Poster Abstracts/Presentations

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October 18-19, 2017 | Toronto, Canada

Kip2 is required for maintenance of normal spindle dynamics and cell cycle progression

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Statement of the Problem: The mitotic spindle is an elegant machine employed by the cell to segregate chromosomes during cell division. It is composed of both nuclear and cytoplasmic microtubules (cMTs), whose movements are regulated by microtubule motor proteins. A key protein that polymerizes and stabilizes cMTs is Kip2p. As most previous studies have focused on the role of *KIP2* in spindle positioning, not much is known about the protein's role during early cell division cycle.

Methodology & Theoretical Orientation: To determine the physiological significance of Kip2p during cell division, we performed genetic studies and examined spindle dynamics in the absence or upon overexpression of KIP2. We used live-cell imaging and confocal microscopy to study spindle dynamics.

Findings: In the absence of *KIP2*, defects in spindle orientation and nuclear migration were observed. Interestingly, overexpression of *KIP2* resulted in a cell cycle arrest.

Conclusion & Significance: Our results indicate that regulation of Kip2p levels is essential to maintain normal spindle dynamics and ensure cell cycle progression. Therefore, Kip2p could have a potential role in anti-cancer therapies.

Speaker Biography

Beryl Augustine is a PhD graduate from the National University of Singapore, where she completed her Doctoral degree in Life Sciences, receiving the prestigious NUS Research Scholarship. Her research work was focused on the molecular regulation of cell division machinery, with potential applications in oncology therapies. Inspired by the power of genetics, whereby one mutation in a gene can impact the whole organism, she did her undergrad in Biotechnology, for which she was awarded the university silver medal. She has a passion to bring the benefits of science and technology to society. She enjoys travelling and exploring different cities and cultures. She has presented her research at several international conferences including Cincinnati, San Francisco and Seattle, the latter with a Travel Fellowship award. She has co-authored two research articles in reputed peer-reviewed journals, one of which is a first-author paper to be published later this year.

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Isolation, identification and antibiotic susceptibility profiles of bacterial strains isolated from supragingival plaque of periodontal patients at dental service and training center of Addis Ababa University

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Periodontal disease is the common oral problem of human being that cause permanent tooth lose. In our study, we have determined the periodontal bacterial pathogens with their susceptibility profiles and the potential risk factors for the disease. Poor oral hygiene practice increases biofilm/plaque formation on the teeth. Dental Plaque formed on the supragingival area can harbor different pathogens that can cause periodontal disease. Microbial infections of the periodontal tissues lead to the destruction of the alveolar bone and cementum accompanied by mobility of teeth. A cross sectional study was conducted from April 2015 to June 2015. A total of 384 clinically confirmed periodontal patients were recruited for the study. 52.9% of them were males and the median age was 35 years. Culture positives were characterized by using standard biochemical tests and API ID Microsystems (bioMérieux, France). Antimicrobial susceptibility test was performed using CLSI and EUCAST 2015. Tested drugs were selected using these guidelines. Microbiological investigations of samples lead to the isolation 459 different types of bacterial strains. The most frequently isolated species were Gram-positive facultative anaerobes and anaerobic gram-negative rods. *Candidia albicans* was also seen in 1.9% (n=9). The antibiotic susceptibility patterns of Gram-positive facultative anaerobes mainly *Streptococcus* species show high resistance rates to ciprofloxacin 20.5% and amoxacillin 20.3%. Drug resistance for a single drug was seen in 56.1% of the isolates and 20.6% of the isolates was susceptible for all the drugs tested. MDR=resistance for ≥2 drugs were seen in 34.7% of the isolates.

Speaker Biography

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In vitro anti-leishmanial activity of *Artemisia dracunculus* and *Heracleum persicum* extracts in comparison with glucantime

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Background & Objectives: Cutaneous leishmaniasis (CL) is one of the most common parasitic diseases. It is one of the major public health in developing countries and throughout the world. Pentavalent antimonial compounds like pentostam and glucantime has been used to treat CL for the last 50 years. The use of these compounds has some limitations such as long duration of treatment, high expenses of drugs, and methods of drug use which are intradermal and intramuscular injection. Beside these, lack of response to the treatment in 10-15% of cases and toxic effects on heart, liver, and kidneys are other possible side effects. Hence, the objective of the present survey was to state the antileishmanial activity of two herbal medicine (*Artemisia dracunculus and Heracleum persicum*) extracts were evaluated against *Leishmania* major and Leishmania infantum using colorimetric MTT (2-(4,5-dimethyl-2-thiazolyl)-3,5-diphenyl-2H-tetrazolium bromide) assay and compared to the glucantime as a reference.

Materials & Methods: The leaves extracts of selected plants were obtained by maceration. The *in vitro* assays were carried out on L. major and L. infantum using colorimetric MTT assay in comparison with glucantime. The concentration-response curves tested extracts and glucantime solutions were designed and IC50 values were located.

Results: Anti-Leishmina effects of *A. dracunculus and H. persicum*) on L. major and L. infantum promastigote were revealed with 50% inhibitory concentration (IC50) values of 49.67 and 42.23 mg ml-1 for *A. dracunculus*, 81.15 and 73.17 mg mg ml-1 for H. persicum. In comparison with the standard drug, glucantime had IC50 value of 40.2 mg ml-1 for L. major and 18.5 mg ml-1 for L. infantum promastigote after 72 hours incubation respectively.

Conclusion: These results revealed that compounds from *Satureja khuzestanica* and *Heracleum persicum* have anti-leishmania properties that necessary to survey the effects of these extracts on *leishmania* genus in animal models in future.

Speaker Biography

Batool Sadeghi-Nejad is working at Abadan School of Medical Sciences, Abadan, Iran. She has published many research papers.

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In vitro activities of six antifungal drugs against *Candida glabrata* isolates: An emerging pathogen

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Background: *Candida glabrata* is pathogenic yeast with several unique biological features and associated with an increased incidence rate of candidiasis. It exhibits a great degree of variation in its pathogenicity and antifungal susceptibility.

Objectives: The aim of the present study was to evaluate the *in vitro* antifungal susceptibilities of the following six antifungal drugs against clinical *C. glabrata* strains: amphotericin B (AmB), ketoconazole (KTZ), fluconazole (FCZ), itraconazole (ITZ), voriconazole (VCZ), and caspofungin (CASP).

Materials & Methods: Forty clinical *C. glabrata* strains were investigated using DNA sequencing. The *in vitro* antifungal susceptibility was determined as described in clinical laboratory standard institute (CLSI) documents (M27-A3 and M27-S4).

Results: The sequence analysis of the isolate confirmed as *C. glabrata* and deposited on NCBI GenBank under the accession number no. KT763084-KT763123. The geometric mean MICs against all the tested strains were as follows, in increasing order: CASP (0.17 g/mL), VCZ (0.67 g/mL), AmB (1.1 g/mL), ITZ (1.82 g/mL), KTZ (1.85 g/mL), and FCZ (6.7 g/mL). The resistance rates of the isolates to CASP, FCZ, ITZ, VZ, KTZ, and AmB were 5%, 10%, 72.5%, 37.5%, 47.5%, and 27.5%, respectively.

Discussion: The intrinsically low susceptibility of C. glabrata, an emerging opportunistic fungal pathogen, to azole antifungals has made its treatment challenging, and infection is accompanied by frequent relapse and failure. The findings indicate that the decreased susceptibility of Candida to azole agents may contribute to the increased proportion of infections caused by these species. Caution is thus recommended with CASP therapy for *C. glabrata* infections when azole resistance is predicted. The resistance of *C. glabrata* clinical isolates to both azoles and echinocandins has emerged over time. This is problematic, owing to its treatment limitations.

Conclusion: These findings confirm that CASP, compared to the other antifungals, is the potent agent for treating candidiasis caused by *C. glabrata*. However, the clinical efficacy of these novel antifungals remains to be determined.

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Isolation of nontuberculous mycobacteria in the waters of a hemodialysis center

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Introduction & Aim: Hemodialysis is a therapeutic manner for chronic renal incompetence patients. The use of poorly treated water during hemodialysis may lead to contamination with nontuberculous mycobacteria (NTM). The aim of this study was to investigate contamination in waters of a hemodialysis center with nontuberculous mycobacteria (NTM).

Methods: A total of 60 samples taken at different points in each hospital's hemodialysis distribution system were collected in Ahvaz, Iran. A volume of 500 mLof the samples were filtered through membrane filters with pores 0.45 mm in diameter. Sediment of each sample was inoculated into two Lowenstein-Jensen medium. Isolated mycobacteria colonies were studied with phenotypic tests, PCR- restriction enzyme analysis (PRA) and rpoB gene sequence analysis.

Results: *M. fortuitum, M. gordonae, M. lentiflavum* and *M. moriokaense* were the most isolated NTM in the waters of hemodialysis.

Discussion: *M. lentiflavum* has mainly clinical importance in young children with cervical lymphadenitis and in immunocompromised patients. *M. moriokaense* first isolated from sputum of a patient with tuberculosis and from soil in Morioka, Japan. Despite its nonvirulent nature, there have been reports of clinically significant diseases caused by *M. gordonae*, including disseminated infections urogenital tract diseases, gastrointestinal tract infections, soft tissue damage, and respiratory and pulmonary infections.

Conclusion: This result demonstrates that dialysis water can be storage of transmission of potential NTM pathogenic among patients with weakened immunity. Suitable monitoring to ensure the best control over the dialysis water system is recommended.

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Peptidoglycan (PG) synthesis interruption in *ΔmrcB* mutant disturbs the bacterial envelope assembly and induces the ECA biosynthesis in *Escherichia coli cells*

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The envelope of Gram-negative bacterium is especially complex and contains two membranes with a thin layer of peptidoglycan (PG) exoskeleton sandwiched in between them. These structures play a key role in maintaining cellular integrity and offer protection from external abuses. Most of our best antibiotics such as penicillin and vancomycin block the biosynthesis of the bacterial envelope and cause cell lysis. Indeed, bacterial envelope biogenesis is one of the best sources of bacterial targets for antibacterial development, because it involves factors that are unique to bacteria and are important for bacterial physiology. In order to determine the role of PG synthesis in envelope biogenesis, *E. coli* WT cells and *ΔelyC* and *ΔmrcB* mutants were grown in LB medium 37°C and 22°C. After that, the hydroxyl radical level was measured by the Flow cytometry (FACS). RNA extraction and purification was achieved and transcriptional analysis by RT-PCR was performed. Then, *murA, mrcB and uppS* genes expression was measured. Our results were shown that these genes were overexpressed at low temperature in WT cells, and highly expressed in *ΔelyC* and *ΔmrcB* mutants. These results show the role of PG and/or ECA synthesis at low temperature. We, therefore observed that the ECA biosynthesis genes was expressed in the WT cells of *E. coli* at low temperature 22°C, and more expressed in *ΔelyC* and *ΔmrcB* mutants associated with the overexpression *of uppS* gene. In addition, uppS gene was too up-regulated at 37°C and 22°C in *ΔelyC* and *ΔmrcB* mutants. So, in the absence of PG synthesis, the lipid carrier Und-P can be produced for the cell wall or more precisely ECA or another polysaccharides biosynthesis. Our results confirm that the cells lacking either of these PBPs are viable, but the simultaneous inactivation of both factors results in rapid lysis and cell death. In addition, the overexpression of ECA biosynthetic cluster, *mrcB* and *uppS* genes in *ΔelyC* mutant confirms the competition between the PG and ECA synthetic pathways for the lipid carrier Und-P. Taken together, these findings suggest that *ΔmrcB* mutant can increase the ECA biosynthesis in the absence of PG synthesis. These results reveal the role of PBP1b protein in the envelope biogenesis correlated with ECA biosynthesis.

Speaker Biography

Khadidja Senouci-Rezkallah received the License (DEA) degree from Mustapha Stambouli University, Biology department, Mascara, Algeria in 2005, Master's degree in Microbiology and Biochemistry from Aix-Marseilles III University, Faculty of Saint-Jerome Marseille, France. After that, she received her PhD degree from Aix-Marseille III, Faculty of Saint-JeromeMarseille, France. The area of her research is microbiology and molecular biology on physiological and molecular characterization of acid tolerance response of *Bacillus cereus*. From 2009 to 2013, she worked as Assistant Professor-Researcher at Mascara University, Algeria. She worked on the characterization of the response to acid and heat stress in bacteria responsible to food-borne illness (*E. coli*, *Stapylococcus aureus* and *B. subtilis*).

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Isolation and characterization of oil degrading bacteria from contaminated soil at oil ARZEW refinery

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Biodegradation by indigenous bacteria represents one of the primary mechanisms by which oil pollutants can be removed from the environment. The aim of our study is the isolation and identification of petroleum hydrocarbon degrading bacteria from oil contaminated soil samples. The samples were collected from differences sites at Arzew refinery Northern Algeria. Bacteriological diagnosis of soils studied corresponding to a biomass 14, 02. 107 CFU/g of soil in the lower polluted soil sample. This biodiversity is inversely proportional to the increase in oil content. Indeed, in the highly contaminated sample, with a biomass of 9.3 .104 CFU/g of soil. The hydrocarbon degrading bacteria isolated and identified belonged to the following genera, *Pseudomonaceae, Bacilliaceae and Staphylococcaceae. Biochimical tests revealed the presence of Pseudomona aeroginosa, Pseudomona fluorecens, pseudomona putida, pseudomona citronéllolis, Pseudomona luteola, pseudomona fluorescens biovare 1, pseudomona fluorescens biovare 3, pseudomona fluorescens biovare 5, Bacillus sp, Staphylococcus hémolytique, Staphylococcus hominis*. The ability of isolates to degrade the crude oil was performed by gravimetric analysis. The biodegradation rate of crude oil by *Pseudomonas aeruginosa* is the best with 82.7%, whereas the lower potential of degradation showed in *Staphylococcus hominis* with 46.63 %. Among the existing strains, *Pseudomonas aeruginosa* have the best production of biosurfactants that reducing the surface tension of culture medium until 19 mN/m, with an emulsion index of 22.72%, and the area of oil displacement (0.9 cm). The strains isolated are capable to produce a biosurfactants that has a great power in the remobilization of hydrocarbons and the acceleration of their biodegradation.

Speaker Biography

Fatiha Dilmi received the license (DES) degree from Mustapha Stambouli University, Biology department, Mascara, Algeria in 2005, Master's Degree in Biology from Department of Biology, Faculty of Sciences, AL al- Bayt University in 2009, Jordan. From 2009 till now, she was worked as assistant professor-researcher at Mustapha Stambouli University, Mascara, Algeria. She worked on the isolation, characterization and biodegradation ability of hydrocarbon degrading bacteria from contaminated soil in petrol station for preparation of phD thesis. She is a member in Laboratory of Microbiology and Plant Science, Department of Biology, Faculty of Natural and Life Sciences, University of Abdelhamid Ibn Badis, Mostaganem, Algeria and Laboratory for Research on Biological Systems and Geomatics (L.R.S.B.G), Department of Biology, Faculty of Natural and Life Sciences, Mustapha Stambouli University, Mascara, Algeria.

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Isolation and identification of *lactobacillus*, which may be potentially prebiotic sources, from the gastrointestinal tract of chicken

Zehranur Yuksekdag
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Antibiotics have been used in poultry industry for decades to promote growth and protect animals from diseases, followed by various side effects. In efforts of searching for a better alternative, prebiotic is of extensive attention. The EPS-based prebiotics that may be used for chicken might been suggested as an effective strategy to decrease infection in chicken. It is only in the last few years that LAB EPS have taken attention with regard to prebiotic potential. For this reason, in experiment 1, 119 bacteria of *lactobacilli* isolated from the gastrointestinal tract of 24 chicken. For experiment 2, the isolates were tested for their exopolysaccharides production levels. In these isolates, exopolysaccharides production were assessed varies from 43-443 mg/L. In experiment 3, for molecular identification, 11 isolates that produced high EPS were selected. These *lactobacilli* isolates were acknowledged using 16S rRNA sequence analysis. As a result of the identification, isolates were identified as *Lactobacillus salivarius* (6 strains), *L. reuteri* (2 strains), *L. aqilis* (2 strains) and *L. saerimneri* (1 strain). These bacteria EPSs may be good alternatives to antibiotics in promoting growth resulting from a beneficial modulation of the intestinal microbiota, which leads to increased efficiency of intestinal digestion in the host animal. Acknowledgements: This research has been supported by General Directorate of Agricultural Research and Policies project coded with TAGEM/15/AR-GE/40.

Speaker Biography

Zehranur Yuksekdag has completed her PhD from Gazi University. She is working as Professor Doctor in Gazi University. Her areas of expertise are probiotics, microbial biotechnology, and food microbiology. She has published more than 30 papers in reputed journals and serving as an Editorial Board Member, referees in different reputed journals, and was worked in 20 research projects.

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Antibody response of dogs to ETHIORAB rabies vaccine

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Background: Rabies is 100% fatal, but it is preventable. More than 95% of human rabies cases occur in improperly treated individuals. This is partly because of modern post-exposure rabies prophylaxis is expensive and therefore not readily available in many endemic regions. Nervous tissue vaccine has been in use for more than 100 years. These vaccines have now been superseded in purity, potency, immunogenicity and safety.

Objective: The objective of this research is to evaluate the efficacy and immunogenicity of inactivated tissue culture rabies vaccine produced in Ethiopia.

Methods: Twelve experimental dogs from local breed were duly conditioned during a quarantine period and assigned to two groups randomly. Animals in group I (cases) were vaccinated subcutaneously with 1 ml of our experimental vaccine. Dogs in group II served as non-vaccinated controls. The immune response of each dog was monitored for 120 days. On the day 120 after final sampling, all dogs were challenged in the masseter muscle with a rabies street virus of canine origin. To evaluate the titer of the rabies virus, neutralizing antibodies (VNA), sera were analyzed by Fluorescent Antibody Virus Neutralization (FAVN) Test. Geometric Mean Titers (GMT) to rabies virus was determined at days 7, 15, 21, 30, 60, 90 and 120.

Results: Geometric mean titers were equal to 1.59, 1.73, 2.19, 3.58, 3.17, 3.35 and 3.56 IU/ml at days 7, 15, 21, 30, 60, 90 and 120 respectively. All dogs showed VNA titers higher than the 0.5 IU/ml mandated WHO recommended threshold. 83.3% vaccinated dogs, survived the challenge virus. In contrast, all dogs in the control (non-vaccinated group), developed rabies.

Conclusions: This study indicated cell culture-based anti-rabies vaccine manufactured at EPHI is efficacious and immunogenic. Field trials should be conducted before mass vaccination of dogs to control rabies cases.

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Antagonism of *Pseudomonas* sp. EMM-1 and its potential as bio-control agent

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Statement of the problem: In nature, plants are subject to several diseases due to the presence of pathogens. Fungal diseases are commonly controlled through the use of pesticides which have resulted in clinical and environmental damages. The use of beneficial bacteria may promote diverse beneficial function in intensive agriculture such as biological control, where bacteria can exhibit antagonistic interactions to compete for space and nutrients in their habitat. The best known antagonistic bacteria are *Enterococcus, Lactococcus, Streptomyces, Bacillus, Pseudomonas, Klebsiella, Escherichia,* and *Burkholderia* due to their potential to produce inhibitory substances such as broad-spectrum antibiotics, organic acids, siderophores, antifungal and bacteriocins. Our study model, *Pseudomonas* sp. EMM-1, is a Gram-negative bacterium isolated from contaminated soil highly competitive due to the production of one or more inhibitory substances. Its antimicrobial activity was demonstrated against diverse beneficial and pathogenic microorganisms including the genera *Bradyrhizobium, Azotobacter, Staphylococcus, Streptococcus, Klebsiella* and *Burkholderia*; as well as the phytopathogenic fungi *Pantoea* and *Fusarium*.

Methodology & Theoretical Orientation: Bacterial competition is mainly evaluated by double-layer agar and simultaneous inhibition assays. In this work the double-layer agar methodology was performed to evaluate the ability of Pseudomonas sp. EMM-1 to antagonize diverse fungi isolated from soil and plants with fungal diseases such as *Aspergillum* and *Fusarium*.

Conclusion & Significance: The results of inhibition assays suggest that *Pseudomonas* sp. EMM-1 is able to produce metabolites that inhibit the growth of diverse fungi, leading us to assume its potential as biocontrol agent.

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The fate of proteins and the involvement in cell death and aging

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Proteins are the major structural and functional players in all organisms. The synthesis and degradation of proteins directly guide the growth, differentiation and death of the cell. During the metabolism pathways of proteins, the aggregation is a special feature of proteins and highly involved in cell death. It has been debated that protein aggregation might be beneficial in aged cells to avoid compromising the protein quality and quantity control meanwhile some evidence indicated the protein aggregation may impair the normal cellular metabolic process. This presentation will discuss the impact of protein synthesis, aggregation and degradation in cell death and their involvement in aging study.

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Antioxidant activity of fungal endophytes isolated from *Kigelia africana, Annona senegalensis* and *Vitex payos*

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The endophytes of medicinal plants are largely underexplored despite their potential as repositories of bioactive compounds including natural antioxidants. The purpose of this study was to evaluate the total antioxidant capacity (TAC) of ethyl acetate extracts of endophytic fungi isolated from the medicinal plants *Kigelia africana* (*Penicillium species*), *Annona senegalensis* (*Epicoccum sorghinum*) and *Vitex payos* (*Epicoccum nigrum*). The TPC was determined using the Folin-Ciocalteu method. The OxiSelect™ total antioxidant capacity assay kit was used to evaluate the TAC. Fourier transform infrared (FTIR) analysis of the crude extracts was also done to determine the possible different functional groups present in the extracts. The extract obtained from the endophyte *Epicoccum sorghinum* isolated from *Annona senegalensis* demonstrated both the highest total phenolic content (28.85±1.14 mg GAE/g dry weight) and total antioxidant capacity (593.46±1.86 µM CRE). A strong positive linear correlation (r=0.95717) was found between total antioxidant capacity and total phenolic content of the tested crude extracts. The FT-IR spectral analysis of the crude extracts confirmed the presence of molecules carrying bonded hydroxyl (-OH) functional group characteristic of phenolic compounds. The preliminary results indicated that the studied endophytic fungi produced metabolites with potential as sources of natural antioxidants and that the TPC influences TAC.

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Study of role of aerobic bacteria *Bacillus subtilis* and *Pseudomonas aeruginosa* on biocorrosion behaviour of stainless steel 304 (SS304)

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This research work has studied the role of two bacteria namley; *Bacillus subtilis* strain S1X and *Pseudomonas aeruginosa* strain ZK in the corrosion behavior of SS304 in minimal salt medium with 1.5% NaCl as a corrosive agent. Electrochemical techniques including Tafel polarization and electrochemical impedance spectroscopy and surface analytical techniques including atomic force microscopy, scanning electron microscopy-energy dispersive spectrum analysis and Fourier transform infrared spectroscopy showed that both bacteria developed a protective layer in the form of biofilm on the surface of SS304 and thus inhibited the corroiosn of underlying surface of alloy. The decrease in pH values for bacterial inoculated systems with increasing incubation time showed the production of some acidic metabolites by bacterial isolates.

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Flagellar Motility plays critical role in biofilm formation of *Bacillus cereus* and *Yersinia enterocolitica*

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Background: Bacteria live either independently as planktonic cells or in organized surface associated colonies called as biofilms. Biofilms play an important role in increased pathogenesis of bacteria and it is assumed that, motility is one of the contributing factor towards biofilm initiation.

Aims: This study was planned to identify the role of flagella in biofilm formation by constructing flagellated (wild type) and physically disrupted variants (non-motile).

Methods: Total 10 clinical bacterial strains were screened. Based on morphological variation and motility, only two highly resistant trains were characterized biochemically, physiologically and genetically. Biofilm formation capacity of strains was analyzed using three methods including Congo red assay, test tube assay and liquid-interface coverslip assay. Afterwards, flagellar disintegration was induced by blending and centrifugation for 5, 10 and 15 minutes.

Results: Our results showed these strains as *Bacillus cereus* and *Yersinia enterocolitica* identified by 16S rRNA sequencing. Both strains produced significant biofilm by all three above mentioned methods. A motility test of these blended variants showed partial leading to completely diminished motility with increased blending time. The significant loss in biofilm formation after 15 minutes of blending confirmed the important contribution of flagella to the initiation of biofilm formation. This biofilm defect observed in flagella paralyzed/minus variants presumably may be due to defects in attachments to surface at early stages.

Conclusion: This study indicated that flagellar motility is crucial initially for surface attachment and subsequently for biofilm formation.

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Resistance to antibiotics of *Staphylococcus* strains isolated from hospitalized patients

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Background: Methicillin resistant *S. aureus* (MRSA) is responsible for hospital (HA-MRSA) and community-acquired infections (CA-MRSA). MRSA strains were identified after the introduction of methicillin in therapy. The purpose was to evaluate the antibiotic resistance phenotypes of CoNS strains isolated from hospitalized patients.

Materials & Methods: The study included strains isolated from hospitalized patients in the Emergency Hospital Prof. Dr. O Fodor Cluj-Napoca. The identification and the antibiotic resistance profiles of the strains were performed by standard and automated methods (ApiStaph galery and Vitek2Compact).

Results: Of all isolates, 37.5% were CoNS: *S. epidermidis* (20.8%), *S. intermedius* (4.2%), *S. capitis* (2.1%), *S. hominis* (2.1%), *S. haemoliticus* (4.2%), *S. saprophyticus* (2.1%) and other CNS (2.1%). From all the CNS strains, 26 strains (27.18%) showed Meticiline resistance (MR). The CNS strains showed high rates resistance to Penicillin (25%), to Erythromycin (22.9%), to Imipenem (16.7%), to Rifampycin (10.41%) and to Fosfomycin (29.16%). The CNS strains resistant to Meticiline were: *S. Epidermidis* (20.8%), *S. Intermedius* (4.2%), *S. Haemoliticus* (4.2%), *S. saprophyticus* (2.1%) and other SCN (21%). The MR CNS strains were resistant to Eritromycin (14.6%), Clindamycin (14.6%), Ciprofloxacin (16.7%), Gentamycin (16.7%), Rifampycin (14.6%), Tetracyclin (25%) and Imipenem (22.9%). The resistance to Moxifloxacin was 10.41%. All strains were susceptible to Teicoplanin and Vancomycin.

Conclusion: Following the strains antibiotics resistance profile, we conclude to the circulation in our geographic area of strains with different resistance phenotypes. This finding indicates the necessity to detect them by PCR, for limiting the spread of these strains in hospitals and community.

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Disinfectant and multidrug resistant aero pathogens in two tertiary health facilities in Abeokuta southwest Nigeria

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Aeromicrobiological survey of indoor and outdoor in two health facilities in Abeokuta, SW Nigeria was conducted using standard methods. Bacterial and fungal isolates sampled from different wards (male, female, children, maternity and gynaecology) and outdoor were subjected to antibiotics, antimycotics and disinfectants susceptibility testing. Resistant strains were identified using standard marker gene sequences for DNA barcoding (16S rRNA for bacteria and internal transcribed spacer (ITS) region for fungi). Multidrug-resistant strains were identified as *Staphylococcus aureus, Klebsiella michiganensis, Escherichia coli, Candida albicans, Aspergillus flavus*. Phylogenetic analyses showed that isolates were specific to their local environment. This is the first report on the presence of *Klebsiella michiganensis*, an emerging clinical pathogen in air samples in many tertiary facilities in Nigeria. Regular disinfection of hospital environment and monitoring of air quality should be given priorities to prevent hospital-acquired infections of resistant pathogens.

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Viral load predicts virological response to therapy in chronic hepatitis C

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Introduction: Hepatitis C is an infectious disease affecting primarily the liver, caused by the hepatitis C virus (HCV). HCV infection is a major problem in Egypt. Egypt has the highest prevalence of the Hepatitis C virus (HCV) in the world, with 14 percent of the population infected and 11.8 million patients, according to the World Health Organization. Every year there are 170,000-200,000 new HVC cases in Egypt. It was first discovered in 1989. The hepatitis C virus (HCV) is a small, enveloped, single-stranded, positive-sense RNA virus. It is a member of the *Hepacivirus* genus in the family *Flaviviridae*. There are seven major genotypes of HCV, which are known as genotypes one to seven. It is transmitted by injection, which means spread primarily by blood-to-blood contact associated with intravenous drug use, poorly-sterilized medical equipment, and transfusions.

Aim of the study: This study aims to determine the common prevalent HCV genotypes among chronic HCV patients in Egypt and to evaluate the rate of sustained virological response (SVR) with some factors that affecting it.

Subject & Methods: In our study, fifty patients were enrolled. Eligible participants were aged ≥18 years, had chronic HCV genotype 4 infection (serum HCV RNA≥2000 IU/mL). All Biochemical tests for liver function, Blood sugar and HBA1C were done for all cases. The recommended regimen was DCV 60 mg plus SOF 400 mg once daily for 12 weeks; at their discretion, physicians could add RBV to the regimen or reduce treatment duration. HCV-RNA (viral load) was measured using RT-PCR (quantitative method) (Qiagen/BD Company) (Before treatment and after 12 weeks).

Results: SVR achieved 12 weeks after the end of treatment. Of the 50 evaluable patients, six received DCV+SOF and 44 DCV+SOF+RBV. Most patients were men (76%). SVR12 (modified intention-to-treat) was achieved by 98% of patients (48/50); one patient had virological breakthrough (was lost to follow-up at four weeks after treatment) and one patients relapsed. There was no statistically significant difference in treatment efficacy between treatment-naive patients (100%, 37 of 37) and those with treatment experience (84.6%; 11 of 13) (P=51). High SVR12 was observed regardless cirrhosis and level of diabetes.

Conclusions: In our study, the most predominant genotype was genotype IV with 86%. Of our HCV-treated patients, had high SVR. HCV genotype-4, and low baseline viral load were predictive of SVR.

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Molecular analysis of aflatoxigenic fungal strains on rice grains

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Aflatoxins have been emerged as a serious threat to food safety and quality assurance. A variety of fungal species i.e., multiple strains of *Aspergillus flavus, Aspergillus niger, Fusarium oxysporum, Alternaria alternata* have been reported as aflatoxigenic. Main objective of this study was to evaluate the genes responsible for aflatoxins production in the fungal strains isolated from rice grains being stored in warehouses of district Lahore, Pakistan. Total five (05) representative samples of rice grains were obtained and analysed for the fungal microflora. Isolation and identification of fungal strains were initially done based on morphological characters, later confirmed by using universal primers of internally transcribed spacers regions (ITS-1 and ITS-4). Eleven (11) fungal strains were identified based on phylogenetic analyses. Potential to produce afaltoxins was checked by using a set of specific primers including genes of aflR, *nor1, omt1, ver1*. Four (04) out of total eleven (11) strains showed the potential to produce aflatoxins. This might be due to humidified environment of warehouse that is helpful for the rapid growth of fungal strains. Research for the root causes for the growth of aflatoxigenic fungal strains in warehouses is continued.

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