EuroSciCon

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AGENDA

Abstract

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Inactivation of a proteorhodopsin-like gene in aurantiochytrium by double homologous recombination

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Aurantiochytrium limacinum, a marine heterotroph which belongs to a crude oil-degrading class of protists called the Labyrinthulomycetes, is one of a variety of thraustochytrids known to produce zoospores that respond to chemical cues, as well as light, but the mechanisms by which they do so are unknown. While many papers have been published concerning how zoospores across different taxa respond to light, little research has been done in investigating the mechanism of light sensitivity of Aurantiochytrium limacinum, which plays an important role in the carbon cycle by decomposing crude oil, tarballs, and other non-living organic matter. Since rhodopsins can be involved in phototaxis, we hypothesized that the gene 7690 in Aurantiochytrium, which encodes a protein with similarity to rhodopsins, serves as a photoreceptor for zoospore phototaxis. By attempting to knockout the 7690 gene through double homologous recombination, this research aimed to determine whether the 7690 protein is required for phototaxis of the zoospores. We extracted, purified and restriction digested a plasmid containing the antibiotic resistance cassette we call 'GZG' (made of promoter and terminator regions of th¬-e Aurantiochytrium GAPDH gene surrounding, and driving the expression of, the shble gene, which encodes resistance to zeocin) in between DNA from upstream and downstream of the 7690 gene, and introduced that whole construct into Aurantiochytrium by electroporation. After testing 6 different isolates using colony PCR to search for double homologous recombinants, we identified a singular potential knockout which can be useful in investigating whether the 7690 gene is required for phototaxis.

Identifying, developing and moving sustainable communities through application of bioenergy for energy or materials: Future perspective through energy efficiency

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The demand for energy continued to outstrip supply and necessitated the development of biomass option. Residues were the most popular forms of renewable energy and currently biofuel production became much promising. Agricultural wastes contained high moisture content and could be decomposed easily by microbes. Agricultural wastes were abundantly by a number of microorganisms. Compost or bio-fertiliser could be produced with the inoculation of appropriated thermophilic microbes which increased the decomposition rate, shortened the maturity period and present research was to promote the biomass technology and involved adaptive research, demonstration and dissemination of results. With a view to fulfill the objective, a massive field survey was conducted to assess the availability of raw materials as well as the present situation of biomass technologies. In the present communication, an attempt had also been made to present an overview of present and future use of biomass as an industrial feedstock for production of fuels, chemicals and other technology must be encouraged, promoted, invested, implemented, and demonstrated, not only in urban areas but also in remote rural areas.

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Antibiotic or a phage? - evaluation of eradication methods of salmonella-derived biofilms under different growth conditions in laboratory environment and

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Salmonella enterica is one of the most common foodborne pathogens associated with contaminated poultry meat and eggs. The genus is subdivided into over 2500 serovars, with different level of pathogenicity. Most common serotypes responsible for the disease in humans are S. Typhimurium and S. Enteritidis. S. enterica commonly live in gastrointestinal tract of farming birds without causing any illness symptoms. However, any damage done to birds' intestines during meat processing may result in bacteria spreading onto the meat and also onto the equipment in the abattoir. S. enterica is able to form biofilm on various surfaces, and thus it can be more resistant to different methods of eradication.In our work, we have analysed the formation of biofilms of S. enterica serotypes commonly associated with salmonellosis in different temperatures, under laboratory conditions. We have also compared the effectiveness of antibiotics, disinfectant and bacteriophages in eradication of biofilms formed by those serotypes under different growth conditions. Moreover, we have analysed the effectiveness of phages and antibiotics against S. enterica in multi-species biofilm in order to compare therapeutic potential of phage therapy as an alternative to antibiotics.We have observed that bacteriophages tended to be equally effective as antibiotics.

Structural basis of interaction between DhHal3p and fungal specific Ser/Thr phosphatase protein DhPpz1p having intrinsically disordered N-terminus from osmotolerant yeast *debaryomyces hansenii*

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Fungal specific Ser/Thr phosphatase 1, DhPpz1p, is negatively regulated by DhHal3p to confer halotolerance in Debaryomyces hansenii. Here we report structurally important pockets and points of interaction between these two proteins. The in silico interaction identified domains and sites of molecular interaction which were corroborated in vitro by Yeast Two Hybrid interaction. Remarkably, a hot spot region residing in the carboxyl end of DhPpz1p was identified to bind DhHal3p. Similarly, from DhHal3p, a region comprising 463-559 residues was identified as vital for binding interaction with DhPpz1p and also with secondary interaction points scattered over N-terminus of DhPpz1p. Loss of binding between proteins was observed for position D443A and D446A from DhPpz1p and R338A, H344A, R348A and R349A from DhHal3p confirming the importance of these docking sites. Our results also revealed the dynamic dual role of short Ser/Arg/Asn motifs from N-terminus of DhPpz1p in selective interaction with DhGlc8p and negative regulator DhHal3p. The DhPpz1NΔ59-75 and DhPpz1NΔ162-183 were clearly refractory to DhHal3p binding and exhibited stronger binding with DhGlc8p. Antagonistically, DhPpz1NΔ27-36, DhPpz1NΔ81-104 and DhPpz1NΔ106-120 showed stronger binding with DhHal3p and no binding with DhGlc8p. Therefore, this study is the first documentation to reveal the regulatory role of N-terminus from DhPpz1p in recruiting regulators via degenerate yet distinct regulatory motifs from its N-terminus. Our work has further opened the room for frontier research in the field of antifungal development against unique N-terminus from each Ppz1p enzyme from diverse fungal species.

The resistance mechanism of *Escherichia coli* induced by ampicillin in laboratory

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Pathogenic *Escherichia coli* often causes diarrhea, sepsis and other clinical symptoms, and is still one of the main intestinal pathogens affecting human and animal health. The aim of this study was to compare the differences in non-synonymous Single Nucleotide Polymorphisms (non-SNP) between drug-resistant strains and sensitive strains, and to understand the function of related genes and the metabolic pathways involved. We simulated the process of clinical antibiotics in organisms by using the method of ampicillin laboratory induction, and explored the relationship between the degree of drug resistance and the mutation site. This study provides a basis for the early detection of drug-resistant strains, the rational and effective application of antibiotics, and a new idea for solving the problem of E.coli resistance. Combined mutations of ftsI and envZ genes were found to induce higher resistance. Mutations in the frdD,OmpD,acrB and VgrG genes may also be linked to antibiotic resistance in β-lactamide antibiotic.

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Molecular characteristics of antimicrobial resistance and virulence determinants of Staphylococcus aureus isolates from clinical infection and food

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Staphylococcus aureus (S. aureus) is an important human etiologic agent. Researching the characteristics of popular genotype of *S. aureus,* relating to the pathogenicity and antibiotic resistance, can provide reference for the prevention. This study collected 275 S. aureus isolates from Zhengzhou city of China, including 148 isolates from patients and 127 isolates from ready-to-eat food. Antimicrobial susceptibility testing was performed using the broth dilution method. Molecular characteristics of antimicrobial resistance, virulence and genotypes were identified by PCR. 34.18% (94/275) of S. aureus isolates were MRSA. Compared with food isolates, clinical isolates had significantly higher antibiotic resistance rates, the carriage rates of resistance genes including acc(6')/aph(2'), aph(3')-Ⅲ, ermA, ermB and virulence genes including tetM, sea, seb, pvl and etb. MRSA-t030-agr Ⅰ-SCCmec Ⅲ and MSSA-t002-agr Ⅱ were the most common types among the clinical strains, and MRSA-t002-agr Ⅱ-SCCmec Ⅲ and MSSA-t002-agr Ⅱ among food strains. Besides, some strains found in agr group were also spa type-specific, suggesting that there may be phenotypic consistency.The clinical isolates contained more resistance genes and had higher antibiotic resistance, while the two sources strains all had high.

Characterization and microevolution of Type I-F CRISPR/Cas system in Group B2 Escherichia coli

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Escherichia coli has become one important model organism for gaining insight into the molecular mechanisms associated with Type I CRISPR/Cas system function. It has been identified to only contain Type I-E and I-F system. However, due to the low incidence of Type I-F system in E. coli, the information on its diversity and immunity role is little known. In this study, we analyzed the occurrence and diversity of Type I-F system and explored its potential for typing strains in 1198 strains of B2 E. coli. We identified 413 strains harboring Type I-F CRISPR/Cas system and 9 strains containing Type I-E system. The components of Type I-F system, including repeat, spacer and cas genes, showed high conservation within single ST or between closely related STs. CRISPR spacer content and polymorphism were instrumental for differentiating highly closely related strain, such as ST141, ST998 and ST1159. The putative acquisition and deletion of spacers could reveal the evolution model between serotypes. The spacers showed more homology with plasmids than phages. The IncF1B-, IncFII- and IncI1-typing plasmids replicons was the predominant challenge for B2 strains, suggesting that Type I-F system may play an important role in the acquisition of antibiotic resistance. Collectively, our data provides one basis for better understanding the characterization and diversity of Type I-F system and its potential for genotyping strains.

Long-noncoding RNAs and mRNAs expression profiles in RD cells infected by EV71 using RNA-seq

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Enterovirus 71 (EV71) is a main pathogen of severe hand-foot-mouth disease (HFMD). Long non-coding RNAs (lncRNAs) are recognized as pivotal factors during the pathogenesis of viral infection. However the critical functions of lncRNAs in EV71-host interactions have not been characterized. Here, we performed global transcriptome analysis of lncRNA and mRNA expression profiles in EV71-infected human RD cells using second-generation sequencing. In our study, 2216 novel lncRNAs were identified. In addition, 96 lncRNAs (58 up-regulation and 38 down-regulation) and 2233 mRNAs (1246 up-regulation and 987 down-regulation) exhibited remarkable differences (fold change≥2.0) in expression levels between infected and uninfected RD cells. Comprehensive bioinformatics analysis included target gene prediction, lncRNA-mRNA co-expression network construction, as well as GO and KEGG pathway analysis mainly focused on differentially expressed genes. Our results suggest that lncRNA may involve with the pathogenic mechanisms of EV71 infection and may be relevant to innate immunity, cellular component biogenesis and transcription-related signaling pathways. The present study provides novel insights into the functions of lncRNAs and the possible pathogenic mechanism following EV71 infection.

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Bioinformatics analysis of *Helicobacter pylori* metalloprotease gene

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University, China

To determine the sequence of the metalloprotease gene (mtp) of Helicobacter pylori MEL-Hp27 strain and investigate the structural characters and biological function of the mtp-encoded protein using bioinformatic methods. The H. pylori mtp gene was applied by PCR from H. pylori MEL-Hp27 strain, and the mtp nucleotide sequence was obtained by gene sequencing. The amino acid sequence, physicochemical properties, transmembrane region, signal peptide, glycosylation and phosphorylation sites, secondary and tertiary structure of the mtp-encoded protein (Mtp) were analyzed using bioinformatics softwares. The coding region of MEL-HP27 mtp gene is 615 bp in length, *encoding a protein comprising 204 amino acids. Bioinformatics analysis resulted in that* the homology of mtp among various H. pylori strains is 91%−98%, the metalloprotease is an unstable and alkaline hydrophilic protein, without transmembrane region and signal peptide, but contains glycosylation and phosphorylation sites. The secondary structure of metalloprotease includes alpha helix, extended strand, beta turn, and random coil, which account for 52.45%, 16.67%, 4.41%, 26.47% of the whole molecular length, respectively. The conserved structures found in Mtp suggested that this protein might belong to the M48 protein family. Mtp contains B cell-associated antigenic epitopes and CTL cell antigenic epitopes. The results indicate that Mtp is alkaline hydrophilic protein with low molecular mass, located in cytoplasm or the nucleus, might play crucial role in cellular signaling, regulation of cellular function, the mechanism of host immune response to H. pylori infection and the pathogenesis. The findings lay novel basis for approaching pathogenic mechanism and immune prevention of H. pylori infection.

To explore the relationship between Shigella tolerance and hipA and hipB genes mutation, and provides a theoretical basis for the solution of bacterial resistance

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To explore the relationship between Shigella tolerance and hipA and hipB genes mutation, and provides a theoretical basis for the solution of bacterial resistance. Shigella bacterias were isolated form suixian county of henan province in 2014 and were biochemical and serological identified. Two strains of Shigella sensitive to ampicillin were selected as sensitive strains , and they were induced by antibiotic concentration intervals of 10MIC respectively, and the tolerance evaluation index was measured. PCR was used to amplify the hipA and hipB of Shigella. The difference of hipA and hipB gene before and after induction was compared. Two strains of Shigella were successfully induced, named mel-ss2014011/YD and mel-ss2014021/YD. The MIC of Shigella before and after induction remained unchanged. The MDK99 of mel-ss2014011/YD and mel-ss2014021/YD were 4 times and 6 times of that before induction.The sequencing results showed that the mel-ss2014021/YD inducer hipA had a single base G insertion at the 226 site, and the insertion region was located in the coding region . There was a missense mutation in the 217th loci of the hipB gene (C to T Pro to Leu) and there was no hipA and hipB mutation found in mel-ss2014011/YD strain. The mutation of hipA and hipB may advance the tolerance of Shigella, and Shigella enters the state of bacterial tolerance before drug resistance occurs.

Trends in antibiotics resistance of *Staphylococcus aureus* at a teaching hospital, China, 2011-2016

Tingting Mao,
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The purpose of this study was to describe the antibiotics resistance trends of Staphylococcus aureus (S. aureus) gathered from a general hospital in Zhengzhou city, Henan province, China during 2011-2016.The resistance of 1406 S. aureus strains detected by Zhuhai Deere DL-96 Bacteria Identification System from 19,260 specimens were analyzed by Minimum inhibitory concentration (MICs). Statistical analyses were performed using the chi-squared test and the chi-squared test for trend.During the study period (2011-2016), the overall detection rate of S. aureus was 7.3% (1406/19,260), of which rates of infected S. aureus increased from 6.72% in 2011 to 8.62% in 2016 ($p=0.0421$), and resistance rates of mostly (14/18) detected antibiotics to S. aureus showed a significant downward trend (all-$p<0.05$). Among these antibiotics, resistance to cefoxitin fastest decreased, from 69.79% in 2011 to 41.9% in 2016. The isolated methicillin-resistant S. aureus (MRSA) overall detection rate was 43.1% (606/1406), which showed a downward trend of resistance rates to 13 antibiotics (all-$p<0.05$), of which levofloxacin fastest decreased from 76.47% in 2011 to 50.89% in 2016. No isolate was detected to be resistant to linezolid and vancomycin.

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Bioinformatics technology in clinical and public health microbiology applying computational methods

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The role of clinical genomics in infectious disease diagnostics and public health microbiology is the topic of discussion during a recent decade. Although much of this work is aimed at describing the structure of outbreak communities, the methodology works equally well to identify pathogens in clinical samples. Clinical genomics is the exploitation of genome sequence data for diagnostic, therapeutic, and public health purposes. Central to this field is the high-throughput DNA sequencing of genomes and metagenomes. The key concept in using clinical genomics methodology is that detection of microbes is independent of culture and is not limited to targets used for in-depth PCR assays. Rather, it is a process of generating large-scale sequence data sets that adequately sample a specimen for microbial content and then of applying computational methods to resolve the sequences into individual species, genes, pathways, or other features.

Direct evidence of viral infection and mitochondrial alterations in the brain of fetuses at high risk for schizophrenia

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There is increasing evidences that favor the prenatal beginning of schizophrenia. These evidences point toward intra-uterine environmental factors that act specifically during the second pregnancy trimester producing a direct damage of the brain of the fetus [1]. The current available technology doesn't allow observing what is happening at cellular level since the human brain is not exposed to a direct analysis in that stage of the life in subjects at high risk of developing schizophrenia. Methods. In 1977 we began a direct electron microscopic research of the brain of fetuses at high risk from schizophrenic mothers in order to finding differences at cellular level in relation to controls. Results. In these studies we have observed within the nuclei of neurons the presence of complete and incomplete viral particles that reacted in positive form with antibodies to herpes simplex hominis type I [HSV1] virus, and mitochondria alterations [2]. Conclusion. The importance of these findings can have practical applications in the prevention of the illness keeping in mind its direct relation to the aetiology and physiopathology of schizophrenia. A study of the gametes or the amniotic fluid cells in women at risk of having a schizophrenic offspring is considered. Of being observed the same alterations that those observed previously in the cells of the brain of the studied foetuses, it would intend to these women in risk of having a schizophrenia descendant, previous information of the results, the voluntary medical interruption of the pregnancy or an early anti HSV1 viral treatment as preventive measure of the later development of the illness.

Experimental research of biogas production by using sewage sludge and chicken manure bioloadings with wood biochar additive

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Bioreactor – special device, which is used for biogas production from various organic material under anaerobic conditions. In this research, a batch bioreactor with a mechanical mixer was used for biogas production from sewage sludge and chicken manure bioloadings. The process of anaerobic digestion was mesophilic (35 oC). Produced biogas was stoted in a gasholder and the concentration of its components was measured with INCA 4000 biogas analyser. Also, a specific additive (pine wood biochar) was applied to prepare bioloadings. The application of wood biochar in bioloading increases the CH4 concentration in the produced gas by 6-7%. The highest concentrations of CH4 were found in biogas produced during the decomposition of sewage sludge bioloadings. The maximum CH4 reached 77.4%. SBioreactor – special device, which is used for biogas production from various organic material under anaerobic conditions. In this research, a batch bioreactor with a mechanical mixer was used for biogas production from sewage sludge and chicken manure bioloadings. The process of anaerobic digestion was mesophilic (35 oC). Produced biogas was stoted in a gasholder and the concentration of its components was measured with INCA 4000 biogas analyser. Also, a specific additive (pine wood biochar) was applied to prepare bioloadings. The application of wood biochar in bioloading increases the CH4 concentration in the produced gas by 6-7%. The highest concentrations of CH4 were found in biogas produced during the decomposition of sewage sludge bioloadings. The maximum CH4 reached 77.4%. Studies have shown that the application of biochar in bioloadings also reduces average CO2 and H2S concentrations in biogas.

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Evaluating Cyanide Biodegradation by Bacteria Isolated from Gold Mine Effluents in Bulawavo. Zimbabwe

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The release of cyanide-rich effluents from gold mines into the environment is a global concern considering the well-known metabolic effects of cyanide. Such effluents need to be treated to remove the cyanide, among other pollutants, before their disposal. This study aimed at evaluating the feasibility of bacterial cyanide removal from cyanide-rich effluents. Firstly, cyanide-degrading bacteria were isolated from gold mine effluents and tested for their ability to grow in and tolerate increasing levels of cyanide. To evaluate each isolate's cyanide-degrading activities, isolates were grown in simulated and actual effluent and a titrimetric method was used to quantify residual cyanide over time. Cyanide degradation efficiency (DE) was then calculated for each isolate. Positive isolates were identified by 16S rRNA gene PCR and sequence analysis through BLAST (Basic Local Alignment Sequence Tool). Six cyanide-utilising bacterial isolates were obtained, two of which were identified as Klebsiella spp while the other two as strains of Clotridium bifermentans. All isolates grew normally with cyanide present, with growth being inhibited at 700 mg/L cyanide and beyond. Cyanide degradation efficiency for all isolates in the simulated effluent ranged from 79% to 97%. All isolates were able to remove cyanide from actual gold mine effluent with very high DE values (90 – 94%) being recorded. Isolates obtained in this study were able to efficiently remove cyanide from effluent, and observation that clearly demonstrates the feasibility of the biological removal of cyanide from cyanide-rich gold mine effluents and should therefore motivate research towards the possible large-scale application of this technology.

A risk-based approach for sterility testing in a small-scale 68Ga radiopharmacy: Evaluation of alternative methods

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Development and availability of radiopharmaceuticals is a key driving force of nuclear medicine establishment and expansion. Recently, the Positron Emission Tomography (PET) has become an accepted tool for diagnosing disease. This study was focused on the sterility testing of the eluate obtained from the newly established 68Ge/68Ga generator for synthesis of 68Ga DOTA-TATE. The sterility testing of the 68Ga eluate commenced on the day of elution using both tryptic soy broth (TSB, suitable for the culture of aerobic bacteria and fungi) and thioglycolate broth (TGB, suitable for the culture of anaerobic bacteria). Six species of microorganisms are proposed by the standard method to be suitable for use in the validation test, i.e.: Staphylococcus aureus, Bacillus subtilis, Pseudomonas aeruginosa, Clostridium sporogenes, Candida albicans and Aspergillus niger. Along with the standard methods approved by *European Pharmacopoeia, additional methods have been evaluated in our study.* Particularly, a suitability of TSB and TGB for growth promotion of Escherichia coli under aerobic and anaerobic conditions was assessed.

Candida albicans and *Non albicans-Candida* Single and dual species formed on catheters

Ouassila Benhabib
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Only few research attempts to study bi or multi species yeast biofilms, especially Candida albicans vs. non-albicans species. In this context, we planned to search multi-species biofilms of Candida which were formed on the same intravascular catheter taken from patients hospitalized in west Algeria.Material and methods: For their ability to form biofilms, the prepared single- or mixed-cell suspension were standardized to 106 yeast cells/mL after counting calculated by measuring OD492 with a spectrophotometer. And mixed biofilm formation was visualized by Scanning Electron Microscope. Candida albicans –Non albicans Candida species together formed more complex biofilms compared to the single-species biofilms, clearly pointing to the mutualism interactions of these dual-species biofilms. We observed the morphological and architectural features formed on between dual yeast cells. Non albicans- Candida biofilm, always in close association with Candida albicans hyphae grown on external and inner surface of catheter after an implanted time of 48 hours .: Results point to the need in-depth studies to combat the mixed-species biofilms responsible of catheter infection.

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Abstract

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Development of eco-friendly and sustainable biostabiliser products for road construction

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The construction industry is rapidly exploring new and exciting opportunities involving the use of biological processes and products to modify the structural properties of the road subsurface, (e.g. strength, volume stability, durability, and permeability) through innovative engineering techniques. Enabled by interdisciplinary research at the confluence of microbiology, civil engineering, and geochemistry, this integrative approach has the potential to meet society's ever-expanding needs for innovative treatment processes that improve soil, supporting new and existing infrastructure. Several microorganisms and other existing bio-enzymatic products such as secondary metabolites, enzymes, endospores, and extracellular polymeric substances have been considered as potential alternatives to conventional chemical soil stabilisers for the development of sustainable road infrastructure. However, the primary challenge with this bio-based approach is the selection of the correct microorganisms which requires medium to high throughput strength testing methodology. This study focused on the testing of fermentation derived fractions of biological materials using in-vitro miniaturised tests on selected soil types and waste (i.e. weathered granite, dolerite and fly ash) to validate screening and selection methodology, using an existing Bacillus strain hypothesised to have strength enhancing properties. Unique miniaturised test equipment was successfully developed using 3D CAD and 3D printing technologies, enabling the successful evaluation of biological components. This work forms the basis for in-vitro selection methodology to enable the development of improved biological stabiliser products for the construction industry.

Beta-lactamase producing bacteria in community and hospital setting in riyadh: Occurrence and susceptibility to antibiotics

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Extended-spectrum β-lactamase producing bacteria (ESBL) poses an increasing challenge to both public health and hospital infection control services. Objective: To determine the prevalence of ESBL producing bacteria, types of infection they cause and their susceptibility patterns to antibiotics in hospital and community settings. This is a cross-sectional study that was conducted at a Medical City in Riyadh. All clinical specimens with positive culture for Gram-negative bacteria were collected from the microbiology laboratory for the year 2013. When bacteria are identified as ESBL strain, the antimicrobial susceptibility is analyzed. Demographic data were collected from patients' records. Overall, 763/6993 (10.9%) were ESBL producing strains. The highest detection of ESBL bacteria were from specimens of patients over sixty years (34.2%), and 23.7% were from 0-<15-year-old. The most frequently detected bacteria was *E. coli* (76.5%) with highest detection from urine, skin swab, blood, wound and ulcer specimens, followed by K. pneumonia (23.1%) with highest detection from respiratory specimens including sputum. The resistance pattern to antimicrobials was (75.5%, 81.3%) to trimethoprim/sulfamethoxazole, (69.7%, 42.6%) to ciprofloxacin, (38.9%, 58.5%) to gentamicin and (8.7%, 30.7) to piperacillin/tazobactam (E. coli, K. pneumonia respectively). However, very high sensitivity to imipenem and meropenem was reported for both bacteria. Generally, ESBL bacteria isolated from outpatients showed significantly higher resistance to ciprofloxacin than the isolates from inpatients ($p=0.02$), conversely is detected with piperacillin/tazobactam ($p<0.0001$). Conclusion: Currently, carbapenems and amikacin are the first line antibiotics that can be used for the treatment of ESBL bacterial infections in both settings.

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Antifungal susceptibility and virulence on murine model of *Aspergillus fumigatus* environmental isolates from a public tertiary hospital in Metro Manila, Philippines

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The increase in the number of invasive Aspergillus infections has been observed among immunocompromised individuals. There is also an elevated incidence of invasive aspergillosis among hospitalized patients (Rajasingham et al., 2017). In the Philippines to date, there is no published data that focused on the prevalence of Aspergillus species or any other thermotolerant fungal species in a hospital environment. Ten isolates of A. fumigatus were preserved from the previous unpublished study of the principal investigator on this recent research, where an environmental air sampling using Andersen Air Sampler was conducted in six wards of a public tertiary hospital in Metro Manila. This research served as a preliminary study to characterize the antifungal susceptibility of environmental isolates of Aspergillus fumigatus from a hospital facility against three antifungal agents. Moreover this study conducted an animal survival analysis to determine the virulence of these isolates on BALB/c mice. Lung tissues of infected mice were also subjected to histopathology. Etest result for antifungal susceptibility testing showed that two isolates were resistant (Non- Wild type) to amphotericin B (AF2-A and AF-3A); one isolate resistant to voriconazole (AF2-A) and an isolate that manifested non- susceptibility to caspofungin (AF2-A). Epidemiological cut-off values were determined for each antifungal following the M38-A2 CLSI guidelines. BALB/c mice survival analysis revealed that the isolate with the highest Minimum Inhibitory Concentration (MIC) for voriconazole resulted to the most number of mortality with the least number of observation days. Gomori Methenamine Silver stain (GMS) and Hematoxylin & Eosin (H&E) histopathology slides showed fungal elements embedded in lung tissue of mice.

Pseudomonas biofilm, swarming motility and biocides Resistance

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Nowadays, it is known that biofilm are potent refuge for the bacterial resistance, making their elimination a big challenge in several macro or micro-ecosystems. However, understanding the mechanisms by which these microorganisms develop biofilm has remained elusive because the role of motility. Swarming motility is one of the most impressive features of microbial life and requires extended investigations. Till now days, many studies have indicated that swarming is the most complex type of bacterial motility, it roles include the colonization of hydrated-viscous surfaces, the formation of biofilms and antibiotics or biocides resistance. Furthermore, the direction of this movement is biased by chemotactic responses to several stimuli. In this study our ultimate goal is to covers recent advances in biofilm formation and to describe certain factors linked to biofilm resistance. A great resistance to 45 components of costus roots separated by GC / MS was recorder. It is important to note that future endeavors are needed to elucidate mechanisms that reduce the susceptibility of biofilms to biocides.

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Abstract

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Detection of androgenic-mutagenic compounds and potential autochthonous bacterial communities during *in-situ* bioremediation of hazardous distillery waste

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Sugarcane-molasses-based distillery waste is well known for its toxicity and complex mixture of various recalcitrant organic pollutants, but the chemical nature of these pollutants is unknown. Distilleries release 12 to 15 liters of spent wash per liter of alcohol produced. Currently, there are more than 319 distilleries in India, reflecting the magnitude of the problem due to the presence of various complex pollutants in anaerobically digested distillery waste. This study revealed the presence of toxic organic acids (butanedioic acid bis(TMS)ester; 2-hydroxysocaproic acid; benzenepropanoic acid, and other recalcitrant organic pollutants (2-furancarboxylic acid, 5-[[(TMS)oxy] methyl], TMS ester; and tricarballylic acid 3TMS, dodecanoic acid, octadecanoic acid, n-pentadecanoic acid, hexadecanoic acid, β-sitosterol, stigmasterol, β-sitosterol trimethyl ether, heptacosane, dotriacontane, lanosta-8, 24-dien-3-one, 1-methylene-3-methyl butanol, 1-phenyl-1-propanol, 5-methyl-2-(1-methylethyl) cycohexanol, and 2-ethylthio-10-hydroxy-9-methoxy-1,4 anthraquinone which are listed as endocrine-disrupting chemicals. In addition, several major heavy metals were detected, including Fe (163.947), Mn (4.556), Zn (2.487), and Ni (1.175 mg l−1). Bacterial community analysis by restriction fragment length polymorphism (RFLP) revealed that Bacillus, Stenotrophomonas, and Enterococcus were dominant autochthonous bacterial communities belonging to the phylum Firmicutes and γ-Proteobacteria. The presence of Bacillus Stenotrophomonas and Enterococcus species in highly toxic environments indicated its broad range adaptation. These findings indicated that these autochthonous bacterial communities were pioneer taxa for in situ remediation of this hazardous waste during ecological succession. Further, a toxicity evaluation showed a reduction of toxicity in degraded samples of distillery waste, confirming the role of autochthonous bacterial communities in the bioremediation of distillery waste in situ.

In vivo profiling of microbial reduced graphene oxide nanoparticles for bone tissue engineering applications

Kavitha Kandiah,
Periyar University, India

Due to the hazards of chemical and physical synthesis of reduced graphene oxide nanoparticles (rGO NPs) needs toward eco-friendly, high yield and potential biological activity of rGO NPs is highly in driving force in orthopedics, drug delivery, cancer treatments and antimicrobial studies. Hence, this study focused on the Indian traditional with medical valuable plants such as Agaricus bisporus, Zizyphus jujube and Cynodon dactylon associated microbial populations (extremophilic actinobacteria; MAA-1, IJLA5 and CDA respectively) were used to synthesis of rGO NPs. The prepared nanoparticles subjected to UV, XRD and FE-SEM characterization study and was exhibited all the biologically synthesized nanoparticles are reduced graphene oxide. The DPPH radical assay of all the prepared NPs at 500 mg concentrations showed better scavenging activity [Agaricus bisporus associated actinobacterial reduced rGO (MAA-1: 70.45%), Zizyphus jujube isolated actinobacterial rGO (IJLA5:65.75%), C. dactylon leaf associated actinobacterial rGO (CDA: 69.57%)]. In addition, In vitro study in PC-12 cell line and In vivo acute toxicity study in Wistar rat conformed non-significant toxicity and the feasibility of the Agaricus bisporus associated actinobacterial reduced rGO in biomedical applications compare than all other microbial mediated rGO, and chemical synthesized rGO respectively.

SPEAKER SLOTS AVAILABLE

Abstract

EuroSciCon

Detoxification of endocrine disrupting chemicals and residual organic pollutants from pulp and paper mill effluent by *autochthonous* bacteria

Pooja Sharma,
Babasaheb Bhimrao Ambedkar Central University, India

Effluent discharged from the pulp and paper industry contains various refractory and androgenic compounds, even after secondary treatment by activated processes prevailing for effluent treatment at industrial scale. Detailed knowledge is not yet available regarding the properties of organic pollutants and methods for their bioremediation. This study focused on detecting residual organic pollutants of pulp and paper mill effluent after biological treatment and assessing their degradability by biostimulation. The major compounds identified in the effluent were 2,3,6-trimethylphenol, 2-methoxyphenol (guaiacol), 2,6-dimethoxyphenol (syringol), methoxy-cinnamic acid, pentadecane, octadecanoic acid, trimethylsilyl ester, cyclotetracosane, 5,8-dimethoxy-6-methyl-2,4-bis(phenylmethyl)napthalen-1-ol, and 1,2-benzendicarboxylic acid diisononyl ester. Most of these compounds are classified as endocrine-disrupting chemicals and environmental toxicants. Some compounds are lignin monomers that are metabolic products from secondary treatment of the discharged effluent. This indicated that the existing industrial process could not further degrade the effluent. Supplementation by carbon (glucose 1.0%) and nitrogen (peptone 0.5%) bio-stimulated the degradation process. The degraded sample after biostimulation showed either disappearance or generation of metabolic products under optimized conditions, i.e., a stirring rate of 150 rpm and temperature of 37 ☐} 1◦C after 3 and 6 days of bacterial incubation. Isolated potential autochthonous bacteria were identified as Klebsiella pneumoniae IITRCP04 (KU715839), Enterobacter cloacae strain IITRCP11 (KU715840), Enterobacter cloacae IITRCP14 (KU715841), and Acinetobacter pittii strain IITRCP19 (KU715842). Lactic acid, benzoic acid, and vanillin, resulting from residual chlorolignin compounds, were generated as potential value-added products during the detoxification of effluent in the biostimulation process, supporting the commercial importance of this process.

Infection control management of infectious diseases

Gampa Vijaya Kumar,
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This study was designed to provide information regarding the management of patients with specified infectious diseases. The Infection Control Management of Infectious Diseases as an informational guide . Standard precautions (SP) must be applied when caring for any patient regardless of their infectious disease and its consequences. Transmission-based precautions are applied in addition to standard precautions and include the basic parameters, Contact Precautions Transmission occurs by either direct or indirect contact, Direct: involves close contact with a colonized / infected patient with transfer of the organism to the, susceptible host, usually in the course of patient care activities e.g. turning a patient. Indirect: occurs if an infectious agent is transferred via a contaminated intermediate object (fomite) or person e.g. when contaminated patient-care devices are shared between patients without cleaning and / or disinfection between patients. Droplet Precautions Transmission occurs through large (i.e.☐ >5 microns in size) respiratory droplets that are generated by an infected person who is coughing, sneezing or talking. The droplets do not remain suspended in the air and are propelled a short distance from the source (approximately 1 metre). There is also the potential for indirect contact transmission as the droplets settle on environmental surfaces. Airborne Precautions Transmission occurs by small (i.e.5microns in size) respiratory droplets which are carried through the air. The droplets can remain suspended in the air for long periods and can be dispersed by currents.

SPEAKER SLOTS AVAILABLE

Heavy metal accumulation by potential by hyperaccumulator weeds & grasses from Endocrine-disrupting chemicals rich complex distillery sludge and their microscopic observations during In-situ phytoremediation

Sonam Tripathi,
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Sugarcane-molasses based distillery waste is a threat to environment for its safe disposal due to complexation of endocrine-disrupting chemicals (EDCs) containing mixture of organic pollutants. This study revealed that distillery sludge contains not only mixture of complex organic pollutants but also retains mixture of heavy metals, Fe (5264.49), Zn (43.47), Cu (847.46), Mn (238.47), Ni (15.60), and Pb (31.22 mg kg−1). The major identified organic compounds were benzene, 1-ethyl-2-methyl, Benzene, 1-ethyl-4-methyl benzoic acid, 3, 4, 5-tris (TMS oxy), TMS ester; Hexanedioic acid, dioctyl ester; stigmasterol TMS ether; 5α-cholestane,4-methylene; campesterol TMS; β-sitosterol and lanosterol. These compounds are listed under the EDCs also as per U.S. Environmental Protection Agency. However, the Phytoextraction potential of growing native weeds and grasses i.e. Argemone mexicana, Saccharum munja, Cynodon dactylon, Pennisetum purpureum, Chenopodium album, Rumex dentatus, Tinospora cordifolia, Calotropis procera and Basella alba revealed the high accumulation of Fe, Zn, Cu, Mn, Ni, and Pb in their root and leaves compared to shoot. This indicated high accumulation and translocation capabilities of these plants. Further, the bioaccumulation coefficient factor (BCF) and translocation factor (TF) was found>1 for majority of plants for various metals. Thus, this given strong evidence for hyperaccumulator tendency of these native weeds and grasses from complex polluted sites. Furthermore, the ultra-structural observations of root tissues also revealed the deposition of heavy metals at various cellular components without any apparent toxic effects. This indicated the variable adaptive characteristics for application of these plants growing at a hazardous waste polluted site.

Structural insight into the enhanced pollutant-degrading capabilities of engineered biphenyl dioxygenases and wild type phthalate dioxygenase

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Biphenyl dioxygenase of Burkholderia xenovorans LB400 BphAE (LB400)) is a multicomponent Rieske-type oxygenase that catalyzes the dihydroxylation of biphenyl and many polychlorinated biphenyls (PCBs). The structural basis for the substrate specificity of the enzyme's oxygenase component (BphAE(LB400)) are largely unknown. BphAE (p4), RR4 and II9, variants obtained through directed evolution, transforms several chloro biphenyls, including more efficiently than BphAE(LB400). Here, we compare the structures of BphAE(LB400) and its variants and examine the biochemical properties of these enzymes. This study provides important insight about how Rieske-type oxygenases can expand substrate the range through mutations that increase the plasticity and/or mobility of protein segments lining the catalytic cavity. Additionally, phthalate dioxygenase system (PDOS) initiates the aerobic breakdown of phthalate by forming cis-dihydrodiol phthalate with consumption of NADH and O2. Here we present the structural insights into phthalate dioxygenase (PDO) from Cupriavidus metallidurans. The crystallographic structure of PDO and PDO-phthalate complex determined to 1.8 A˚ and 2.2 A˚ respectively, revealed an overall unique fold and unusal dioxygenation position of 3, 4 compared to other gram negative bacterial strains. We have depicted that catalytic domain features the largest substrate binding cavity characterized so far within oxygenase family, where part of cavity is lined with polar residues for interaction with phthalate.

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Abstract

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Structure-assisted discovery of antivirals targeting *chikungunya virus* protease

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Chikungunya virus (CHIKV), a pathogenic arbovirus that poses a public health threat. Currently, no specific antivirals are available against CHIKV infection. CHIKV nsP2pro is the virus specific protease, which splices the nonstructural polyprotein into individual non-structural proteins essential for the viral replication complex formation. Hence, constitutes an attractive target for antiviral drug development. In this study, the crystal structure of nsP2pro has been determined and structure analysis done that revealed the presence of a variable loop gating the active site. Structural comparison of CHIKV nsP2pro with other alphavirus nsP2pro has disclosed the presence of substrate binding residue Asn547 on this variable loop. The Asn547Ala substitution led to three fold reduction in nsP2pro activity, indicating the specificity of Asn in substrate recognition & binding. Furthermore, based on the crystal structure of CHIKV nsP2pro, two peptidomimetics compounds (PepI & PepII) were identified and a fluorescence resonance energy transfer (FRET) based CHIKV nsP2 protease assay was developed to assess the nsP2pro activity with its fluorogenic substrate peptide. This FRET assay was utilized to evaluate the inhibition potential of Pep I & Pep II. Both the compounds were found to inhibit nsP2pro with IC50 values of 34μM and 42μM, respectively. The inhibition constant (Ki) value is 33.34±2.53 μM for Pep-I and 45.89±4.38 μM for Pep-II. Moreover, plaque reduction assay and RT-PCR analysis revealed that these compounds specifically inhibit CHIKV replication. Our studies of structure-asisted identification of nsP2pro inhibitor molecules pave way to the rational approach for development of novel antivirals against CHIKV.

Combined effect of linolenic acid and tobramycin on *Pseudomonas aeruginosa* biofilm formation and quorum sensing

Warren Chanda,
Dalian Medical University,

Pseudomonas aeruginosa is a ubiquitous Gram negative opportunistic pathogen capable of causing severe nosocomial infections in humans, and tobramycin is currently used to treat P. aeruginosa associated lung infections. Quorum sensing regulates biofilm formation which allows the bacterium to result in fatal infections forcing clinicians to extensively use antibiotics to manage its infections leading to emerging multiple drug resistant strains. As a result, tobramycin is also becoming resistant. Despite extensive studies on drug discovery to alleviate microbial drug resistance, the continued microbial evolution has forced researchers to focus on screening various phytochemicals and dietary compounds for antimicrobial potential. Linolenic acid (LNA) is an essential fatty acid that possesses antimicrobial actions on various microorganisms. It was hypothesized that LNA may affect the formation of biofilm on P. aeruginosa and improve the potency of tobramycin.

Pharyngeal colonization and drug resistance profiles of morraxella catarrrhalis, *streptococcus pneumoniae*, *staphylococcus aureus* and *haemophilus influenzae* among hiv infected children attending art clinic of felegehiwot referral hospital, ethiopia

Derese Chekol,
Bahir Dar University,

Asymptomatic pharyngeal colonization by potential bacteria is the primary reservoir for bacterial species within a population and is considered a prerequisite for development of major childhood diseases such as sinusitis, otitis media, pneumonia, bacteremia, and meningitis. However, there is dearth of data on the colonization and drug resistance pattern of the main bacterial pathogens in the pharynx of HIV infected children in Ethiopia. Therefore, this study determined the pharyngeal colonization and drug resistance profile of bacterial pathogens in HIV infected children attending ART clinic of Felegehiwot Referral Hospital (FHRH), Amhara Region, Ethiopia

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Abstract

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Enterococcus faecalis as nosocomial pathogen

Fatoba Johnson Sunday,
University of Benin,

Enterococcus faecalis is Gram-positive, catalase-negative, non-spore-forming, facultative anaerobic bacteria, which usually inhabit the alimentary tract of humans in addition to being isolated from environmental and animal sources. They are able to survive hostile environments, such as in extreme temperature (5-650C), pH (4.5-10.0) and high NaCl concentration, enabling them to colonize a wide range of niches. Depending on the site of infection this organism colonizes, invades the host tissue using their surface adhensin causing pathological changes in the host. Enterococcus faecalis is the leading causative agent of serious nosocomial infections such as urinary tract infection (UTIs), endocarditis, bacteremia, intra-abdominal and intra-pelvic abscesses. This organism may frequently be acquired by cross-infection from other patients and through contaminated medical equipments. Diseases cause by this organism can be treated with antibiotics such as gentamycin, vancomycin and daptomycin. Cautious use of antibiotics and implementation of infection control measures are ways of preventing this infection. Understanding the pathogenicity and antibiotics resistance of this organism will help in preventing it from causing nosocomial infection

The Influence of CD4 cells count on bacteriuria Among HIV/AIDS individuals

Zenoh Danjuma,
Taraba State University Jalingo,

Urinary tract infections (UTIs) is defined by a bacterial count of ≥105 CFU/mL, or 103 CFU/mL in pregnant women; the threshold defining UTIs in HIV positive individual is rare. This work attempts to investigate the bacterial count diagnostic of UTIs in HIV/AIDS individuals. Methods: Over 220 HIV/AIDS positive (test subjects) and 180 negative (control subjects) individuals attending Government House Clinic Jalingo Taraba State, Nigeria between February and July, 2017 were sampled. A mid-stream clean catch urine and 3mLs of blood were collected from each subject. The urine was examined for the presence and enumeration of bacteria by culturing 0.001mL on CLED and blood agar; and the blood was analysed for the CD4 cell count using Partec CD4 cyflow counter machine. Alere Determine HIV-1/2 rapid test kits were used to authenticate the status of the subjects, and data were analysed statistically. Result: The prevalence of significant bacteriuria (≥105 CFU/mL) does not vary significantly with CD4 count level. Statistical analysis shows no significant association between bacteriuria and the host's CD4 cells level. (X=1.96 df = 6 P=0.37). Symptoms of UTIs were observed only among those with bacteria count of 104 CFU/mL and above in the control subjects, in the test subjects however, subject exhibited symptoms even at low bacterial count of ≤103 CFU/mL. Conclusion: Data obtained in this study showed that CD4 level may have little or no effect on bacteriuria, but with low CD4 count, subjects are more likely to exhibit symptoms of UTIs even at a low bacterial count.

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Abstract

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Antibiotic Resistance and Potential Role of CRISPR Type Mechanisms

Simon Raymond,
Scientific Research and an Alumnus of Melbourne University, Australia

There has been increasing attention directed toward antimicrobial resistance as a contributory factor with respect to current severity level issues (as defined by UN and WHO) in regards to infectious disease type situations globally.This presentation discusses the possibility that pathogens may contain mechanisms similar to that of the CRISPR type category which conduct analysis of the human genes in assessment of what genes contribute the robustness of human cells with regards to antibiotics, as a means to determine how to enhance functioning in a manner as to achieve sturdy and robust protection against the anti-replicative (and toxic) effects of antimicrobials by way of mimicking the genetic functions of human beings.The above is as opposed to development of pathogen resistance being based simply on random mutation and survival of microorganisms that have (through random mutation) come to contain enhanced survival functioning.This research however is only in the early phases.Previous research has already shown that micro-organisms through actual molecular mimicry have managed to develop the ability to perform voltage gated ion channel communications to each other. Other current research by the presenting author: 1.Application of Quantum Physics to Medicine and Surgery-To advance into the future the practice of medicine and surgerySite Attachment Inhibition Therapeutics Development of the third branch of antimicrobial therapeutics. As opposed to the two historic methods, site attachment inhibition focuses on negation of attachment by the micro-organism to the human cellular biology. Site attachment inhibition includes new generation immunization which utilises stem cell therapy in the period of embryogenesis, spanning back to oogenesis and spermatogenesis. In conclusion, This presentation discusses new areas of research with regards to antibiotic resistance.

Molecular investigation of *Mycobacterium avium subsp. paratuberculosis* infection and its associated pathological lesions in small ruminants

Farhan Anwar Khan
The University of Agriculture

Paratuberculosis (ParaTB) is a chronic granulomatous infectious disease of animals also known as Johne's disease (JD), caused by Mycobacterium avium subsp. paratuberculosis (MAP). Paratuberculosis is also a serious public heallth concern as MAP is responsible for Crohn's disease in human beings. This infectious disease is one of an unexplored disease so far in Khyber Pakhtunkhwa (KPK) Province of Pakistan either in large or small ruminants. Therefore this study was proposed for an investigation of presence of MAP by indirect ELISA (iELISA), associated histopathological lesions, and PCR in sheep and goats at district Peshawar, KPK, Pakistan. Serum (n=75) and faecal (n=75) samples were collected separately at random from goats (n=150) and sheep (n=150) from farms situated in the urban and rural areas of district Peshawar, while tissue samples (n=100) (intestine, mesenteric lymph node) as well as serum samples (n=100) were collected at random from goats (n=200) and sheep (n=200) at abattoirs of district Peshawar. By iELISA seroconversion at farm level was determined in 6% and 8% of goats and sheep, respectively, whereas serum samples from abattoirs exhibited prevalence of MAP antibodies in 8% and 9% of goats and sheep, respectively. Ziehl Nielsen (ZN) staining showed acid-fast bacilli (AFB) in 11% of goats and 13% of sheep's faecal samples. Gross pathology (thickness, corrugation) and histopathological lesions (infiltration of polymorpho-nuclear and mono-nuclear cells, micro-granulomas) were observed in 22% and 30% of goats and sheep intestinal samples, while MLN exhibited pathology (haemorrhages, oedematous swelling, infiltration of polymorpho-nuclear and mono-nuclear cells, micro-granulomas) in 27% and 30% goats and sheep respectively. Additionally, PCR confirmed 3% goats and 5% sheep faecal samples positive for MAP. It is concluded that seroprevalence of MAP specific antibodies in small ruminants, presence of lesions and AFB in tissue samples associated with MAP, and confirmation of MAP by PCR in this study indicated the presence of MAP in local animals of district Peshawar. This could be a serious threat to livestock as well as public health in a region.

SPEAKER SLOTS AVAILABLE

Abstract

Bioconversion of feather wastes to potential feed supplement using *keratinase* from *Bacillus licheniformis*-K51

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University of Ibadan

Bacterial keratinases are important hydrolytic enzymatic tools produced only in the presence of keratin-containing substrates such as feathers. Accumulation of chicken feather waste generated by commercial poultry processing plants leads to wastage of the protein-rich substrate. Keratinase producing bacteria can play an important role in the removal of poultry feather waste by recycling them into useful byproducts. Ten grams of white native chicken feathers were treated with keratinase from Bacillus licheniformis-K51 (EZYKer-51). The degraded keratinase-treated feathers were analysed using Fourier-Transform Infrared Spectroscopy (FTIR). Amino acid profile of keratinase-digested feathers was determined using gas chromatography and the energy profile, proximate content and in vitro protein digestibility were determined using standard methods. EZYKer-51 completely degraded 10 g of white native chicken feathers within 48 h at pH 8, 50oC and 150 rpm. FTIR of digested feather confirmed stages in feather degradation. Eighteen amino acids, including all the essential amino acids were obtained from EZYKer-51-digested feather which also had energy content of 4.4 kcal/g compared to unhydrolysed feather (0.9 kcal/g). The digested feather yielded 88.7% crude protein and had 78.0% in vitro digestibility which was higher than the crude protein (13.4%) and in vitro digestibility (6.8%) of unhydrolysed feather. Keratinase from Bacillus licheniformis-K51 shows great suitability for conversion of feather waste to easily digestible proteins with high nutritional and energy content which can serve as potential supplements for animal feeds

Isolation and characterization of *Klebsiella pneumonia* bacteriophage

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Palestine Polytechnic University, Palestine

Klebsiella pneumonia is a Gram-negative, non-motile bacteria that are found ubiquitously in nature. It frequently causes human nosocomial infections especially in immune-compromised patients, leading to respiratory tract, urinary tract and blood stream infections. Due to the extensive usage of broad-spectrum antibiotics in hospitalized patients, the incidence of multidrug-resistance producing strains among clinical isolates has been increasing. Consequently, this has rekindled the interest in using phage therapy as a safe and effective treatment for multidrug resistance pathogens. The rapid ability of phages to lyse bacteria and their specificity make them effective alternative to antibiotics. Results demonstrated a successful isolation of a Klebsiella bacteriophage isolated from sewage water. The bacteriophage was able to host and completely lyse the Klebsiella bacterium as a first case reported in Palestine. The results were confirmed several times to ensure consistency. It also gave positive results when spotted on different Klebsiella strains. In addition, one-step growth curve using a double layer plaque assay was performed to determine the phage life cycle phases of infection. It showed a latent period of about 3.5 h, burst period of 10 h and a burst size of about 102.5×106 PFU /plaque, Furthermore, SDS-PAGE results reveled that four major bands have been detected for phage structure proteins their size : 75KDa,100KDa,135KDa,and 180KDa.

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Abstract

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Impact of resistance genes (L119F-GSTe2, Cyp6p9a and Cyp6p9b) mutations on blood meal process of Anopheles funestus, major African malaria vector.

Lynda Nouagea,
University of Yaoundé,

Mosquito species such as, Anopheles funestus have adopted haematophagy to ensure egg development and high reproductive rate. Recently, two mutations that confer resistance to insecticide in Anopheles funestus mosquito, were reported to significantly impact the longevity and reproductive performance of Anopheles funestus mosquito species. In this study, we aimed to assess the impact of these two mutations on blood meal size An. funestus mosquito.

F1 progenies from blood feed field-collected mosquitoes were used to assess the impact of L119F-GSTe2 mutation, whereas for Cyp6p9a/b, we used F4 females from crossing between insecticide susceptible and resistant An. funestus lab strains. Mosquitos were allowed to feed on the arm of human for 30 minutes. The size of blood meal measured by quantifying human hemoglobin in the abdomen of feed mosquitoes. DNA extracted from head and thoraces of each mosquito was used for genotypying of L119F-CSTe2 or Cyp6p9a/b mutations. For the L119F-GSTe2 the size of blood meal was not significantly different between homozygote resistant 3.9 µl/mg), heterozygote (3.74 µl/mg) and susceptible (3.48/mg) mosquitoes. This suggest that the L119F-GSTe mutation has no impact on the size of blood meal in An. funestus. The analyse combined of Cyp6p9a/b show a significant difference of blood meal volume in the tree genotypes.

This study seems to indicate that some detoxifications enzymes, such as, cytochrome P450 implicated in insecticide resistance could be impact the blood meal size of An. funestus mosquito species. However further studies are needed to be more informative on the consequence in the vectorial capacity.

Human *Papillomavirus* Infection in genital women in four regions of Senegal

El Hadji Seydou Mbaye,
Aristide Le Dantec Hospital

Cervical cancer is the most frequent cancer among women in Senegal. However, there are few data concerning the HPV types inducing neoplasia and cervical cancers and their prevalence, in the general population of Senegal The aim of this study is to determine the prevalence of HPV infection in Senegalese women aged from 18 years and older.A study was performed on 498 cervix samples collected from healthy women aged 18 and older in Dakar. 438 other samples were collected from three other regions, Thiès, Saint Louis and Louga. The samples were screened for 21 HPV genotypes using an HPV type-specific E7 PCR bead-based multiplex genotyping assay (TS-MPG) which is a laboratory-developed method for the detection of HPV.The prevalence for pHR/HR-HPV in the region of Dakar was 20.68%. HPV 52 (3.21%) was the most prevalent HPV type, followed by HPV 16 (3.01%) and HPV 31 (3.01%). In the regions of Thiès, Louga and Saint Louis, the prevalence for pHR/HR-HPV was 29.19%, 23.15% and 20%, respectively. The study revealed the specificity of the HR-HPV prevalence in Dakar and other regions of Senegal. The patterns differs from the one observed in the other regions of the world and rise the issue of the development of vaccination program in the country. Such a program should take into account the real HPV prevalence for an effective protection of HPV-associated diseases.

SPEAKER SLOTS AVAILABLE

Abstract

EuroSciCon

Antimicrobial susceptibility pattern of *Enterobacteriaceae* isolated at the french medical institute for mothers and children Kabul, Afghanistan

Mohammad Khalil Elaj,
French Medical Institute for Mothers and Children

Antibiotic resistance in Enterobacteriaceae is a serious global concern. Enterobacteriaceae are responsible for a large proportion of serious, life-threatening infections and resistance to multiple antibiotics in these organisms is an increasing global public health problem. The quick emergence of resistant bacteria is happening worldwide, risking the efficacy of antibiotics. Execution of recommended steps, such as rapid diagnosis, implementation of antibiotic stewardship programs and better infection control measures, are likely to be effective to prevent the spread of ESBLs and other forms of resistance in Enterobacteriaceae. The aim of this study was to determine the frequency of causative organisms belonging to Enterobacteriaceae among patients who are suspected having bacterial infections and susceptibility pattern of the isolated bacteria for the commonly used antibiotics. A descriptive Cross sectional study was conducted. Records of all patients referred or admitted to FMIC and undergone for culture and sensitivity tests on their clinical samples, including blood, urine, sputum, pus, wound and exudates during January 2016 to December 2016 were reviewed. Data was entered and analyzed with the help of SPSS version 22.0. The approval for the data collection was obtained from the Ethical Review Committee of FMIC. A total of 2500 blood culture, 3600 urine, and 3541 cases of pus and vaginal which was suspected bacterial infection. Totally 6048 cases of blood, urine and miscellaneous identified gram negative bacteria consecutive. All isolated organism were highly resistant to commonly used empirical antibiotics for treatment of Enterobacteriaceae like Augmentin, cephalosporin, inappropriate use of antibiotics by physicians is leading to resistance, mortality and morbidity.

Why Our body acts against Facts of Physics in Fever

Yacob Mathai,
Marma Heatth Centre

According to the facts of physics, if temperature increases, thermal expansion of an object is positive it will expand and with decrease of temperature it will shrink. Pressure will increase due to increase of temperature.On the contrary, during fever we can see blood vessels and skin are shrunk, pressure decreases, body shivers, sleep increases, motion decreases, inflammation increases, body pain increases, blood circulation decreases, dislike cold substances etc...In fever, the firing rate of Warm sensitive neurons decreases, and the firing rate ofCold sensitive neurons increases.At the same time if we apply hotness from outside by thermal bag or if we drink hot water, our body acts according to the Facts of Physics- increase of temperature pressure will also increase, expands blood vessels and skin, body sweats, motion will increase , inflammation will decrease , body pain will decrease, blood circulation will increase, like cold substances etc..During fever, why our body acts against Facts of Physics? when disease increases, pressure and temperature will decrease. Blood circulation will decrease due to decrease of pressure. If the essential temperature of the body is going out, essential temperature and pressure will further decrease. This will further endanger the life or action of organ. when disease increase, it is the sensible and discreet action of brain that tends to act against facts of physics to sustain life or protect organ .There is no way other than this for a sensible and discreet brain to protect the life or organ.We will get a clear answer if we find out the purpose of fever, sensible and discreet action of brain . No medical books clarify this1During fever, if the temperature of fever is not a surplus temperature or if it is not suppose to be eliminated from the body, the shrinking of skin and blood vessels, shivering of body, dislike towards cold substances etc are a protective covering of the body to increase blood circulation to important organs of the body it is against the facts of physics.

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