo). Journal of comparative pathology 09/2013; 149(4)., DOI:10.1016/j.jcpa.2013.06.004

5. Mudenda B Hang'ombe, James C L Mwansa, Sergio Muwowo, Phillip Mulenga, Muzala Kapina, Eric Musenga, David Squarre, Liywali Mataa, Suzuki Y Thomas, Hirohito Ogawa, Hirofumi Sawa, Hideaki Higashi: Human-animal anthrax outbreak in the Luangwa valley of Zambia in 2011. Tropical Doctor 04/2012; 42(3):136-9., DOI:10.1258/td.2012.110454

Biography

David Squarre is currently the head wildlife veterinarian for the Department of National Parks and Wildlife in Zambia. He previously worked and managed the wildlife veterinary service department at the Zambia Wildlife Authority. He works mostly with free ranging wildlife in National Parks and protected areas in Zambia. He is currently a PhD candidate at Hokkaido University, Japan, focusing on vector bourne zoonotic parasites. He is also persuing his MSc in Conservation Genetics and Wildlife Forensics at the University of Edinburgh, Scotland. He has published more than 15 peer reviewed papers on subjects related to wildlife health and conservation. He has presented his work at several conferences on wildlife health and conservation at the Society for Wildlife Forensics, Scotland (2017), Japan Graduate (JGRID) and society for conservation GIS 2014 (california). He has received several awards including the Hashimoto award, Japanese Society for the Promotion of Science (JSPS) and Society for Conservation GIS (SCGIS).

Notes: