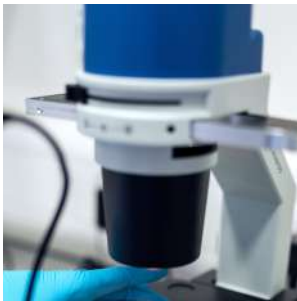


Poster

Microbiology 2022



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Antagonistic effect of lactic acid bacteria extracted from pulque

Ana Rosa Huezo Sánchez

Universidad Popular Autónoma del Estado de Puebla, México

The current research refers to the evaluation of the antagonistic effect of a synbiotic beverage made from aguamiel, mainly, the bactericidal effect of a functional beverage on pathogens. Aguamiel is a Mexican millenary drink, whose consumption has declined significantly in recent years. To study the effect of this drink, it is necessary to mention the causes that precede it, one of them been the high number of foodborne diseases, followed by poor hygiene practices and indiscriminate use of antibiotics that ultimately constitute a health and economic problem of global relevance.

There are few studies about the functions, properties and impact of Mexican endemic foods and human health, for this reason, the purpose of this research is to generate documentation in response to the following research question: Is the synbiotic beverage based on aguamiel able to inhibit the growth of pathogens of clinical importance?

The study is developing in five phases which consisted on the selection and growth of five probiotic microorganisms and seven pathogens, production of the synbiotic drink, antagonism tests against pathogens in microplate and by antibiogram method following by the identification of the metabolites in charge of the inhibition and finally a step of intervention with murines. The tests are being carried out in triplicate.

Speaker Biography

Ana Rosa Huezo Sánchez, 28 years, is a Ph.D. student in biotechnology at UPAEP university in Mexico. Her area of research is focused on probiotics and their use as adjuvants in the treatment of gastrointestinal infections. Currently, she is a thesis advisor for undergraduate and master's students. She studied her bachelor's degree in food science and technology at Zamorano university, Honduras.

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Enhanced activity of the plant-growth promoting rhizobacteria (PGPR) affect cannabis flower biomass and cannabinoid accumulation

Dongmei Lyu and Donald L. Smith

McGill University, Canada

Plant growth-promoting rhizobacterium (PGPR) as a sustainable approach has been used to improve plant growth and enhance yield and quality. However, some of isolated PGPR activated in laboratory condition are hardly colonization into host plants in field. Inoculating PGPR with microbial growth medium (King's B) could contribute to its survival under the undomesticated growth condition. Cannabis was selected to test the efficiency of PGPR because its production was prohibited which caused the shortage of knowledge about this plant. This study evaluated three individual PGPR (strain 1, strain 2 and strain 3) and King's B inoculation, and two different inoculation timings (vegetative and flower stage) on the growth and development of cannabis (cv. CBD Kush). Inoculated PGPR at vegetative stage had better performance on yield attributes, and physiological variables but flowering inoculation contributed to better cannabinoids concentration. At vegetative stage inoculation, we observed the significance difference between PGPR

inoculated and mock-inoculated (sterile water) plants. Among different PGPR inoculations, strain 3 enhanced the plant height and stem weight, while strain 2 significantly increased flower dry weight. In conclusion, a slow-growing PGPR with the presence of microbial growth medium has improved cannabis' flower yield at early inoculation; whereas the fast-growing PGPR barely changed the plant growth and yield compared with the growth medium, this result will be necessary to be considered in future studies to verify if this type PGPR produce some compounds caused the slowness of plant growth.

Speaker Biography

Dongmei Lyu is PhD student at McGill University. She has been working on the plant growth promoting rhizobacteria and associated crop (hops, and cannabis production) for three years. She has published eight peer-reviewed papers in international journals, with two currently under review.

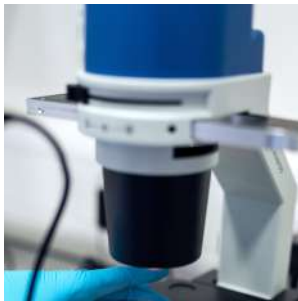
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Vitamin K accelerates wound healing process on rat skin achieved by common wound dressing agents in Erbil city/ Kurdistan

Shokhan Osman and Zahra Abdulqader Amin

Hawler Medical University, Iraq

Vitamin K is a fat-soluble vitamin which plays an important role in coagulation pathways of living organisms. The aim of the study was to test the wound healing effect of Vitamin K and some common wound dressing agents available in hospitals and private pharmacies of Erbil City/ Kurdistan which were; the Moist Exposed Burn Ointment (MEBO) and the Cica silver spray and to test their combination with vitamin K injection.

Methods: Six groups of albino rats were used. Group M: Mebo ointment, Group C: Cica silver spray, Group K :Vitamin K injection, Group MK: Mebo ointment+Vitamin K injection. Group CK: Cica silver spray +Vitamin K Group, and N:(No-treatment group). The duration of the experiments was as 7,14, and 21 days post wound surgery. The percentage of wound contraction was measured and the blood serum was collected to test the level of transforming growth factor- β (TGF β) and platelet-derived growth factor (PDGF).

Results: The results showed that best wound contraction

percentage was given by the MK treated rats in comparison to the not treated rat's group. Similar results were obtained from TGF β and PDGF data in which MK group showed significant highest levels of these growth factors.

Conclusion: Application of MEBO ointment showed significant results during the wound healing process when it used separately but the best result of MEBO ointments was given when it used in combination with vitamin K in treating excisional wound model on rat skin. therefore, our results provide a scientific basis of co-administration of vitamin K and MEBO in the management of wounds. Keywords: Wound healing; Rat; cskin; vitamin K; MEBO; Cica silver spray.

Speaker Biography

Shokhan Osman is currently a lecturer in Hawler Medical University, Iraq.

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Adaptation of microalgae to extremely polluted waterbodies from radionuclides

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Water pollution is an important cause of the phytoplankton decline. Consequently, the effect of anthropogenic contaminants on microalgae and cyanobacteria has been studied in detail. An alternative approach is to study the mechanisms that allow adaptation of phytoplankton to anthropogenic pollution. Adaptability of microalgae to contaminated environments is very relevant to understand the evolutionary ecology of phytoplankton under anthropogenic global change. Little is known about the mechanisms that allow rapid adaptation of microalgae to these extreme environments. An outstanding example of the adaptation of microalgae to extreme anthropogenically-generated environments (i.e., residual waters from radiochemical plant with extremely high levels radionuclides contamination, severe acidity and elevated conductivity) has been discovered in a huge evaporation pond at some plant atomic industry near the Yenisei River. Although it is usually assumed that

extremophile species inhabit these extreme environments, all the microalgae living in these ponds are mesophile species that have developed a very fast adaptation to extreme waters. Experiments have proven that only a single, rare, spontaneous mutation is necessary to produce the adaptation to the extreme contamination in evaporation pond. Microalgae living in the extreme ponds of residual waters from radiochemical industry could be the descendants of mutants with changes on a single-gene or few genes that confer a large adaptive value under extreme contamination.

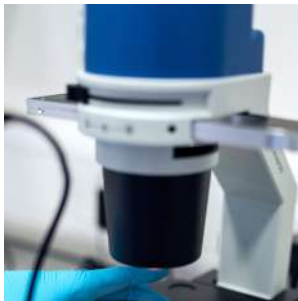
Speaker Biography

Lydia Bondareva is a specialist in the field of the environment, studying the effects of anthropogenic pollution of various natures on the health of the population. She is the author of over 150 scientific articles and monographs.

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Accepted Abstracts

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Structure-Activity-Mechanism Studies for Various Natural Compounds: Phenol Group Is Crucial for the Antimicrobial Activity

Bengü Ergüden

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Pandemic we are facing today increased our awareness about the antiviral, antibacterial and antifungal compounds. Bioactive molecules having antimicrobial properties are of special interest for the control of pathogens that cause infections in humans. We focus on the mode of action of these compounds and especially relation between structure-activity-mode of action trio.

Terpenoids, secondary metabolites abundantly found in plants, are known to possess antibacterial activity against both Gram-negative and Gram-positive bacteria, and antifungal activity against pathogenic fungi. Recently, we studied the structure-activity relation of various substituted diterpenes and showed that phenolic structures are superior to their relatives against both bacteria and fungi. We also analyzed effect of these compounds on the microbial cell wall structure and maintenance of homeostasis. Free hydroxyl group of the phenol moiety was essential for this effect, since neither the O-methyl derivatives nor the benzylic partners were as effective. We demonstrated that phenols increase membrane permeability and cause leakage of ions. We thus propose that perturbation of ion homeostasis upon increase in cell wall permeability is key for the action of terpenoids against bacteria cells.

On the other hand, chalcones, valuable precursors for flavonoids, have important antibacterial and antifungal activities against bacteria, pathogens, harmful fungi, and even

antibiotic-resistant microorganisms that cause food spoilage and infectious diseases. It is widely known that chalcones target various vital metabolic pathways of the bacterial cells. We aimed to study their action on the cell wall architecture, and studies various substituted chalcones. Similar to the case for terpenoids, phenolic chalcones proved to be superior to other substituted derivatives against both Gram-negative and Gram-positive bacteria. We also demonstrate that the cell wall is the first barrier that the chalcone molecules face for their action, and that phenolic chalcones increase ionic cell wall permeability to a greater extent than the other substituted members. Especially, against Gram-positive bacteria ion leakage can be detected at lower concentrations than the minimum inhibitory levels. Even though, disruption of metabolic pathways may be the principal mode of action of chalcones; in accord with our observations, we propose that the ion leakage precedes other inhibitory effects and contribute to the antibacterial action of phenolic chalcones.

Since, plant derived active reagents can be used as food preservatives and pharmaceutical agents, it is very important to understand their mode of action and their main target sites in the cell. Thus, this research not only opens new perspectives to understand antimicrobial activity mechanisms of these compounds, but also help widen their use.

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Toll-like receptor 2 activation in monocytes of alcohol use disorder patients contributes to systemic inflammation and alcohol-associated liver disease

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Background and Aims: A minority of alcohol use disorder (AUD) patients develops progressive alcohol-associated liver disease (ALD) potentially linked to gut barrier dysfunction, microbial translocation, and activation of systemic immune responses. Activation of circulating monocytes by microbial products might contribute to systemic and liver inflammation leading to ALD progression. Human data linking monocytes to early stages of ALD are lacking. We explored the links between changes in monocytes, microbial translocation, systemic inflammation, and monocyte-derived macrophages in early human ALD.

Method: We included n=123 AUD patients following a highly standardized rehabilitation program and n=26 healthy controls. We determined the total number of monocytes and proportion of monocytes subsets by FACS. Serum microbial translocation markers and cytokines were measured by ELISA and multiplex assay, respectively. Cytokines reflecting activation of monocytes were assessed by qPCR. Toll-like receptor (TLR) expression in monocytes and activation as well as phagocytosis were assessed *in vitro*. ALD severity and liver inflammatory responses were analyzed in liver biopsies by histology, qPCR, immunohistochemistry, and ELISA.

Results: In AUD patients, the number of blood monocytes increased ($p < 0.0001$). Among the 3 monocyte subpopulations,

intermediate and non-classical increased while classical monocytes decreased compared to controls. Monocytes from AUD patients up-regulated IL1 β and IL8 together with TLR2, down-stream AP-1 and inflammasome NLRP3. IL1 β and IL8 were actively secreted by those monocytes upon stimulation *in vitro* with the TLR2 ligand Peptidoglycan. Stimulation with *E. coli* confirmed preserved bacterial phagocytic activity. Systemic levels of cytokines and alterations in monocytes correlated with microbial translocation markers.

In parallel, IL1 β and IL8 were increased in ALD livers together with activation of intrahepatic macrophages (CD163+, iNOS+, TREM1+). Liver chemokines (MCP1, CX3CL1) involved in monocytes attraction were induced in liver tissue. IL1 β and IL8 correlated with liver chemokines, iNOS+ up-regulation in macrophages and ALD severity markers (e.g., fibrosis, AST/ALT, CK18-M65 and M30).

Conclusion: Our results point to a contribution of activated monocytes to systemic and liver inflammation. Monocytes likely infiltrate the liver, transform into monocyte-derived macrophages and release IL1 β and IL8 in response to Peptidoglycan and TLR2 activation, ultimately leading to ALD progression.

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Rhizospheric microbiome: Bio-based emerging strategies for sustainable agriculture development and future perspectives

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In the light of intensification of cropping practices and changing climatic conditions, nourishing a growing global population requires optimizing environmental sustainability and reducing ecosystem impacts of food production. The use of microbiological systems to ameliorate the agricultural production in a sustainable and eco-friendly way is widespread accepted as a future key-technology. However, the multitude of interaction possibilities between the numerous beneficial microbes and plants in their habitat calls for systematic analysis and management of the rhizospheric microbiome. This review exploits present and future strategies for rhizospheric microbiome management with the aim to generate a comprehensive understanding of the known tools and techniques. Significant information on the structure and dynamics of rhizospheric microbiota of isolated microbial communities is now available. These microbial communities have beneficial effects including increased plant growth, essential nutrient acquisition, pathogens tolerance, and increased abiotic as well as biotic stress tolerance such as drought, temperature, salinity and antagonistic activities against the phyto-pathogens. A better and comprehensive understanding of the various effects and microbial interactions can be gained by application of molecular

approaches as extraction of DNA/RNA and other biochemical markers to analyze microbial soil diversity. Novel techniques like interactome network analysis and split-ubiquitin system framework will enable to gain more insight into communication and interactions between the proteins from microbes and plants. The aim of the analysis tasks leads to the novel approach of Rhizosphere microbiome engineering. The capability of forming the rhizospheric microbiome in a defend way will allow combining several microbes (e.g. bacteria and fungi) for a given environment (soil type and climatic zone) in order to exert beneficial influences on specific plants. This integration will require a large-scale effort among academic researchers, industry researchers and farmers to understand and manage interactions of plant-microbiomes within modern farming systems, and is clearly a multi-domain approach and can be mastered only jointly by microbiology, mathematics and information technology. These innovations will open up a new avenue for designing and implementing intensive farming microbiome management approaches to maximize resource productivity and stress tolerance of agro-ecosystems, which in return will create value to the increasing worldwide population, for both food production and consumption

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