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الجامعة الاسلامية العالمية ماليزيا
INTERNATIONAL ISLAMIC UNIVERSITY MALAYSIA
يونيبرسيتي اسلام انتارابغسا مليسيا

ÜSKÜDAR ÜNİVERSİTESİ
İSTANBUL 2011

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Özet Kitabı

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Prof.Dr. Muhsin KONUK
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Dear Participants,

On behalf of the Executive Committee and the Local Organizing Committee, we are delighted to invite you to participate in the 8th International Molecular Biology and Biotechnology Congress, which will be held in Afyon on 17-20 December 2019.

Following the success of previous meetings, the scientific program will focus on Keynote/ Plenary Lectures given by distinguished speakers, as well as on paper submissions from all over the world.

Comprehensive whole day course aimed at younger colleagues will also be a part of our Congress. The scientific program would, however, be incomplete without your participation, without Paper presentations and Posters.

We encourage all of you to submit abstracts of your work, so that we can put together an exceptional scientific program.

We look forward to meeting you in the remarkable city of Afyon for the 8th International Molecular Biology and Biotechnology Congress.

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INVITATION SPEAKER

BROMELAIN: FROM MOLECULAR BIOLOGY TO COMMERCIALIZATION

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Abstract

Bromelain is an enzyme that has vast applications in industry. Studies on its application in animal feed, food, pharmaceutical and medical industries have been conducted by many researchers worldwide. However, those researches remain as bench-scale research output because it is hard to produce bromelain at high purity, high activity and at a large scale. Most bromelain in the market is produced from pineapple waste that has low activity. The highest bromelain enzyme activity available in the market is only 300 GDU. Therefore, through molecular biology and bioprocess engineering, our team developed recombinant bromelain with the enzyme activity that can be custom-made and high purity. Through the 10 years of research, the cloning, functional activity, upstream and downstream processing and the scaling-up studies have been carried out to ensure that recombinant bromelain produces suitable for the commercial market. This paper presents the whole 10 years of research activities for others to benefit.



Research for Making Life Better

Evaluation of Insecticides Used in Agricultural Areas in Turkey and Investigation of Alternative Biotechnological Products

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Abstract

Efficient use of agricultural areas to feed the growing population in Turkey is very important. In order to produce high quality and efficient agricultural products, It is necessary to management pest insects. For this reason, insecticides are used in pest control in agricultural areas. However, intensive use of insecticides causes environmental pollution. When the use of insecticide was examined; about the use of insecticides was determined that the last 10 years in Turkey increased by 37%. In 2009, 9914 tons of insecticides are used to management pest insects in Turkey. In 2018, this amount increased to 13583 tons. Also; In 2018, arable land decreased significantly. According to these data; increased use of insecticide in the last 10 years can cause environmental pollution. Therefore, the importance of using chemicals that have less toxic effects to the environment has increased. These chemicals can be plant extracts and some antibiotics. In the investigation of these chemicals, model insects are used in laboratory conditions. In agricultural pest control research; Galleria mellonella has been preferred model insect in recent years. Under laboratory conditions, low toxic chemicals investigated on G. mellonella may be an alternative to insecticides and may reduce the amount of insecticide used in agricultural areas. In this study; it was determined that increases the amount of insecticides used in pest control and decreased agricultural areas in Turkey last 10 years.

Keywords: Insecticides, Model insects, Environmental pollution, Turkey

A Comparative Investigation into Macroalga Vallisneria Spiralis in Biotechnology Uses to Remove Heavy Metal Ni (II) in Aqueous Media

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Abstract

Alongside increasing agricultural, industrial, and municipal activities water pollution arising from these activities has threatened mankind and the ecosystem environment on a serious level. Nonbiodegradable heavy metals such as lead, cadmium, chrome, arsenic, mercury, copper, zinc and nickel, unlike organic contaminants, cause to accumulate in living organisms when they are released into ecosystem. Environmental, economic and political pressures have driven the interest towards the search of sustainable, cheap, easy to regenerate adsorbents. At present, macroalgae (green, brown and red marine) are getting growing consideration as an alternative resource for algal biomass to remove heavy metals in aqueous media in biotechnology uses. In this study macroalga Vallisneria Spiralis has been employed as an effective adsorbents for the elimination of Nickel (II) as pristine, chemical- and microwave-treated forms. All the batch biosorption experiments were conducted to optimize different factors affecting biosorption. To enlighten the biosorption mechanism the biosorbents were characterized by Scanning Electron Microscope (SEM), Transmission Electron Microscope (TEM), Fourier Transform Infrared Spectroscopy (FTIR). The candidate macroalga was found to be feasible and efficient biosorbent in the light of further studies such as kinetic, isotherm, and desorption studies.

Keywords: Macroalga, Vallisneria Spiralis, Biosorption, Biosorption Mechanism, Characterization

A PRELIMINARY STUDY: CREATING PHARMACOGENETIC ALGORITHM FOR WARFARIN USE IN TURKISH SOCIETY

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Abstract

Background: Warfarin is an oral anticoagulant widely prescribed for the prevention and treatment of thromboembolic diseases under certain conditions, despite the presence and ease of use of Vitamin K oral anticoagulants as an alternative. Warfarin dosage adjustment is also a leading element of serious adverse drug events due to the narrow therapeutic window and complexity of pharmacokinetics and pharmacodynamics. Some genetic variations are known to be associated with warfarin metabolism are effective in dose adjustment and predicting the risk of adverse treatment. However, these genetic variations differ between populations and block the establishment of a stable pharmacogenetic algorithm. So far, although the most common strategy for dose determination in warfarin treatment is the standard fixed dose method, this does not guarantee successful treatment for every patient. Although polymorphisms in the VKORC1 and CYP2C9 genes constitute approximately 40% of the inter-individual variability in warfarin dose requirement, this value is observed only for certain variants. The aim of this preliminary study is to reveal the prevalence of the polymorphisms involved in warfarin metabolism in patients on warfarin therapy in the Turkish population and to propose a pharmacogenetic algorithm for clinical use of drug specific to our society.
Material Methods: 24 warfarin treated patients (16 female, 8 male) from Cardiology Clinic of Florence Nightingale Hospital, Istanbul Bilim University were included in the study. For each patient the clinical data and drug-drug interactions were evaluated as a response to CYP2C9 star alleles (2, 3, 4, 5, 6, 11) and VKORC1 polymorphic regions (-1639 G>A, 5808T>G, 1173C>T, 6853G>C, 6009 C>T, 8773C>T, 3730 G>A and 7566C>T). Genomic DNA was isolated from peripheral blood using Qiacube with QIAamp DNA Mini Kit. For the detection of polymorphic alleles, automated, multiplexing, continuous flow, random access microarray platform, the INFINITI-Plus System (Autogenomics) was used.
Results: According to our results, the number of patients carrying CYP2C9 * 2 variant was found 6 (5 heterozygous, 1 mutant); patients with variant CYP2C9 * 3 were 6 (6 heterozygous); the number of patients carrying VKORC1 3673 variant was found 14 (9 heterozygous, 5 mutant). According to considering these results the safe dose of warfarin was recommended to be 0.5-2 mg for 14 patients. According to the analysis includes other gene regions, 100% similar genotype was observed in VKORC1 1639 G>A, VKORC1 1173C>T, VKORC1 6853G>C, VKORC1 7566C>T gene regions in 4 of 6 patients whose INR value was less than 2. The INR values of 4 patients were found higher than 3, but there was no 100% common genotype, but at least one variant was found in VKORC1 1173C>T, VKORC1 5808T>G, VKORC1 1173C>T, VKORC1 6853G>C and VKORC1 7566C>T regions in these patients.
Conclusions: Pharmacogenetic dosing algorithm is being developed all over the world to define the individual dose of warfarin in order to reduce the risks of its overdose. It is clear that this case may show variations between populations. This preliminary research is the first comprehensive study for use in clinical pharmacogenetics of warfarin in Turkey. According to our results, we believe that the warfarin pharmacogenetic algorithm specific to the Turkish population is efficient and necessary due to the fact that the variants used in dosing determination in most populations were not detected, whereas the rare variants were available in our society.

Acknowledgement: This study was supported by Istanbul Development Agency, Project No. TR10/16/YNY/0030.

Genetic polymorphisms of CYP2D6 gene and breast cancer risk in Moroccan population.

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Abstract

Breast cancer is the most common cancer among women worldwide, the etiology of breast carcinoma is still poorly understood. Hereditary breast cancer of high penetrance genes constitute only 5-10%, low penetrance genes therefore account for the most of sporadic breast cancer form. Cytochrome P450 (CYP) enzymes are the most important xenobiotic metabolizing enzymes involved in carcinogen metabolism and detoxification. The CYP2D6 gene is highly polymorphic, and individuals can be extensive, intermediate, or poor metabolizers of endogenous and exogenous substrates that potentially activate carcinogenic forms. The aim of the present study was to assess the association between CYP2D6 and breast cancer susceptibility in Moroccan population. We conducted a case-control study including 400 participants (200 breast cancer patients and 200 matched-age healthy controls) to evaluate three polymorphisms of CYP2D6 gene: CYP2D6*3 (rs35742686), CYP2D6*4 (rs3892097) and CYP2D6*10 (rs1065852) by PCR-RFLP. Our preliminary results suggest that the A/- genotype of CYP2D6*3 is significantly associated with breast cancer susceptibility. However, no association was shown for the other polymorphisms. This suggest a possible implication of polymorphisms of CYP2D6 in the occurrence of breast cancer in Moroccan population.

Keywords: CYP2D6, Breast cancer, CYP2D6 polymorphisms, Moroccan population.

Characterization of high antibiotic producer Streptomyces coelicolor strain which have one extra lon gene in its genome

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Abstract

Streptomyces are gram positive bacteria belonging to actinomycetales species that reproduce vegetatively through flamentous structures. Streptomyces are medically and biotechnologically important bacteria because they are the producers of a wide variety of bioactive compounds (anticancer agents, immunosuppressant drugs, herbicides etc.), including 75 % of the commercialized antibiotics. Streptomyces coelicolor is used as a model organism for studies on the regulation of antibiotic production and these studies have shown that a diverse set of genes and external factors that cause stress affect secondary metobolite biosynthesis. From bacteria to human, ATP dependent Lon proteases are one of the important proteases in protein degradation and play essential roles in different physiological processes. In a previous study, we obtained a high antibiotic producer Streptomyces coelicolor recombinant strain which have one extra copy of lon gene integrated to its genome. In this study, we analyzed the transcription of genes involved in stringent response (relA), polyphosphate metabolism (ppk), secondary metabolite production (actII-ORF4, redK) and stress response (sigB) in this recombinant strain. We have seen a significant increase in the expression of these genes compared to wild type.

Keywords: Streptomyces, antibiotic, Lon, polyphosphate, stringent response, stress.

In-silico aptamer design targeting human DNA topoisomerase II

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Abstract

Cancer is one of the major health problems in modern society and currently lots of strategies are used to overcome. Among these strategies, targeting DNA topoisomerase enzymes is one of the best approaches because of their roles in replication, transcription and chromosome stability. Therefore, numerous chemical-based drugs, such as camptothecin and its derivatives, have been developed and utilized to target DNA topoisomerases. However, chemical-based strategies are failed due to drug resistance. In this regard, biotherapeutics provide a suitable alternative to chemical-based therapies. In this work, we have designed DNA aptamer candidates that target human DNA topoisomerase II through bioinformatics tools. We first have gathered the protein sequences that have already had designed DNA aptamer against them. Then we used phylogenetic approaches to generate evolutionary trees which would explain the similarities between these proteins and human topoisomerase II. Based on evolutionary relation we have generated a DNA aptamer consensus sequence. The consensus sequence has provided us over 5000 different aptamer sequences in the length of 20 bases. We have generated 2D and 3D structures of these sequences based on modeling and used them in docking analysis. According to docking analysis, we have chosen up to 20 sequences and we are going to analyze them in in-vitro topoisomerase enzyme assays.

Keywords: DNA Aptamers, DNA Topoisomerase II, in-silico Modelling, in-vitro Topoisomerase Enzyme Assay

Plant Pectate Lyases: What is Their Role in Development and Ripening?

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Abstract

Plant cell walls are highly complex structures that are modified throughout development. They are a major contributor to the properties of plant structure and act as barriers against microbial pathogens. The primary cell walls of plants are composed of polysaccharides and proteins. The polysaccharide fraction is divided into three components which are cellulose, hemicelluloses and pectin that are all modified during fruit ripening. There is strong evidence that pectin plays an important role in intercellular adhesion and controlling the porosity of the wall. A large number of pectin degrading enzymes have been characterised from plants and they are involved in numerous aspects of plant development. The role of pectate lyases in plant development has received relatively little attention, probably because they are normally associated with the action of plant pathogenic organisms. However their importance in plant development and ripening is now becoming well established and new information about the role of pectate lyases in plant development forms the focus of this presentation.

Keywords: Pectate lyase; Plant cell walls; Plant Development; Fruit Ripening; Fruit Softening.

Production of Recombinant and Nano Recombinant 1,4-β-endo Xylanase from Bacillus subtilis BTX6 (MH101286) and Comparison of Enzyme Activities

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Abstract

Enzymes in a constantly growing world are used in a large area for reasons of use. There is a wide and widespread use of enzymes in the growing world market sector. In addition to product costs and stability, the need for continuous need has increased the interest in enzymes. Enzymes, which are often used at lower temperatures, can not work in certain environments requiring high temperatures. Considering all these negativities; The need for new enzymes that can operate at higher temperatures and which can show activity at different pH values has increased. The aim of this study; Obtaining 1,4-β-endo xylanase enzyme from Bacillus subtilis BTX6 (MH101286) microorganism, which can grow between 35 °C and 85 °C, is a comparison of this enzyme with nano enzyme. PCR amplicons obtained from Bacillus subtilis BTX6 (MH101286) were transferred to carrier vectors followed by E. coli DH5-α and plasmid isolation was performed. As a result of the sequence analysis, it was determined that the targeted gene was the desired gene sequence. As a result of cloning, the insert was ligated to pET 16b and then transformed into E. coli Rosetta. Protein isolation and subsequent purification of recombinant proteins with 6X-His tag with Nickel affinity were performed. The presence of pure enzyme; protein isolation was determined by methods such as purification, SDS Page and Western Blotting. The recombinantly obtained enzyme is then described in Say et al. (2015)1 by ANADOLUCA. ANADOLUCA method; biotechnology is a method that improves the stability and effectiveness of products obtained in fields such as genetics and molecular biology, such as oligomers, enzymes, amino acids and other biotechnological products; ruthenium-based, light-sensitive, conjugation and cross-linking. The obtained recombinant enzyme is surrounded by ruthenium based amino acid monomers by means of cross-linked structures; activities, stability, sensitivity and reusability. The enzyme caged by ANADOLUCA method, zeta size analysis with recombinant enzyme and CD spectroscopy were compared. In zeta size analysis, the size of recombinant enzyme was measured as 400.3 nm. Nano recombinant enzyme was measured as 422.6 nm. When analyzed by CD analysis, the positive peak and negative peak occurring in the spectrum indicate differences in structures. The activity of the enzyme at optimum pH, substrate amount and temperature were tested in both enzymes. As a result, it was determined that the activity of caged enzyme by ANADOLUCA method was higher than recombinant enzyme.

Keywords: Western Blot, SDS Page, Transformation, Bacillus subtilis, Activity, ANADOLUCA

Acknowledgements: This work was supported by Kafkas University Scientific Research Projects Office (KAU BAP-Project No: FM-24)

Reference: 1- Say, R., Unluer, O.B., Ersoz, A., Ozic, C. and Kilic, V., 2015. Reusable Nanocopy Machine Particles for the Replication of DNA. Biotechnology Progress, 31 (1), 119-123.

Effects of Selective Serotonin Reuptake Inhibitors on Electricity Generation in Microbial Fuel Cells

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Abstract

Microbial fuel cells (MFC) have recently emerged as renewable energy sources. MFCs consist of electrochemically active anode and cathode parts converting organic subrates into electricity via the catalytic activity of microorganisms. This technology is also useful for biological removal of environmental pollutants. Selective serotonin reuptake inhibitors (SSRIs) are a group of drugs commonly used in the treatment of moderate to severe depression in various mental disorders. However, metabolites of SSRIs are discharged into environment causing biological accumulation in the long term damaging the ecosystem. In this study, MFC performance using urine samples containing SSRI drugs, O-desmethylvenlafaxine (ODV), paroxetine and venlafaxine was examined as the mixture. Human urine samples containing 0-10-50 ng/mL of SSRIs were examined, and removal of SSRIs were monitored using liquid chromatography tandem-mass spectrometry (LC-MS/MS). The removal rate of SSRIs in combination were investigated during MFC operations. Cytotoxity analysis of both mixture and individual SSRIs was performed using ECV 304 (human endoterial) cell lines at a concentration range of 10-250 ng/mL using the MTT assay. Our results show that increasing concentration of SSRI drugs decreased voltage generation. 94% of paroxetine, 66% of venlafaxine and 48% of ODV removal was achieved. The removal rate of paroxetine was faster when compared to the other SSRIs. Cell viability decreased when SSRI concentration increased. In conclusion, MFC technology can be used for bioremediation of wastewaters contaminated with SSRIs.

Keywords: electricity; microbial fuel cell; selective serotonin reuptake inhibitors (SSRIs); urine; wastewater

Low-Moderate Doses of H_2O_2 Arrest Cell Cycle in hFOB 1.19 Osteoblast Cells without Apoptosis

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Abstract

Reactive oxygen species (ROS), e.g. H2O2, are the main cause of some metabolic diseases in humans such as bone and cartilage degeneration via oxidative stress and eventual cell loss. Cell cycle arrest, cell viability reduction, and increased cell death are consecutive events eventuating after short or long-term exposure of oxidative stress. In this study, it was aimed to check 24 hour-effect of H2O2 on cell viability, cell cycle arrest, and apoptosis in hFOB 1.19 osteoblast cell line. Seven concentrations of H2O2 (5, 10, 25, 50, 60, 75, 100 µM) were tested and IC50 (75.74 µM) was calculated via MTT assay. 75 and 100 µM H2O2 concentrations were found to significantly reduce cell viability after 24 hours. Sub-IC50 values (50 and 60 µM) were picked as low/moderate concentrations to check the effect of H2O2 on the gene expression levels of apoptotic (caspase-3, Bcl-2) and cell cycle arrest (p21) markers. RT-qPCR results revealed that, both 50 and 60 µM H2O2 concentrations increased p21 mRNA levels whereas there was no change in caspase-3 or Bcl-2. In previous studies, H2O2 could trigger cell cycle arrest, autophagy or apoptosis depending on its concentration. While high H2O2 concentrations lead to apoptosis, its low or moderate concentrations can result in cell cycle arrest. In conclusion, low/moderate H2O2 doses led to cell-cycle arrest after 24h in hFOB 1.190 instead of apoptosis. The following pathways (apoptosis, autophagy, senescence, etc.) under longer exposure times and higher concentrations of H2O2 in hFOB 1.19 osteoblast cells should be further investigated.

Keywords: Osteoblasts, autophagy, apoptosis, hydrogen peroxide stress, hFOB.

Antioxidant and mutagenic activities of freshwater microalgae Chlorella vulgaris and Chroococcus limneticus isolated from Diyarbakir region

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Abstract

The antioxidant and mutagenic activities of methanol extracts from the freshwater microalgae Chlorella vulgaris Beyerinck [Beijerinck] and Chroococcus limneticus Lemmermann were investigated. The species were isolated from Kabaklı Pond (37° 55' 23N, 40°17' 40E, Diyarbakır, Turkey) and identified according to Prescott (1973). Microalgae samples were grown in BG-11 medium under laboratory conditions. After harvesting, their extracts were used for antioxidant and mutagenic activities. The antioxidant activities determined by using 2,2´-diphenyl-1-picrylhydrazyl (DPPH), 2,2'-azino-bis-3- ethylbenzthiazoline-6-sulphonic (ABTS•+) and copper (II) reductive antioxidant activity (CUPRAC) assays. Their mutagenic activities were investigated by the Ames Salmonella/microsome mutagenicity assay test on Salmonella typhimurium strains TA98. The antioxidant assays were carried out at concentrations ranging from 10–100 µg/ml and for mutagenic activities 12.5-1000 µg/plate. The study revealed that the highest antioxidant activities recorded on ABTS assay of C. vulgaris (36.63%) and C. limneticus (28.48%) for 100 µg/ml concentration. On the other hand DPPH and CUPRAC assays showed weak activity. Antioxidant activities don't seem significant for both species if compare them to positive controls (Butylhydroxyanisole (BHA) 89.74%, Butylatedhydroxytoluene (BHT) 69.74%). There seems to be no mutagenic activities, otherwise C. limneticus would exhibit an effect on colony structure of S. typhimurium strains TA98.

Keywords : Microalgae , antioxidant, mutagenicity, C. vulgaris, C. limneticus.

Association of IL-6 rs1800795 and IL-10 rs1800871 Polymorphisms with Breast Cancer Risk in Moroccan Women

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Abstract

Breast Cancer (BC) is the most common malignancy in women worldwide. The incidence of this condition continues to increase rapidly. Although it has been established that BC onset and progression are multi-step processes resulting from a series of epigenetic, genetic, endocrine and external environmental factors.
Understanding the molecular mechanism of carcinogenesis BC is still complex so far. Several recent studies have highlighted the importance of the immune system in the etiology of BC.
Interleukin-6 (IL6) and Interleukin-10 (IL10) are a multifunctional immuno-regulatory cytokines with antiangiogenic functions involved in the development and progression of various tumors it may act as a two-edged sword. On one hand it exhibit cancer promoting immunosuppressive effect and on the other hand, it has cancer inhibiting anti-angiogenic property.
Considering the diverse roles of these cytokines, we proposed that polymorphisms in the cytokine genes could affect the risk of BC. Therefore, the aim of the present study was to assess the association between IL6-174 (rs1800795; G/C) and IL10-819 (rs1800871; T/C) polymorphisms, and the BC susceptibility in Moroccan women.
We conducted a case-control study including 577 study participants (263 BC patients and 314 female controls without cancer). The samples were genotyped by means of polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP).
To our best knowledge, this is the first time such studies are conducted in Morocco. This preliminary result show that the CC and GC genotype of IL6-174 polymorphism and CT genotype of IL10-819 polymorphism significantly reduced breast cancer risk however no association was observed for the TT genotype of IL10-819 polymorphism.

Keywords: breast cancer, genetic association, polymorphism, Moroccan population, IL6 (rs1800795), IL10 (rs1800871)

The Effects of Food Preservative-Ethoxyquin on Zebrafish Early Development and Gene Expression Profiles

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Abstract

Ethoxyquin (EQ) is a synthetic antioxidant used as preservative in animal feed. EQ is not permitted to be used in human food, however, it may reach to and be detected in human system via food chain and environmental contamination. Although EQ has been shown to have negative effects on different animal models, there are still limited studies on its adverse effects in aquatic animals. In this study, we analyzed the effects of EQ on developmental abnormalities and behavior as well as gene expression profiles in zebrafish. For this purpose, we exposed zebrafish eggs to various concentrations of EQ ranging from 1 to 100 µM for six days. We observed 90 and 100 % mortality in eggs treated with 100 µM EQ following 24 and 48 h exposure, respectively. After 48 h exposure to 50 µM EQ, developmental delay and decreased pigmentation were apparent in the eggs. We also determined pericardial edema in larvae exposed to 50 µM EQ. We observed a distinct locomotive pattern both in light and dark in larvae. Meanwhile, we analyzed the gene expression profiles for 1, 10 and 25 µM doses of EQ. We showed that EQ affected several genes associated with different physiological pathways such as stress response, cell cycle and DNA damage. These results demonstrate that EQ results in toxicity by inducing oxidative stress, DNA damage and apoptosis and could be detrimental to aquatic system.

Keywords: Gene expression, toxicity, development defects, mortality, behaviour

Identification of a cell surface receptor CuRe1 homolog as a candidate loci for broomrape (Orobanche cumana Wallr.) resistance breeding in sunflower (Helianthus annuus L.)

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Abstract

Broomrape (Orobanche cumana Wallr.) is an important parasitic plant causes reduction in sunflower yield. Natural resistance genes confer resistance to parasitic plant is the most effective method to control the disease. Although several resistance genes and QTLs were identified in sunflower genome, molecular mechanism of resistance is not known. Recently a cell surface receptor-like protein CUSCUTA RECEPTOR 1 (CuRe1) confers resistance to Cuscuta reflexa which is a parasitic plant were identified in tomato. CuRe1 recognizes the parasitic plant similar to gene for gene interactions in plant resistance to microbial pathogens. Despite its importance, none of the homologs were identified in sunflower genome. In the present study, homologs of this gene were identified in newly assembled sunflower reference genome by using bioinformatics tools. As results, a gene had 12 exons and 5.1 kb in size were identified in linkage group 4. This is the first report of identification of CuRe1 homolog in sunflower. CuRe1 homolog identified in this study provided valuable target for development of molecular tools for broomrape resistance breeding in sunflower.

Keywords: Molecular breeding, genome annotation, Helianthus annuus L

Computer-Aided Engineering of Candida parapsilosis Alcohol Dehydrogenase for Hydroxy-Fatty Acid Methyl Ester Oxidation

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Abstract

Oxidation of alcohols to their corresponding carbonyl compounds (aldehydes or ketones) is one of the essential reactions in industry for the synthesis of many important building blocks and intermediates. Enzymatic oxidation through alcohol dehydrogenases offers an alternative route for eco-friendly and sustainable production of carbonyl compounds from alcohols. Alcohol dehydrogenase 5 of Candida parapsilosis (cpADH5), a zinc dependent medium chain alcohol dehydrogenase, accepts diverse range of substrates such as aliphatic or cyclic ketones, keto esters, and aryl or aromatic substituted secondary alcohols. Up until now, cpADH5 has been engineered for asymmetric reduction of prochiral ketones to their corresponding chiral alcohols.
Herein, we report the semi-rational engineering of cpADH5 for oxidation of 3-hydroxy fatty acid methyl esters. In this concept, computational analyses were performed in order to determine amino acid positions which could involve in the oxidation of the target substrate methyl 3-hydroxyhexanoate. Later on, single and double site saturation libraries of two identified positions (L119 and W286) were generated and screened in order to obtain variants that oxidize the substrate methyl 3-hydroxyhexanoate. Afterwards kinetic characterization of cpADH5 variants with improved activity was performed. Furthermore, substrate specificity, selectivity and enantiopreference of improved variants were identified. Finally, structure-function relationships of the selective oxidation of 3-hydroxy fatty acid methyl esters were elucidated by employing substrate docking studies.

Keywords: protein engineering, directed evolution, alcohol dehydrogenase, fatty acid methyl ester

In Silico Analysis and Modeling of Missense Single Nucleotide Polymorphisms (SNPs) in Human CALML6 (calmodulin-like 6) gene

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Abstract

CALML6 gene (also known as CAGLP) encodes the EF-hand protein calmodulin-like 6 which is a calcium binding protein roles in various pathways such as calcium signaling pathway, cAMP signaling pathway and Ras signaling pathway etc. The purpose of this study is to predict the effect of each single nucleotide polymorphism (SNP) on the structure and function of the protein encoded by CALML6 by using computer-based bioinformatics tools.
SNPs in the CALML6 gene and FASTA format sequence of the CALML6 protein were obtained from NCBI dbSNP and UniProt databases, respectively in June, 2019. Deleterious/damaging effects of missense SNPs were determined using SIFT (Sorting Intolerant From Tolerant) and PolyPhen-2 software tools. I-Mutant 3.0 and MUPro Software tools were used to predict the decreasing/increasing effects of SNPs on the protein stabilization. Three-dimentional (3D) models of both wild-type and mutant type proteins were built and structural information was obtained using Project HOPE software tool.
Among 156 missense SNPs in the CALML6 gene, 11 SNPs were determined to be deleterious/damaging by both SIFT and PolyPhen-2 software tools and 3D models confirmed those effects. 7 SNPs of them were found to decrease the protein stabilization according to I-Mutant 3.0 and MUPro Software tools. These findings are suggested to provide data for further experimental validation studies.

Keywords: CALML6, single nucleotide polymorphism (SNP), In silico, calcium signaling pathway

Characterization of new bacteria with biosurfactant/bioemulsifier production potential from used engine oil contaminated areas

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Abstract

Surface active agents (surfactants) have long been used as one of the most commonly consumed chemicals of everdaylife. However, toxicity and accumulation of these synthetic substances in the environment restrict their consumption. Sharing similar functionality with many advantages like less toxicity, biodegradability and renewability leaded biosurfactants from microorganisms to gain widespread interest in many fields of industry for their emulsifying, foaming, wetting, and numerous other biological activities. In this study, discovery of novel biosurfactant producing bacteria was aimed. To do that, total of sixty-three bacteria were isolated from soil samples contaminated with used motor oil. Biosurfactant production potential of each bacterial isolates were screened using various methods such as oil displacement assay, drop collapse test and parafilm M test. Determination of emulsification index against several hydrocarbons including kerosene, xylene, diesel and motor oil were carried out for evaluation of bioemulsifying activity and the highest emulsification index (E24=56.6%) was observed for xylene. Promising isolates giving the best screening results were subjected to molecular identification, and sequencing of 16S rDNA regions suggested that these bacterial isolates were included in Serratia, Klebsiellla, Stenotrophomonas, Raoultella, Trabulsiella and Enterobacter genera.

Keywords: Biosurfactant, bioemulsifier, screening, bacteria, 16S rDNA sequencing

Investigation on Biotechnological Application Possibilities of Paenibacillus and Brevibacillus Isolates

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Abstract

The aim of this study is to determine the potential of certain isolates for use as plant growth promoter, compost enhancer and biocontrol agent. Isolates utilized in the study were obtained from sediment. These isolates were also potential candidates as new species. Enzyme tests were applied to Paenibacillus and Brevibacillus isolates obtained from Sakarya River sediment. Tests were conducted to determine potential biotechnological utilization possibilities of isolates. Taxonomic position of Paenibacillus and Brevibacillus isolates was detected by 16S rRNA sequence analysis. Selective isolation of Paenibacillus and Brevibacillus strains was performed from sediment samples collected from 4 different points of Sakarya river in Çifteler, Eskişehir. Isolates were tested against cellulase activity, indole acetic acid production, phosphate solubility (PGP) and caseinase activity.
Phylogenetic analysis of 16S rRNA gene sequences showed three isolates (S1I41, S1S24 and S3S32) closely related to Brevibacillus genus in the range of 99.4-99.58% resemblance and 6-8 nt differences. S1S22 isolates were also closely related to the genus Paenibacillus (99.58% resemblance and 6 nt difference). Enzyme tests revealed variant results for isolates. Among all, only S1I41 isolate was positive against cellulase activity. S1I41, S1S22 and S3S32 isolates were positive against caseinase activity while S1S24 indicated negative result. S1S24 and S1S22 isolates were determined to produce indole acetic acid. All of the isolates were found to be negative against phosphate solubilization.

Keywords: Biotechnological Application, Brevibacillus, Paenibacillus, River sediment, Selective isolation

Acknowledgements: Financial support of Bilecik Seyh Edebali University (Project no. 2016-01.BŞEÜ.13-01) was gratefully acknowledged.

Elucidating the Analogues of 3-bromopyruvate (3-BP) as Inhibitors Against Human Hexokinase II for the Development of Anti-Dengue Drugs

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Abstract

Dengue is one of the most severe febrile diseases caused by Dengue virus (DENV), a single-stranded RNA virus of Flaviviridae family. Recently, it has been declared that glycolysis exhibited perturbation during DENV infection, which is explicitly governed by human hexokinase II (HKII). Our aim is to identify HKII inhibitors based on 3-bromopyruvate (3-BP), a known HKII inhibitor, as a query molecule through virtual screening and verified by inhibition assays. Virtual screening method comprised of ligand and structure-based analyses, while inhibition studies were conducted by using personal glucose meter (PGM) and enzymatic assay. Firstly, the analogues of 3-BP were screened through ligand-based screening using Ultrafast Shape Recognition CREDO Atom Types (USRCAT) program and compounds were selected based on similarity scores. Subsequently, all selected compounds were docked through structure-based screening using AutoDock4 software and selected based on the best binding energy, to be tested using enzymatic assay. Compound 8 (ZINC78456436) and compound 10 (ZINC39416010) have been selected based on the similarity scores (0.838 and 0.836) respectively, and the best binding energy, -4.05 kcal/mol and -4.80 kcal/mol, whereas 3-BP itself was shown to be -3.66 kcal/mol. At 1 mM concentration, both compounds 8 and 10 showed inhibitory effects on HKII with PGM reading signal of 29.9 mM and 31.9 mM, respectively. Meanwhile, the IC50 values for both compound 8 and 10 were determined to be 1.6 mM and 7.4 mM. In a nut shell, selected compounds have fruitfully shown inhibitory effects on HKII, which paved the way towards the discovery of new dengue therapeutics.

Keywords: Dengue, Human Hexokinase II (HKII), 3-Bromopyruvate (3-BP), virtual screening, enzymatic assays

AN EVALUATION OF BASIC FOOD SCIENCE AND FOOD BIOTECHNOLOGY PROCESSES IN THE DIET

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Abstarct

Food biotechnology comprise sorts of scientific disciplines including food chemistry, biochemistry, molecular bıology, microbiology, bioreactors, fermentation process, nutrition and food quality assurance. In the Daily diet, fermented food and drinks have and special importance because of their functional properties and biochemical compounds. In Turkish traditional fermented foods such as yogurt, kefir and kımız, boza, shalgam and tarhana and special pickles etc. contain various functional properties and biochemical compounds that have beneficial effect to organism. They contain lactic acid bacteria, probiotics, B complex vitamins, nutritive minerals, and some specific compounds which can prevent to development of cancer and tumors, cardiovascular diseases, cholesterol reducing effect. In the healthy diet, essential food elements; essential amino acid vitamins, essential fatty acids, nutritive minerals must be taken with other nutrients that sufficient carbohydrate, lipids and protein content in the diet. Food biotechnology also includes Genetically Modified Organism (GMO). Studies are evaluated in food biotechnology too. On the other hand, the another significant and common fermented product types are beer, wine, wine agar, even distilled alcohol drinks those produced ethyl alcohol from carbohydrates sources e.g. gape fig, barley, wheat, rice or any carbohydrate sources. Food biotechnology can be evaluated in basic food science and food biotechnology process. Functional properties and medicinal compounds are known as anti-aging, and functional agents which affected health in positive way and preventive and protecting effect to organism. The process of the each of fermented food biotechnology products are established by the enzymes in aerobic and anaerobic conditions. Fermentation includes such a complex long ways to be able obtain products. The mentioned topics were reviewed in detail.

Keywords: Food biotechnology, food science, process, functional properties, nutrients, health.

Thermal Conductivity of Titanium Matrix Composites

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Abstract

Titanium (Ti) and its alloys are used in aerospace and biomedical applications as matrix material due to their high strength, high corrosion resistance and light weight. In this study, it was aimed to produce Ti-graphene composites with superior thermal conductivity (> 4500 W / mK) graphene reinforcement.
For this purpose, graphene with a thickness of 5-8 nm and a diameter of 10 µm was used. Powders of different graphene ratios were reinforced to Ti and sintered by vacuum sintering method. The composites were characterized by microscopic and non-microscopic methods and the structure-property relationship between thermal properties and microstructure was investigated.
By adding 0.15% and 0.30% graphene to pure titanium, thermal diffusivity and thermal conductivity were increased at room temperature. While there was a significant decrease in thermal diffusivity with the addition of 0.45% graphene, there was also a decrease in 0.6% graphene addition. When the microstructure images were examined, it was found that the graphene was agglomerated and did not spread homogenously. Homogeneous distribution is observed in 0.15% and 0.30% graphene added samples. As a result, optimum graphene amount was determined as 0.30% in order to increase thermal diffusivity.

Keywords: Graphene, titanium matrix composite, thermal conductivity

KNOCK-OUT OF APOBEC1 GENE BY CRISPR/Cas9

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Abstract

RNA editing, besides the known post-transcriptional modifications, is known as the replacement of a single base on the post-transcriptional messenger-RNA transcript. The first known protein of RNA editing, APOBEC1, physiologically deaminates Cytosine(6666) to the Uracil base in the transcript of the human apolipoprotein B protein. In this study, we aimed to generate a suitable cellular model for the analysis of RNA editing induced by the RNA editing enzyme APOBEC1. In general, this study includes the knock-out of the gene encoding APOBEC1, the catalytic element of RNA editing. For this process, a very popular genome editing tool derived from bacterial CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) / Cas9 (CRISPR-associated 9) system was used. Surrogate reporters were used to facilitate the identification of clones in which the knock-out of the gene of interest occurred. Subsequently, Caco-2 cells which assumed to lack APOBEC1 protein were cultured in a specific medium for sequence analysis of the knocked-out gene of interest. According to the results of the sequence analysis after cell culturing, gene silencing was effective on the reporters but not on the APOBEC1 gene on the genome.

Keywords: Caco-2, RNA Editing, CRISPR/Cas9, Gen Silencing, Surrogate Reporters.

Marker assisted selection and molecular markers in plant biotechnology

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Abstract

In recent years, biotechnology is one of most popular and innovative scientific fileds. Plant biotechnolohy is one of these fields too and Molecular markers that is used in this field appears to be an important biotechnological tool. Molecular makers are described as any gene in the genomes or gene region which is related with any piece of DNA. Today, Molecular markes are used for in plant systematics, breeding and the evalulation of gene resources effectively. Molecular marker technology led to the adoption of new practices to develop a comprehensive strategy for selection in plant breeding. As a result, plant biotechnology studies have brought expansive dimensions in molecular markers, enabling to get more efficient and rapid scientific results.
In this review, it is mentioned that principles and advantages and disadvantages of molecular markes which are used in biotechnology studies and application of marker assisted selection in plant breeding.

Keywords: plant biotechnology, molecular marker, marker assisted selection

Biochemical and Functional Analysis of Recombinant T169V and P172H Mutant Bile Salt Hydrolases (BSHs) from Lactobacillus plantarum B14

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Abstract

Bile salt hydrolase (BSH), synthesized by some intestinal bacteria, catalyzes the deconjugation of glycine- or taurine-conjugated bile acids into the amino acids and free bile salts in human intestine. Deconjugated bile salts potentially play an important role in the reduction of blood cholesterol level and formation of some gastrointestinal diseases such as cholestasis, gallstone formation and colon cancer. Because of the link between BSH and human health, the functional and biochemical features of BSHs necessitate an intensive study. Although BSHs exhibit variations in their catalytic activities, threonine-169 (T169) and proline-172 (P172) amino acids are strictly conserved in all members of the N-terminal nucleophile (Ntn) hydrolase superfamily. However, their functions are remain to be elucidated. In order to analyze the correlation between these two conserved amino acids and catalytic activity or stability of BSH, they were mutated by PCR-based site directed mutagenesis. The negatively charged polar T169 and hydrophobic P172 were substituted for the hydrophobic valine-169 (V169) and histidine-172 (H172) respectively. The mutant recombinant BSHs were expressed in Escherichia coli BLR(DE3). While the effects of the mutations on catalytic activity were detected by the ninhydrin assays, the effects of the mutations on formation of the BSHs were visualized by SDS-PAGE analysis. Although both mutations resulted in stable recombinant BSHs, P169V and T172H mutations reduced the catalytic activity 97% and 63% respectively and altered substrate specificity of BSH. This is the first experimental report indicated that the T169 and P172 are critical amino acids for the catalytic activity of the BSH.

Keywords: Bile salt hydrolase, Human bile acids, Catalytic activity, Lactobacillus plantarum, Site-directed mutagenesis

Development and testing of new SSR (simple sequence repeat) markers to use in phylogenetic analyses for breeding studies in *Triticum aestivum*

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Abstract

In recent years, DNA-based markers become crucial to select parents in breeding studies. To determine genetic polymorphism situations of the parents are very important for elapsed time in the selection of suitable candidates. SSR (simple sequence repeat) markers are widely used in phylogenetic analysis or genetic polymorphism studies, and each SSR marker has got the different distinction ability according to organism variety. In this study, it was aimed for development and testing of new SSR markers to use in phylogenetic analyses for breeding studies in *Triticum aestivum*. For this aim, new designed or modified primers, and some resistance gene markers (SSR-based) in *T. aestivum* were used as candidate primers. DNA amplifications were performed in eighteen wheat varieties using ten candidate primers. It was determined that the tested SRR primers have got high polymorphism rate. Band profiles for each SSR primers were analysed by using the software Phoretix 1D Pro for band counting and size assignment. The band data were used for evaluating the genetic similarity between samples and for constructing a dendrogram by UPGMA (the unweighted pair group method with arithmetic mean) clustering analysis method. The dendrogram showing genetic divergence among samples was drawn using MEGA 6 software. The genetic relationship among wheat varieties according to branching forms on the dendrogram was revealed and analysed.

Keywords: SSR markers, Phylogenetic analysis, *Triticum aestivum*, Plant breeding.

Design of nickel modified non-enzymatic sensor platform towards electochemical glucose detection

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Abstract

Producing sensitive and selective glucose sensors is very significant in the food industry, in the development of renewable, sustainable fuel cells. The enzyme based amperometric electrochemical glucose biosensors have extensively been examined for glucose level detection. However, enzyme sensors have some disadvantages, such as instability due to the presence of interfering chemicals and changes in the pH and temperature of the sample. To overcome these disadvantages, metal oxide sensors have been proposed which is determined by direct electrochemical oxidation of glucose using non-enzymatic glucose sensors [1].
In this study, nickel metal modified new enzymeless glucose sensor (POM@Ni) has been fabricated by using the drop-casting method. Then, electrocatalytic oxidation of POM@Ni sensor has been investigated in alkaline medium directly on the graphide rode electrode. The prepared POM@Ni sensor exhibited high electrocatalytic activity, selectivity and good detection range. Here, we utilized the advantages of Ni's electrocatalytic activity to generate a high potential for a non-enzymatic electrochemical glucose biosensor.

Keywords: Non-enzymatic, sensor, nickel, electrochemical detection

Anti-oxidative Effects of Gypsophila perfoliata on D-Galactose Induced Aging in Rat

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Abstract

D-Galactose (D-GAL), a monosaccharide, induces the oxidative stress and results in the mimicked aging model in rats. Gypsophila perfoliata belongs to Caryophyllaceae family and a perennial plant. The content of this plant is rich in saponarin and phenolics, therefore scientist has been focused on its possible antioxidative effects. In this study, we studied the antioxidant effect of Gypsophila perfoliata on aging mimicked rats induced by D-GAL. Wistar-albino rats were divided into 4 groups, with 8 rats each: Control, D-GAL, GYP, D-GAL+GYP. The rats have been applied D-GAL (150 mg/kg/day) subcutaneously (s.c.) and Gypsophila extract (100 mg/kg/day) via gavage for 12 weeks. Blood serum and brains used to determine Glutathione (GSH) and Malondialdehyde (MDA). The data were analyzed by use of the SPSS software package (20th version) One-way ANOVAs followed by post-hoc Bonferroni tests were used, and $p< 0.05$ was considered as significantly different value. When the data of examined groups compared to the control, we observed a significant increase in the MDA while significant decrease in the GSH levels. However, when we compared the Gypsophila group with D-GAL, the levels of both the GSH and MDA varied significantly. Our findings showed that the extract of Gypsophila could be used in reducing the oxidative stress during the aging.

Keywords: Aging, D-galactose, Gypsophila perfoliata, lipid peroxidation, glutathione

NLRP3 Inflammasome Activity on the Physiopathology of Posttraumatic Osteoarthritis

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Abstract

Osteoarthritis (OA) is a degenerative joint disease characterized by progressive and irregular cartilage loss, osteophyte formation, subchondral sclerosis, periarticular structures and a number of abnormalities in the synovial membrane. Posttraumatic osteoarthritis (PTOA) is one of the common causes of osteoarthritis, which can be acute or chronic after joint damage due to traumatic cases. PTOA leads to loss of performance and long treatment processes especially in athletic people and animals (horses, dogs, cats, etc.). Therefore, biomarker studies for early diagnosis remain important. In the pathophysiology of PTOA, an inflammatory response occurs in the region, engaging elements of the innate immune system. Although biomarker studies in recent years have focused on matrix metalloproteinases, aggrecanases, and proinflammatory cytokine families. The pathway of inflammation activated by cytosolic nod-like receptor proteins (NLRP) by members of the family of inflammatory cells has become more important than other pathways among the early detection biomarkers. NLRP3 inflammasome is a member of this family that activates the proinflammatory cytokines IL-1B and IL-18 through caspase-1 activation, stimulating macrophage infiltration and accelerating the inflammatory response. In this review, we aimed to discuss the role and diagnostic and therapeutic importance of NLRP3, which a member of the family of the inflammatory response, in the early diagnosis of PTOA.

Keywords: Arthritis, Inflammation, physiopathology, toll-like receptor.

Magnetic Nanoparticles in Image-Guided Biomedical Applications

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Abstract

Using engineered nanoparticles with unique physicochemical features such as ultrafine sizes and a large surface area to mass ratio, recent advances in nanomedicine have shown promises for a vast variety of biomedical applications including magnetic resonance imaging, targeted delivery of drugs or genes, tissue engineering, hyperthermia of cancer, magnetic transfections, among others. Among the engineered nanoparticles (organic nanoparticles (lipids, polymers, liposomes, polymeric micelles, dendrimers, and engineered peptides and nucleic acids); inorganic nanoparticles (carbon nanoparticles, metal and metal oxide nanoparticles)), magnetic nanoparticles have special advantages; they can be manipulated using magnetic fields, can be used in magnetic hyperthermia, in which an alternating magnetic field is used to heat the nanoparticles, can be used to enhance contrast and improve diagnostic sensitivity in magnetic resonance imaging (MRI). Thus, magnetic nanoparticles have a great potential for theranostics to enhance contrast and improve the diagnostic sensitivity of MRI, as well as to provide targeted delivery of drugs and implementation of hyperthermia, under magnetic fields. Herein, a methodology for the design and image-guided biomedical applications of magnetic nanoparticles will be discussed.

Keywords: Magnetic Nanoparticles; Theranostics; Targeted Drug Delivery; Magnetic Hyperthermia; MRI

Biochemical Characterization of Metagenomic ß-D-Glucosidase and Endo-1,4-D-Glucanase from Malaysian Palm Oil Mill Effluent

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Abstract

Palm oil mill effluent (POME) functional metagenomic library was constructed and screened to bioprospect cellulose-degrading enzymes. Using bioinformatic tools, the sequence analysis of identified genes indicates that the metagenomic cellulose-degrading enzyme 1 (MCDE1) is a putative ß-D-glucoside glucohydrolase and the structural based modeling analysis confirms that this enzyme belongs to GH3 familly with the presence of the active site from 273-290 amido acids and it shares TM-score of 0.95 with a novel dimeric GH3 beta-glucosidase isolated from compost using metagenomic analysis. For MCDE3, it is similar to non-characterized endo-1,4-D-glucanase from Serratia sp. and the strucural based modeling analysis indicates that the closest protein in the PDB is an endo-1,4-D-glucanase from Pseudomonas putida with TM-score of 0.914. The expected molecular weight of MCD1 is 84.3 kDa and the biochemical characterization shows that MCDE1 is highly active at pH 7 and at 50 °C and it shows a good and fast fluoresence in the presence of the fluoresence substrate 4-methylumbelliferyl β-D-glucopyranoside (MUGlc). For MCDE3, the expected molecular weight is 40.5 kDa and the biochemical characterization shows that MCDE3 is highly active at pH 4 and at 70 °C. These two metagenome-derived enzymes are expected to be relevant in different industrial processes depending on the required pH and temperature and further characterization such as influence of metal ions of their enzymatic activity may place them in the favorable industry.

Keywords: Metagenomics, 3D Modeling, TM-score, Glycoside hydrolase, Biochemical characterization

Functional Analysis of Arabidopsis Immune-Related Molecular Signatures In Arabidopsis thaliana In Response To Four Different Pathogens

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Abstract

Plants are attacked by diverse pathogens such as virus, bacteria, fungus, oomycetes, and nematodes. Although plants' physical and chemical barriers can eliminate some of these attacks, some aggressive ones can cause catastrophic losses on agricultural fields. Understanding how plants recognize and response to diverse pathogens can elaborate the genetic mechanisms of plant immunity. With the enormous effort on bioinformatics approaches and availability of whole genome sequences, a global set of gene expression data is getting available for plants exposed to various biotic stresses. In the present study, we collected data from published *Arabidopsis thaliana* transcriptomic data against virus (*Turnip crinkle virus* (*TCV*)), bacteria (*Pseudomonas syringae* pv.tomato strain *DC3000*), fungus (*Golovinomyces orontii*), and oomycetes (*Hyaloperonospora arabidopsidis* isolate *Noco2*). The transcriptome data and functional networks that specific to those pathogens or common expressed genes were identified and compared. According to results; 14 genes were commonly upregulated by four different pathogens. Additionally, plants also induce distinct transcriptomes for each pathogen; 180 genes for Pst, 338 genes for fungus, 3241 genes for oomycetes and 72 genes for virus. Functional characterization of those genes can reveal mechanisms of plant defense system for different pathogens uniquely.

Keywords: ***Arabidopsis thaliana*****, Biotic stress, Transcriptomics data, computational analysis**

Molecular Methods Used in Diagnosis of Plant Pathogenic Bacterial Diseases

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Abstract

There are many disease factors that negatively affect yield and quality in crop production. One of these diseases is caused by plant pathogenic bacteria. Nowadays, besides the classical methods used to determine the physiological, morphological and biochemical properties of bacterial diseases, the use of molecular biology methods which give faster and more accurate results has accelerated. In this study, molecular biology techniques used in the diagnosis of bacterial plant diseases are reviewed.

Keywords: Plant, Bacteria, Disease, Molecular Biology Techniques

Genotoxic characteristics of urban wastewater sludges of open drying beds

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Abstract

Open-air drying beds are the main and only technique used in the treatment of sewage sludge in Algerian wastewater treatment plants (WWTP), a valuable technique to reduce organic load. The effectiveness of this operation on the cytotoxic, mutagenic and genotoxic sludge qualities is studied with the Ames and *Allium cepa* tests. the number of revertants for the two strains (TA 98 and TA 100) tested induced by raw sludge is statistically significant, the number of revertant strains decreases significantly with and without metabolic activity in the sludge samples treated by the drying bed but it still mutagen. The *Allium cepa*- chromosome aberration test performed with different samples of raw and open drying bed treated sludge indicated the effectiveness of this treatment in reducing cytotoxicity but not the genotoxic effect expressed by a significant amount of chromosomal aberrations. Although the treatment of open-air beds reduces toxicity in a very effective way, sludge mutagenicity and genotoxicity remain significant.

Keywords: Open air-drying bed**,** wastewater sludge, Ames test, *Allium cepa* test.

In silico biosynthetic gene cluster analysis of a novel actinobacterium *Nonomuraea* sp. CH32

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Abstract

The genus *Nonomuraea* is a rare actinobacterial taxon with high potential to synthesize wide range of bioactive compounds. In this study, strain CH32 was isolated from an arid soil sample and identified by 16S rRNA gene sequence analysis. Pairwise sequence comparison conducted on EzBioCloud server (https://www.ezbiocloud.net/) indicated that the strain is a novel member of the genus *Nonomuraea* and the pairwise sequence identity of the strain to the most closely related type strain of *Nonomuraea gerenzanensis* was found to be 98.75%. Whole genome sequencing was carried out in MicrobesNG service (Birmingham, UK) to determine biosynthetic potential of strain CH32. Genomic DNA libraries were prepared using Nextera XT Library Prep Kit (Illumina, USA) and sequenced on the Illumina HiSeq using a 250 bp paired end protocol. *De novo* assembly was performed on samples using SPAdes version 3.7 and contigs were annotated on RAST server (http://rast.theseed.org/). In addition, the genome sequence consisting of 468 contigs with 71.0% GC content was analyzed on antiSMASH server (https://antismash.secondarymetabolites.org/#!/start) to detect biosynthetic gene clusters. In conclusion, strain CH32 was found to have bacteriocin, NRPS, PKS, siderophore and terpene biosynthesis gene clusters. Thus, strain CH32, which is a novel member of the genus *Nonomuraea*, promises to be a valuable source for novel bioactive secondary metabolites.

Keywords: *Nonomuraea*, **biosynthetic gene clusters, genome mining**

A study on the evaluation of micropropagation efficiency of some artichoke (*Cynara scolymus* L.) cultivars

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Abstract

Artichoke (*Cynara scolymus* L.), widespread in the Mediterranean basin, contributes greatly to the agricultural economy of the region. Artichoke is mainly grown for its heads and its stem and leaves are seen as the waste materials although they are also rich in polyphenols. Therefore it has gained more and more commercial importance in recent years and in addition to its consumption as food, it has started to attract attention in pharmaceutics. Micropropagation method, which is one of the *in vitro* techniques, enables the production of healthy, pathogens-free plants on a large scale, and is a fast, reliable and realistic alternative method to classical propagation method. The aim of the present study was to evaluate the micropropagation efficiency of some artichoke cultivars based on media and subcultures. In the present study, two different media combinations and seven important cultivars ('Bayrampaşa', 'Sakız', 'Olympus', 'Madrigal', 'Sambo', 'Green Globe' and 'Imparator') were used to serve the purpose. During the study, 15 subcultures were applied and the average numbers of shoots per explant, the average number of leaves per shoot, infection, old and undeveloped plantlet rates were assessed for each subculture. According to obtained data, Murashige and Skoog (MS) basic media supplemented with 0,05 mg L^{-1} 6-benzyladenine (BA) and 0,005 mg L^{-1} indole-3-butyric acid (IBA) was more effective than the media supplemented with 0,25 mg L^{-1} BA and 0,025 mg L^{-1} IBA. Results revealed that Imparator and Bayrampaşa gave the highest total number of plants. In terms of the number of shoots per explant, Imparator with 12,33 shoots/explant gave more positive results than others. Sakız was the best in terms of leaf formation with 20,8 leaf/explant. Results obtained from present study clearly demonstrated that total number of plant obtained showed variation based on cultivar and number of subcultures.

Keywords: Artichoke, ***In vitro*** **propagation, Plant tissue culture, Plant growth regulators**

Therapeutic effects of plant-edible exosomes

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Abstract

Exosomes are nano-scaled extracellular vesicles. The secretion of exosomes from the cells is mediated by the fusion of multivesicular bodies which contain many exosomes. Not only animal cells but also plant cells produce exosomes to communicate with neighbouring and distant cells by the transfer of the nucleic acids and proteins. Besides communication, plant cells utilize the exosomes for the conveyance of antimicrobial agents to the invading pathogen microorganisms. Beyond the activities on the invading pathogens, edible-plant derived exosomes can act on the intestinal system of the recipient body. Moreover, these edible-plant derived exosomes have been reported to function as an anticancer drug and/or drug delivery vehicle. In this study, the reviews and original articles in PUBMED were searched for bringing together the information about the edible plant-derived exosomes which have the therapeutic effects on various diseases. It was observed that exosomes that are from broccoli, carrot, ginger, grapefruit, and lemon are functional in various diseases, particularly in cancer management. Further studies can be conducted to increase the utilities of these exosomes in order to produce effective drugs.

Keywords: Exosomes, edible-plants, cancer

MicroRNAs as Biomarkers for the Prediction of Pesticide Toxicity

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Abstract

MicroRNAs (miRNAs) are small (18-26 nucleotides long) non-coding single-stranded RNAs that are found in all organisms. Function of these molecules is to regulate the gene expression at the posttranscriptional level. Several toxic agents including air pollutants, food contaminants, metals and pesticides have effect on expression of miRNAs. Recently, miRNAs have been attracted a great deal of interest as biomarkers in toxicological researches. miRNAs have several advantages when considered as biomarkers for pesticide exposure due to their specific properties including stability in biofluids, tissue-specific expression, accurate measurement and evolutionarily conserved in organisms. This review aimed to conduct a general assessment of the scientific studies related to miRNAs as potantial biomarkers for predicting of pesticide toxicity in model animal species and in human. For this purpose, some of the scientific research reports published between 2010 and 2019 were reviewed. Studies showed that some pesticides may cause alteration in expression of miRNAs and genes in model mammalian cell cultures, in model fish and mammalian species also in biofluids of human. As a result, expressions of some miRNAs were significantly affected by pesticide exposure and alterations in expression of miRNAs may have potential to be used as biomarkers for predicting of pesticide toxicity. It was concluded that further researches are needed to clarify the relationship between pesticide toxicity and miRNAs.

Keywords: Epigenetic, miRNAs, pesticide toxicity, biomarker

Pb(II) Resistance and Bioaccumulation by Using Thermophilic *Bacillus firmus*

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Abstract

In this investigation, a thermophilic *Bacillus firmus* was isolated from mud sample of Omer thermal spring in Afyonkarahisar, Turkey. This thermophilic isolate was identified by morphological, biochemical and 16S rRNA analyzes. After isolation procedures, the resistance and bioaccumulation of Pb(II) was studied. The minimum inhibition concentration(-MIC) of Pb(II) was 145 mg/L and 22.5 mg/L in solid and liquid medium, respectively. The effect of different Pb(II) concentrations on the growth of thermophilic *B. firmus* was investigated. The highest Pb(II) bioaccumulation capacity was determined as 104.27 mg/g of dry bacteria at 24th. Before and after bioaccumulation studies, SEM analyzes were tested. The effect of Pb(II) on antioxidant enzyme superoxide dismutase(SOD) and catalase(CAT) was also tested.

Keywords: Thermophilic, *Bacillus firmus*, Pb(II), heavy metal resistance, bioaccumulation

Oral Presentation

Ellagic Acid Ameliorates Pancreatic Damage in Rats via Up Regulate of Nrf-2 and Caspase-3, Down Regulate of NF-kB, Tnf-alpha, Bcl-2 and Akt Protein Expression

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Abstract

Pancreas is the control center of energy consumption and metabolism. Carbon tetrachloride (CCl4) is a potent carcinogenic agent that causes the production of reactive free radicals and initiates cell damage. Recent studies have found that ellagic acid (EA) has a variety of biological activities including antioxidant, anti-inflammatory, anti-fibrosis and anticancer properties. The aim of this study was to examine whether EA plays a protective role against pancreas damage induced with CCl4 in rats. 36 Wistar albino rats (n = 36, 8 weeks old) were used to determine whether or not EA had a protective role against pancreatic damage in rats induced with CCl4. The animal experiments section of this study was carried out by Firat University Animal Experiments Ethics Committee. With the permission dated on 06.03.2019 and numbered 53 decisions, F.U Experimental Animal Research Center. Rats were separated into 4 groups and 9 rats included each group. Groups: (i) Control Group: Standard diet; (ii) EA Group: Standard diet + EA group; (iii) CCl4 Group: Standard diet + CCl4 group; (iv) EA + CCl4 Group: Standard diet + EA + CCl4 given group. Animals were decapitated after 8 weeks and their pancreas tissues were received and investigated. In pancreas tissue, TNF-alpha, Nrf-2, NF-kB, Caspase-3, Bcl-2, VEGF and Akt expression levels were analysed by western blotting technique, lipid peroxidation was detected by MDA (malondialdehyde) and catalase and GSH level was determined by spectrophotometer. As a results, Nrf-2, Caspase-3 protein expression, GSH and catalase activity increased, Tnf-alpha, Bcl-2, Akt, NF-kB, VEGF protein expression and MDA levels decreased in EA + CCl4 group compared to CCl4 group. These results suggest that EA reduces the rate of pancreas damage in rats and that EA can also be used as a potential drug to protect against to pancreas damage in the future.
Information: The article supported by Firat University Scientific Research Projects Unit (FUBAP) with FF.16.42 project number

Keywords: Carbon tetrachloride, Ellagic Acid, Pancreas damage, NF-kB, VEGF

Single Dose Lithium Borate Treatment Protects the Kidney from Ischemia Reperfusion Injury in Rats

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Abstract

Boron and some boron compounds have antioxidants and anti-inflammatory properties, and they are widely used in medical applications. The aim of this study was to explore the effect of lithium borate on the levels of oxidative stress and inflammation markers in the rats of renal ischemia-reperfusion injury. Female Sprague-Dawley rats were randomly divided into three groups: the group of control (sham–operation), the group of renal ischemia-reperfusion injury, and the group of renal ischemia-reperfusion injury treated with lithium borate. 50 min before the ischemia-reperfusion procedure, the rats in the last group were treated with lithium borate (50 mg/kg) orally once. At the end of the experiment, the animals were sacrificed and rat kidney was harvested for biochemical (SOD, GSH, MDA, and MPO) and inflammation (TNF-α and IL-6) analysis. The ischemia-reperfusion significantly altered oxidative defence (increased MDA, MPO, and decreased GSH, SOD) and pro-inflammatory cytokines levels (increased TNF-α and IL-6) in the rat kidney. Lithium borate significantly attenuated these alterations in oxidative stress and inflammatory markers in rat kidney. This study showed that lithium borate can protect the kidney against ischemia-reperfusion damage, ameliorate the oxidative damage and inflammation in the rats of renal ischemia-reperfusion.

Keywords: Ischemia-reperfusion, lithium borate**,** kidney, oxidative defence, inflammation.

Stabilized hypochlorous acid induces apoptosis or necrosis in *Saccharomyces cerevisiae* depending on its concentration

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Abstract

Hypochlorous acid (HOCl) is a strong oxidant produced by neutrophils at the sites of inflammation in order to fight against infections. Stabilized HOCl was synthesized as a wound care and protection agent owing to its antimicrobial activities. Unlike many antimicrobial agents, it provides antisepsis without damaging the healthy tissue. Although, the microbiocidal activities of stabilized HOCl preparations were reported previously, mechanism(s) of cell death mediated by HOCl is not clear. The aim of this study was to investigate the mode of cell death triggered by stabilized HOCl in Saccharomyces cerevisiae. The effect of various dilutions (1:2, 1:4, 1:8, 1:16, 1:32 or 1:64) of stabilized HOCl on the viability of wild type yeast cells were examined by the spotting assay. Mode of cell death triggered by HOCl at lethal concentrations was investigated by Hoechst 33342/PI staining. Finally, whether the apoptotic pathway induced by HOCl was dependent on the yeast metacaspase (Yca1) or apoptosis inducing factor (Aif1) was determined using yca1Δ and aif1Δ mutants. Our data revealed that 1:32 and above diluted HOCl led to cell death in yeast. Specifically, 1:16 diluted HOCl caused necrosis in 99,83% of cells, whereas at 1:32 diluted HOCl led to apoptosis in 99.02% of cells. Furthermore, apoptosis induced by HOCl at 1:32 dilution was caspase-dependent and Aif1 independent.

Keywords: Hypochlorous acid, Apoptosis, *Saccharomyces cerevisiae*

The effects of Salvia officinalis extract on Galleria mellonella phenoloxidase activity

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Abstract

The leaves and flowers of common sage (*Salvia officinalis L.)*are evaluated economicall and the oil obtained is also used in the treatment of throat infections and oral wounds due to its antiseptic and antibiotic effects. In addition, there are studies indicating that it treats skin diseases with its antifungal effect, supports the excretion of toxins from the body and improves brain functions. *Galleria mellonella* is a model organism used for immunological experiments. Insect immune responses are evaluated in two categories; humoral and cell mediated. Phenoloxidase is a key element of the melanogenesis process with insect humoral immune response. In this study, 70% ethanolic extraction of *S. officinalis* was dissolved in 40% dimethyl sulphaphoxide at 0.1%, 0.25%, 0.5% and 1%. These extracts were injected into the larvae of *G. mellonella* last instar (0.18 ± 0.02 g) with 5 µl per dose. It was waited for 24 hours for the extracts to take effect. At the end of this period, 10 µl of larvae were collected and injected into ependorf tubes containing 10 µl of anticoagulant. 80 µl of phosphate buffer solution was placed on it. This mixture was read on ELISA plate reader for 30 minutes every 5 minutes at 492 nanometer wavelength to determine phenoloxidase activity. According to the our results, a significant increase in phenoloxidase activity was observed at a dose of 1% compared to the control group. Our results support the literature information. Further studies will reveal the effect of *S. officinalis* on the immune system.

Keywords: *Salvia officinalis*, Phenoloxidase, *Galleria Mellonella*, immune system

Investıgatıon of SNPs Wıth Functıonal Effects In GZMB (Granzyme B) Gene Usıng In Silico Methods

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Abstract

The GZMB gene encodes a member of the granzyme subfamily of proteins that are part of the peptidase S1 serine protease family. The encoded preproprotein is regularly expressed by cytotoxic T lymphocytes (CTLs) and activates target cell apoptosis by caspase-dependent and independent means. This protein, which also processes cytokines, plays a role in chronic inflammation and wound healing by reducing extracellular matrix proteins.The aim of this study was to determine single nucleotide polymorphisms (SNPs) in the GZMB gene by using in silico methods and to estimate SNPs that have a damaging effect on the protein structure and stabilization.SNPs in the GZMB gene were obtained from the NCBI dbSNP database in March 2019. Functional effects of SNPs known to cause amino acid change were determined using SIFT (Sorting Intolerant From Tolerant) and PolyPhen-2 software tools. I-Mutant 3.0 and MuPRO software tools were used to determine the effect of these SNPs on protein stabilization and Project HOPE were used to construct three-dimensional modeling.187 missense SNPs were found in the GZMB gene. It has been found that 5 SNPs have a deleteriorus/damaging effect in common with SIFT and PolyPhen-2 software tools. It has been concluded that I-Mutant 3.0 and MuPRO software tools reduce protein stabilization in 5 SNPs. Using the Project HOPE software tool, wild and mutant types of 5 SNPs were evaluated in terms of size, charge and hydrophobicity.These findings showed that 5 SNPs in the GZMB gene may have a damaging effect on protein structure and stabilization.

Keywords: GZMB, apoptosis, single nucleotide polymorphism (SNP), *In silico*

Protein and Carbohydrate content of thermophile *Geobacillus toebii* strain E134

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Abstract

Geobacillus toebii strain E134 is a gram-positive, obligately aerobic, non-pathogenic, spore forming, thermophilic bacilli. The isolate was isolated from a water sample of Kozakli (Nevşehir), Turkey hot spring. The isolate's optimal growth values are 0% NaCl, pH 8.5, and 65°C. Bacteria move on surfaces with the flagella and migrate to new places. According to conclusion showed that the E134 isolate had monotrichous flagella and produced a fragile pellicle at 55°C for 4 days in the air-liquid interface. Thermophilic bacteria produce extracellular polymeric substances (EPSs). Protein and carbohydrate are available in EPS structure. Determination of carbohydrate content in EPS component was carried out by phenol-sulfuric acid method. The amount of carbohydrate corresponding to the absorbance value read was calculated with the help of the standard curve ($R^2 = 0.99$). Furthermore, amount of protein corresponding to the absorbance value read was calculated with the help of the standard curve ($R^2 = 0.98$). The concentrations of total protein were quantified as 163 µg/mL. Moreover, the concentrations of total carbohydrate were quantified as 22.1 µg/mL. It seems that the amount of protein was much greater than the amount of carbohydrate.

Keywords: Geobacillus toebii E134, protein, carbohydrate

Production of 2-hydroxyethyl methacrylate-g-poly(ethylene terephthalate) nanofibers by electrospinning and characterization of the obtained nanofibers

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Abstract

In this study, it is aimed to synthesize and characterize nanofibers of 2-hydroxyethyl methacrylate-g-poly(ethylene terephthalate) (PET-g-HEMA) copolymers containing different amounts of HEMA. Firstly, PET-g-HEMA graft copolymers were obtained by radical polymerization technique using benzoyl peroxide as the initiator and the obtained copolymers were characterized by fouirer transform infrared spectrophotometer (FTIR) and scanning electron microscopy (SEM) investigations. The solubility of the PET-g-HEMA copolymers in various solvents was then investigated and the graft copolymer was best dissolved in trifluoroacetic acid (TFA). The PET-g-HEMA copolymers containing different amounts of HEMA were dissolved in TFA at different concentrations (10, 15 and 20% w/v) and the electrospinning of nanofibers from polymer solutions was investigated under different conditions. In the electrospinning process, when the solution concentration was 20%, the solution feed rate was 5 µL/min, the applied voltage was 12 kV, and the distance between the needle tip and the collector plate was 12 cm, continuous, smooth, bead-free nanofibers were obtained from the original PET and PET-g-HEMA copolymers containing 20 and 55% (w/w) HEMA. The morphological structures and mean fibre diameters of the obtained nanofibers were determined by SEM analysis. Thermal properties of nanofibers were investigated by thermogravimetric analysis and water retention capacities and surface contact angles of nanofibers were determined to investigate surface properties. In addition, the porosity properties of the synthesized nanofibers were investigated using mercury porosimetry and their mechanical properties were determined by tensile test. According to the results of the analysis, the average fibre diameters of PET-g-HEMA nanofibers increased, thermal decomposition properties changed and surface contact angle decreased while the water retention capacities of the nanofibers increased compared to original PET nanofibers. In addition, the porosity of PET-g-HEMA nanofibers was considerably increased compared to the original PET nanofibers. Finally, although the mechanical properties of PET-g-HEMA nanofibers, such as elastic modulus and tensile strength, were decreased compared to the original PET nanofibers, the obtained PET-g-HEMA nanofibers still have high mechanical properties. PET-g-HEMA nanofibers obtained in the this study are suitable materials for application in many biomedical fields due to their superior mechanical properties, porous structure and thermal resistance.

Keywords: Poly(ethylene terephthalate) fibers; Grafting copolymerization; HEMA, Electrospinning, Polymer characterization

Decreasing stress level of *Lactococcus lactis* N8 caused high nisin yield

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Abstract

Certain strains of *Lactococcus lactis* produce nisin which is the only food additive bacteriocin approved by World Health Organization (WHO). Nisin cannot be produced chemically, so the methods that aim to increase nisin yield are very attractive. Growth and nisin production are directly proportional in *L. lactis* cells. We hypothesized that molecules decreasing the stress level of *L. lactis* would affect the growth positively causing increased nisin production. In this study, the genes that encode stress-related enzymes were transcriptionally analyzed to describe the effect of glutathione (GSH) and pyruvate on the defense system of *L. lactis* cells. The selected genes are; *sodA* (superoxide dismutase), *ahpF* (H_2O_2-forming NADH oxidase), *ahpC* (NADH peroxidase), *gshR* (glutathione reductase), *trxB1* (thioredoxin reductase), *noxE* (H_2O-forming NADH oxidase), *recA* (recombinase) and *relA* (pppGpp synthetase). The expression of these genes was found to be apparently upregulated in *L. lactis* cells grown in GM17 medium supplemented with GSH or pyruvate. Transcription of one of the biosynthetic gene in nisin cluster, *nisZ* was significantly increased in *L. lactis* cells grown in pyruvate containing medium. *nisZ* expression was also higher at 4th and 8th hour of growth in the presence of GSH. Nisin production was also measured at the protein level. It can be concluded that the antioxidant molecules, GSH and pyruvate, contribute to the defense system of *L. lactis* cells, as a result, higher nisin yield was obtained.

Keywords: glutathione, *Lactococcus lactis*, nisin production, pyruvate, stress, transcriptional analysis.

The Protective Effects of Ellagic Acid in Testicular Damage Injury in Rats

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Abstract

Male reproductive system consists of testis, genital excretory channels, sex glands (vesicula seminalis, prostate and bulbourethral glands). Carbon tetrachloride (CCl_4) is a strong carcinogenic agent that causes the production of reactive free radicals and initiates cell damage. Ellagic acid (EA), which is known as a polyphenol compound with its antioxidant properties, has a protective effect against oxidative stress of the testes. The aim of this study was to examine whether EA plays a protective role against testis damage induced with CCl_4 in rats. In this study, 36 male wistar albino (n=36, 8 weeks old) rats were used. The animal experiments of this study was carried out by Firat University Animal Experiments Ethics Committee with the permission dated on 06.03.2019 and numbered 54 decisions, F.U Experimental Animal Research Center. The rats were divided into 4 groups, and 9 rats involved in each group. The groups were: (i) Control Group: Fed with standard diet; (ii) EA Group: Fed with standard diet+EA; (iii) CCl_4 Group: Fed with standard diet+CCl_4; (iv) CCl_4+EA Group: Fed with standard diet+CCl_4+EA. After 8 weeks, the rats were decapitated and the testis tissue were examined. Expression levels of caspase-3, bcl-2, Tnf-alpha, nrf-2, VEGF and NF-kB in testis tissue were determined by western blotting technique, lipid peroxidation was determined by MDA (malondialdehyde), catalase activity and GSH levels were determined by spectrophotometer. As a results, nrf-2 and caspase-3 protein expression, GSH level and catalase activity increased, but Tnf-alpha, VEGF, NF-kB, bcl-2 protein expression and MDA levels decreased in EA+CCl_4 group compared to CCl_4 group. These results show that EA reduce testis damage ratio at wistar albino rats and also these results suggest that ellagic acid may be a potentially protective drug against to testis damage in future.

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Keywords: Carbon tetrachloride, Ellagic acid, Nrf-2, Testis damage, Tnf-alpha

Immobilization of Catalase Enzyme from Sunflower Seeds on Stable and Friendly Target

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Abstract

In the last period, the approach to green chemistry is increasing rapidly; the main target of which is to utilize raw materials for the significant application. The catalase has been used in many biotechnological applications such as removal of hydrogen peroxide residue from milk, production of gluconic acid, phenyl pyruvic acid and dihydroxyacetone phosphate combined with oxidases. In the present study, the catalase enzyme was immobilized onto friendly target. The influence of pH, temperature stability, thermal stability, half-life, storage stability, reusability and FTIR analyses of the immobilized catalase were done for characterization the structural modifications. The residual immobilized catalase activity onto friendly target was 79% after 15 cycles, respectively. The present study concludes that covalent cross-linking of catalase with friendly target by a cross-linker was found to improve its stability along with increase recycling efficiency. The obtained immobilized catalase can be used in the different industrial processes such as food, detergent, also in bioremediation processes and other commercial application.

Keywords: immobilizing enzyme, catalase; commercial application.

Design of modified Fe_3O_4 magnetic nanoparticles as supports for bi-enzyme systems permitting improved cascade biocatalysis

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Abstract

Magnetically separable bi-enzyme systems prepared by co-precipitation of enzymes and modified Fe 3 O 4 magnetic nanoparticles. In this work, two different enzymes were used for cascade biocatalysis. Horseradish peroxidase (HRP) was selected for the first enzyme and glucose oxidase (GOx) as a second enzyme was used to complete the cascade reaction. The bi- enzyme@mFe 3 O 4 was prepared wherein HRP and GOx immobilized in the mFe 3 O 4 layer. The properties of the bi-enzyme@mFe 3 O 4 were characterized by scanning electron microscopy, thermal gravimetric analysis, vibrating sample measurement, X-ray diffraction, Fourier transform infrared spectroscopy. The optimum enzyme's activity was detected at a temperature of 25°C and pH=7. The bi-enzyme@mFe 3 O 4 showed highly operational stability comparing to the free GOx and HRP. The present work provides greatly improved the general biocatalytic efficiency.

Keywords: glucose oxidase; horseradish peroxidase; magnetic nanoparticles; and bi-enzyme systems.

Role of Medicinal Aquatic Plants in Biotechnology

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Abstract

Aquatic biotechnology is one of important discipline of Biotechnology and known as blue Biotechnology. It contains application of biotechnolgical approaches towards aquatic plants, animals, algae and microorganisms. Aquatic plants are rich in diversity including 87 families, 168 genera, and 1022 species with varied distribution worldwide. They have the potential to offer solutions to several problems in the field of aquatic biotechnology. The aquatic plants are highly significant for humans due to their impact on aquatic ecosystem and high nutraceutical values. These aquatic plants have been an important source of medicine since ancient times. Over 3.000 years ago, extracts from aquatic plants were used as medicine. Several aquatic plants are unique sources of new genes, proteins and metabolic processes that may have significant applications in medicine. For example, anticancer compounds have been discovered in certain species of marine plankton and plants. Similarly, efforts on developing new novel compounds from these aquatic plants have been done by researchers to cure different diseases and disorders. Thus, research on this field is vital to tap the vast potential of the aquatic environment to improve human life in any way possible.

Keywords: Aquatic plants, Biotechnology, Medicine, Neutraceutical



ABSTRACT for

POSTER PRESENTATION

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Research for Making Life Better

Bio-ecology of Leptocybe invasa on Eucalyptus globulus in the North-East of Algeria

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Abstract

The Eucalyptus species are endemic to Australia, although a few were introduced into Algeria by the Frensh colonization at the 19th century. In the last 10 years, an invasive insect have been discovered in the Algerian Eucalyptus leaves (North-East region). Leptocybe invasa Fisher & La Salle 2004 (Hymenoptera: Eulophidae) appears to be a widespread species in Australia, ranging from northern Queensland to Victoria and Western Australiahas, as it has been detected from Algeria in 2010, The dynamics of L. invasa and its field infestation rate were followed since 2017, in Eucalyptus globulus plantation in the North-East Region in Algeria(Msila, Setif and Beni Aziz). Some bio-ecological parameters and control strategies of thes new pest is reviewed and discussed.

Keywords: Eucalyptus, parasitic insects, parasitoids, biological control.

Antibacterial Activity and Cytocompatibility of Silk Sericin-Capped Gold Nanoparticles Synthesized Under UVC Radiation

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Abstract

Biosynthesis of metal nanoparticles is gaining importance in view of their biocompatibility, good colloidal stability and eco-friendly features. In our previous work, sericin-capped gold nanoparticles (S-AuNPs) were synthesized by an easy one-pot synthesis method involving only gold salt and sericin extracted from silk worm cocoon in the presence of UVC light at different sericin solutions (0.25, 0.5, 1% w/v). According to the physicochemical test results, S-AuNP0.5 group was selected as the most suitable group and in this work, the colloidal stability, antibacterial and cytotoxicity effects of S-AuNP0.5 were investigated. The colloidal stability of S-AuNPs was determined in both high ionic strength solution and cell culture medium for either short and long-term incubation periods. Characterization results from UV-Vis spectroscopy showed that the synthesized AuNPs were stable in both at high salt concentration or in cell culture medium. The antibacterial properties of S-AuNPs and mixtures of S-AuNPs and streptomycin antibiotic were determined by minimal inhibitory concentration (MIC) test on *Bacillus subtilis* and *E. coli* bacteria. According to the MIC tests performed, the synthesized S-AuNP0.5 group had no antibacterial effect on *B. subtilis* and *E. coli* when used alone but, when it was used with streptomycin, it decreased the MIC value of the antibiotics for *B. subtilis* and *E. coli*. In addition, in-vitro biocompatibility of S-AuNPs were assessed with WST-1 assay, proliferation (xCELLigence microelectronic system) and apoptosis/necrosis observation. Cytotoxicity assays carried out with L929 cells demonstrated the non-toxic nature of S-AuNPs. As a whole, the synthesized S-AuNPs could be proposed as potential candidates for many biological applications due to their good colloidal stability, ability to act as reinforcing agents for the streptomycin antibiotic and biocompatible features.

Keywords: *Bombyx mori* silk sericin; Gold nanoparticles; Aqueous stability; Biocompatibility; Antibacterial activity

Molecular detection for Methylation Pattern of MTHFR gene in Infertile Men

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Abstract

In more than half of infertile men, the cause of their infertility is unknown. Several studies revealed the role of epigenetic especially DNA methylation in male infertility. The aim of the present study was to determine the Methylation Pattern of MTHFR gene in semen from asymptomatic infertile male patients, and its association with altered semen parameters. A total of 100 semen samples were collected from Kamal AL-Samaree for fertilization and infertility Hospital and the Medical City Teaching Hospital, Iraq. Semen analysis and detection for Methylation Pattern of MTHFR gene by real-time PCR were performed. Comparison of semen parameters between patients and control samples were performed, The MSP results revealed that (25) samples of patients with percentage (33.33%) and (2) samples of control with percentage (8.00%) were positive for methylation while (50) samples of patients with percentage (66.67%) and (23) samples of control with percentage were negative for methylation. The result of the study show a differences in the distribution MTHFR gene promoter methylation between patient and control .also the result show that the presence of MTHFR gene promoter methylation was significantly high and at the level of ($P<0.01$). The findings suggest that Hypermethylation of the promoter region of MTHFR gene is strongly associated with idiopathic male infertility.

Keywords: Infertility, Herpes Simplex Virus, Real-time PCR, Semen.

Usage of Biotechnology in Agriculture and Animal Production

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Abstract

Today, biotechnological studies provide important opportunities for facilitating human life, eliminating health problems and increasing the productivity of agricultural products. The most important development in the agricultural field is the transfer of genes that protect plants against pests. However, the long-term detrimental consequences of these studies are unknown. New studies are needed because transgenic plants can be harmful to non-target organisms. Another important development in agricultural biotechnology is the mass production of biological agents against agricultural pests. Mass production of parasitoid under laboratory conditions in biological control of pests in agricultural areas is one of the important biotechnological developments that will reduce insecticide use.
Biotechnology in animal production has been directed towards research on the isolation and characterization of growth hormone genes from various animal species. One of these biotechnological studies that bovine somatotropin hormone was isolated and injected into cows and it was stated that it increased milk production. In another study; Porcine Somatotropin has been reported to increase the amount of protein in meat. Biotechnological studies in agricultural and animal production may be a solution to countries suffering from food shortages, however new studies are needed to eliminate ethical concerns.

Keywords: Agricultural, biological control, Animal biotechnology

Comparison of the effectiveness of open-air drying beds and silver nanoparticles treatments in reducing the microbiological load of wastewater treatment sludge

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Abstract

Wastewater sludges are very rich in different types of microorganisms principally pathogenic ones in very important amounts which were isolated from treated wastewater and concentrated in sludge especially: *Salmonella arizonea, Salmonella Spp., Aeromonas hedrophila, Escherichia coli, Vibrio cholerae, Vibrio parahaemolyticus, Burkholderia cepacia, Pseudomonas aeruginosa, Pseudomonas luteola, Pseudomonas fluorescens, Staphylococcus lentus, Staphylococcus xylosus, Staphylococcus aureus, Candida parapsilosis, Cryptococcus albidus, Enterobacter cloacae, Chryseomonas luteola*. In the present study, we compared the effectiveness of sludge treatment in open-air drying beds during 1 to 6 months with treatment by silver nanoparticles (Ag-NP) during 24h. The microbiological study of liquid and solid sludge demonstrates the ineffectiveness of the treatment carried out at the wastewater treatment plant in Guelma's city, only by drying the bed. This treatment results in an increase in contaminating flora (indicators of faecal contamination) and pathogenic bacteria despite the saprophyte flora (especially *Streptomyces*) due to the ambient temperature of drying beds and static conditions in addition to the presence of a significant organic load in the sludge. Treatment by liquid Ag-NP allows a total elimination or significant reduction of microorganisms present in the sludge to 90% for most bacteria.

Keywords: wastewater sludge, microorganisms, open-air drying bed, silver nanoparticle

Evaluation of Anti-Inflammatory, Anti- arthric and Analgesic Activities of Helichrysum stoechas (L.) Moench Extracts

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Abstract

In the course of the valorization of Algerian medicinal plants, this study was conducted on Helichrysum stoechas species (Asteraceae) to validate its uses in traditional medicine by evaluating its anti-inflammatory, anti-arthritic and analgesic activities. Two different extraction methods using ethanol as solvent were carried out by maceration and Soxhlet apparatus. Phytochemical screening revealed the presence of polyphenols, flavonoids, alkaloids, tannins, sterols and triterpenes. The anti-inflammatory activity of the ethanolic extracts was investigated in vivo by induction of paw edema and in vitro according to the anti- hemolysis test (red blood cells membrane stability) induced by hypotonic and heat. Anti-arthritic capacity was evaluated by the protein denaturation test. The analgesic activity of the ethanolic extract of the plant was evaluated using the method of tail immersion, hot plate and torsion test in mice. At the third hour, ethanolic extracts reduced the edema 72% at a dose of 1mg/g. However, this inhibition was more effective than that observed with diclofenac (100mg/kg) during the same period. The inhibition of red blood cells hemolysis as well as albumin denaturation by H. stoechas was found to be almost similar to that exhibited by diclofenac. Results showed that H. stoechas alcoholic extract increased reaction time in the analgesic test, deducing its centrally mediated analgesic activity. The ethanolic extract reduced the number of spasms induced by acetic acid, suggesting its peripheral analgesic activity. It can be concluded that H. stoechas posses protecting effects against these affections.

Keywords: Helichrysum stoechas (L.) Moench, phytochemical screening, anti-inflammatory activity, anti-arthritic activity, analgesic activity

The Exposure to Chemically Polluted Environment Alters the Composition of Gut Microbiota in Rattus rattus (Rodentia: Muridae): Next-Generation Sequencing Study

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Abstract

Humans and mammals are holobionts living in symbiosis with numerous and diverse microorganisms, all of which are called microbiota. The ecological environment and nutritional diets of many species such as Rattus rattus of Rodentia class are different. The impact of these variables on the gut microbiota was defined for the first time by the examples of natural life. In this study, the differences in the microbiota of Rattus species living in a chemically polluted environment and natural habitat were revealed and compared to illuminate the influence of ecological factors on the bacterial composition in genus and species levels. Bacterial species of gut microbiota were identified by the next-generation sequencing method of V3-V4 hypervariable region in 16s ribosomal RNA. The findings of the study will significantly contribute to comprehend the cellular mechanisms and develop novel strategies in the treatment of intestinal diseases in terms of animal models. The study is also valuable for the determination of molecular phylogeny of taxonomically problematic species on the ground of microbiota status.

Keywords: Microbiota, Next-generation sequencing technique, Rodentia, Nature Life

Funding: This study was funded by Scientific Research Project fund of Bilecik Şeyh Edebali University [grant number 2019-01. BŞEÜ.01-01].

Effects of *Ferula assafoetida*, *Rosa canina* and a microalgae isolate on ECV 304 and Ishikawa Cell Lines

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Abstract

Ferula assafoetida and *Rosa canina* plants are widely used in many different industries, especially in pharmacology and medicine fields. Antioxidant, antimicrobial and anticarcinogenic features of different extracts obtained from this plants have been reported. Microalgae which contain various enzymes, pigments, fatty acids and minerals are important microorganisms for the ecosystem. In this study, the effects of dimethylsulfoxide (DMSO) and methanol extracts obtained from *Ferula assafoetida*, *Rosa canina* and a microalgae isolate on ECV 304 and Ishikawa cells was investigated using MTT Assay. Essential oils of this three extracts were analysed using gas chromatography mass spectrometry (GC-MS). The DMSO extract of *Ferula assafoetida* decreased the cell viability to 76.7% in Ishikawa cells, while it decreased to 66% in *Rosa canina* extract. The cell viability of ECV304 of *Ferula assafoetida* was around 111.2% at a concentration of 0,5 mg/mL, while *Rosa canina* was 135 %. The DMSO extract of the microalgae prepared by lysis was found to be 147% in the ECV 304 cell line at a dose of 0,005 mg/mL compared to the control group. According to GC-MS results of the DMSO extracts obtained, the compounds were found major; phenol, hexadecanoic acid, oleic acid and stearic acid and 2-hydroxy-1-(hydroxymethyl) ethyl ester for the microalgae extract.

Keywords: Cytotoxicity, GC-MS, *Ferula assafoetida*, *Rosa canina*, Microalge.

An insight into Phytoremediation Potential of Aquatic macrophyte – Ceratophyllum demersum L.

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Abstract

Heavy industrilization in both developed and under developing countries in recent decades lead to soil and water contamination more rapidly than compared to past. To overcome this issue, number of techniques have been employed to overcome this issue with moderate success. The problem of contaminated sites with different pollutants is more prone to aquatic ecosystem through drainage and these pollutants are directly affecting the human health by contaminating water for drinking. Phytoremediation using palnts for cleaning the contaminated sites with differrent types of polluters is an important and eco-friendly technique with other biological and economic advantages. However, the selection of proper plant for phytoremediation along with its availability are highly significant. Coontail (Ceratphyllum demersum L.) is an important aquatic macrophyte used for phytoremediation studies against different pollutants like heavy metals. The plant has been reported for the phytoremediation of nickel (Ni), lead (Pb), cadmium (Cd), aluminium (Al) and chromium (Cr). Besides that, number of studies also revealed the use of coontail plant for contamined sites. This study enlightens the use of coontail plant for phytoremediation studies.

Keywords: Aquatic ecosystem, Coontail, Healy metals, Phytoremediation, Pollutants

A magnetized thermophilic Bacillus cereus for determination and preconcentration of uranium and thorium from environmental samples by magnetic solid phase extraction (MSPE)

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Abstract

A novel magnetic solid phase extraction (MSPE) was developed for simultaneous preconcentration of U(VI) and Th(IV) by ICP-OES. Thermophilic Bacillus cereus SO-14 was immobilized to γ-Fe2O3 nanoparticles and applied for MSPE. The recovery of the radionuclides increased with increasing pH and reached a peak at pH 5.0 (%100). A 3.0 mL min-1 was used as flow rate. A 100 mg of B. cereus SO-14 and γ-Fe2O3 nanoparticles were used all preconcentration experiments as MSPE column. Preconcentration factors were determined as 100 for Th(IV) and U(VI). The quantitative recoveries of U(VI) and Th(IV) were achieved both 5 mL of 1 mol L-1 HCI and 5 mL of 1 mol L-1 HNO3 solution. U(VI) and Th(IV) were recovered quantitatively (≥95%) when using up to 500 mL of the sample solution. The magnetized biosorbent could be quantitative after 35 cycles of biosorption and desorption. The results indicate that the new method could be accepted as a green method with high accuracy and it can be used for preconcentration of radionuclides from environmental patterns.

Keywords: Thermophilic, Bacillus cereus, U(VI), Th(IV), preconcentration

Acknowledgements: This study was supported by the Research Fund of Mersin University in Turkey (Project No. 2018-3-AP4-3092).

The Effect of Kefir on Oxidative Stress Mimicked Aging Model by Induced D-Galactose in Rats

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Abstract

D-Galactose (D-GAL), is a monosaccharide that mimics the natural aging process in rodents by increasing the oxidative stress. We investigated the effect of daily kefir consumption on oxidative stress caused in aging related damage model. Rats received D-GAL (300 mg/kg/day, 5 days), low dose of kefir (0.7 ml/kg/day, 5 days) and high dose of kefir (3.5 ml/kg/day, 5 days) during 8 weeks. At the end of the 8 weeks period, obtained in brain tissue samples Glutathione (GSH) and Lipid peroxidation (LPO) levels, Superoxide dismutase (SOD) and Acetylcholinesterase (AChE) activities were measured. The control group was compared with the D-GAL group, a significant decrease in GSH levels and SOD activities were observed, but LPO levels and AChE activities were increased ($p < 0.05$). Both doses of kefir in D-GAL groups were decreased LPO levels as compared to D-GAL group ($p < 0.05$). The D-GAL group was compared with the D-GAL received low dose of kefir, a significant increase in SOD activity, a siginificant decrease in AChE activity were observed ($p < 0.05$). At the same time, in histopathological findings of kefir have supported the decline of oxidative stress by showing a protective effect on the mimetic aging model. These results indicated that kefir may have some favorable effects on aging-induced oxidative damages in especially brain tissue.

Keywords: D- Galactose, Kefir, Aging, Oxidative stress, Rat

Contribution to the study of harmful insects on Eucalyptus gomphocephala (Myrtaceae) in Algeria

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Abstract

Eucalyptus gomphocephala is an essence of the family Myrtaceae. It resists a certain salt content and the sea wind. Despite that, it subject to many factors of degradation as parasitic and harmful insects. Field trips (Batna, Ras El Oued and Jijel in the North Est of Algeria) from September 2017 to September 2018. The results made it possible evidence the presence of 2 harmful species: Leptocybe invasa, Ophelimus maskelli (gallicolous insects , Hymenoptera, Eulophidae). A procession of other species has been studied highlighting the presence of parasitoids such Closterocerus chamaeleon (Hymenoptera) parasitoid of Ophelimus maskelli. To these pests of other insects live on this essence permanently or temporarily. In all 5 orders divided into 12 families comprising 14 species that have been determined. Three main orders, Hymenoptera, Coleoptera, and Collemboles alone represent 12 species, while Lepidoptera and Hemiptera, are represented by only one species.

Keywords ; Eucalyptus gomphocephala, harmful insects

*This work was made by Laboratory ADPVA

Pestalotia Fruit Rot on Strawberry plant in Iraq

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Abstract

Result showed the presence of many pathogens infected Strawberry plants, *Fusarium solani* , *Fusarium oxysporum* followed by *Pestalotia longisetula* was most frequently pathogenic fungus isolated from strawberry fruits.
Incidence of Fusarium root rot in the field survey of three sites showed that highest infection (60%) While as *P. longisetula* (66%) in plastic houses at Horticulture Departments, College of Agriculture & Forestry, Mosul University.
The present of fungus *P. longisetula* as our knowledge is the first record on Strawberry in Iraq.
Regarding the effect of some fungal biocides on growth of *F. solani* and *P. longisetula* revealed that 100 mg active ingredient / liter was enough to discourage growth and potent as biocide and there were some significant differences between bacterial biocides in the percentage of inhibition of pathogenic fungi. Bacterial and fungal biocides were found to combat Fusarium root rot and Pestalotia Fruit rots disease in Strawberry plants.

Keywords: Strawberry, Fusarium root rot , Pestalotia Fruit rot, biological control.

Synergy study, plant extracts and antibiotics against bacteria

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Abstract

Antimicrobial drugs effective for treatment of pathogenic bacterial infections are limited, thus it is important and valuable to find compounds that potentiate antimicrobial activity of antibiotics against this bacteria. So, our study aims to evaluate the synergistic effect between antibiotics and extracts of pine resin and propolis against five strains of bacteria, using the diffusion method disks. This study constitute a confirmation of the synergistic effect of the two extracts with antibiotics especially against *Staphylococcus aureus*, *Bacillus cereus* and *Pseudomonas aeruginosa* (with 10-30mm diameters of inhibition zones) which were resistant to several antimicrobial agents and antibiotics. Our results seem to validate the traditional use of the resin and propolis in modern medicine.

Keywords: *Pinus halepensis*, resin, propolis, antibiotic, antibacterial activity, synergistic effect

Antimicrobial Activity of Helichrysum Stoechas (L.) Moench Extracts

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Abstract

Helichrysum stoechas (L.) Moench (Asteraceae) a medicinal plant belonging to Asteraceae family is used to trait several diseases related to urinary tract. Recent works suggest that this species bears antifungal and antibacterial properties towards plant and animal pathogens. The aim of this work was to evaluate the antimicrobial activity of aqueous and hydroalcoolic extracts from H. stoechas (L.) Moench against a panel of Gram+ and Gram- bacteria such as Staphylococcus aureus ATCC6538, Klebsiella pneumoniae ATCC4352, Escherichia coli ATCC25922, Bacillus cereus (ATCC10876) and Enterococcus faecalis ATCC2035 and a yeast C. albicans according to the disk diffusion and microdillution methods. The minimal inhibitory and bactericide concentrations were also determined as well as the ratio CMB/CMI. These findings suggest that inhibition zone was dose dependent. Ethanolic extract obtained by Soxhlet was the most effective against Gram+ bacteria, Staphylococcus aureus (25,333mm), E. faecalisi (21± 0.5mm) and B. cereus (22±0,964mm). However, S. aureus, E. coli and C. albicans were the most sensitive strains with MIC values in the range 0.019- 2.5mg/ml. In contrast, the aqueous extract was effective only against K. pneumonia with an inhibition zone diameter ranging between 13-14,333 mm. It can be concluded that the sensitivity of these microorganisms tested can be classified as follows S. aureus > E. faecalis > B. cereus > K. pneumonia> E. coli. These results are in accordance with previous works.

Keywords: Asteraceae; Helichrysum stoechas; aqueous extract; hydroalcoolic extract; antimicrobial activity

Chemical Composition of Essential Oil of *Turgenia latifolia* (L.) Hoffmann

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Abstract

The essential oil of the aerial parts of *Turgenia latifolia* (L.) Hoffmann (Synonym : *Caucalis latifolia* L.) collected from Setif, (Algeria) was analysed by gas chromatography and gas chromatography–mass spectrometry. Thirty compound representing 98.8% of total oil were identified. The oil yield of dried plant (volume/dry weight) obtained by hydrodistillation was 0.09%. The predominant components in the oil were, spathulenol (18.3%), α-pinene (15.7%), verbenone (8.8%), trans-verbenol (5.9%), and α-cadinol (4.9%). The oil consisted of oxygenated sesquiterpenes (41.6%), oxygenated monoterpenes (25.0%), monoterpenic hydrocarbons (21.7%) and sesquiterpene hydrocarbons (10.5%)

Keywords: Apiaceae, *Turgenia latifolia*, essential oil, spathulenol

The Effects of Some Preservative Food Additives on Viability of Saccharomyces cerevisiae

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Abstract

Preservative food additives are substances or mixtures of substances which are commonly used by food industry to increase food resistance against bacterial growths and to preserve natural characteristics and appearances of foods. However, the adverse health effects of many artificial additives are controversial, especially among researchers specializing in food science, toxicology and biochemistry. From this point of view, in this research, we aimed to investigate the potential toxicities of three chemical preservative food additives including sodium benzoate (SB), potassium sorbate (PS), and sodium nitrite (SN) on eukaryotic model Saccharomyces cerevisiae. For this aim, yeast cells were grown in YPD medium (1% [w/v] yeast extract, 2% [w/v] peptone, 2% [w/v] glucose) until early-exponential phase and then treated with various concentrations of the agents for 12 h. Based on our data, SN did not cause any significant change in yeast viability except the highest dose (50 mM) which resulted in about 15% decrease. In PS treatments, it was observed that viability decreased slightly with the increasing concentration of the agent. On the other hand, SB showed its toxic effect even at 1 mM and in a concentration dependent manner. 50 mM SB decreased the yeast cell viability approximately by %85. Collectively, it can be certainly said that all three agents at the concentrations tested have impacts on healthy cell model viability and further studies must be conducted to understand their biochemical effects on cells.

Keywords: Sodium benzoate, Potassium sorbate, Sodium nitrite, Saccharomyces cerevisiae, Toxicity

Investigation of Mesenchymal Stem Cells Differentiation Under Static Magnetic Field Induction

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Abstract

Mesenchymal stem cells (MSCs) are important biological tools for regenerative medicine or cell therapies. Static Magnetic Field (SMF) is one of the biophysiological stimulants to modulate physiological processes in different cell lines. In vitro conditions, SMFs, according to their intensity and duration, change cellular membrane polarization, oxidative product concentrations, gene expression patterns and cell propagation rates. In this study, human bone marrow derived MSCs were grown under 328 mT SMF by using Neodymium Iron Boron (NdFeB) magnets to investigate SMF influance on their proliferation rates, morphologies, osteogenic differantiation capacity. The proliferation rate was analysed by MTT 24 hours and 6 days after SMF induction. Although preliminary results showed that cells with spindle shapes in SMF treated group gained an oriantation according to magnetic field direction, SMF influence did not significantly changed proliferation rates. It was analyzed and compared alkaline phosphatase (ALP) activity in the cells grown for 14 days under both continual SMF and chemically osteogenic induction. It was observed that ALP activity in this group decreased compared to the control groups. Also, Alizarin Red S staining showed that mineralization decreased in the cells grown under the same conditions compared to control cells.
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Keywords: Mesenchymal Stem Cells, Static Magnetic Field

Anti-glycation study of hydro-alcohol and aqueous extracts of Moroccan plant species

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Abstract

Inhibition of advanced glycation end products (AGEs) and free radicals generated during diabetes represents a major therapeutic target in the prevention and treatment of diabetic complications. Natural molecules pre- sent in fruits, vegetables and herbs and which are usually safe for human consumption, could represent a strong glycation inhibitor. Anti-glycation effect of nine plant species used in traditional medicine has been evaluated after extraction by hot (HAE) or cold (CAE) maceration and by ethanol (HE). Anti- glycation activity performed on a model system of bovine serum albumin, and methylglyoxal was measured by fluorescence and native electrophoresis. Total phenolic and flavonoid contents were assessed as well. Except for Sesamum indicum, all the species studied have an Anti-glycation effect. The highest effect was recorded in Laurus nobilis and was dose-dependent, inhibiting both formations of Amadori products and fluorescent AGEs. HPLC analysis revealed a richness of Laurus nobilis EE in phenolic compounds such as quercetin, vanillin and gallic acid. A strong correlation was registered between antioxidant power and phenolic/flavonoid content. In contrast, there was no correlation between antioxidant and anti-glycation power. Phenolic and flavonoid compounds were strongly involved in the observed anti-glycation effect. However, the anti-glycation activity obtained is probably attributed to non-antioxidant compounds.

Keywords: Anti-glycation, Antioxidant, Ethanol extracts, Polyphenols, Water Extracts.

Myrtus nivellei Essential Oils and Ethanolic Extract Activities

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Abstract

This work aims to study the chemical composition and the antioxidant, antimicrobial activities of the essential oils and hydroethanolic extract of a local medicinal plant Myrtus nivellei. The plant material was harvested from central Sahara of Algeria and identified by the National Institute of Forest Research. Aerial parts of this plant were submitted to hydro-distillation by Clevenger apparatus. Essential oil obtained was analysis by GC-MS and identification of compounds was based on mass spectra (compared with Wiley Registry 9th Edition/NIST 2011 edition mass spectral library) and published data spectre with those of NIST 2011 and willey and by the literature. Antimicrobial screening of oil and crude extract were evaluated on Gram positive and negative bacteria. Three tests were used for the investigation of antioxidant activity of extract and oil. This one was obtained by hydrodistillation of the aerial part of Myrtus nivellei yielded 0,75%(w/w). The GC-MS revealed that 1,8 cineole is the main component for Myrtus nivellei oils (53,44%). Other compounds were present in high contents: 2,2, 6,7-tetramethyl-10-oxatricyclo [4.3.0.1(1,7)]decan-5-one (11,73%), trans ocimene (7,54%), linalyl propirionate (6,81%) and lavandulyl acetate (5,24%). Strong antioxidant activity was showed mainly by crude extract. Ethanolic extract and oil were active especially on Staphylococcus aueus.

Keywords: Antioxidant activity; Antimicrobial activity; Essentiel oil; GC-MS; Ethanolic extract, Myrtus nivellei.

Clean Extraction of Pectin from Fruit Peels

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Abstract

Pectin is the main constituent of the fruit peels and contributes to the solid and firm shape of the fruit due to its complex structure. Pectin has wide applications in the industry, inclusive but not limited to food, pharmaceutical and cosmetics. In this study, aqueous extraction of pectin from dragon fruit peels was performed using water and ultrasonication. Morphological screening with electron microscope (SEM) and FTIR showed that the extracted pectin has a similar surface when compared to the commercial pectin and is completely dissolved in water to form a homogenous suspension. The pectin yield was 60±2.00 wt% with degree of esterification at about 66-72%. This study introduces a a clean extraction of which could substitute solvents in the food industry. Pectin may be used as source of safe fiber for human consumption, as food additives, stabilizer and gelling agent.

Keywords: extraction, pectin, fruit, aqueous, biomaterial

Reduced expression of PEDF and ALDH1A1 in cancer spheroids originated from A549 cells

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Abstract

"Cancer stem cell" (CSC), accepted as ancestor of various cancers, can initiate tumor and metastasis due to its invasiveness. CSC is resistant against anti-tumorigenic drugs owing to several drug transporter proteins. Thus, CSC shows resistance against chemotherapy and causes cancer relapse even after a tumorectomy. CSCs highly express stem cell markers providing self-renewal. Our target molecule PEDF is a neurotrophic, antitumorigenic, and antimetastatic multi-factorial protein. PEDF levels in aged and malignant cells decrease but its status in A549 spheroids is still unknown. Our aim was to compare PEDF, Oct4, and ALDH1A1 mRNA levels between A549 and spheroids cells with qRT-PCR. After we produced spheroid cells in serum-free low binding conditions, we performed spheroid and colony formation assays with spheroids and A549 cells and found that clonogenic ratios of A549 and spheroids were ~% 60 and ~1 % respectively. We also found that in spheroids Oct-4 mRNA level did not change but PEDF and ALDH1A1 levels decreased significantly compared to A549 cells ($p<0.05$). Although "stemness" of CSC is characterized by elevated stem cell markers e.g. Oct-4 and ALDH1, spheroid cells consist of heterogeneous population in which only "side population" has these specific stem cell characteristics. Since we could not enrich or isolate these specific SP cells, overall we did not observe an increase in either of markers. Reduced PEDF levels, however, can be a suppression mechanism of spheroid cells against anti-tumorigenic effects of PEDF. For a better understanding, PEDF effect on spheroids should be evaluated at both gene and protein levels.

Keywords: Lung cancer stem cell, PEDF, A549, Spheroid cell.

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