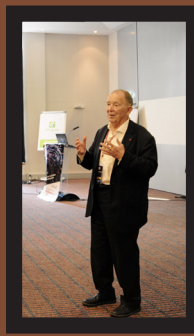


POSTER

Abstracts



EuroSciCon Conference on

VIROLOGY AND INFECTIOUS DISEASES

April 22-23, 2019 | Athens, Greece

April 22-23, 2019
Athens, GreeceSecil Sevinc et al., Arch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

THE DETECTION OF BOVINE CORONAVIRUSES IN FECAL AND NASAL SPECIMENS FROM CATTLE IN TURKEY

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Coronaviruses have been described in many mammalian species, including humans, and have gained prominence in zoonotic preserve viruses, especially after SARS-coronavirus (Severe Acute Respiratory Syndrome) and MERS-coronavirus (Middle East Respiratory Syndrome) outbreaks. Bovine infectious coronaviruses (BCoV), often have been described as an important cause of diarrhea, especially in newborn calves, in many countries including Turkey. Besides the newborn calves' diarrhea, BCoV also causes digestive system infections (winter dysentery) and respiratory system infections in adult cattle. In this study, we aimed to investigate the presence of coronavirus as an aetiological agent in cattle with respiratory disorders or diarrhea and to analyze the relationship with other coronaviruses reported before. Therefore, 50 feces samples and 50 nasal swab samples from calves with diarrhea and adult cattle with respiratory disorders, respectively, were tested for the presence of coronavirus. Among the nasal samples and fecal samples, 5 (10%) and 8 (16%) were positive based on the results for BCoV N gene by nested RT-PCR (Reverse Transcription-Polymerase Chain Reaction). Sequence analysis was performed via service procurement. Comparison analysis completed with the web tool NCBI-BLAST, BioEdit and MEGA-X programmes for phylogenetic analysis. Our results demonstrated that BCoV is a pathogen having a role in mentioned disorders alone or along with other possible viral or bacterial pathogens. The phylogenetic analysis of N gene region of detected BCoVs indicated that all of them were related to the reference strain Mebus. Further studies on the epidemiology and molecular characterization of different gene regions will provide a better understanding of the importance of BCoVs in these cases and the pathogenetic mechanism that provides sensitivity to different systems. Thus, the analysis of S gene, coding the protein which has several important functions during virus-host interaction are still continuing for BCoVs detected in this study.

Biography

Secil Sevinc is a PhD student and also Research Assistant at Faculty of Veterinary Medicine, Department of Virology, Ankara University. She is a Member of the Society of Veterinarians in Turkey. Also she is a Member of the Society of Veterinary Microbiology in Turkey.

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April 22-23, 2019
Athens, GreeceEmile Barrias et al., Arch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

NEW PHOSPHOLIPIDS ANALOGUES AS CANDIDATES TO AN ANTI T. CRUZI CHEMOTHERAPY: IN VITRO TEST AND ULTRA-STRUCTURAL ANALYSIS

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Chagas disease is a systemic and endemic neglected tropical disease, caused by *T. cruzi*, an obligate intracellular parasite. Nowadays, 8-10 million people in Latin America suffer with this trypanosomiasis and it is considered a major parasitic disease burden in the American continent. The treatment is based on two nitroheterocyclic compounds and both are ineffective against late chronic phase of the disease. Besides, the toxicity of these compounds is high. Thus, the need for more efficient, safe, and accessible drugs is urgent. Phospholipids analogues (PAs) have been shown to be effective against malignant mammalian cells and some pathogenic protozoa as *Leishmania*. Here, we analyzed the effects of new phospholipids analogues on the epimastigotes, trypomastigotes and intracellular amastigotes of *T. cruzi*. TC 387, TC388, LDT10 and LDT137 which were able to inhibit the in vitro growth of epimastigotes and amastigotes with IC50 in the nanomolar range. Trypomastigote lysis was also observed. Ultrastructural analysis demonstrated that these compounds affected the parasite's membranes. Mitochondrial and Golgi cisternae swelling and the formation of membrane blebs, ultimately leading to parasite death, were observed. The Golgi complex of parasites, but not that of the host cells, was affected suggesting a specific mechanism of action possibly due to interference in two different phospholipid biosynthesis pathways used in the distinct cell types. Our observations show that the trypanocidal activity of the PAs investigated herein is higher than that of previously reported PAs in the literature. In conclusion, this work shows that these compounds are potent and fast acting inhibitors of the growth of the proliferative developmental forms of *T. cruzi* (associated with several alterations in the parasite structural organization) and cause lysis of the highly infective trypomastigote form. The effects observed support the assertion that interference with the phospholipids of the membranes is important as a potential route for the development of new therapeutic agents to treat Chagas disease.

Biography

Emile Barrias is a Researcher in the area of optical microscopy-Inmetro with emphasis on optical microscopy of biological material. She holds a Bachelor's degree in Biological Sciences from the Federal University of Rio de Janeiro (2006), a Master's degree (2008) and a PhD (2014) in Biological Sciences (Parasitology and Cell Biology Program) from the Federal University of Rio de Janeiro at Carlos Chagas Filho Institute of Biophysics. She has experience in the areas of Cellular Biology, with emphasis on Parasitology, Cell Biology of parasites, working mainly on the following topics: *Trypanosoma cruzi*, *T. cruzi* interaction-host cell and anti-parasitic chemotherapy using optical microscopy techniques, super-resolution (STORM, SIM and GSD), transmission electron microscopy, scanning electron microscopy (SEM), multiparametric cell sorting and flow cytometry publishing 15 articles in international journals and three book's chapters. She participates in the BIPM (Cellular Analysis Working Group) research group in cellular quantification pilot studies involving microscopy techniques.

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EuroSciCon Conference on

VIROLOGY AND INFECTIOUS DISEASES

April 22-23, 2019 | Athens, Greece

April 22-23, 2019
Athens, GreeceKhashaiar Mansouri et al., Arch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

ISOLATION AND IDENTIFICATION OF *MYCOBACTERIUM* FROM CAPTURED CATS BELONGING TO TUBERCULOSIS INFECTED FARMS

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Background & Aim: Bovine tuberculosis is one of the most important zoonotic diseases in Bovidae. Humans and animals that transit to the farm can transfer *Mycobacterium* to the cattle. Hence, the aim of this study is to evaluate the possible role of cats in transferring the *Mycobacterium* infection in dairy farms.

Methods: From a dairy cattle farm with more than 20% infection of *Mycobacterium*, seven cats were captured and their gastric juice cultured in the LJ and LG medium. The acid-fast staining of the isolates prepared to identify *Mycobacterium* and PCRs were carried out afterwards.

Results: Five out of seven cultures were positive in direct smear by acid fast staining and in PCR-16SrRNA, which indicates that the above-mentioned isolates belong to the *Mycobacterium* genus. Also, positive PCR-IS6110 confirmed that the isolate species are identified as *Mycobacterium tuberculosis* complex. Currently, we are conducting sequencing for the exact identification of these isolates.

Conclusion: Animals such as mice and cats that live in the farm can harbour *Mycobacterium*. In this study, it has been proven that cats certainly transfer *Mycobacterium* to the cattle farms.

Biography

Khashaiar Mansouri is currently studying Doctor of veterinary medicine at the Islamic azad university Garmsar branch. His Research focus is on zoonotic diseases particularly *Mycobacterium* in cat and mice, as well as *Bukholderia mallei* in Guinea pig. Recently, he has given poster presentation in the 19th international and Iranian congress of microbiology.

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April 22-23, 2019
Athens, GreeceVirna Maria Tsitou et al., Arch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

PCR DETECTION OF *STAPHYLOCOCCUS AUREUS* AND *MECA* GENE IN PATIENTS WITH INVASIVE INFECTIONS

Virna Maria Tsitou, Ivan Mitov and Raina Gergova

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Invasive infections caused by methicillin resistant *Staphylococcus aureus* and coagulase-negative Staphylococci (MRSA/MRSCoN) require fast laboratory detection and start of adequate treatment. The aim of this study was to develop a new faster protocol for direct detection of MRSA/MRSCoN in blood cultures and in abscess punctures. For this purpose were used polymerase-chain reaction (PCR) by primers for species specific identification of *S aureus* and methicillin resistance gene *mecA*. We examined 85 growth-positive BACTEC blood cultures and 56 abscess punctures by routine microbiological assay and simultaneous PCR detection of MRSA/MRSCoN. The specificity of the PCR was evaluated by using DNA from another 16 microbial species for negative controls. We determined the susceptibility to methicillin by disc ceftoxime according EUCAST 2019 criteria and minimum inhibitory concentration (MIC) of oxacillin against the *S aureus* isolates using the E-test. In the blood cultures, the two methods detected near 40% MRSA, resp. 94% MRSCoNS. In the punctures, the PCR assay identified near 20% MRSA. The PCR and the routine microbiological results for the blood samples are fully consistent but the new method was faster (only a few hours were need). Among the punctures, there were five PCR MRSA positive and culture negative samples. The new PCR protocol was more sensitive and again faster for detecting MRSA from abscess punctures than the routine microbiological techniques. This molecular-genetic test will speed up the right choice of empirical therapy, which is extremely important for saving patients' lives

Biography

Virna Maria Tsitou has completed her Specialty Doctor of Medicines from Medical University of Sofia- Bulgaria in 2011. She worked in Emergency Department in "Prevent DCC" hospital from 2009-2012. She has also worked as Intern in Dermatology Department in "Tokuda Hospital" in Sofia Bulgaria from 2010-2013 and Intern in Microbiology Department in "ISUL-TSARITSA IOANNA" hospital in Sofia Bulgaria from 2013-2014. She has served as a Specialist Microbiologist in the Department of Medical Microbiology in Medical University Sofia-Bulgaria from 2014-2018. She is working as an Assistant Professor in the Department of Medical Microbiology in Medical University Sofia-Bulgaria since 2016. She is fluent in Greek, English and Bulgarian language. Her participation in Congresses is very active because she wants to share her research findings with other scientists from the Microbiological Community and also keep up with the scientific innovations in Bulgaria but also abroad.

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April 22-23, 2019
Athens, GreeceNibedita Das, Arch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

STUDY OF COVARIATES OF BACTERIAL VAGINOSIS IN FEMALES ATTENDING STI CLINICS IN EASTERN INDIA

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Sexual transmitted infections (STI) have a profound impact on reproductive health worldwide. India is witnessing a chronic disease burden due to sexual transmitted infections. It ranked among the top five disease categories for which healthcare is required. This study was done to understand the impact of bacterial vaginosis in females suffering from STIs. 1074 female patients, who attended two STI clinics in Kolkata, India were included in this study. The vaginal discharge samples were collected by swab sticks from patients and immediately transferred to Sexual Transmitted Infection (STI) Laboratory at Institute of Serology, Kolkata, India. The samples were processed according to the Standard Laboratory Procedures. 57.82% females were symptomatic and presented with vaginal discharge. The prevalence of bacterial vaginosis was 11.26%. The detection rate of bacterial vaginosis among symptomatic patients was 19.48%.

Biography

Nibedita Das is a Medical Microbiologist working with the Government of India. She now works in Sexual Transmitted Infections (STI) and Measles and Rubella eradication. She has experience in antibiotic resistance management and has published a monograph on antimicrobial resistance pattern. She has articles in national and international Journals of repute. She also has experience in disaster management for Govt of India.

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April 22-23, 2019
Athens, GreeceKiyemba Ronald, Arch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

EFFECT OF SUBSTANCE ABUSE ON SPORTS (PERSONNEL) IN UGANDA

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Statement of the problem: Substance abuse is popular on the increase in our low income setting today for various reasons and is associated with poverty as a major risk factor. In Uganda mental illness has become common in sports and is often associated with substance enhancement from alcohol and marijuana intake. Some of the factors that have promoted this rise include physical pain, chronic injuries and pressure to produce results. The overall effect of this problem has led to addiction, low productivity, social dissociation and finally failure to perform in sports.

Methodology and theoretical orientation: We reviewed articles and references of related topics finding those relevant to the scope of the subject. Objectively closed ended questioners were given to 380 sports participants chosen from 12 sports centers (Pilot) areas under random distribution in 4 different regional urban setting in Uganda. They were assessed on modified additional and productivity scales.

Findings: Northern region n=60 12 normal 48(80%) Addiction low productivity 0.83(83.3%), Eastern region n=100 20 normal subjects, Addiction 40(40%) low productivity 47(47%). Western region n=90 Addiction 23(25.5%) low productivity 52 (57.7%) Central region n=130 Addiction 68(52.3%) low productivity 39(30%) Conceptual frame work

Conclusion: Urban region e.g. Central have highest rates of Addiction with low productivity due availability of drugs and cheap alcohol/spirits on the market. Restrictions on alcohol is not observed within the local communities in the rural regions Sports men have highest low productivity due to poor social support, unemployment and no formal infrastructure.

Biography

Mr Kiyemba ronald DOB, 07-02-1979 in Uganda Kampala. Coach for Uganda cycling national teams, holding a degree in sports science. President, KITANDA CARE for HIV/Aids & UTI infections control Owner of, Bike 2 Bike tours (U) LTD.

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EuroSciCon Conference on

VIROLOGY AND INFECTIOUS DISEASES

April 22-23, 2019 | Athens, Greece

April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

MICROALGAE AS AN IMPERATIVE TOOL FOR NEW DESIGN AND BUILDING OF BIOLOGICAL SYSTEM

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The environment is one of the main current challenges as critically imperative for economic and social progress. Microalgae (*Cyanobacteria* and single-cell green algae) production is one-third of total biomass worldwide and contributes 50% of atmospheric oxygen. Their composition may consist from 50-70% protein, more 30% lipids, and vitamins B, E, K, D, etc. in comparison with other plants or animals. Algae have remained also the most effective tool for the primary accumulation of bioenergy. We use nature's models (biomimicry) and developed Theory of global sustainable development based on involvement of microalgae in bio and industrial cycles. New design and building of biological system that organically runs through the use of the microalgae as general natural creator of life conditions aimed to GHGs emission and waste mitigation through the production of food, feed, biopharmaceuticals, fertilizers, cosmetics ingredients and biofuels (2012-2013). Further application of system analysis aimed to assessment algae technologies, resources, economics, policy and regulations influences show big potential microalgae application to solve human problems (book by Avagyan AB entitled Algae to energy and sustainable development, technologies, resources, economics and system analyses. New Design of Global Environmental Policy and Live Conserve Industry, Amazon). The analyses showed that development of microalgae producing have all necessary unlimited resources such as land and water (wastewater and groundwater). According to the our approach, a spread of algae global scale cultivation can promote new design and building of biological systems as well as an opening possibility for the shift from non-efficient protection of the environment to its cultivation in a large scale with mitigation of GHG emission and waste as well as generating of O₂ and value-added products. This is the non-alternative path with significant longer-term effects.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

THE NEED FOR NEW VIRUS VACCINES IN HUMAN AND VETERINARY MEDICINE WITH NOVEL APPROACHES TO DESIGN AND VALIDATION

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New vaccines are required in both human and veterinary medicine. Measles virus (MV) is the only human virus within the Morbillivirus genus of the *Paramyxoviridae*. The virus can cause severe neural complications such as measles giant cell pneumonia, acute post measles encephalitis, subacute sclerosing panencephalitis and in immunosuppressed individuals, measles inclusion body encephalitis. The World Health Organization has set goals towards the complete eradication of MV. However, there are potential problems following MV eradication as the closely related veterinary members in the genus share common cell entry receptors raising the risk of zoonotic infection. MV is thought to have evolved from the now eradicated cattle Morbillivirus, Rinderpest and to have entered the human population during cattle domestication. Veterinary Morbilliviruses have recently jumped into new species including non-human primates. This highlights the possibility of zoonosis and the potential consequences of complete withdrawal of MV vaccination (which gives some cross protection to other morbilliviruses) after measles eradication. The MV vaccine is live attenuated and has very low risk of reversion but is still unlikely to be acceptable in a measles free world raising the need for alternative approaches to human protection from veterinary Morbillivirus infection. Other vaccines for diseases such as Respiratory syncytial virus and Nipah virus are also urgently needed. We are carrying out research into recombinant vaccines using virus vector systems which can be used in both humans and animals but do not cause disease themselves and can be delivered mucosally. These vectors can incorporate various foreign genes to protect against viruses or other pathogens.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

BENEFICIAL MICROBES IN AGRICULTURE: SYMBIOSIS FOR SUSTAINABLE SOIL MANAGEMENT AND CROP PRODUCTION IN CHANGING CLIMATES

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Soil fertility and health is continuously declining due to removal of essential plant nutrients from the soils in the current changing climate scenario. Low and high water and temperature stresses results in the deficiencies of essential plant nutrients, organic matter and beneficial soil microbes that had negative impact on soil health, crop productivity and grower's income especially under arid and semiarid climates globally. Integrated nutrients management in arid and semiarid climates increase soil fertility and health, increase crop productivity and grower's income. Integrated nutrients management refers to the maintenance of soil fertility and improvement in crop productivity with application of plant nutrients through combined application of organic manures, inorganic/chemical fertilizers and bio-fertilizers (beneficial microbes). Beneficial microbes are known to play several vital roles in soil fertility; crop productivity and profitability. Bio-fertilizers are the products containing living cells of different types of beneficial microbes (bacteria, fungi, protozoa, algae and viruses). Some of the commonly used beneficial microbes in agriculture include Rhizobia, Mycorrhizae, Azospirillum, Bacillus, Pseudomonas, Trichoderma, Streptomyces species etc. Beneficial microbes are essential for decomposing organic matter in the soil and increase essential macro-nutrients (nitrogen, phosphorus, potassium, sulfur, calcium and magnesium) and micro-nutrients (boron, copper, chlorine, iron, manganese, molybdenum and zinc) availability to crop plants. Beneficial microbes also play significant role in solid wastes and sewage management. Beneficial microbes increase plants tolerance to different environmental stresses (drought, heat, cold, salinity etc.) and increase plant resistance to insects and diseases attacks. Beneficial microbes not only improve crop growth and productivity by increasing photosynthesis and producing hormones and enzymes, but also improve crop quality by controlling different insects and various plant diseases. Beneficial microbes reduce the use of chemical fertilizers and thereby reduce environmental pollution caused by chemical fertilizers. Beneficial microbes reduce cost of production and so increase grower's income and profitability. Beneficial microbes are therefore very important for increasing crop productivity, profitability and sustainability. Applications of organic manures such as crop residues, animal manures, chicken manures, green manures, composts, farm yard manure, biochar, ash etc. increases the beneficial microbes in the soil and improves soil health and sustainability. Our long-term field experiments on field crops e.g. cereals crops (rice, wheat & maize), oilseed crops (canola, sunflower & soybean) and grain legumes/pulses (chickpea, mungbean & mashbean) confirmed a significant increase in yield per unit area with integrated nutrients management under semiarid climate in Peshawar Valley. The combined application of plant nutrients especially major nutrients (nitrogen, phosphorus and potash) along with different organic sources (farmyard manure; animal manures: poultry manure, cattle manure, sheep manure, goat manure etc., plant residues: onion residues, garlic residues, wheat residues, rice residues, chickpea residues, fababean residues, canola residues etc.) into the soil plus application of beneficial microbes had significantly improved crop growth and increased productivity and profitability.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

VACCINATION VERSUS NON-VACCINATION

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For several years in Romania there has been a trend of opinion of a part of the population against vaccination. I will mention some arguments that combat this opinion based on personal examples. The main issue is the occurrence of cases of autism after ROR (Rougeole, oreillons, rubeole) vaccination, scleroderma after HBV vaccination and various effects due to adjuvants. To be able to say that these cases of autism occur after vaccination, it should be studied in detail all the determinants of this disease and how much every one of the percent affects the onset of the disease. In the so-called cases of post-vaccination autism, do we have all the data about the immune status of the vaccinated persons and the genetic profile at birth, as well as the impairment of this predisposition due to the influences of the environmental pollution, the eating disorders and in particular the continued irradiation of organisms? A lot of things are known about acute irradiation syndrome. What happens after many irradiations, or after their accumulation as an important factor in the half-life of various radioactive elements and the occurrence of systemic, degenerative and cancer diseases? As far as my country is concerned, I know the appearance of many cases of neoplasms immediately after the 1986 Chernobyl explosion. How long did nuclear explosions have not occurred since then? Has it really been studied what these factors actions over time? Of course, there is the likelihood that vaccine production today will also be based on more in-depth studies regarding each person vaccinating, especially children. However, this does not prevent continued vaccination, especially as it has had beneficial effects over the years, and many medical personalities both internationally and nationally have contributed to their introduction into the population.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

ISOLATION, PURIFICATION, STRUCTURAL ELUCIDATION AND ANTIMICROBIAL ACTIVITIES OF KOCUMARIN, A NOVEL ANTIBIOTIC ISOLATED FROM ACTINOBACTERIUM KOCURIA MARINA CMG S2 ASSOCIATED WITH THE BROWN SEAWEED PELVETIA CANALICULATA

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Aim: Screening of seaweed-associated bacteria capable of producing antimicrobials.

Methods & Results: Fifteen microbial strains, associated to the brown seaweed *Pelvetia canaliculata* (Linnaeus) attached to the rocks of Sonmiani Beach (Karachi, Pakistan), were screened. Crude extract filtrates of CMG S2 strain grew on Zobell marine agar (ZMA) had the most remarkable antimicrobial activity. Based on its phenotypic aspects (e.g. Gram-positive, microcoid form), biochemical characteristics (e.g. halotolerance) and genetic analyses, CMG S2 is identified as a putatively new *Kocuria marina* type strain belonging to the actinobacteria's class and micrococcaceae family. Thereby, the nucleotide sequence analysis of its full-length 16S ribosomal ribonucleic acid (rRNA) gene (GenBank accession number EU073966.1) displayed highest identity (i.e. 99%) and score (2630) with *K. marina* KMM 3905. Phylogenetic trees analysis using the neighbor-joining method showed closest evolutionary distance of CMG S2 with KMM 3905 strain and *K. carniphila* (DC2201) species. Interestingly, a unique ultraviolet (UV)-bioactive compound was purified from CMG S2 crude extracts by flash silica gel column and thin-layer chromatography (TLC) techniques. Its chemical structure was unravelled as 4-[(Z)-2 phenyl ethenyl] benzoic acid (PEBA, later named kocumarin) by nuclear magnetic resonance (NMR) spectroscopy techniques. Importantly, kocumarin demonstrated prominent and rapid growth inhibition against all tested fungi and pathogenic bacteria including methicillin-resistant *Staphylococcus aureus* (MRSA), with a minimal fungal inhibitory concentration (MFC) of 15-25 µg/mL and a minimal (bacterial) inhibitory concentration (MIC) of 10-15 µg/mL.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

PLANT VIRUS NANOPARTICLES: NEW APPLICATIONS FOR DEVELOPING COUNTRIES

Kathleen Hefferon

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For over two decades now, plants have been explored for their potential to act as production platforms for biopharmaceuticals such as vaccines and monoclonal antibodies. Without a doubt, the development of plant viruses as expression vectors for pharmaceutical production have played an integral role in the emergence of plants as inexpensive and facile systems for the generation of therapeutic proteins. More recently, plant viruses have been designed as non-toxic nanoparticles which can target a variety of cancers and thus empower the immune system to slow or even reverse tumour progression. The following presentation describes the employment of plant virus expression vectors for the treatment of some of the most challenging diseases known today. The presentation concludes with a projection of the multiple avenues by which virus nanoparticles could impact developing countries.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

GENTAMICIN ENHANCES TOXA EXPRESSION IN *PSEUDOMONAS AERUGINOSA* ISOLATED FROM COW MASTITIS

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The present study was undertaken in order to investigate the role of gentamicin in the gene expression of *toxA* in *Pseudomonas aeruginosa* isolated from cow mastitis. A total of ten *P. aeruginosa* strains originally isolated from cows infected with mastitis. Agar dilution methodology was performed to determine the minimal inhibitory concentration of gentamicin, all of which developed resistance toward gentamicin. The findings presented here demonstrated that all these strains harboured *toxA* depending on PCR-based assay. Nonetheless, RT-PCR technique revealed a wide variation in expression of *toxA*. Moreover, the cultivation of *P. aeruginosa* in the presence of gentamicin, significantly ($P < 0.05$), induced the expression of *toxA*, in addition to the possibility of enhancing the virulence of this bacterium. In conclusion, using gentamicin to treat infections caused by *P. aeruginosa* may participate in more severe outcomes.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

HIV-1 VPR TARGETS TET2 FOR DEGRADATION BY CRL4VPRBP E3 LIGASE TO SUSTAIN IL-6 EXPRESSION AND ENHANCE HIV-1 PATHOGENESIS

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HIV-1 expresses several accessory proteins to counteract host anti-viral restriction factors to facilitate viral replication and disease progression. One such protein, Vpr, has been implicated in affecting multiple cellular processes, but its mechanism remains elusive. Here we report that Vpr targets TET2 for polyubiquitylation by the VprBP-DDB1-CUL4-ROC1 E3 ligase and subsequent degradation. Genetic inactivation or Vpr-mediated degradation of TET2 enhances HIV-1 replication and substantially sustained expression of the pro-inflammatory cytokine interleukin-6 (IL-6), correlated with reduced recruitment of histone deacetylase 1 and 2 to and enhanced histone H3 acetylation of the IL-6 promoter during resolution phase. Blocking IL-6 signaling reduced the ability of Vpr to enhance HIV-1 replication. We conclude that HIV-1 Vpr degrades TET2 to sustain IL-6 expression to enhance viral replication and disease progression. These results suggest disrupting the Vpr-TET2-IL6 axis may prove clinically beneficial to reduce both viral replication and inflammation during HIV-1 infection.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

BUNYAVIRUS: A GROUP OF ANCIENT, BUT NEWLY DEFINED VIRUS

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B*unyavirales* order is one of the largest groups of RNA viruses, including more than 350 members distributed among ten families according to the latest International Committee on Taxonomy of Viruses (ICTV) report. Some of them can cause disease in humans, including highly pathogenic Crimean-Congo hemorrhagic fever virus (CCHFV) in the *Nairoviridae* family; the Rift Valley fever virus (RVFV), the severe fever with thrombocytopenia syndrome virus (SFTSV) in the *Phenuiviridae* family; Lacrosse virus and Oropouche virus in the *Peribunyaviridae* family and several hantaviruses such as Hantaan virus, Sin Nombre virus, Andes virus in the *Hantaviridae* family. Only vaccines for HTNV and SEOV have been developed in Asia. And no specific drugs are available against these contagious Bunyaviruses. The glycoproteins (Gn and Gc) on the Bunyaviruses play an important role in particle entry into the target cells. They are also the major antigens which arise neutralizing antibodies in human body against the infection. This research focuses on the structural and functional studies of the envelope proteins of RVFV and SFTSV and fished the neutralizing antibodies from the RVFV infected patients' PBMCs using the recombinant glycoproteins and then explored the neutralizing mechanisms based on the antigen-antibody complex structures. These studies provide potential specific drugs against RVFV and also provide the detailed information of epitope of the antigen, thereby paving way on the vaccine development.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

MICROBIAL ETIOLOGY OF CHILDHOOD PNEUMONIA IN DEVELOPING COUNTRIES

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Childhood community acquired pneumonia (CCAP) is a significant public health challenge in developing countries. Determination of microbial etiology is critical to develop evidence-based treatment and vaccination policies. Due to paucity of well-designed studies, it is generally believed that bacterial etiology dominates in unvaccinated children. Our research group sought to address the following research gaps.

Etiology of Pneumonia: In the community acquired pneumonia etiology study (CAPES), 4045 children with pneumonia underwent blood and nasopharyngeal aspirate (NPA) culture, and NPA PCR for 26 species. Gram-negative bacilli predominated in blood, followed by *S. aureus*, pneumococcus and Hib. Blood and NPA cultures were discordant in most cases. Multiplex PCR revealed viruses in 46.5% children viz RSV, rhinovirus, PIV, HMPV, coronavirus, influenza virus, and combinations. This confirmed that viruses dominate in NPA and *S pneumoniae* is not as frequent as expected.

Reliability of NPA for etiology: In 222 children with severe pneumonia, we examined blood culture, NPA culture and NPA viral PCR in all. Additionally lung aspirate, BAL, pleural fluid, sputum, and induced sputum were processed where feasible. Etiology was assigned using a hierarchy of biological specimens and three distinct etiology assignment models. Irrespective of the model used, viral etiology dominated and RSV was the most frequent organism. Gram-negative bacteria outnumbered Gram-positive organisms and *S pneumoniae* was identified in very few children. This confirmed that RSV and not bacteria is the dominant pathogen in pneumonia, even in the lungs or lower airways.

Bacterial vs Viral Etiology: We did not find any differences in demographic characteristics, clinical features, and radiographic findings in children with bacterial vs viral pneumonia. Although CRP and Procalcitonin were higher in bacterial pneumonia, there was no clinically useful discriminatory level. However, IL-6>5000 pg/ml, IL-8>1000 pg/ml, and their combination could reliably distinguish bacterial from viral etiology. Thus, systemic biomarkers can help to establish etiology at the time of presentation itself.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

ISOLATION AND IDENTIFICATION OF *MYCOBACTERIUM* FROM CAPTURED CATS BELONGING TO TUBERCULOSIS INFECTED FARMS

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Background & Aim: Bovine tuberculosis is one of the most important zoonotic diseases in Bovidae. Humans and animals that transit to the farm can transfer *Mycobacterium* to the cattle. Hence, the aim of this study is to evaluate the possible role of cats in transferring the *Mycobacterium* infection in dairy farms.

Methods: From a dairy cattle farm with more than 20% infection of *Mycobacterium*, seven cats were captured and their gastric juice cultured in the LJ and LG medium. The acid-fast staining of the isolates prepared to identify *Mycobacterium* and PCRs were carried out afterwards.

Results: Five out of seven cultures were positive in direct smear by acid fast staining and in PCR-16SrRNA, which indicates that the above-mentioned isolates belong to the *Mycobacterium* genus. Also, positive PCR-IS6110 confirmed that the isolate species are identified as *Mycobacterium tuberculosis* complex. Currently, we are conducting sequencing for the exact identification of these isolates.

Conclusion: Animals such as mice and cats that live in the farm can harbour *Mycobacterium*. In this study, it has been proven that cats certainly transfer *Mycobacterium* to the cattle farms.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

ANTIVIRAL ACTIVITY OF CARIBBEAN SEaweEDS AGAINST HUMAN VIRUS WITH CLINICAL AND EPIDEMIOLOGICAL SIGNIFICANCE

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Marine ecosystems represent a promising source of organisms with a wide spectrum of biomedical applications. The brown seaweeds of *Sargassum* genus embrace a varied biochemical composition and synthesize metabolites with antiviral activities. Becoming then in potential candidates for searching and developing drugs against viral diseases that show drug resistance or lack of therapy. The goal of this work is to evaluate and characterize the antiviral activity of different extracts from seaweeds of the Caribbean against reference and clinical strains of some human enterovirus and respiratory virus. The qualitative determination of secondary metabolites (phytochemical identification) from the extracts was made according to Rondina and Coussio, 1969. The cytotoxicity of the extract was evaluated in Vero, RD and Hep-2 cells by MTT method and the CC50 was calculated by lineal regression analysis. Determination of antiviral activity (EC50) was made by means of cytopathic effect inhibition in cells. The extracellular virucidal activity of the extract and the reduction of viral yield were determined by viral titration through final dilution assay. The antiviral activity was characterized by an addition of time assay. The preliminary characterization of the extract showed compounds such as tannins, quinones, proanthocyanidins/catechins, triterpens, proteins and polysaccharides. The extract was non-cytotoxic at the evaluated concentrations and showed an inhibitory activity against the viruses. Besides, it showed virucidal activity and diminished the viral titer more than three log compared to the control. The extract was active on the early and late stages of viral replication. The presence of actives compounds might be related to the showed antiviral activity, supporting so the potential of these seaweeds as a source of antivirals.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

RELATIONSHIP BETWEEN DIFFERENT ENTERIC VIRAL INFECTIONS AND THE OCCURRENCE OF DIARRHEA IN BROILER FLOCKS IN JORDAN

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The aim of this study is to determine if enteric viruses are the cause of diarrhea in broiler flocks in Jordan. Intestinal content samples were collected from 101 broiler flocks from different regions of Jordan to detect the presence of astrovirus, coronavirus, reovirus, and rotavirus, by using reverse transcriptase polymerase chain reaction (RT-PCR). Forty six of these flocks were clinically healthy with no enteric disease and the other 55 flocks were clinically suffering from diarrhea. The samples were collected between 5 and 16 days of age. The results showed that 79% of these flocks were infected with one or more of the above enteric viruses. Coronavirus was the most common virus, detected in 56.4% of these flocks, with astrovirus in 29.7% of the flocks, and rotavirus (9.9%) and reovirus (5.6%) being the least common. None of these flocks were found to be infected with all four viruses, but one of the flocks was found to be infected with astrovirus, coronavirus, and rotavirus simultaneously. Individual infection was noted with astrovirus, coronavirus and rotavirus but not with reovirus, whereas all flocks infected with reovirus were also infected with coronavirus. There was no statistical evidence to link these viruses as the main cause of diarrhea in the flocks tested. This is the first study in Jordan to detect all of these viruses and to correlate their presence with diarrhea in chicken flocks.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

DRUGS SIDE EFFECTS IN PREGNANT WOMEN INFECTED WITH HIV REFERRED TO IMAM KHOMEINI HOSPITAL, VOLUNTARY COUNSELING AND TESTING CENTER TEHRAN, IRAN 2009-2013

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Objective: To obtain enough information about the prevalence of the ARV side effects in pregnant women infected with HIV and their infants and also evaluate drug efficacy in decreasing HIV infection in their children.

Method: This descriptive study was based on information of 40 pregnant women infected with HIV files at voluntary and counseling center, Imam Khomeini Hospital, Tehran, Iran during 2009 -2013. In this study, we evaluated epidemiologic, demographic, clinical, laboratory data and drugs side effects.

Results: The most commonly used drug group was AZT/3TC/EFV. About 75.5% of patients received mother to child prevention and 27.5% received ARV Antiretroviral therapy treatment. 5% anemia, 2.5% rash and 2.5% pre rupture of membranes were reported and no preeclampsia or gestational diabetes was reported in patients' files. Only one abortion (2.5%) was occurred in late first trimester. Except rash, other adverse effects were solely reported in ARV treatment group. All neonates had normal Apgar score. Fetal defects were not reported at birth.

Conclusion: In this evaluation, safety of ARV in pregnancy period and at birth was observed especially in the group received prevention of mother to child transmission (PMTCT). So we advise ARV treatment or PMTCT in pregnancy period.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

IDENTIFICATION OF *PELARGONIUM SIDOIDES* ROOT-ASSOCIATED MICROBES AND THEIR POTENTIAL FOR ANTIFUNGAL LIPOPEPTIDE PRODUCTION

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Emerging and persistent fungal pathogens increasingly threaten human health, agriculture and natural biodiversity on a global scale. It has been suggested that this is due to a gradual loss in drug efficacy as microbes adapt to evade familiar antifungal treatments. In addition to this, slow antifungal drug development has led to developed antifungal drug resistance in a range of fungal pathogens. For this reason, medicinal plants and plant-associated microorganisms are being investigated as sources of novel antifungal compounds. Antifungal peptides (AFPs), for example are rapid acting, biodegradable microbiocides. This study evaluates potential AFP production in microbial isolates associated with *Pelargonium sidoides*. Crude extracts of bacterial and fungal isolates were cultured using a variety of different growth conditions and tested against a panel of medicinally and agriculturally important fungal pathogens. Extracts were also tested for haemolytic activity, biofilm eradication capabilities and analysed by LC-MS to detect known antifungal peptides. Molecular techniques were used to identify microbial isolates using multiple gene regions (16S, Gyr B, Rec A, Atp D, ITS and β -tubulin). Some microbial isolates produced a crude extract with fungistatic activity. The crude extracts inhibited the growth of fungal pathogens *Cryptococcus neoformans*, *Candida albicans*, *Botrytis cinerea* and *Fusarium oxysporum* when grown on solid media. Microbial isolates identified were *Bacillus*, *Pseudomonas* and two *Penicillium* species. Surfactins and fengycins A and B were detected in one very potent *Bacillus* extract called YC2. These compounds are known lipopeptides and with further optimisation could be implemented agrochemical applications and perhaps future medicinal drugs.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

DIMINISHED ANTIMICROBIAL DEFENCE IN DIABETES MELLITUS

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It is widely accepted that people with diabetes (DM) bear an increased propensity to develop infections and the magnitude of the diabetes effect on the risk, remains an active research question. Besides cardiovascular causes and cancer, infectious diseases substantially contribute to the reduced life expectancy for DM. Diabetes enhances the susceptibility to significantly higher rate of osteomyelitis, pyelonephritis, cystitis, pneumonia, cellulitis, sepsis or peritonitis and therefore to lower respiratory and urinary tract, bacterial skin and mucous membrane infections. There are several additional aspects that link diabetes to rare infections such as emphysematous pyelonephritis, invasive otitis externa, emphysematous cholecystitis or rhinocerebral mucormycosis. Host- and organism-specific factors may explain why DM are more susceptible while are immunocompromised and recurrent infections can pose a problem. Although diabetes seems to predispose to some infectious diseases and possibly to a worse outcome thereof, several lines of evidence suggest that diabetes comorbidities importantly contribute to this phenotype. Many factors could predispose to infections, including genetic susceptibility, altered cellular and humoral immune defence, plus poor blood supply and nerve damage. Alterations in metabolism contribute significantly and improvements in metabolic control is limiting the development of an infection. The reasons why DM presents with an increased susceptibility to frequent and protracted infections remain still far from being understood. Studies have shed light to the diminished defective chemotaxis, bacterial killing, superoxide production, leukotriene release, lysosomal-enzyme secretion and endoplasmic reticulum stress, which is related to the degree of glycaemic control and is reversible. Further on hyperglycaemia leads to more pronounced activation of coagulation, while at the same time neutrophil degranulation is reduced. Infections continue to bear a serious hazard for the DM but remains difficult to comprehend the underlying problem and explain why epidemiologic studies yielding conflicting results.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

ANTIBIOTIC RESISTANCE AND POTENTIAL ROLE OF CRISPR TYPE MECHANISMS

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Potential role of CRISPR type mechanisms in antibiotic resistance: 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: application of quantum physics to medicine and surgery; to advance into the future, the practice of medicine and surgery; site 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.

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April 22-23, 2019
Athens, GreeceArch Clin Microbiol 2019, Volume:10
DOI: 10.4172/1989-8436-C1-018

IDENTIFICATION OF ONCOLYSIS EFFECT IN COLORECTAL CANCER CELLS BY ORF VIRUS STRAIN NA1/11 *IN VITRO* AND *IN VIVO*

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Oncolytic viral therapies against cancers, using variously attenuated or recombinant viruses, have appeared as a promising method in cancer treatment in recent years. Orf virus (ORFV) strain NZ2 has been shown to have antitumor effects in animal models mediated by immunoregulation profile, however, little is known about the molecular cellular mechanism of orf virus's anti-cancer effect. Here we report ORFV strain NA1/11, isolated from a sheep in Jilin province of China, inhibited the growth of colorectal cancer (CRC) cells lines including Caco-2, HCT116, LoVo, RKO, SW480, SW1116 cells. ORFV strain NA1/11 also significantly inhibited the growth and the pulmonary metastasis of CRC cells *in vivo*. The inhibitory mechanism of ORFV strain NA1/11 involved apoptosis and autophagy induction. Besides, we utilized a cytokine antibody array to develop a more comprehensive description of the cytokines by ORFV, which indicated that ORFV likely plays roles in the regulation of key factors relevant to apoptosis, autoimmunity/inflammation, angiogenesis and the cell cycle for further molecular mechanism studies. These results suggested that ORFV could be an oncolytic virus for CRC therapy.

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