21st National
9th International
Congress on Biology

Cell & Molecular

Semnan University, Semnan, Iran

16-19 Feb. 2021

Semnan University

Iranian Biology Society

FIBS Federation of Iran Bioscience Societies

United Nations Educational, Scientific and Cultural Organization

UNITWIN Network in Global Pharmacy Education Development

Iranian Society of Plant Physiology

I.G.S. انجمن ژنتیک ایران Iranian Genetics Society

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انجمن علمی بانک های علوم شناوری و مراکز رشد ایران

IAPCT Iranian Association for Plant Cell and Tissue Culture

IPPA AltitudeClinic

IBIS Iranian Bioinformatics Society (IBIS) انجمن بیوانفورماتیک ایران

ICTCA Iranian Cell & Tissue Culture Association

انجمن ایرانی ژنتیک گیاهی ایران ۱۳۷۶

BIOTECHNOLOGY GENERATIONS

انجمن قارچ شناسی ایران

Iranian Society of Microbial Sciences

Welcome to

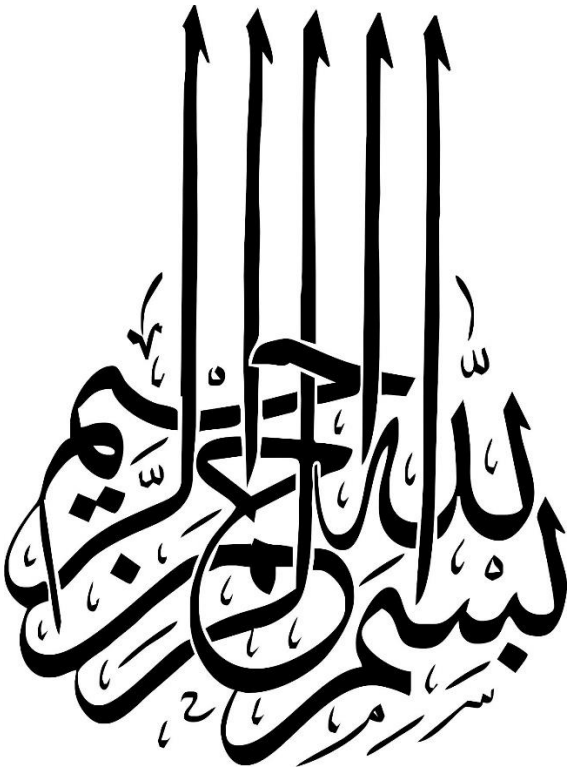
IBS

2021

Conference On

Cell & Molecular

21st National & 9th International Congress On Biology


بسم الله الرحمن الرحيم

Abstracts

of

21st National and 9th International Congress on Biology

Conference on Cell and Molecular Biology

16-19 Feb. 2021

Semnan

IRAN

Websites: http://ibs2020.semnan.ac.ir/en/; https://ibs.org.ir/; https://semnan.ac.ir/; https://biology.semnan.ac.ir/

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Preface

The Iranian Biology Society and Semnan University are honored to held the **21st National and 9th International Congress on Biology** on 16th to 19th February 2021 inclusive, in Semnan, Iran. The main aim of the event is to present frontline bioscience helping to acknowledge sever challenges dealing with global environmental treats in our planet. Also, we aimed to provide a way of communication among peers of young scientists and students locally and internationally. It also intends to provide an interdisciplinary platform to present and discuss the most recent innovations, trends, and concerns along with practical challenges surrounding biological sciences. The congress consists of four concurrent conferences on major Biology disciplines (Plant Biology; Animal Biology; Cell and Molecular Biology; and Conservation and Environmental Biology). Meanwhile, a prominent event includes a special panel on coronavirus disease 2019 (COVID-19) concerning molecular and cellular approaches. In the amid of the current global pandemic, Semnan University and Iranian Biology Society hold on an *International Virtual Symposium on the Biological, Clinical and Basic Science approaches to Covid-19*, at the 21st National and 9th International Congress on Biology in Semnan University, Semnan, Iran.

This proceeding is one the six abstract books, including abstract books for Plant Biology, Animal Biology, Cell and Molecular Biology, and Conservation and Environmental Biology conferences and a Persian version of the content of the abstracts altogether, and one last booklet for COVID-19 symposium. We hope the knowledge and experience of biologists to be shared during the 21st National and 9th International Congress on Biology benefits all parties involved and beyond.

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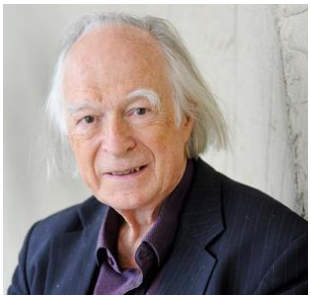

Prof. Denis Noble; CBE, PhD, FRS

Emeritus Professor of Cardiovascular Physiology
https:/www.dpag.ox.ac.uk/team/denis-noble

Denis Noble developed the first mathematical model of cardiac cells in 1960 using his discovery, with his supervisor Otto Hutter, of two of the main cardiac potassium ion channels. These discoveries were published in Nature (1960) and The Journal of Physiology (1962). The work was later developed with Dick Tsien, Dario DiFrancesco, Don Hilgemann, Yung Earm, Ten Tusscher & Panfilov, and others to become the canonical models on which more than 100 cardiac cell models are based today. All are available on the CellML website.

More recently he has focussed on developing skeletal muscle models, with articles published in the ground-breaking PHYSIOME journal: formulation of the model and its use in the relief of muscle cramp. More information on this project on https://www.denisnoble.com/systems-biology/

He was elected President of the International Union of Physiological Sciences (IUPS) at its Congress in Kyoto in 2009. He was then elected for a second term at the 2013 Congress in Birmingham, UK. He also delivered the opening plenary lecture at the Congress (see Music of Life link) which is also published as an article in Experimental Physiology (2013). He is the author of the first popular book on Systems Biology, The Music of Life, and his most recent lectures concern the implications for evolutionary biology. To follow the debate on this see the FAQ (Answers) pages on the www.denisnoble.com website.His book, Dance to the Tune of Life. Biological Relativity, extends the systems approach to biology, including evolutionary biology.

KN1 Why does the world need an integrative system approach to biology

Denis Noble -Department of Physiology, Anatomy & Genetics, University of Oxford, Oxford, UK.
E_mail: nobleoxford@gmail.com

It is now 20 years since the first human genome sequence was announced in 2001. The expectation was that, by now, we would have cures for cancer, heart disease, and for most of the major diseases of the organs and systems. We have made *incremental* progress, but nothing like the *major change* that was predicted. WHY? We got genetic causation the *wrong way round*, Genes are *used* by organisms, not the reverse. The organism activates, controls, and modifies its genome. What is the evidence and what are the implications for Biology in the 21st century? Those are the topics of this Lecture. I will then address the question of sustainable development.

Prof. Ali A. Moosavi – Movahedi

Professor of Biophysical Chemistry
UNESCO Chair on Interdisciplinary Research in Diabetes, University of Tehran, Tehran, Iran
Institute of Biochemistry and Biophysics, University of Tehran, Tehran, Iran
https://www.researchgate.net/profile/Ali-Moosavi-Movahedi

Ali A. Moosavi-Movahedi is currently Professor of Biophysical Chemistry in IBB, University of Tehran. Born in Shiraz, Iran, in 1953, graduated from National University of Iran (NUI) with a BSc in Chemistry, 1975, from Eastern Michigan University (EMU), USA, with a MSc in Chemistry (Bioanalytical Chemistry), 1979 and from University of Manchester, UK, with a PhD in Biophysical Chemistry, 1986. His research career has been mostly marked on thermodynamics of protein folding/unfolding. In recognition of his outstanding research in the field of science, he was awarded International Khawrazmi Prize, 1990, National Distinguished Professor, 1997, the first class medal for research, University of Tehran, 2003, National Eminent Character 2003, first rank medal for basic science research in Razi Medical Science National Festival 2005, Elsevier-Scopus International Award for Top Researcher in the Field of Biochemistry, Genetics & Molecular Biology 2007, Avicenna Festival First Rank Award for Top Researcher-2008, Member of Iran Academy of Sciences, 2009 and first rank award and national eminent researcher 2009 is conferred in National Research Festival by Ministry of Science, Research and Technology of Iran, selected as Eminent Professor of University of Tehran 2010, prominent Professor appointed by Iran National Elites Foundation 2012 and Essential Science Indicators (ESI) 1% citation scientist in the field of Biology and Biochemistry, TWAS (The World Academy of Sciences) Fellow 2015, IAS (The Islamic Academy of Sciences) Fellow 2016 . He has supervised PhD and MSc students and guides postdoctoral researchers in the cited area. He is the author of 17 books and numerous research full papers published in mostly international research journals mainly in the area of structural elucidation of protein, enzyme and DNA. He is a member of Biophysical Society (USA), Protein Society (USA), Iranian Chemical Society, Iranian Biochemical Society, and is currently the president of Iran Society of Biophysical Chemistry. He is already the president of National Member Committee of International Council for Science (ICSU) at University of Tehran.

KN2 Wisdom-based Outlook on Biological Sciences

Ali Mosavi-Movahedi -. *UNESCO Chair on Interdisciplinary Research in Diabetes, University of Tehran, Tehran, Iran. Institute of Biochemistry and Biophysics, University of Tehran, Tehran, Iran. E.mail: moosavi@ut.ac.ir*

Today, the planet Earth suffers from the man-made technology and industry and this planet is under pressure and suffers from various diseases.

Since the principles and rules of nature and existence have been made correctly, so It should be bio-modeled the science and technology in order to have a prosperous and comfortable life. Therefore, Biomimetic and Bioinspiration should be emulated and scientific and technology centers should be developed on this basis. Biological phenomena must be discovered through basic and fundamental science and interdisciplinary knowledge. This approach should be disciplined in universities and scientific centers towards bio-modeling of nature, and extended in social life.

To discover biological phenomena, it is necessary to educate the knowledge-man scientists with high potential in basic, biological and interdisciplinary sciences.

Prof. Alastair Summerlee

professor emeritus *biomedical* science
University of Guelph, UOGuelph, Department of Biomedical Sciences
https://www.researchgate.net/profile/Alastair_Summerlee

A passionate humanitarian, dedicated teacher, and internationally renowned researcher, Alastair Summerlee served as president and vice-chancellor of the University of Guelph (2003-14), interim president and vice-chancellor Carleton University (2017-2018) and professor of Biomedical Science (1989-2017). He is currently an adjunct professor in the Sprott Business School at Carleton and a professor emeritus biomedical science at Guelph.

Summerlee spent six years on the board of the World University Service of Canada where he became involved in humanitarian issues in the refugee camps in Kenya. His work to raise funds to support education and women and girls in the campus attracted international investment from the governments of Canada and the United Kingdom and from private individuals. Summerlee is part of the international movement to unite universities worldwide in fighting hunger and poverty known as the PUSH Initiative (President's United to Solve Hunger) and was the International Quality of Life Laureate at the United Nations in 2012.

Summerlee has published numerous scientific articles and book chapters, written about teaching and teaching practice, advocated in the media for better conditions for people in refugee camps and is regularly invited to speak on teaching, research, accountability, fund-raising and sustainable business. His current research focuses on iron deficiency and a simple innovation, known as the Lucky Iron Fish®which has the capacity to alleviate the condition for almost 2 billion people worldwide. He is also serving as a Special Advisor to Carleton on the capital campaign and the interim leader of Education City– an initiative to provide educational innovation in the Ottawa region.

KN3 The imperative to develop a sustainable solution to iron deficiency

Alastair JS Summerlee - *Department of Biomedical Sciences, University of Guelph, Guelph, Canada.*
E-mail: alastair@luckyironfish.com

Prof. Ian Adcock

Professor of Respiratory Cell & Molecular Biology
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Ian Adcock graduated from St Thomas' Hospital Medical School in 1987 with a PhD in Molecular Pharmacology. After MRC-funded spells in Edinburgh and at St Georges' Hospital in London he moved in 1990 to the National Heart and Lung Institute to work with Professor Peter J Barnes on the molecular mechanisms of glucocorticoid action in the lung. In 2004 he became Professor of Respiratory Cell & Molecular Biology at Imperial College London. Dr Adcock serves on the Editorial Board of several Journals including the AJRCCM and ERJ, is a former Head of Assembly 5 (Airway Diseases) (2014-2017) within the ERS and on the ERS and ATS Programme Committees. Dr Adcock is a PI and WP Leader in the EU/EFPIA IMI UBIOPRED initiative to determine biomarkers of severe asthma using integrated 'omics and clinical features; PI in the MRC-ABPI COPD MAP initiative; PI in the MRC-Asthma UK Centre for Asthma and Allergy and a PI in the CRF at the Royal Brompton and Harefield Hospitals.

KN4 Immune cell types in severe asthma

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Asthma is a chronic inflammatory disease of the airway associated with the recruitment and activation of a large number of diverse immune cells including eosinophils, macrophages, mast cells, neutrophils and T cells. These play divergent roles in the various sub-types of asthma that exist and make excellent potential therapeutic targets for specific patients. The advent of single cell sequencing and associated bioinformatics tools has enabled the interrogation of immune cell subtypes in asthma samples that were previously difficult to either access or isolate sufficient immune cells from such as bronchial biopsies, BAL and sputum. The presentation will highlight how distinct we can use information from single cell analysis to identify groups of severe asthmatics associated with key cell-types that are driven by specific driver mechanisms. This has implications for personalised medicine.

Prof. Fatemeh Maghuly

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She holds a habilitation in Plant Functional Genomics at BOKU, Vienna. She is the author and co-author of more than 40 peer-reviewed papers and monographs. She was/is the PI or team member of several national and international projects supported by FWF, FFG, EU. As Principal Investigator, F.M. was responsible for the genetic characterization of an extensive collection of apricot accessions and several hundred transgenic stone fruits and grapevine plants. Since 2005, F.M. joined the allergen research efforts, intending to develop improved detection methods for traces of food allergens in fresh and processed plant-derived products. Since 2009, F.M. was responsible for targeted genotyping of a bioenergy plant (J. curcas), to discover SNPs using TILLING and EcoTILLING approaches, as well as GBS and double digest GBS sequencing (ddGBS). The whole transcriptome of different developmental stages of J. curcas seed was studied using NGS. Technical expertise in population genetics, molecular marker development, and NGS allows her to handle the diverse bioinformatics approaches. She is familiar with all resources, genomics, phenomics, and gene editing (CRISPR/Cas) to study gene function. F.M. has also stayed as a visiting professor at several institutions abroad.

KN5 Multi omics approaches to improve none-domesticated Jatropha curcas: Challenges to counteract land degradation

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With increasing human activities, the most significant challenges are facing energy demand, fuels and CO2 emission from fossil fuel, which resulted in the release of the high amount of greenhouse gases. To solve this problem, it is necessary to design and use more efficient machines, processes and alternative fuels.

In the last years, biofuel crops received more attention in transferring crude fossil oil to more sustainable resources. Among different oil-rich seeds plant, *J. curcas* is considered a promising source of non-edible oil, which can be used for biodiesel production. It is an extremely drought-tolerant plant that can grow in places where other plants fail to be cultivated. Jatropha thrives on almost any soil and can prevent soil erosion and therefore can be considered an effective option for rehabilitating wasteland. It has also been found as a suitable plant for cultivation, not interfering with food crop agricultural production. Its seeds contain 20% to 50% oil and 22to35% proteins, even higher than soybean. Thus, the wish to take this plant into culture has been steadily increasing. However, *Jatropha* has not really been domesticated. Its seeds contain a range of toxins and anti-nutritional compounds, which render the seedcake and oil unsuitable for animal feed and human consumption. Besides, the lack of knowledge of the quantitative genetic variations and gene expression patterns makes it difficult to predict its seeds' oil and toxin levels.

Therefore, optimizing *Jatropha* yield and seed quality to identify key enzymes invoking in the seed maturation process is important. Moreover, in-depth knowledge of the *J. curcas'* genomic approaches needs to be complemented by qualitative and quantitative analyses at several omic levels to obtain functional genomics information, which will accelerate breeding efforts in this biofuel crop.

Prof. Abdolhassan Kazemi

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Administrative experience: Research vice-chancellors, Tabriz University of Medical Sciences (2004-2006); Director of International Relation Affairs, Tabriz University of Medical (2002- 2004); Dean of Medical Mycology Dept., Tabriz University of Medical Sciences (2003-present); Dean of Medical Ethics Research Team - Tabriz Uni. of Med. Sci.(2007-present); Dean of Medical Ethics & History Research Center - Tabriz Uni. of Med. Sci.(2009-present), Dean of Bio-Medical Ethics Dept. - Tabriz Uni. of Med. Sci.(2011 –present).
Award: National Selected Lecturer & Academic Staff (Iranian Ministry of Health, Treatment & Medical Education-2005); National Selected Lecture in Educational Motahhary Award (2009); National Selected Lecture in Educational Motahhary Award (2011)

KN6 Biological supertrends, futures studies and futures perspectives of human society and civilization

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The subjects like Synthetic biology, Mimic biology, Artificial biology, and Virtual biology actually refer to the realization of "second nature, new nature" or the attempt to recreate nature.

Forms the basic super-framework in the field of life and medicine sciences and with synthetic synthesis or genomic manipulation; A minimal genome called the “Biological chassis” and then the “Cell chassis”; the back cell creates the desired or ideal base for specific defined purposes.

These initial steps (bio-chassis, cellular chassis) eventually lead to the final step, the Homosyber human (Techniqueno species), which is the descendant of Homo sapiens, the product of natural evolutionary processes, natural selection, and evolutionary pressures over species evolution during billions years. Is alive, transforms into a homosyber human being who in his realization and belly; of course, the concept of Trans Humanism follows and also leads to the objectivity of genetic doping, genetic fabrication, trait selection, infant design, and so on. The objectivity of the above concepts, of course, leads to the realization of live machines, which in turn blurs the line between the non-living machine, the robot, and the human free agent, especially since living machines have a Dignity identity and are considered citizens. Therefore, along with human dignity, human dignity is the subject of machine dignity and of course, consequently, the discussion of machine ethics and the values and moral norms related to the interaction of human and human society with the society of living machines with identity and dignity. The combination of the above ideas will lead to a change in the structure and basic concepts related to human civilization, culture, society, education, moral and legal values, the concept of normative and moral virtues and ugliness, idolatry and the perception of human beings as the end of creation. All familiar concepts in the history of civilization will advance human societies, as in the case of non-human species of living organisms, the emergence of chimer species, microorganisms with no history of vacuolar life chain and biological cycles, new equilibrium and unknown areas in biology. One of the most important issues to consider is the manner of communication and interaction without the biological and ecological background of this "secondary nature or new nature" with each other and with the "primary nature" or existing nature, and in the meantime, of course, the possibility or impossibility Symbiosis is a point of contention between these two areas, because the establishment of “Biological apartheid” is not considered a solution to the dilemma of this area.

Keywords: Biological Supernatants, Secondary Nature, Biological Synthetics, Biological Apartheid, Human Dignity

INVITED SPEAKERS

IS1 Pneumolysis in COVID-19: pathophysiology and high altitude implications

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Severe lung compromise in COVID-19 patients often evolves to life-threatening hypoxemia. The mechanisms involved are not fully understood. Their understanding is crucial to improve the outcomes. Initially, past-experience lead to the implementation of standardized protocols assuming this disease would be the same as SARS-CoV. Impulsive use of ventilators in extreme cases ended up in over 88% fatality. Medical and physiological high altitude acute and chronic hypoxia experience with COVID-19 hypoxemia grants a new insight. A pathophysiological analysis is performed based on literature review and histopathological findings. Application of the Tolerance to Hypoxia formula = Hemoglobin/$PaCO_2$ +3.01 to COVID-19, enlightens the critical hypoxemia. ***Pneumolysis*** is an acute infectious disease marked by ***inoculation of the Coronavirus-2 RNA or other viruses within the pneumocytes, viral*** intra-cellular replication and ***pneumocyte destruction (***generally not compromising the bronchioles), accompanied by ***inflammation, edema,*** capillary vasodilatation, the formation of hyaline membranes, and micro-abscesses, nuclear atypia, characterized by non-productive cough, initial silent hypoxemia, and sudden onset of difficulty in breathing, fatigue, tachycardia and rapid progression to a reduced lung gas exchange area and subsequent fibrosis. First known use: Jun 13, 2020. The adequate interpretation of the histopathological lung biopsy photomicrographs reveals these alterations. The three theoretical pathophysiological stages of progressive hypoxemia (silent hypoxemia, gasping, and death zone) are described. At high altitude, normal low oxygen saturation (SpO_2) levels (with intact lung tissue and adequate acid-base status) could be considered *silent hypoxemia*. Several factors influence a lower incidence of COVID-19 at high altitude. At sea level, in COVID-19, the *silent hypoxemia* starting at SpO_2 =< 90% (comparable to a normal SPO_2 {88-92%} at 3,500m) suddenly evolves to critical hypoxemia. This, as a consequence of progressive *pneumolysis* + inflammation + overexpressed immunity + HAPE-type edema resulting in pulmonary shunting. The proposed treatment is based on the improvement of the Tolerance to Hypoxia (Hemoglobin factor), inflammation reduction, antibiotics, rehydration and anticoagulation if required. Understanding the pathophysiology of COVID-19 may assist in this disease's management.

IS2 Applying behavioral insights to control COVID-19 epidemic in I.R. of Iran

Seyed Abbas Motevalian -*Professor of Epidemiology, Iran University of Medical Sciences . E-mail: amotevalian@iums.ac.ir*

The trend of epidemic changes in COVID-19 is influenced by the trend of changes in people's behavior. Understanding the process and planning properly to control the epidemic requires correct and accurate information about people's behaviors and the trend of its changes. In the COVID-19 Population Survey of Iran (COPSIR study), the trend of changes in the behavior of the Iranian adults in relation to COVID-19 has been examined. Serial cross-sectional studies in 9 consecutive waves with telephone interviews have been carried out on Iranian adults aged 18 years or older. The survey instrument is adapted from German COSMO (COVID-19 Snapshot MOnitoring) study. In each wave, 515 individuals and 4605 in total participated in the study. Knowledge about COVID-19 symptoms, routes of transmission, and its preventive measures among Iranian adults was high and stable in all nine waves of the study, with little increase in knowledge about the symptoms. Risk perception and severity perception of Iranians was generally lower than expected, with a little increase in waves 7 to 9 (July 2020 to February 2021). Preventive behaviors were high and constant in the first four waves (April to May 2020) with a decrease in 5th to 7th waves (May to July 2020). The most trusted and mostly used media for receiving COVID-19 related information was national television channels. Low perceived risk caused people to downplay the risk of COVID-19. So, by easing social restrictions, Iranians quickly put aside their preventive behaviors which led to the second and third waves of COVID-19 epidemic in Iran. Risk communication strategies and public health measures must be strictly followed to prevent the fourth wave or reduce its severity.

IS3 Emission, effects and mitigation of greenhouse gases (GHGs) in agriculture

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The main sources of Green House Gases (GHGs) emission are burning of fossil fuels (for industrial use, transportation, electricity etc.), clearing the land to produce wood (domestic, industrial, or crop husbandry etc.), industrial developments, energy sector and agriculture. *Carbon dioxide*, *methane*, *nitrous oxide*, *ozone* and Chlorofluorocarbons (CFCs) are the primary GHGs in our atmosphere. GHGs absorb and emit the solar radiations within thermal infrared range which is the basic cause of greenhouse effects. It is reported that since pre industrial, there is an increase of 31%, 151% and 17% in CO_2, CH_4 and N_2O, respectively.

Land clearing for crop husbandry is responsible for high CO_2 in atmosphere. Land clearing disturbs the soil and increases the organic matter decomposition which results in release of high quantity of CO_2. It enhances the soil erosion which limits the soil's ability to uptake carbon. Crop husbandry includes the slash and burning the residues which further add up CO_2 in the atmosphere. Methane (CH_4) is produced as by product in several agricultural activities. Rice culture, livestock and termite mounds are the main sources of methane emission while biomass burning also contributes significantly. Standing water with a lot of organic water creates anaerobic conditions where anaerobic bacteria utilize CO_2 as source of O_2 and release huge amount of methane. In traditional rice culture, rice crop is submerged for four months a year. This practice adds 50-100 million tons of methane in atmosphere and reported to be the largest anthropogenic source of methane. Termite mounds are a significant methane release process in tropics due to abundant plant residues. The bacterial activity in the animal's stomach and intestine (particularly the cows and buffalos) is another source of methane emission (about 100 million tonnes per year) to atmosphere. Further the decomposition of livestock wastes is another significant source of methane emission. N_2O is the third important GHG released by agriculture. Bacteria in low/zero-oxygen environments convert nitrite (NO_3) to nitrogen gas (N_2) and nitrous oxide (N_2O) under anaerobic conditions. Inorganic fertilizers and animal manure are the main source of N_2O release in the soil.

Among the cereals, rice is the main staple food more than half of world population, mainly in Asia and Africa. To feed 9 billion world population, 25 % increase in rice yield is required in 2050. Tropics contribute 75 % of world rice production. The effects of climate change are expected to be more severe in tropics. Intergovernmental Panel on Climate Change (IPCC) reported an increase in global temperature (0.6 °C) during last century and predicted a further increase about 5 °C during this century. This climate change will affect the rice productivity severely due to sensitivity of critical stages of rice crop. The optimum temperatures for germination, tillering, pollination and ripening are 18-40 °C, 25-31 °C, 30-33°Cand 20-29 °C, respectively. The current temperatures are already approaching critical levels in different countries e.g. Pakistan/ India (September, October), South India (April, August), East India/Bangladesh (March–June) in subcontinent. Several researchers reported negative effects at different growth stages which resulted poor rice productivity due to low germination, poor tillering, high panicle sterility etc. Water shortage, increased soil salinity, flooding, increased risk of disease infestation and pest attack and enhanced rice-weed competition are the others outcomes of climate change. These factors will affect the rice productivity severely. To face the future challenges in rice productivity, development of tolerant varieties to environmental stresses (temperature, salinity, lodging, and drought) and biotic stresses (disease and insect-pest resistance) is only option either through hybridization or genetic transformation. Climate smart agriculture (CSA) is an integrated approach to manage landscapes, croplands, livestock, forests, and fisheries that address the interlink challenges of food security and climate change with aim to achieve simultaneously achieve three outcomes; increased productivity, enhanced resilience and reduced emissions. Emission of methane may be reduced by keep low numbers of animals with high productivity of milk and meat, establishment of rangelands for grazing, generation of biogas and biofertilizer form the animal wastes. Similarly, dry rice culture may be adopted by introducing the climate resilient varieties with tolerance to biotic and abiotic stresses. The nitric oxide emission may be reduced by intruding the organic fertilizers, optimum dose and right time for application of chemical fertilizers, increasing the soil organic matter, use of slow-release fertilizers. However, CO_2 may be managed by AGRO FORESTORY, encouraging the home gardening, rooftop gardening, urban farming etc. Last but foremost, a comprehensive awareness campaign may be initiated worldwide to raise such a generation who can be CLIMATE GUARDIANS, as mindset and attitudes would be the key elements in mitigation process.

IS4 Characterization of the complete chloroplast genome sequence of the IRLC species and its phylogenetic implications

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Fabaceae (legumes) are the third largest family of angiosperms which have shown the most structural variation. Currently accepted classification of the legumes based on plastid gene *mat*K includes six subfamilies: Caesalpinioideae, Cercidoideae, Detarioideae, Dialioideae, Duparquetioideae, and Papilionoideae. Gene order and gene content in plastomes of all subfamilies except Papilionoideae are highly conserved and similar to the ancestral angiosperm genome organization. Papilionoideae exhibit numerous rearrangements and gene/intron losses and have smaller genome. The remarkable loss of the one of the plastid inverted repeats in the inverted repeat lacking clade (IRLC), a largest legume lineage, is an example of genome variation in papilionoids. This clade comprises 52 genera (e.g., *Wisteria*, *Glycyrrhiza*, *Astragalus, Colutea, Trifolium, Lathyrus, ...*) and ca 4000 species divided into eight tribes. Furthermore, plastome in IRLC show other rearrangements of gene order and gene content. For example, *ycf*4 in some species of *Lathyrus* and *Pisum* (both from the tribe Fabeae) is either absent or a pseudogene. Comparative analysis of the chloroplast genomes across the IRLC revealed that *ycf*1 gene, which is located in the IR region, is more variable than *mat*K in many taxa and thus suitable for molecular systematics at low taxonomic levels. Furthermore, the monophyly of the IRLC and all its tribes is in accordance with all previous studies.

IS5 DNA Barcoding: An Effective Molecular Tool to Identify Gene Expression Host Organisms

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Lemnaceae family members (commonly called as duckweed) are characterized as the world's smallest and fastest growing flowering plants. It consists of monocotyledonous aquatic members, representing a vast range of potential applications like production of feed and food, biofuel and biogas alongside the molecular biotechnology, because of possessing a noteworthy capacity of huge biomass production. The first stage of all of the above-mentioned approaches is to obtain the appropriate species selected based on suitable strategies. Since a high degree of reduction in their anatomical complexity and minimalization of the morphological units make it hard to identify the closely related species of duckweeds based on morphological markers, different molecular taxonomic tools are introduced to require a solution of the problem. DNA barcoding is one the molecular taxonomy techniques using sequences of plastidic DNA fragments. Till now, there is no evidence on molecular identification of the Iranian native duckweed species based on sequence polymorphisms. In this study, we collected some Iranian samples and applied divergent marker categories such as non-coding spacers to achieve reliable successful identification based on direct sequence comparison. Our final goal in this project is to present identified optimal and sustainable strains of the duckweed with acceptable relative growth rate and doubling time in which recombinant pharmaceuticals can expressed in additional related studies.

IS6 The fate of silver nanoparticles in *Lycopersicon esculentu*

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The advancement of nanotechnology has resulted in the application of nanomaterials in a diverse area including medicine, industry, or agriculture. The vast application of nanomaterials and their potential release into the environment can affect soil and water quality, plants, and subsequently human health through the food chain. Silver nanoparticles (AgNPs) are among the most commonly used nanomaterials. AgNPs released into the environment can be oxidized and be transformed into the ionic form (Ag^+) which is more interactive than the particulate form. This study investigated the molecular and physiological responses in tomatoes (Lycopersicon esculentum) exposed to 30 mg/L AgNPs (20nm) for seven days. Plants exposed to $AgNO_3$ and Hoagland media were subsequently used as positive and negative controls. To determine the concentration of Ag and to distinguish between the particulate and the ionic form of Ag in plant tissues an ICP-MS (NEXION

350X) equipped with a nano-detector was used. The concentration of H_2O_2 and MDA, as well as the activity of antioxidative enzymes catalase and peroxidase, were investigated to determine the level of oxidative stress in plants. The expression of membrane transporters H^+-ATPase and V-ATPase as well as the expression of enzymes catalase and mitochondrial IDH were studied using RT-q-PCR. Immunofluorescent labeling was used to study the expression of proteins. The analytical analysis showed that both particulate and ionic forms of silver were accumulated in plant tissues confirming that AgNPs can be oxidized in the environment. The physiological analysis showed that the oxidative stress caused by Ag^+ was more significant than the particulate form. The expression of H^+-ATPase was significantly upregulated upon exposure to AgNPs and $AgNO_3$ compared to the control group. This study suggests that the higher concentration of Ag^+ in plants exposed to all forms of silver changed the electrochemical potential of cells and resulted in the upregulation of H^+-ATPase to send more H^+ out of cells. This study provides invaluable information to better understand the fate of metal-based nanomaterials and their effects on plants.

Keywords: Analytical analysis, Membrane transporters, Nanoparticles, Oxidative stress

IS7 Plant life on gypsum: living at the edge

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The occurrence of special substrates such as saline, serpentine, dolomite or gypsum soils, with a distinct flora associated to them, has puzzled naturalists for centuries. Some of these substrates, and the adaptations displayed by plants to cope with them, are quite well understood. Such is, for example, the case of saline and serpentine soils, where distinct traits have been identified as characteristic of plants adapted to them. However, other substrates like gypsum soils are still poorly understood, and the mechanisms displayed by plants to survive on them pose intriguing questions to ecologists. Gypsum ($CaSO_4 \cdot 2H_2O$) is a rock-forming mineral that also occurs in soils. Gypsum outcrops are widespread throughout the Earth, being present in the five continents. They are particularly prevalent in arid and semi-arid regions of Africa, Western and Central Asia, where they account for ca. 40%, 75% and 25% of the total surface, respectively. Gypsum is also a key water-holding mineral of Mars, and a targeted substrate in the search of extra-planetary life. Due to its particular physical and chemical properties and the aridity typical of the areas where gypsum soils develop, this type of soil poses very restrictive conditions to plant life, yet it hosts a highly diversified flora, rich in endemic and rare species. This talk is an invitation to discover the most recent advances on the ecology and evolution of gypsum plants throughout the world. We will take a closer look at the diversity of gypsum plant communities, examine the different limitations that restrict plant growth on gypsum soils, explore the various mechanisms displayed by plants to cope with them and analyze the dangers that threaten the conservation of these unique environments.

IS8 Using Protected Areas to Secure Forest Tree Genetic Diversity in Hyrcanian forest (Application to the endemic and endangered *Populus caspica*

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The planning of the protected areas and their effectiveness in maintaining the genetic diversity of species remain challenging. The severe degradation and anthropogenic activities in plain regions of the Hyrcanian forest and designing several national parks that have been proceeding for at least three decades provide an opportunity to assess the role of protected areas in conserving genetic diversity. *Populus caspica* Bornm. is an endemic species from Hyrcanian forests and classified as endangered in Iran. For this study, 359 trees from 20 populations (including three national parks from eastern, central, and western parts) distributed throughout the plain region of the Hyrcanian forest, were selected to evaluate the genetic diversity parameters using 14 microsatellite markers. The highest allelic richness, private alleles, and gene diversity were observed in populations located

within national parks, i.e. Ashrafieh, Noor and Loove. Significant reduction in effective population size and a genetic bottleneck were not observed in popualtions in national parks, while about 50 percent of other populations (8 from 17) are under bottleneck effect. STRUCTURE analysis showed the existence of at least two genetic clusters with strict geograohic background but estimated average gene flow was low - the average proportion of the migrants detected among populations was 0.008. We concluded that designing a protected area for the maintenance of the genetic diversity of *Populus caspica* is a very good strategy to reduce the risk of the extinction of this species in the near future.

Keywords: Caspian poplar, endemic species, Genetic conservation, Protected area, Hyrcanian forests.

IS9 Molecular Biophysics of SARS-CoV-2 virus and its susesepibiliy

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SARS-CoV-2 corona virus that caused the Covid-19 Pandemic, is composed of the lipid bilayer membrane and several constituent antigenic proteins including; Spike, Orf3a, and other envelope (E) proteins that can be used as potential targets for treating the virus in a non-clinical and genetically manner. The known atomic structure of the mentioned molecules at atomic level has made it possible to take biophysical approaches focusing on the charges, intra and intermolecular electrostatic interaction and forces, as well as their physico-chemical interactions with the medium co-ions and counter-ions, pH, temperature and water status as the neutralizing, destructing and treating agents. Furthermore, due to the atomic and molecular characteristics and configuration of virus, it can be considered likewise solid state materials and expect to affect its electrical status by exposing it to external electrical, magnetic and elecromagnetic fields for the detection and inactivation purposes. The conformation of the spike protein and its functional antigenic status is achieved and stabilized by intra-molecular and inter-molecular forces that are susceptible to the external fields. Here, the ultrastructure of the virus will be discussed and different approaches considered to study and treat its membrane and constituent proteins for detection and inactivation purposes are presented. Our voltage clamp experiments have shown EMF effect on the lipid membrane integrity and voltage-dependent channel activities leading to pore formation and ultimate destruction of the membrane. Furthermore, the applied EMF caused decreased voltage sensitivity and long lasting inactivation of the voltage dependent OmpF voltage gated channel. Accordingly, although, the actual contribution of the voltage-gated rectifier OrfA channel is not fully known yet, we expect that exposing it to the external EMF can interfere with its activity and possible deviation of the virus functionality and ingrity and corresponding response be used for detection purposes.

Keywords: Biophysics, SARS-CoV-2, Covid-19, EMF, Membrane, Voltage Clamp, Virus.

IS10 Role of HMGB1 and decorin in preeclampsia

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Preeclampsia (PE) is a common, pregnancy-specific disease that belongs to the family of “hypertensive disorders in pregnancy” and is characterized by hypertension, proteinuria and other systemic disturbances at or after 20 weeks of gestation. PE is a major contributor to maternal and fetal morbidity and mortality. Eventhough the precise mechanisms of PE pathogenesis remains unknown, it is widely acknowledged that the placenta is the central organ in its pathogenesis, and PE is caused by maternal responses to abnormal placentation and associated with an increased inflammatory state. Pre-eclampsia is closely related to maternal malfunction of the vasculature and is a major cardiovascular risk for the duration of the pregnancy, post-parturition and in later life. Also, endothelial dysfunction may contribute to elevate the peripheral resistance of blood vessels, which forms an essential component of the maternal syndrome. This study is aimed at the study of sterile immunomodulatory profile of normal-pregnant versus pre-eclamptic subjects and focuses on the identification of potential biomarkers for the early detection of PE and the changes in the hemodynamic parameters leading to the pathophysiology of PE. There have been a lack in the proper understanding of the pathophysiology of PE & hence, no effective therapy or treatment is available so far. The levels of NO were significantly decreased in PE as compared to healthy pregnant subjects. As NO is a potent vasodilator, when its level in circulation

decreases, the contraction of blood vessels increases which leads to elevation in the blood pressure. In our study, we observed that there is a marked increase in the expression level of SI markers (DAMPs) such as HMGB1, HSP90, vWF and DCN in plasma as well as in the placental tissue. From these observations, we can conclude that these inflammatory markers play an important role in the commencement of the pathophysiology of PE. We observed a decreasing trend in all SI markers when the pre and post-delivery samples of PE patients were compared, however significant reduction was seen only in the case of DCN for the SI markers. Therefore, it can be deduced that the DCN is one of the most important molecules which plays a significant role in the pathophysiology as well as progression of PE. On comparing the biochemical reports of the PE and normal subjects we have found that there is statistically significant increase in the biochemical parameters of the patients versus normal subjects. We observed that certain biochemical parameters such as S. Alkaline phosphate, SGOT, SGPT and protein concentration were significantly increased in PE as compared to healthy controls while no significant change was observed in blood urea and serum creatinine levels. We also analysed the blood parameters from the CBC (complete blood count) reports of patients. On comparing both the reports we observed that the NLR (neutrophil to lymphocyte ratio) was significantly increased in PE as compared to healthy pregnant subjects. On combining all the observations, we can conclude that low levels of NO lead to placental hypoxia which induces DAMPs expression. Increased expression of DAMPs in turn acts as a stimulus for neutrophil activation in increasing the NLR in PE patients

IS11 Oxygen sensing and Lead (Pb) toxicities: Molecular interactions, cell signaling & antioxidant defense

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Hypoxia is one of the most serious factors that can directly impair the function of metabolic pathways in the cell. Cellular hypoxia causes an initiation of hypoxia-response genes responsible for angiogenesis, oxygen transport, and metabolism. Hypoxia leads to alter intracellular chemical microenvironment by increasing calcium concentration ([Ca2+]i), 5-lipoxygenase, lipid peroxidation, cycloxygenase (COX), constitutive nitric oxide synthase (cNOS), leukotriene B4 (LTB4), prostaglandin E2 (PGE2), interlukins, tumor necrosis factor-α (TNF- α), caspases, complement activation heat shock protein 70 kDa (HSP-70), and hypoxia-inducible factor-1α (HIF-1α). Another key molecule within this hypoxia-induced response is the presence of nitric oxide (NO). It is synthesized by nitric oxide synthases (NOS) and its release can be stimulated as a result of inflammatory responses, sympathetic activation and drop in oxygen levels. Interestingly hypoxia and divalent heavy metal like lead (Pb) generates ROS and disturbed oxidant/antioxidant balance which is linked to the transcriptional factor hif- 1α. The results from the author's study showed both divalent cationic heavy metal (Pb) or chronic sustained hypoxia stimulates the production of hif-1α transcription factor and VEGF gene expression in metabolically active tissues in similar molecular mechanism.

IS12 Proteomic dissection of signaling pathways in cancer cells

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Protein interaction networks underlie most cellular processes, and in many diseases, including many cancers, protein networks that mediate signal transduction pathways are inappropriately activated or rewired. We are interested in how mutations alter protein interaction networks, and we are focused on understanding the role of the Wnt signaling pathway in solid tumors using both proteomic and bioinformatics techniques. In this presentation, I will describe our contributions to developing proteomic and bioinformatics approaches as well as our identification of novel protein-protein interactions that drive oncogenesis.

IS13 Integrated Biorefineries

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Biorefineries are industrial plants, which are based on the use of biomass, instead of fossil fuels, for production of fuels, chemical base materials and energy. These are comparable with petrochemical refineries in many aspects of their operations and products. It is said that the era of the fossil fuels is at its end, not because of its ending resources, but because of finding new technologies that are more environmentally friendly and economic. Biorefineries are not yet fully operational but are in the midway. Many exhibition pilot-plants are made and working, while a lot of experimental tests are yet on the way. The carbon is the essential material for production of the organic substances and products. We have an enormous source of carbon in the biosphere in the form of CO_2 of the atmosphere and carbonates of the earth crust. Both of these sources are continuously adsorbed by plants, algae and autotrophic microorganisms by the use of solar energy. The biomass of these organisms has an amount of carbon around 50% percent of its weight. This carbon can be converted into a wide spectrum of useful products like biofuels, bioplastics, organic acids, solvents, etc. Different processes are used for these conversions: physical, chemical and biological. Biological processes are more advanced and produce less environmental problems. The diverse metabolic power of microorganisms is used here to produce the products. Nearly, all of the routine refinery's products can be produced by the biorefineries. In this lecture specifications of the biorefineries and some examples of working ones in the world and Iran will be presented.

IS14 Antimicrobial resistance (AMR) and Role of the laboratory in AMR control

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IS15 Survey of Microorganisms' World in Kerman Desert

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Microorganisms have a crucial role in soil processes. Information about soil microbiota in arid and semiarid area, especially in Iran is limited. The aim of study was to determine microbial diversity of soil biological crusts (SBC) of Khabr and Ruchun National Park. First, microorganisms of SBC were identified through culture-dependent and culture-independent techniques. Then, microbial diversity was tested by Next Generation Sequencing (NGS) technique. After that, nitrogenase activity of the isolated Cyanobacteria strains was determined *via* acetylene reduction and expression of *nif*H gene by using real time-PCR. Next, desiccation stress was performed on the isolated Cyanobacteria and the superior strain was selected. Whole genome of the tolerance strain of Cyanobacteria to the desiccation stress was sequenced. Afterward, its transcriptional response to the desiccation stress was assayed. Finally, by lab modelling of the desert soil inoculated with the selected Cyanobacteria concerning to the nitrogen fixation, the growth of model plant was evaluated. The results indicated that this area has vast diversity of different phylum of microorganisms. Furthermore, changes in the composition of microbial communities due to the climate fluctuations or other stresses can be shown before any changes in chemical and biochemical properties of soil. The soil treated with Cyanobacteria especially when accompanied with chemical fertilizer showed well increasing of model plant growth and improving soil properties as well. The comparative genome analysis showed the presence of genes involved in the biosynthesis of mycosporines, trehalose and phycobilisome. Transcriptomics and comparative genome analysis showed that 397 genes such as genes encoding catalase and chaperons were differentially expressed in response to the desiccation stress. Transcriptomics and comparative genomic studies can open a new window to the adaptation mechanisms of cyanobacteria studies in terrestrial ecosystems.

Keywords: Cyanobacteria, Acetylene Reduction, Real Time-PCR, Nitrogenase Activity, *nif*H, Khabr and Ruchun Park

IS16 The resulting experience of wildlife management and biodiversity conservation to maintain quality habitat in Semnan province

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According to the Koppen-Geiger climate classification, the world is divided into five major climatic regions. Iran's biodiversity is the result of the aggregation of three of these five climatic zones. Dry, temperate and continental climates. The result of this climatic diversity is 197 species of mammals, 535 species of birds, 227

species of reptiles, 21 species of amphibians and 160 species of fishes. Thirteenth century Hijri was a century of rapid development and extensive land use, especially in the plains of Iran. Contrary to the explosive growth of hunting equipment and prolonged droughts, this phenomenon has pushed large populations of the country's biodiversity to the brink of extinction. Semnan province is the only province in the country that has all three major climatic regions of Iran. For this reason, the fate of many animal species, especially in the category of mammals, is tied to the habitats of this province. The Asian cheetah is the rarest cat species in the world. It is the flagship species, the umbrella species, the flag species and the focal species of Iran. Unfortunately, the evidence shows that during these twenty years, the reproduction of the Asian cheetah to the protected area of Turan in Semnan province in other habitats of the world and six of the seven provinces of Iran has been lost and the hope for the return of this species to those habitats is very low. The Asian cheetah is now at the top of the ecological pyramid of Iranian steppe animals, and the removal of such blows will inflict severe blows on the body of this pyramid. Therefore, any effort that leads to the conservation of the remaining population of this species will play an effective role in the population dynamics of other species in the food chain ecosystem. This presentation demonstrates the successful results of the efforts made by the General Department of Environmental Protection of Semnan Province, which has led to the conservation of Asian cheetah regeneration and thus the conservation of other species of the ecological pyramid in three areas and its experiences for use in other habitats. Iran and the world consider it usable.

IS17 Regulatory mechanisms of sperm motility initiation in fishes – a review

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Fish spermatozoon is differentiated into a head, a midpiece and a flagellum. The head does not have the acrosome, and contains nucleus which transferring haploid set of the chromosome into the next generation. Mitochondria, proximal centriole and distal centriole are located in the midpiece. Mitochondria supply energy for the flagellar beating. Both proximal and distal centrioles consist of nine peripheral triplets of microtubules. The distal centriole organizes formation of the sperm motility apparatus called *"axoneme*" with "9+2" microtubules structure. Fish spermatozoa are immotile in the sperm duct due to osmolality or presence of high potassium (K^+) ions in the seminal plasma. Spermatozoa motility is triggered *in* hypo-osmotic and hyper-osmotic environments in freshwater and marine fishes, respectively. Duration of spermatozoa motility is generally limited to a short period due to adenosine triphosphate (ATP) content. After initiation of motility, percentage of motile spermatozoa, spermatozoa velocity and beating frequency of the flagellum decrease due to rapid depletion of ATP stores. When motility of spermatozoa activated by a change in the environmental osmolality, K^+ and water effluxes occur in freshwater and marine fishes, respectively, which trigger spermatozoa motility signaling. Generally, initiation of axonemal beating is associated with an increase in intracellular calcium (Ca^{2+}) ions and pH in spermatozoa of both freshwater and marine fishes, while cyclic adenosine monophosphate (cAMP) remains unchanged. However, it has been shown that axonemal beating is cAMP-dependent in demembranated spermatozoa of salmonid and sturgeon fishes. Extracellular or intracellular stores of Ca^{2+} supplies required Ca^{2+} concentration for axonemal beating. Several axonemal proteins have been so far identified that are activated by Ca^{2+} and cAMP, directly or mediated by protein kinase C and protein kinase A, respectively. The present study reviews differences and similarities in complex regulatory signals controlling spermatozoa motility initiation in fishes, and notes physiological mechanisms that await elucidation.

Keywords: ATP, Axoneme, cAMP, Ions, pH, Osmolality, Seminal plasma

IS18 Making Meaningful Decisions for Life: Epigenetic Monoallelic Gene Expression in Mammals

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Monoallelic gene expression or allelic exclusion, once known to be restricted to random X chromosome inactivation in female mammals, seems to be more common than thought with crucial effects in embryonic development, apparently as a way to increase the repertoire of variations in gene expression patterns. Monoallelic expression of immunoglubin genes and T-cell receptors is responsible for huge diversity of

antibody production and antigen recognition, respectively, through DNA rearrangements. However, other patterns of monoallecic gene expression all come in effect via epigenetic mechanisms employ on similar genetic backgrounds. Among these phenomena, *mammalian X chromosome inactivation* in female tissues and the parent-specific *genomic imprinting* considered as classic paradigms for epigenetic gene regulation. While X chromosome inactivation occurs via "*random choice*", however, genomic imprinting exhibits a *deterministic choice* for the expression/repression of the respective genes through a parent- of- origin specific pattern during gametogenesis. Interestingly, X chromosome inactivation shows both patterns of random choice in mammalian somatic tissues, the paternally imprinted form of X chromosome inactivation occurs in marsupials, and also in rodents and human placentas. The last category encompasses stochastic allelic exclusion of a plethora of different autosomal genes, including genes for odor sensing in olfactory sensory neurons, as it seems the rule of one neuron-one receptor gene is essential for odor perception. All kind of epigenetic monollelic gene expression share similar epigenetic signatures, including the expression of long noncoding RNAs, DNA methylation and extensive chromatin modifications, polycomb protein bindings, etc. Also, their organization along the genome and mechanisms involved show considerable parallels. In current lecture, along with a brief introduction of various instances of epigenetic allelic exclusion, its various roles in growth and development of embryos and its some evolutionary implications are discussed.

Keywords: Allelic exclusion, Monoallelic gene expression, X-chromosome inactivation, Genomic imprinting, olfactory receptor genes

IS19 Consequences of Simulated Microgravity in Biosystems: Structural Effects and Cellular morphology

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Enhancements in technology have offered extraordinary opportunities for the human to travel more rapidly on or near the surface of the Earth. The primary goals of space travel are the search for life, planetary exploration, and more significantly safe return to Earth. Humans on Earth are adapted to the constant gravitational force (9.8 m/S2). Nevertheless, in space, gravity is much weaker than on Earth which is known as microgravity. Presently, investigations on the growth and development of cells as well as bio-macromolecules structure exposed to microgravity, as biophysical force, is a hot topic in cell biology and astronauts' health. Consequently, we first investigate the probable impacts of simulated microgravity on the structure of human serum albumin (HAS), histone H3, and DNA by multiple spectroscopic techniques. Subsequently, we analyzed the effects of simulated microgravity on the growth of MCF7 and T47D breast cancer cell lines. Our results exposed that the structure of HAS, histone H3, and DNA subjected to simulated microgravity changed significantly. Furthermore, our results showed that microgravity simulation did not have a remarkable effect on the viability of cells, but cells were grouped and linked to each other making multicellular spheroids. The findings achieved from this investigation can open fascinating research lines in biophysics, astrobiology, and biology and can be utilized to enhance survivability and life quality for space travelers.

Keywords: Astrobiology, Cell viability assay, DNA structure, Protein structure, Microgravity

IS20 Bone Tissue Engineering; Advances and Challenges

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Tissue engineering is a multifaceted, interdisciplinary discipline that uses the principles of engineering sciences and natural sciences to repair the structurally and functionally damaged tissues. In order to achieve satisfactory results in tissue engineering, simulation of the natural extracellular environment is essential. To achieve this goal, the development of appropriate cell differentiation protocols as well as scaffold design similar to the natural matrix should be carefully considered. Stem cell differentiation into the bone line is enhanced by many inducers, including biochemical agents, biomechanical stresses, and electrical stimuli. Based on our studies, the synergistic effects of anti-mir221, hydroxyapatite nanoparticles and electrical induction in improving the bone differentiation of mesenchymal stem cells in vivo have been confirmed. Considering the functions and positions

of markers in ossification signaling pathways, it can be concluded that hydroxyapatite cooperates in allocating stem cells to bony progenitors in the early stages of ossification while electrical stimulation to more mature cells in achieves functional phenotypes. In general, the study of synergies between different stimuli and the exploitation of interactions in an optimal way can lead to the production of efficient ossification protocols for bone tissue reconstruction and engineering.

Keywords: osteogenic differentiation, electrical stimulation, anti-mir221, hydroxyapatite nanoparticles, regenerative medicine

IS21 The importance of Bioinformatics and Computational Biology in Systems Biology

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Nowadays, a huge amount of data such as multi-omics data including gene expression, DNA sequences, and demographic information are available that need analysis in order to find latent patterns that give rise to solving biological issues. To this aim, state-of-the-arts approaches such as modeling using graph, machine learning, and deep learning can help to find novel methods for modeling biological systems. Some hot topics in this field are drug-drug interaction prediction, precision medicine, and cancer biomarker detection that can be solved by using the mentioned computational strategies. In this lecture, we going to briefly discuss aforementioned topics and explain a computational solution for some of them.

Keywords: Biological networks, Machine learning, Precision medicine, Drug recommendation, Cancer

IS22 Development of artificial enzymes with biomedical and industrial applications; Perspectives and future challenges

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Natural enzymes, most of which are proteins, are catalysts that can speed up chemical reactions rate by reducing activation energy and mediated the biological processes under mild conditions. However, these biomolecules have some drawbacks including the high cost of synthesis, purification and low stability in extreme conditions of pH or temperatures for performing catalytic functions. So, due to these disadvantages and to overcome these limitations, easily synthesized, highly stable and low cost enzyme mimetic from molecules to inorganic nanomaterials have been developed. Developing many manmade enzymes (artificial enzyme mimetics), as alternatives to natural enzymes, using non-protein molecules become an interesting field for researchers. However, the disadvantages of enzyme mimetics are that the catalytic efficiency, specificity, and selectivity are relatively low. To date, many enzyme mimetics have been prepared and have activities analogous to cytochrome P450, serine protease, dioxygenase, phosphodiesterase, lipase, acylase, ligase, hydrolase, aldolase, superoxide dismutase, and nitrile hydratases. Nanomaterials are chemical entities at least one dimension smaller than 100 nm. With such an extremely small size and large surface area per unit of volume, nanomaterials have characteristic physical, chemical, photochemical, and biological properties that are very different from those of the same material in bulk form. Nano-based materials due to their physicochemical properties relative to bulk materials including large surface/volume ratios, optically active, mechanically strong and chemically reactive have various applications in different areas, including biosensing, catalysis, textile industry, drug delivery and water treatment. Enzyme mimetic behavior of some nanomaterials is one of the most interesting features of these materials which make nanomaterials as potential alternatives for natural enzymes. Nanomaterials, with enzyme mimic activities, which are called nanozymes, have gained much more attention among the researchers during the past decades because of their unique properties such as low-cost, high stability and simple preparation. Also, nanozymes have their catalytic activity even in the harsh environmental conditions of pH and temperatures. Nanoparticles' catalytic activity and intrinsic ability in generating or scavenging reactive oxygen species (ROS) in general can be used to mimic the catalytic activity of natural enzymes. To date, many nanoparticles with enzyme-like activities have been found, potentially capable of being applied for commercial uses, such as in biosensors, pharmaceutical processes, and the food industry. The reported enzyme-like activities for nano-sized materials includes the superoxide dismutase-like (SOD like), oxidase-like, catalase-like, glucose

oxidase-like and peroxidase-like activities. Also, enzyme-mimic activity of some metal-protein complexes have been reported, too. In general, artificial enzyme mimetics have been developed by using different non-protein molecules such as metal-complexes, metal-nanomaterials, polymeric and supramolecules.
Key Words: Artificial enzymes, nanomaterials, nanobiosensors, enzyme mimetic acticity

IS23 Biophysical understanding and control of living systems

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The physical nature and biophysics of the living systems in micro-organisms, plants and animals make them very susceptible to the various external irradiation sources including; electric, magnetic and electromagnetic fields. They also possess and make use of their own intrinsic fields for functioning, healing, communication and defend purpose. This is the way we can detect and recognize their functional state and control and manipulate their activities at organ, cellular, molecular, atomic and even subatomic levels. Clinical application of these very characteristics has mad us use EEG, EMG, EKG and Squid Magnetometers to detect the functional state of brain, muscles, heart and brain by means of their bioelectric and biomagnetic activities and status in a non-invasive and real time manner in animals and human being. Dolphins, sharks, electric Eeles, bats, honey bees and others rely on their intrinsic fields potentials to communicate, detect, navigate, defend and manage their life. In plants, squeezing, cutting and burning of the leaves have caused corresponding electrical signals comparably to electrical signals in animals nervous systems to transfer the information across the plant body. Magnetoproteins in certain strains of bacteria makes it possible to navigate using Earth magnetic field in oceans. Water, forming about 70% of the biological systems, possess magnetic momentum, electrical dipole characteristics, diamagnetic nature and provides appropriate platform for polyelectrolyte charged biological macromolecules such as enzymes, pumps, channels, robotic nano-motor proteins and so on to take appropriate conformation and dynamics and function properly. Here, the importance of biophysics in understanding the structure and function of living organisms and its application in the detection, control and treatment is discussed at atomic, molecular, cellular, organ and whole body levels. It will be shown that the above knowledge is necessary for all the undergraduate and postgraduate students in various fields of biological sciences to enable them solving corresponding problems living organisms are suffering from on the Earth in an efficient manner.
Keywords: Biophysics, Zoology, Botany, Microbiology, Environment, Clinical Sciences, Electric, Magnetic, Electromagnetic fields

IS24 Signaling pathway modeling for systematic study of diseases

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Signaling pathways are a sequence of actions inside a cell, usually responsible for the transmission of a message from outside world to the nucleus. Finding disease-related signaling pathways is helpful in discovering the mechanism of the diseases, creating better drugs, and personalizing drugs for patients. Different Pathway analysis methods have been proposed to find and rank signaling pathways perturbed in a given phenotype. In this article, we review the approaches proposed by our research team to analyze the signaling pathways. These approaches are based on graphical models and formal methods for modeling signaling pathways. In the first method, a new pathway enrichment analysis method, BNrich, is introduced. This method has been applied on data related to systemic lupus erythematosus (SLE), to underscore key molecular characteristics of SLE pathogenesis, which may serve as effective targets for therapeutic intervention. After that, two formal methods are introduced, the first one models the signaling pathways using PRISM language and assign weights to gene-gene interactions, and the second uses Petri net for modeling, which have advantages over other formal methods, because of its graphical and hierarchical structure. Based on these proposed methods, two tools called FoPA and PAPet have been developed, in Python and R programming languages.
Keywords: signaling pathway, graphical model, formal method, petri

IS25 Design of antimicrobial and anticancer peptides based on membrane and peptide biophysical properties

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Peptides are a unique group of pharmaceutical compounds whose intrinsic function and nature in regulating the cellular and physiological processes of the human body have made it possible to mimic and benefit from these characteristics in the treatment and drug design. Therapeutics peptides due to their small size, ease of synthesis, ability to penetrate cell membranes, high activity, specificity and biological and chemical diversity are suitable candidates for the treatment of many diseases. Antimicrobial and anticancer peptides are a group of therapeutic peptides that in addition to antibacterial, fungal, and viral properties can affect the immune system and have an effective role in the removal of cancer cells. Due to the expansion of databases in the field of therapeutics peptides, the use of computational methods such as artificial intelligence and machine learning has made it possible to design and modify the performance of these peptides. The cell membrane is the first barrier to penetrate and binding the factors that cause cell destruction. Changing the membrane content and its physical properties determines how the therapeutics peptides interact with the membrane. The interactions between proteins and membranes play critical roles in signal transduction, cell motility, and transport, and they are involved in many types of diseases. Molecular dynamics (MD) simulations have greatly contributed to our understanding of protein–membrane interactions. In this study, the binding, penetration, and interaction of natural and designed antimicrobial and anticancer peptides with different membranes was investigated by the molecular dynamics simulation. All the simulations were run for at least 200 ns using the GROMACS package and then peptide penetration in the membrane was evaluated by different analyses. The results show that the penetration rate, mechanism of action of the peptide, and interaction peptide with membrane depends on the characteristics of the peptide such as sequence length, hydrophobicity, charge, peptide orientation on the membrane, amino acidic composition, and its concentration. The lipid composition of different membranes, the presence of cholesterol in the membrane, and fluidity and symmetry in the membrane will be important factors affecting the interaction of peptides with membrane.

Keywords: molecular dynamics, membrane, therapeutics peptides, penetration

IS26 Pan-cancer analysis of microRNA expression profiles highlights microRNAs enriched in normal body cells as effective suppressors of multiple tumor types

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MicroRNAs (miRNAs) are frequently deregulated in various types of cancer. While antisense oligonucleotides are used to block oncomiRs, delivery of tumour-suppressive miRNAs holds great potential as a potent anti-cancer strategy. Here, we aim to determine, and functionally analyse, miRNAs that are lowly expressed in various types of tumour but abundantly expressed in multiple normal tissues. By compiling all publicly available miRNA profiling data from The Cancer Genome Atlas (TCGA) Pan-Cancer Project, we reveal a small set of tumour-suppressing miRNAs (which we designate as 'normomiRs') that are highly expressed in 14 types of normal tissues but poorly expressed in corresponding tumour tissues. Interestingly, muscle-enriched miRNAs (*e.g.* miR-133a/b and miR-206) and miRNAs from *DLK1-DIO3* locus (*e.g.* miR-381 and miR-411) constitute a large fraction of the normomiRs. Moreover, we define that the CCCGU motif is absent in the oncomiRs' seed sequences but present in a fraction of tumour-suppressive miRNAs. Finally, the gain of function of candidate normomiRs across several cancer cell types indicates that miR-206 and miR-381 exert the most potent inhibition on multiple cancer types *in vitro*. Overall, our results reveal a pan-cancer set of tumour-suppressing miRNAs and highlight the potential of miRNA-replacement therapies for targeting multiple types of tumour.

Keywords: tumorigenesis, cancer cell, miRNA, cell viability, proliferation

IS27 From Birth to Birth

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Newborn screening is the practice of testing every newborn for certain harmful or potentially fatal disorders that aren't otherwise apparent at birth. With a simple blood test, doctors often can tell whether newborns have certain conditions that eventually could cause problems. Although these conditions are rare and most babies are given a clean bill of health, early diagnosis and proper treatment sometimes can make the difference between lifelong impairment and healthy development. **Child package** A successful future begins when parents understand and devote themselves to develop the potential their child possess since birth. The Inborn Talent Genetic Test (ITGT) helps parents like you to discover your child's talents that may not be obvious at a young age along with personality traits that they have. Knowing your child's genetic make-up allows you to take control of their development to nurture their talents. It also allows you to intervene in their weaknesses at an early stage before it takes root in your child. With the career profiling report that comes with the genetic test, this test package is the roadmap for you to plan your child's future towards success. **Preconception Gene Profile** is a genetic test aimed at prospective parents to determine if they are **carriers** or not for certain hereditary diseases. Preconception Gene Profile allows establishing the genetic risk of having affected offspring and, thanks to adequate genetic counselling, offering to the prospective parents the different **reproductive options** available according to their situation, in a personalized manner. **Non-Invasive Prenatal Tests (NIPT)** which allos the genetic analysis of the fetus early in pregnancy by carrying out a fetal genetic analysis using a maternal blood sample that contains cell-free fetal DNA. SG Baby Test is designed to assess the risk of the fetus of being a carrier of aneuploidy (abnormal number of chromosomes) **Multifactorial Disorders Nutrition and sport Skin and beauty Cancer Genetic ancestry** testing, or genetic genealogy, is a way for people interested in family history (genealogy) to go beyond what they can learn from relatives or from historical documentation. Examination of DNA variations can provide clues about where a person's ancestors might have come from and about relationships between families. Certain patterns of genetic variation are often shared among people of particular backgrounds. **DNA paternity** testing determines the biological father of a child. We all inherit our DNA from our biological parents — half from our mother and half from our father. A DNA paternity test compares a child's DNA pattern with that of the assumed father to determine if there is a match.

IS28 Scale-up Production of Liver Organoids

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Liver organoids (LOs), are attracting growing interest for drug screening and disease modeling or transplantable constructs for tissue regeneration. Hepatocytes, the key component of LOs, isolated from liver or generated by differentiation of pluripotent stem cells (PSCs). PSCs are preferable because of their availability, scalability, and potential for personalized treatments. However, maturation of the PSC-derived hepatocytes to functional unites in LOs has yet remained challenging. Incorporation of cell-sized microparticles (MPs) derived from liver extracellular matrix could provide a tissue-specific microenvironment for further maturation of hepatocytes inside the LOs. The MPs were fabricated by chemical cross-linking of a water-in-oil dispersion of digested decellularized liver tissue. These MPs were mixed with human PSC-derived hepatic endoderm cells, human umbilical vein endothelial cells and mesenchymal stromal cells to produce homogenous bioengineered LOs (BLOs). BELOs showed enhanced maturation of hepatocytic specific genes and function e.g., CYP activities, Alb secretion and metabolism of xenobiotics. Efficient hepatic maturation and integration resulted after *in vivo* and *ex ovo* transplantation either. Ectopic transplantation of BELOs in mice with acute liver injury improved survival rate. In conclusion, MPs incorporated in BLOs improved maturation of hepatocytes compared to LOs. BELOs represents a novel tool for drug screening, toxicology and potential translational applications. Moreover, this approach could be likely implemented as a versatile strategy to produce functional organoids from different sources.

Keywords: Liver organoid, Tissue specific Microparticle, Pluripotent stem cell, Hepatic differentiation, Tissue engineering

IS29 Structure function relationship in active and inactive Apaf-1 in apoptosome formation

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In multicellular organism, apoptosis is one of the programmed cells death pathway in which is vital for development and regulation of homeostasis. During apoptosis and other programmed cell death pathways formation of large protein complexes is one of the main hallmarks. We have used split luciferase complementary assay to monitor protein-protein interactions in mentioned complexes like apoptosome, necrosome and inflammasome. During apoptosis, apoptosome formation is the main bottleneck for cell death progress, in which Apaf-1 is an adaptor that activates caspase-9. Structural studies suggest that normally Apaf-1 is held in an inactive conformation (Latent form) by intramolecular interactions between Apaf-1's nucleotide binding domain and one of its WD40 domains (WD1). Based on molecular model of Apaf-1 activation, cytochrome *c* binds to sites in WD1 and in Apaf-1's second WD40 domain (WD2), moving WD1 and WD2 closer together that allows Apaf-1 to bind dATP or ATP and to form the apoptosome then activates caspase-9. We investigated the effect of one WD domain (Apaf-1 1-921) deletion on Apaf-1 interactions and caspase cascade activation. Trucated Apaf-1 (1-921) could not activate caspase-9, even in the presence of cytochrome *c* that suggest a single WD domain is sufficient to lock Apaf-1 in an inactive state and that this state cannot be altered by cytochrome *c*.

IS30 Applications of integrative biology to address global challenges

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As the name "Integrative Biology" reflects the belief that the study of biological systems is best approached by incorporating many perspectives like communicative and integrative biology, cellular biology, molecular biology, tissue biology, developmental biology, evolutionary biology, computational biology, structural biology, mathematical biology, and integrative and comparative biology. We bring together a diversity of disciplines that complement one another to unravel the complexity of biology. The concept includes anatomy, physiology, cell biology, biochemistry and biophysics, and covers all organisms from microorganisms, animals to plants. Our broad range of expertise includes cell biologists, geneticists, physiologists, behaviorists, morphologists, microbiologists, computational biologists, systems biologists, structural biologists, ecologists, biophysicists, and biotechnologists. IB is a multi- and interdisciplinary approach for researches using experimental or computational quantitative technologies to characterize biological systems at the molecular, cellular, tissue, and population levels. It mainly included investigations that contribute to a quantitative understanding of how component properties at one level in the dimensional scale (nano to macro) determine system behavior at a higher level of complexity. Today, more than ever, biology has the potential to contribute practical solutions to many of the significant challenges confronting the world. IB for the 21st Century recommends greater integration within biology, and closer collaboration with physical, computational, and earth scientists, mathematicians, and engineers be used to find solutions to five vital societal needs: sustainable food production, climate change, ecosystem restoration, optimized biofuel production, and improvement in human health.

IS31 Ecological Responses of Algal Community to Hydrological Changes in the MacKenzie River, Australia: Implications for River Basin Management

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Today, many rivers and wetlands have been heavily regulated to ensure adequate provision of water resources for anthropogenic uses. Aquatic ecosystems, especially those in arid and semi-arid regions, are experiencing severe stress due to the increasing demands on the ecosystem services they provide. In this study, samples of diatoms, soft algae and measurements of water quality were analysed at ten sampling sites for three years (between February 2012 and November 2014) along the MacKenzie River to understand the spatial and

temporal variation in the relationship between algal communities, water quality and stream condition. Baseline information on algal communities and water quality was collected during base flow conditions, while experiments on the effect of water releases on algal communities were based on flow regime variations (manipulated flow regimes), specifically on the algae community structure, water quality and ecosystem function. Algal species composition changed along the river under different flow regimes and different seasons. Under base flow, diatoms were more abundant upstream and filamentous green algae were more abundant downstream. The results showed that the algal composition shifted downstream after water release events. Green algae, Cyanobacteria and Chrysophyta gradually increased from upstream to downstream under base flow conditions, and before water releases, whereas diatoms were greater upstream and increased downstream after water releases. The results suggest that by tailoring the discharge and duration of the river flows, through the amalgamation of consumptive and environmental flows would improve the condition of the stream, and supplementing the positive effects of the flows dedicated to improving environmental outcomes.
Keywords: Algae, Ecology, River management, Biodiversity

IS32 Identification of Medicinal Plants Value Chain, Challenges and Opportunities (Case Study of Thyme)

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Nowadays, 80% of the world's population, especially in developing countries, are dependent on medicinal plants for treatment. According to the World Health Organization, about 25% of all medicines used worldwide are derived from plants and their derivatives. Preserving the genetic resources of plant species in natural habitats is essential. Therefore, with the aim of increasing the quality and quantity of the final product and achieving homogeneous and uniform medicinal plant to meet the growing global demand, the policy of cultivation and domestication of medicinal plants in the agricultural conditions was prioritized. Thyme species are important medicinal plants in the world due to their various valuable compounds. In this paper, the research path from identifying different thyme wild populations, studying germination needs, seedling production and establishing different populations in one place, multiple species evaluations to identifying superior and compatible ones in Semnan province as a practical example of the medicinal plant breeding program will be reported in this presentation.
Keywords: domestication, breeding, thymus spp, essential oil, thymol

IS33 15 years of taxonomic study on the genus *Silene* (Caryophyllaceae) in Iran a pattern for taxonomic studying of species rich genus in Iran

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The genus *Silene* (Caryophyllaceae) with about 118 species, is an important and problematic taxon in Iran. 15 years taxonomical studies in different aspects of the genus in Iran including; extensive new collection, herbarium specimens examination, nomenclature, morphometry, anatomy, ecology, chromosome features, Seed and pollen micromorphology, and phylogeny has led to changes in its taxonomy. During these studies, 3 new species; *S. mishudaghensis, S. oxelmanii* and *S. circumcarmanica were* described, 2 sections (*Scorpioideae* and *caespitosae*), 9 *Silene* species and *S. odontopetala* subsp. *congesta* were recorded for the first time from Iran. *S. eremicana* has been considered as distinct taxon and 3 species has been determined as synonymous of other species. At all, chromosome number information of 70 species was reported for the first time from Iran. Anatomical features of 45 species was studied and leaf and stem epidermis characteristics of 75 Iranian *Silene* species was described. Seed and pollen micromormorphology of 65 and 70 species respectively was studied and described by using scanning electron microscope. According to the available information, about 60% of species of this genus have been studied up to now, so that providing a new and complete classification at the section level and intraspecific variations requires more information. Considering the existence of about 20 genera with more than 40 species in Iran, the step by step model of taxonomic study performed in the genus *Silene* includes; Extensive sampling at population level from all natural habitats, detailed study of morphology and correct determining of taxa, resolving the nomenclatural problems of taxa, description of habitat features,

phtyogeography, anatomy, chromosome features, micromorphological studies of Seeds and pollen, embryology and reproductive systems and finally phylogenetic study can be a suitable model.

Keywords: *Silene*, Taxonomy, species rich genus, Seed micromorphology, Iran

IS34 The Value of Micromorphological Studies in Poaceae

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Poaceae is the fourth largest flowering plant family in the world that is adapted to different types of habitats. There are 12 subfamilies with 50 tribes and 81 subtribes in Poaceae. The efficiency of micromorphological data in systematic studies of the Poaceae is documented for the leaf blade epidermis, Glumes, lemmas, and paleas especially at the subfamily and tribal levels. Micromorphological features in lemma and palea as shape and distribution of silica bodies, long and short cells, different hair types as prickles, macro-hairs, and crown cells are of taxonomic importance. Intercoastal long cells are show different outlines and wall shapes. Straight wall and different undulation as curved, U-shaped, V-shaped, and especially Ω-shaped are found in Poaceae. In intercoastal zone, short cells are of diagnostic importance in form of their presence or absence and their shape. Silica bodies as an anti-feedant agent in the grasses caused enhanced strength and rigidity. By the presence of silica bodies, the water loss via cuticle is decreased. It is especially very functional in tolerance to the lodging, fluctuation in temperature, radiation, and drought stresses. Different shapes of silica are of taxonomic importance. Epicuticular wax is a functional tool in confrontation with the environmental aridity by decreasing the water loss via epidermis surface and stomata. The presence of diketone-tubules, platelets, and longitudinally aggregated rodlets types in the grass family have been documented. The micromorphological variation in different groups of Poaceae taxa in Iran will be discussed to show the taxonomic value of several micromorphological characteristics of the leaf blade, lemma, and palea.

Keywords: leaf epidermis, glume surface, diagnostic features, Iran

IS35 The phylogeny of Rosoideae (Rosaceae) in Iran, based on cpDNA and nrDNA sequenced data

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The present survey deals with phylogenetic analyses of Rosoideae from Iran. A total of 34 taxa from 6 tribes and 4 subtribes of Iranian taxa plus 36 previously sequenced data were analyzed for *trn*L-F, *rpl*32-*trn*L (UAG) PsbA-trnH and nrDNA ITS regions. For data analysis, both Maximum parsimony (as implemented in PAUP) and Bayesian method (using MrBayes program) was used. In all the reconstructed phylogenetic trees, the following clades are given phylogenetic definitions: Colurieae, Agrimonieae, Potentilleae and their subclades. The monophyly of Colurieae, Agrimonieae, Potentilleae were well documented.The current results support circumscriptions of the genera *Geum*, *Agrimonia* and *Aremonia* (presented in Flora of Iran). However, it displays divergence of the genus *Sanguisorba* in to two monophyletic groups (a) *Sanguisorba minor* and three subspecies b) *Sanguisorba officinalis* group) and the union of the genera *Fragaria, Alchemilla, Aphanes, Drymocallis, Sibbaldia* and *Sibbaldianthe* within *Fragariinae* and *Duchesnea, Ivesia , Horkelia* and *Argentina* within *Potentilleae*. In this study, the evolutionary trend of exin sculpturing was discussed.

Keywords: Cladistics analysis, Rosaceae, Colurieae, Agrimonieae, Potentilleae

IS36 Inhibitory effects of some mosses extracts on phytopathogenic fungi *in vitro* and *in vivo*

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Mosses are a group of simple, small and xerophyte plants that have been shown to have anti-cancer, anti-microbial and anti-fungal effects.In order to evaluate the antifungal effects of mosses, the extracts were made

using ethanol, methanol, acetone and distilled water then they were tested against four phytopathogenic fungi *Rhizoctonia solani*, *Fusarium solani*, *F. pseudograminareum*, and *Bipolaris sorokiniana* on PDA medium by using disc-diffusion method and compared with the effects of industrial fungicides Benomyl, Difenoconazole and Tetraconazole. The experiment was conducted with three replications. Finally, data were processed using SAS 9.2 software. Statistical analysis of results was based on Duncan significance test. Differences of $p<0.05$ were considered significant. The results showed that, ethanolic extracts produced significant inhibitory effects on tested fungi. In order to investigate the effect of moss extracts *in vivo*, wheat seeds of "Chamran" cultivar were implanted into moss extract and then transfered into pots containing 1: 10 mixture of soil and soil contaminated with tested fungi. After 35 days, the root and crown of wheat plants were examined. *In vivo* observations had also indicated that, ethanolic extracts can control the root and crown rot significantly.

Keywords: Mosses, Extract, Benomyl, Difnoconazole, Tetraconazole

IS37 A Survey of Moss flora of Zagros Mountains in Khouzestan Province

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Khouzastan Province is situated in South-west of Iran. It covers an area of 63633 km^2, which lies between the latitudes of 29° 57´ N and 33° 00´ N and the longitudes of 47° 40´ E and 50° 33´ E. The elevation varies between sea level in Persian Gulf beaches to 3500 m in Sefidkoh Mountain.For this study, the moss samples were collected from seven location during summer 2018-2020. Samples were collected in paper bags and field data were recorded. The samples were air-dried in room temperature and stored in the standard paper packet. For morphological observations, the samples were soaked in hot water for a few minutes for their revival. Identification of the specimen was made with the help of Smith (2004) Frey *et al*. (2006), Kürschner (2007), ،((Athertonn *et al*., 2010) and Kürschner and Frey (2011). The voucher specimen is preserved in the herbarium of the Ministry of Jihad-e Agriculture ("IRAN") at the Iranian Research Institute of Plant Protection (Tehran, Iran). After field trips in suitable seasons, 12 species belong to 11 genus and six families were identified. One species belonging to Pottiaceae namely *Dialytrichia mucronata* was new to Iran.

Keywords: Mosses, Khouzastan Province, Zagros Mountains, Acrocarpous, Pleurocarpous.

IS38 OMICS approaches towards deeper insight into cellular processes: genome projects and decoding the genomic and transcriptomic data

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Cellular processes are controlled at various levels and consequent of a series of hierarchical processes related to genome, transcriptome, proteome and metabolome ultimately determines the phenotype of an organism. The ultimate aim of genomics and transcriptomics is to identify the structure and function of all the genes of all organisms. In recent years, the emergence of new high- throughput technologies such as Next generation Sequencing (NGS) along with various OMICS approaches has revolutionized molecular biology. Complete genome sequences will provide powerful tools for biologists. The sequences will aid in understanding how gene families have been created, amplified, and diverged, resulting in the creation of new biological activities and specificities. The gene content of related species can be compared to identify which pathways are shared among many species and which are restricted to some parts of the kingdom. The new tools and approaches that are available for investigating gene structure and function have been steadily developed over the past 20 years. Today the molecular tools include various cloning systems like GateWay and TOPO cloning, micro array, high-throughput Next Generation Sequencing, and mass spectroscopy (MS) which led to a great revolution in biology along with gene and genome editing approaches like CRISPR-Cas9. The application of these methodologies results in the generation of very large amounts of data i.e. data tsunami that need to be stored, processed and analysed. On the other hand, these challenges led to the development of various bioinformatics algorithms and it has made the computational biology and big data more prominent. The wealth of data generated by high-

throughput methodologies will advance our understanding of gene structure and function. In addition, the ability to change gene expression in vivo, by using insertional mutagenesis, RNA interference, or other silencing mechanisms, will be crucial in determining the specific function of a particular gene. Therefore, at the present time, techniques are available to identify a specific phenotype. In the past the genome projects were limited to a few organisms such as Arabidopsis, human, rice and wheat, while, with the advent of Next and Next-Next Generation Sequencing technologies, complete sequences of genomes and transcriptoms of many organisms have been released in shorter intervals.

Keywords: Databases, Gene network, Big data, Computational biology, Algorithm

IS39 SARS-CoV-2: genome evolution, possible causes of divergenve and expansion of somelinage, and the pathogenic importance of different variants

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IS40 Prefrontal cortical-hippocampal-amygdala functional loop in memory formation

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The involvement of the prefrontal cortex, the hippocampus and the amygdala in learning and memory processes has been studied over the past 30 years. However, the neurotransmitter mechanisms underlying functional interactions among these brain sites in memory formation are not fully understood. Our studies using animal models suggest that the direct and indirect pathways among the prefrontal cortex, the hippocampus and the amygdala, which form a functionally important loop, may be critically involved in cognitive functions. It seems that the loop activation occurs when the hippocampus encrypts new information to store as long-term memory. The hippocampal projections to the PFC and the amygdala can change their activities to generate synaptic long-term potentiation or depression which is necessary for memory formation. The hippocampus is functionally divided into the dorsal part which is necessary for memory formation and the ventral part which is associated with both memory and emotional behaviors. The prefrontal cortex (PFC) as an important component in the central nervous system plays a key role in long-term and short-term memory. The amygdala connects with the PFC and the hippocampus through the efferent and afferent projections to create long-term emotional memory. The dysregulation of the PFC/hippocampal/amygdala neurotransmission may be a major reason for the memory loss. We found that there is an association between memory formation or impairment with the changes of BDNF/cFOS/CAMKII/CREB signaling pathways in the PFC, the hippocampus and the amygdala. Moreover, the different neurotransmitter systems including glutamatergic, GABAergic, dopaminergic and endocannabinoid systems in these brain areas have critically been involved in the reward-related memory. Taken to gather, these findings support the existence of a functional loop among the PFC, the hippocampus and the amygdala during processing learning and memory.

Keywords: Learning and memory, Neurotransmission, Signaling pathways, Animal models

IS41 Wnt signaling in dopaminergic neuron development and degeneration

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Parkinson's disease (PD) is one of the most common neurodegenerative diseases in elderlies. Degeneration of dopamine-producing cells in the midbrain nucleus of the substantia nigra during years of the disease progression results in PD. Among the signaling pathways, the Wnt pathway have been suggested to modulate the differentiation and survival of dopaminergic neurons, both during embryonic development and adulthood. Activation of the Wnt pathway requires phosphorylation and inactivation of the enzyme glycogen synthase kinase 3 beta (GSK-3β) at serine 9 which leads to the expression of Wnt target genes such as C-myc and cyclin D1. Wnt pathway is activated by variety of ligands, such as lithium and the indirubins, natural alkaloids extracted from the indigo colored plants and molluscs. While lithium is a general activator of the Wnt, the indirubin BIO is a specific inhibitor of GSK-3β, both of which lead to the expression of Wnt target genes. Using the SH-SY5Y cell line with dopaminergic differentiation potential, we showed that lithium enhanced their

dopaminergic differentiation and BIO protected them from toxicity induced by MPP+, a dopaminergic neurotoxin. We have further showed that the effect of BIO is mediated by microRNAs as novel diagnostic and therapeutic candidates for PD. Altogether, Wnt pathway efficiently modulates survival and differentiation of dopaminergic neurons.

Keywords: Parkinson's disease, SH-SY5Y, lithium, 7-BIO, MPP^+

IS42 Role of non-coding RNAs in morphine function

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Morphine is widely used in medicine to control moderate to severe pain. However, long-term administration of morphine is accompanied by unfavorable phenomena like tolerance and dependence to the drug. The exact molecular mechanisms underlying morphine tolerance and dependence have remained unclear. The effects of morphine are mediated via its binding to opioid receptors, which are distributed throughout the central and peripheral nervous systems. Further, data also indicates that alterations at other neurotransmitter receptors and downstream signaling pathways are also involved in morphine tolerance and dependence. Changes in gene expression have been reported in different brain areas, including the midbrain, striatum, hippocampus, and cortex following tolerance and addiction to morphine. However, central epigenetic changes during tolerance and addiction to morphine remain unclear. non-coding RNAs (ncRNAs) constitute the majority of the transcriptome in the brain and play essential roles in regulating cellular processes. ncRNAs are commonly linear molecules that are divided into housekeeping and regulatory subgroups. The former includes ribosomal (rRNA), transfer (tRNA), small nuclear (snRNA) and small nucleolar (snoRNA) RNAs that are ubiquitously expressed and contribute to structural and functional homeostasis. On the other hand, regulatory ncRNAs are involved in gene regulation and are typically divided into two categories based on their length. The first category includes RNAs with lengths fewer than 200 nucleotides; these RNAs include micro-RNAs (miRNAs), small interfering RNAs (siRNAs), and RNAs associated with the Piwi protein or piRNAs. ncRNAs containing more than 200 nucleotides are referred to as long ncRNAs (lncRNAs), which are involved in a variety of biological processes, including gene expression. It is also worth noting that circular RNAs (circRNAs) are a unique class of ncRNAs covalently-linked ends with having more than 200 nucleotides that are produced due to a back-splicing process. Reports during the past two decades indicate the involvement of ncRNAs in addiction to morphine, alcohol, methamphetamine, cocaine, and heroin. Our data indicate the involvement of different miRNAs, including miR-124, miR-133, miR-339, miR-365. Others and we have also shown that changes in the expression of long non-coding RNAs such as BC1, H19, MALAT1, and MIAT1 as well as circular non-coding RNAs such as CircOprm1 in different areas of the brain and spinal cord after morphine treatment in rats, which indicate the involvement of these RNAs in the effects of morphine. It can be concluded that the analgesic effects of morphine and its adverse effects such as addiction resulted from its repeated use are mediated by changes in the expression of various genes and non-coding RNAs have a significant role in the effects of morphine due to their regulatory role in regulating gene expression processes in the nervous system. Therefore, they should be given more attention in future research and their performance in morphine function needs further investigations.

Keywords: Pain management, Tolerance, Addiction, Gene regulation, non-coding RNAs

IS43 Selection of competent oocytes for assisted reproductive technologies

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Oocyte competence or quality have defined as the ability of oocyte to resume meiosis, cleave following fertilization, develop and differentiate into blastocyst stage, induce pregnancy and finally bring healthy offspring. Oocyte maturation is one of the most important processes of oogenesis, since it leads to the generation of "competent fertilizable oocytes". Oocyte maturation include nuclear maturation, cytoplasmic maturation, and Epigenetic maturation which is precisely regulated by molecular factors. Invasive and noninvasive methods are commonly used to select developmentally competent oocytes that can improve the take-home baby rates in assisted reproductive technology (ART) centers. One of the noninvasive methods conventionally utilized to

determine competent oocytes is the morphological analysis of cumulus complex, first polar body, zona pellucida, perivitelline space, meiotic spindle, and ooplasm. however, all morphological criteria that are currently used for the grading and screening of oocytes are not able to eliminate the subjectivity. Despite recent studies of the molecular factors related to oocyte quality, it is technically difficult to develop an index based on these factors, and new indices that reflect intracellular conditions are necessary. The numerous transcriptomics, proteomic and metabolomic studies have been conducted in the follicular fluid and follicular cells (granulosa and cumulus cells) in order to find non-invasive biomarkers of oocyte quality. Recent studies have uncovered the presence of cell-secreted vesicles in follicular fluid. Moreover, these cell-secreted vesicles contain small non-coding regulatory RNAs called microRNAs, which can be shuttled between maturing gametes and surrounding somatic cells. In humans, it is known that extracellular microRNAs of follicular fluid are associated with fertilization ability and early embryo quality. Recently, oocyte condition can be evaluated noninvasively using a temperature imaging system. The dynamic changes in the cytoskeleton and mitochondrial activity are considered to contribute to intracellular thermal variations. Intracellular temperature in mature oocytes was higher in fresh oocytes immediately after PB1 extrusion, and the temperature decreased with time after polar body release. The differences in oocyte intracellular temperature can correlate with developmental competence. Fresh oocytes had high-temperature regions localized around the cell membrane and around the spindle. Further studies should evaluate the link between temperature and cellular phenomena to establish its use as an indicator of quality.

Keywords: Oocyte quality, oocyte maturation, follicular fluid, microRNA, temperature

IS44 A review on the role and importance of oribatid mites, taxonomy and status of species reported from Iran

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Acari (Ticks & Mites) are an important group of arthropods, and along with scorpions, tarantulas, spiders, etc. situated in the class of Arachnida. These tiny creatures are cosmopolitan, and so far more than 50,000 species have been reported worldwide, and it is estimated that the number of mite species reaches half a million. Among the mites, Cryptostigmata, which also known Oribatida (Order Sarcoptiformes), as one of the largest groups, occupies the predominant fauna of most soils. So far, more than 11,000 species and subspecies of these mites have been described. These mites benefit from a wide range of food and feed on fungi, mosses, lichens, plants and sometimes carrion, and are actively involved in the decomposition of organic matter and the formation of soil nutrients and soil texture. In addition to the effective role of these mites in the decomposition of organic matter, their importance as bioindicators in soil and air management, control of some pests, diseases and weeds, as well as being in the cycle of transmission of animal parasites as intermediate hosts, is considered. Is. However, unfortunately, in our country, no comprehensive scientific research has been done on the taxonomy of these mites, and only a few species have been reported in the form of master's and doctoral dissertations from different parts of the country. At present, about 400 species of oribatid mites are reported from Iran, of which approximately 30% belong to the primitive group (Macropylina) and the rest to the higher group (Brachypylina). The family Oppiidae is known as the richest family in terms of number of species. Among the species reported from Iran, about 40 new species have been described, most of which have been named "Iran". Due to the diversity of habitat and climate in Iran, it is expected that there are many unknown species in this vast and ancient land.

Keywords: Arthropod, Cryptostigmata, fauna, Distribution, taxonomy

IS45 An overview of assisted reproductive technology procedures

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Infertility is a major issue in the lives of couples who suffer from it and endure a lot of social and psychological pressures. Unfortunately, 1 to 6 couples remain in infertile societies and 10% of them need assisted reproductive technology. The birth of Louis Brown in July 1978 with the help of this technology was an important turning point for infertile couples, which is now considered as an important and internationally recognized treatment

option. Since then, significant improvements have been made in the knowledge of reproductive biology and biotechnology. The outcome of treatment is not very satisfactory and the average pregnancy rate worldwide is 30-34%. The rate of congenital anomalies and abnormalities is slightly higher than the normal population, which is related to a woman's age and has nothing to do with this treatment. Assisted reproductive techniques include ICSI, IUI, IVF, ZIFT, GIFT, IVM, PGD, PICSI, assisted hatching and embryo cryopreservation. In vitro fertilization and intracytoplasmic injection are the most common methods of treating infertile couples and allow artificial insemination outside the body. Indications for IVF include absent fallopian tubes or obstruction of bilateral. Endometriosis, male infertility, secondary infertility, unexplained infertility and genetic diseases leading to miscarriage or abnormal birth. The injection of an immobilized mature sperm into the cytoplasm of a mature metaphase II oocyte is known as intracystoplasmic sperm injection. Indications for ICSI include recurrent failure in IVF, severe oligospermia, severe asthenospermia, sperm obtained by TESE, PESA, TESA methods in obstructive and non-obstructive azoospermia, and frozen sperm. The steps of assisted reproductive techniques include ovulation stimulation, ovarian response assessment, oocyte retrieval, sperm preparation, IVF / ICSI, and embryo transfer.

Keywords: ICSI, IVF, Severe Oligospermia, Non-obstructive azoospermia, Unexplained infertility

IS46 Exosome application in cancer diagnosis and therapy

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Exosomes are natural nanovesicles with 50-100 nm sizes, which contain proteins, nucleic acids, and microRNAs. Exosomes originate from multivesicular bodies (MVB), which release their contents outside the cell. These nanovesicles can fuse with the membrane of the recipient cell to pass their information. Exosomes can be used as diagnostic biomarkers since they have a broad range of macromolecules and are proper candidates to provide information about the tumor from which they were originated. Moreover, Exosomes can be used as nanocarriers to deliver therapeutics to the target cell or tissue, such as tumors. Since these nanocarriers are naturally isolated from body cells, they exert fewer side effects than synthetic nanoparticles.

Interestingly substances carried by exosomes also have therapeutic effects on some lesions. Exosomes' immunogenicity is very low, resulting in their low cytotoxicity. Since exosomes are derived from cell membranes, they are not captured by the reticuloendothelial system. Therefore, exosomes' half-life in the blood is longer compared to other nanocarriers. Also, many studies have found that exosomes can spontaneously migrate toward unhealthy tissues. Exosomes containing chemotherapy reagents or phytochemicals such as curcumin or anti-tumor miRNAs were effective in inhibiting tumor growth. To conclude, exosomes hold high promises for cancer diagnosis and therapy.

IS47 The effect of green nanoparticles on the aggregation of protein

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The aggregation of proteins, including amyloid fibril formation, is the cause of many age-related diseases encompassing Alzheimer's (AD), Parkinson's (PD) and cataract. These human diseases involve the conversion of a specific protein or protein fragment from a soluble native state into insoluble amyloid fibrils that are deposited in a variety of organs and tissues. Nanoparticles interfere with protein amyloid formation and can significantly influence the nucleation and aggregation process of peptides. In this study protective ability of synthesize green nanoparticles of plant origin, using an extract derived from natural products that are powerful antioxidants, against amorphous aggregation and amyloid fibril formation of proteins are discussed. Green synthesis nanoparticles had a potential inhibitory effect on the aggregation of reduced protein in a concentration-dependent manner. This inhibitory effect of nanoparticle probably caused by decreasing the rate of fibrillation through surface absorbing of free monomeric peptides and prevents amyloid fibril formation. The surface properties of the green nanoparticle and the interaction between both nanoparticle and protein determine the potential inhibitory effect of green nanoparticles in preventing the aggregation of reduced protein. Thus, green synthesized nanoparticle as nano chaperone, can be used as a therapeutic approach in the treatment of amyloid disease such as Alzheimer disease.

Keywords: Nanoparticle; Alzheimer disease; Amyloid; chaperone

IS48 Herbal research: Important forgottens

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The Iranians were the first tribes who discovered the properties of medicinal herbs. The history of Persian medicine dates back to three thousand years ago and many centuries before Christ. The school of Zoroaster (Mazdayasna) existed long before the medical schools of Greece. The 2500-year antiquity of Simorgh is more than some medical symbols in the world and Greece.

According to Cyril Elgood, the Iranians taught the Greeks the fundamental of Greek medicine to the Greeks. Cyril Elgood and John Bernal cite the unfamiliarity with the Pahlavi or other ancient Iranian languages, and the destruction of ancient Iranian books as the reasons for the neglect of Persian medicine. It seems that the unfamiliarity and alienation with historical sources and scientific-cultural history still exist in the Iranian scientific community. The history of Iranian traditional medicine as well as Iranian endemic herbs have not been properly considered by Iranian researchers. While in modern ethnopharmacology, familiarity with historical sources is known as one of the important ways in discovering of natural-based drugs.

The safety of all herbal medicines due to their natural origin is a misconception. Biological and chemical contaminants, drug interactions, and misidentification of medicinal herbs are among the dangers associated with using herbs. However, these items, perhaps for economic reasons, are not the main subject of all herbal research. Nevertheless, there are items with impact on the validity and reproducibility of the results of herbal research and studies, such as the correct identification of medicinal herbs, scientific nomenclature, and detailed explanation of experimental methods (such as location and source of plant samples or the processing steps of herbs). These important details are also of forgotten in some publications on herbal medicines, although there is no extra cost to mentioning them. Paying more attention to the education and research of graduate students and paying attention to the above-mentioned items can have a significant impact on the international validity of herbal research.

Keywords: medicinal herbs, validity, reproducibility, scientific nomenclature

IS49 Drug Delivery Using Nanoparticles

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Various nano-sized protein and lipid complexes are being investigated as drug delivery systems. The encapsulation of more than one drug in a single nanocomplex carrier could enhance the therapeutic potency and afford synergistic therapeutic effects. In this study, we developed a novel protein-lipid nanocomplex as a controlled drug delivery system for two important cancer drugs, doxorubicin (DOX) and mitoxantrone (MTO). Apoferritin (AFr) functionalized with folic acid (FA) was used to encapsulate DOX to create the targeted protein nanocomplexes (TPNs). The encapsulation was achieved by the disassembling of apoferritin into subunits at pH 2 followed by its reformation at pH 7.4 in the presence of the DOX drug. The second drug, MTO, was loaded into the cationic solid lipid nanoparticles (cSLN) to form the liposomal drug nanocomplex particles (MTO-cSLNs). Two complexes were then assembled by tight coupling through ionic interactions to obtain the final drug delivery system, the dual targeted protein-lipid nanocomplexes (DTPLNs). It is notable, the toxicity of the anticancer drugs can be decreased by utilizing nanocarriers and targeted drug delivery systems. UV-Vis and fluorescence spectroscopy were used for structural characterization of TPNs and DTPLNs. Transmission electron microscopy (TEM) was used for comprehensive analysis of the final DTPLNs. We confirmed that the DTPLNs display desired time-dependent and pH-dependent drug release behaviors. We also demonstrated the improved anti-cancer efficacy of DOX and MTO in their encapsulated DTPLNs as compared to their free forms. Our results provide promising prospects for application of the DTPLNs as efficient drug delivery systems.

Keywords: Apoferritin; Doxorubicin; Mitoxantrone; Cationic solid lipid nanoparticles; Dual targeting; pH-responsive

IS50 A review on history and taxonomic status of bats in Iran

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Bats (order Chiroptera) are one of the most diverse, abundant and widely distributed orders of mammals and the only one with the capacity of powered flight. Nearly, 1400 species of 230 genera and 21 families can be found all over the world except in the northern and southern polar areas, representing approximately 20%of all mammalian species. Chiroptera can be divided into the two suborders Megachiroptera (old world fruit bats) are represented by only one family with 46 genera and 191 species and Microchiroptera (echolocating bats) comprise 20 families include 184 genera with 1210 species. Despite the importance of bats in providing ecosystem services as well as natural hosting reservoirs, so far the least study has been done on them compared to other mammals. Diverse physical geography and close vicinity of the Iranian plateau to the major biogeographic zones has caused this country to possess a variety of fauna unequaled in other parts of the Middle East. Bat biodiversity, like many other taxa is considerably high. Bats of Iran have been thoroughly studied since long time ago, both by Iranian and foreign zoologists. By the present taxonomic arrangement finally, 51 species of bats have been reported from Iran. These bats belonging to the families of Pteropodidae (1 species), Rhinopomatidae (3 species), Emballonuridae (2 species), Rhinolophidae (5 species), Hipposideridae (3 species), Vespertilionidae (34 species), Miniopteridae (1 species), and *Molossidae* (2 species). However, our knowledge about distribution and abundance of bats in Iran is far from adequate. For example from the 51 species of bats reported of Iran, six species have been reported only once, 17 species are known from less than 10 localities and only seven species are known from more than 50 localities. There may be further possibility to observe more bat species to occur in Iran because there are several species reported from neighboring countries in bordering areas to Iran. These species include *Rhinolophus lepidus* from Afghanistan to be seen in the northeast (Khorassan province), *Plecotus turkmenicus,* and *Rhinolophus bocharicus* from Turkmenistan to be present in similar habitats of NE and *Pipistrellus rueppellii* from Iraq to be found in western Iran. Also, *Myotis myotis* occurs in western Turkey, It's occurrence in NW Iran is possible. Only recently, intensive studies on bats have provided opportunities to make available new data on the taxonomy and ecology of bats. Future studies on bat research require much attention on involving ethical values in scientific studies, their importance in providing ecosystem services, expanding molecular studies, a survey of their viruses and their relationship to emerging diseases, re-organizing current conservation assessments, evaluating the effect of land use alternation, global warming and caves destruction on the Iranian bats, and also to enhance public attention to conservation oriented research projects.

Keywords: Mammalia, Chiroptera, Taxonomy, Conservation, Viruses and emerging diseases

IS51 Animal models in physiological studies: Challenges and prospects

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The animal model is widely used in physiology and pharmacology research. Although the use of animals in research can be an advantage for other animals, it is more useful for the advancement and improvement of human life. Even in many investigations, animal studies is considered as an introduction to clinical trials. But first of all, the use of animals as research tools requires to make a mutual relationship between humans and animals, so, ignoring safety and health and neglecting the ethical considerations of working with animals can have problematic consequences. From the past until now, these models have been divided into different groups, including experimental models, breeding and transgenic, etc., but undoubtedly any research at the beginning should have a proper reason for the use of the animal model, and the ethical and legal concerns of working with animals should be considered (such as a place for keeping and free access to water and food and many physical and environmental factors ..), which may affect the physiological and behavioral responses of the animal. The first models may have simulated part of the disease, but over time most of the key features of the diseases were replicated in the models to make them appear to be very creative and useful. However, due to limitations such as mismatching of animal and human, these models have been revised many times and with recent advances, computer simulations, and 3D printing of biocompatible materials with the help of bio 3D printer as a new

technology have replaced animal models and through eliminating the previous restrictions can be used to design and build cellular constructions and living components.

Keyword: Animal model, Ethical considerations, 3D Printer

IS52 Royan Kidney Group (RKG): Cells Therapy and Tissue Engineering in Renal and Urinary Tract Diseases: Stem cells as a new trend

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Kidney and urinary tract research group is one of the established groups in Royan Institute, and at present, most of its activities have focused on the administration cell therapy in patients with renal transplantation, acute and chronic renal failure and urinary incontinency. Kidney and urinary tract research group started its activities in the basic and clinical sciences by the research charity institute support from 2012. Our final goal in kidney group is to use the cell therapy as an alternative therapeutic for treatment of different renal disease. Based on this, the group's strategy has mainly focused on the following topics: 1- Development and generate of renal stem cells and differentiation of pluripotent stem cells into renal cells, 2- Create animal models of acute and chronic renal failure and transplantation of stem cells for therapeutic effects, 3- Transplantation Immunology and provided solutions for clinical studies using animal models of transplantation, 4- Understanding the mechanisms involved in the pathogenesis of polycystic kidneys to aid to the healing process of the patient and 5- Cell therapy in urinary tract diseases. Several projects have designed related to with different renal cells and their transplantation in animal models of acute and chronic renal failure. According to above goals, after equipping the non-human primate animal's lab, the model of renal failure was established in these animals as a way to study the effects of mesenchymal stem cells (MSCs) transplantation in decrease of inflammation and increase of regeneration. The results show that injection of bone marrow MSCs (BM-MSCs) as intra-renal vascular effectively reduce cisplatin-induced acute renal failure. Although our histological findings did not show significant differences between cell injected group with the control group, but it seems to reduce inflammation and prevent apoptosis through cell immune regulatory mechanisms, reducing symptoms and improving quality of life of treated animals. Also, there are also clinical trials using MSCs in acute and chronic renal failure. Differentiation of pluripotent stem cells into renal cells, is be designed for differentiation of embryonic stem cells into tubular cells. The proposal has been trying to plan the initial differentiation of pluripotent cells into renal progenitor cells. We are also trying to provide the normal kidney tissue engineering scaffolds. In this study we want to transfer of progenitor cells on acellular renal tissue scaffold of monkey kidney and evaluate the renal function with new cells. Immunomodulatory properties of mesenchymal stem cells are evaluating for kidney transplantation. The effects of immune regulation will be evaluated by transplant of different sources of mesenchymal stem cells such as bone marrow or adipose tissue in animal models. Our goal is decrease the use of immunosuppressive drugs in patients receiving kidney transplants by administration of mesenchymal stem cells. Mutation analysis of coding region in PKD1 and PKD2 genes in autosomal dominant polycystic kidney disease is other study to detect the mutations in Iranian patients with renal polycystic disease. There are also clinical trials and several projects using MSCs in animal model of polycystic kidney disease. In urinary tract diseases field, almost 30 patients have been treated in the clinical trial for evaluation of the safety and efficacy of intramuscular injection of muscle stem cells in improving incontinence and the primary results show that this method can improve the patients 'symptoms without any special complication.

IS53 Novel Cellular Strategies for Generation of Human Cardiomyocytes in Vitro

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The human heart has very limited regenerative capacity, and the low rate of carcinogenesis is not sufficient to compensate for the enormous loss of cells after injury such as myocardial infarction. Despite advances in cardiac treatment, myocardial repair remains severely limited by the lack of an appropriate source of viable cardiomyocytes (CMs) to replace damaged tissue. Human pluripotent stem cells (hPSCs), embryonic stem cells (ESCs) and induced pluripotent stem cells (iPSCs) can efficiently be differentiated into functional CMs

necessary for cell replacement therapy and other potential applications. The number of protocols that derive CMs from hPSCs has increased exponentially over the past decade following observation of the first human beating CMs. A number of highly efficient, chemical based protocols have been developed to generate human CMs (hCMs) in small-scale and large-scale suspension systems. To reduce the heterogeneity of hPSC-derived CMs, the differentiation protocols were modulated to exclusively generate atrial-, ventricular- and nodal-like CM subtypes. Recently, remarkable advances have been achieved in hCM generation including chemical-based cardiac differentiation, cardiac subtype specification, large-scale suspension culture differentiation, and development of chemically defined culture conditions. All highlight the possibility that hPSC-derived CMs may be very close to implementation in cell-based replacement therapies and other applications. Herein we review recent progress in the in vitro generation of CMs and cardiac subtypes from hPSCs and discuss their potential applications and remaining limitations.

Keywords: Heart Regeneration, Human Pluripotent Stem Cells, Direct Reprogramming, Cell Therapy

IS54 Wnt signaling in development and stem cell control

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The Wnt signaling pathway is one of the central signaling pathways regulating early vertebrate development. The role of this signaling pathway on the specification of embryonic axes, especially in *Xenopus* embryo, is well documented. In recent years, it has become clear that the Wnt pathway also regulate many aspects of stem cell behavior and adult tissue homeostasis. Since stem cells are an ideal candidate for cell therapy, it is important to identify the signaling network that controls the activity of these cells. Our recent works have shown that activation of Wnt/β-catenin signaling pathway in adipose tissue-derived mesenchymal stem cells (AD-MSCs) resulted in a decrease in bone matrix synthesis and expression of osteogenic specific genes in these cells. Moreover, while the expression of *BMP* and its target gene (*ID3*) was decreased, the expression of BMP antagonist, *Noggin*, was significantly increased in Wnt activated AD-MSCs. Altogether, our recent results suggest that activation of Wnt signaling in osteogenic induced AD-MSCs inhibits osteogenic differentiation through inducing the expression of BMP antagonist. These results provide further insight into the role of Wnt signaling in stem cell differentiation.

Key words: Mesenchymal stem cells, Wnt signaling pathway, osteogenic differentiation

IS55 Wolbachia in scale insects: A unique pattern of infection prevalence, high genetic diversity, and host shifts

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Wolbachia is one of the most successful endosymbiotic bacteria of arthropods. It is a master manipulator, modifying its hosts' biology in many ways to increase its vertical (maternal) transmission. Wolbachia can also undergo host shifts that can be mediated by ecological vectors such as shared host plants or parasitoids. Here, I screened 687 specimens from 151 scale insect species that were mostly collected in Asia and Australia for Wolbachia infection. I fitted the distribution of within-species prevalence of Wolbachia to our data and compared it to distributions fitted to an up-to-date dataset compiled from surveys across all arthropods. In contrast to other hemipteran groups, the prevalence of Wolbachia in scale insects follows a distribution similar to exponential decline (most species are predicted to have low prevalence infections). By conducting Illumina pooled amplicon sequencing of 59 infected scale insect samples and 16 direct associates of scale insects (including wasps and ants), I determined 63 Wolbachia strains in these species belonging to supergroup A, B and F. I observed a lack of congruency between Wolbachia and scale insect phylogeny and identified several putative host-shifts events. Finally, I fitted a Generalised Additive Mixed Model (GAMM) to assess factors influencing Wolbachia sharing among scale insect species. I found strong effects of host phylogeny without any significant contribution of host geography. There were high rates of Wolbachia sharing among closely related species (i.e., host-shifting mostly happens between species of the same genus) with a sudden drop-off in sharing with increasing phylogenetic distance. This finding can explain a large number of reported Wolbachia host-shifting among congeneric species.

IS56 Molecular data proves successful in resolving taxonomy, phylogeny and biogeography of Pompilidae (hymenoptera)

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During recent years, using molecular data for taxonomic questions has proved successful. Pompilids are difficult hymenopteran group that are understudied in Australia. Here we used a combined dataset of Mitochondrial, nuclear and UCE markers to delineate two closely related genera of Heterodontony and Cryptocheilus. We also used DNA data for species delimitation and biogeography reconstruction. The results suggest that Heterodontonyx distribution is mainly limited to Australia whereas Cryptocheilus is distributed in Palearctic, nearctic, Africa and Oriental region. Three new potential species discovered using PTP and bPTP plus BioGeoBEARS analysis suggest that Australian species may have oriental origin.

Keywords: Pompilid phylogeny

IS57 Mass production of live food and their by-products in semi-arid areas

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The semi-arid area possesses several key factors such as sun light, suitable temperature, nutrient rich soil, saline or brackish water, land availability which make it candidate for certain organisms biomass production. In this talk, production of unicellular algae, Rotifer, some crustacean, insect and fish will be discussed. The priority is given to job enhancements for local community using traditional experiences and advanced methods in closed culture systems. The advantages of using locally available species greatly help the sustainable use of resources and their conservation in the nature. In addition, due to unique adaptation of species, there is an opportunity to establish a Bio-Bank for genetic and natural resources. Apart from biomass production, the by-products of these farms are used in pharmaceutical and medicinal industries and green fuel production.

As an example, some comparative added values to land use, level of biomass production and economical investments from other countries achievements are given.

IS58 A review on the effects of the herbal active molecules, pectins and flavonoids on the mammary gland epithelial cells and cancer cell; targeting these cell in cancer cells

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Human History always was related to the use of herbal medicine which was the main treatment of diseases. Chemical drugs applying became popular along with developing science and industry. As such drugs contained side effects, using herbal medicine resume.

There are two kinds of herbal effective substances: the first one is the primary metabolic substances such as polysaccharides (pectins). The other is the secondary metabolic substances as flavonoids.

We assessed the effects of these herbal effective molecules on cancerous and healthy cells. The polysaccharides (pectins) were studied on GH3/B6 cells which are capable of secret Prolactin and Growth Hormone. The data were shown the effect of pectins on these cells.

In the second group, we studied the flavonoid named Salvigenin. In cancer cells, Salvigenin could link to P53 following cycling-CDK linkage to inhibit the cell cycle in G,M and S phase. In such conditions, P53 plays an apoptotic role while it plays an anti-apoptotic role in normal cells. Our results declared that salvigenin accompany magnetic nano-particles promoted the apoptotic effects of this molecule alone. It is worth mentioning that such effects were not seen in normal cells. The PLGA synthetic polymer with sedimentation method used to prepare Fe3O3@mPEG-b-PLGA.

IS 59 The effect of Mouse Embryonic Stem Cells (mESCs) transplantation on ischemic tolerance in animal stroke model

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The number of people affected annually by stroke, actually over 2 million worldwide. This is because of the increase in the mean population age, the persistence of unhealthy habits, and the emerging risk factors that will affect young patients particularly. The previous studies have shown that cell transplantation can improve neurological function after cerebral ischemia and therefore extend the therapeutic time window for intervention. The development of stem cell-based therapies for cerebral ischemia aims to replace lost neurons and/or to prevent cell death. Embryonic Stem Cells (ESCs) are a good source for cell therapy and regenerative medicine. Mouse Embryonic Stem Cells (mESCs) possess stem cell properties, can be cultured in abundance in vitro and contains an inexhaustible, noncontroversial source of stem cells for therapy. 35 adult male rats weighing between 300-250 grams were used. The rats were divided into 3 groups. Control, sham and Mouse Embryonic Stem Cells (mESCs) transplantion-recipived groups. Rats of Mouse Embryonic Stem Cells (mESCs) transplantion-recipived were divided into 2 categories for evaluation of infarct volume and neurological deficit scores. In the control group, only the effect of cerebral ischemia surgery and in the sham group, the effect of injection of Mouse Embryonic Stem Cells medium (non-ischemic and transplantation) were evaluated. In the control and Mouse Embryonic Stem Cells (mESCs) transplantion-recipived groups, the rats were subjected to 60 min of right middle cerebral artery occlusion (MCAO). In the present study, Mouse Embryonic Stem Cells (mESCs) were transplanted into right rat's striatum by using stereotaxic surgery. After 7 days pretreatment, the rats were subjected to 60 min of right middle cerebral artery occlusion (MCAO). After 24 h ischemia induction, neurological deficit scores (NDS) and infarct volume (IV) in total, cortex, piriform cortex-amygdala, and striatum areas of hemisphere were assessed. In this study, a significant reduction in neurological defects was observed in the Mouse Embryonic Stem Cells (mESCs) transplantion-recipived compared to the control group. The volume of infarction was significantly lower in the Mouse Embryonic Stem Cells (mESCs) transplantion-recipived group compared to the control group in the striatum, cortex and piriform cortex-amygdala. For the first time, the present results indicate that transplantation of Mouse Embryonic Stem Cells (mESCs) before ischemia induction resulted in a significant reduction in NDS and IV, in comparison with the control group. Our study showed that Mouse Embryonic Stem Cells (mESCs) can protect neural cells against undesirable impacts of cerebral ischemia. It seems that Mouse Embryonic Stem Cells (mESCs) due to exerts decremental effect on ischemic damages.

Keywords: Cerebral Ischemia; Embryonic Stem Cells (ESCs); middle cerebral artery occlusion (MCAO); Infarct volume (IV); Neurological Deficits.

IS60 Cerebral folate and cerebrospinal fluid: essential components of normal brain development

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The cerebrospinal fluid (CSF) system has been largely ignored as a physiological fluid of any importance. However, CSF is made specifically for the cerebral cortex from the initiation of cortical development and its production continues throughout life. CSF has been shown to be a growth medium for brain stem cells and has also been shown to be essential to normal migration of cells as the cortex develops. Many conditions of poor brain development and neuropsychiatric conditions have been associated with abnormalities in the fluid system and hydrocephalus, the extreme of these, has been shown to dramatically affect cerebral folate supply. In this talk I will present evidence for the critical role of CSF and cerebral folate in the development of the cerebral cortex and how this can go wrong

in the aetiology of some neurological conditions. Addressing this specific cerebral folate issue, which is independent of folate status in the rest of the body, can prevent or treat such conditions.

IS61 Novel strategy for reduction of morphine dose in pain relief: the underlying mechanisms

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Pain, an unpleasant sensory and emotional experience, is a wide prevalence syndrome impairing different aspect of patient's life quality and associated with the economic and sociality burden. Morphine is one of the most well-known and potent analgesic agents for treatment of acute or chronic pain; however, it can also induce various side effects. Thus, finding new treatment and mechanisms for pain management as well as drugs which potentiate the analgesic effects of low doses of morphine and reduce its side effect will be good strategies. Nociceptors transmit information about noxious stimuli from mechanical, thermal, and chemical sources to the central nervous system and higher brain centers via electrical signals. Nociceptors express various channels and receptors including voltage-gated sodium channels (VGSCs), voltage-gated sodium channels (VGCCs), transient receptor potential channels (TRP channels) and NMDA receptors which inhibition or alteration of these pain targets can attenuate the pain response. The other potential new targets for pain relief are miRNA replacement therapy and nanomedicine approach. Also, combining a suboptimal dose of morphine with another drug providing additive analgesic effects with less side effect will be useful method for pain management. The molecular players in the above mentioned approaches are diverse and complex. Thus, it can be concluded that the future of pharmacological pain therapies will be multidirectional.

Key words: Pain relief; Morphine; Side effect; Nociceptors

IS62 Investigation of the effect of point mutations on human transthyretin protein structure and aggregation

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In cell proteins will be synthesized away the nascent chain to folded state. For almost all proteins, based on appropriate conditions, there would be an aggregated state, generally called amyloid can lead to neurodegenerative diseases such as Alzheimer's and Parkinson's diseases. Generally, aggregations causing these pathological conditions are initiated from intrinsic disorders (e.g., mutations). Transthyretin, a tetrameric transporter protein that in its monomeric form can self-associate to shape amyloid-beta aggregation is one of these proteins. All the point-mutations that can expose buried hydrophobic region, unstable tetrameric formation, and ultimately cause aggregation can lead to pathological conditions such as Transthyretin amyloidosis disorders or transthyretin amyloid cardiomyopathy (TAC). This study focuses on producing and isolating recombinant human transthyretin in *E.Coli* by making specific amino acid alternation via site-directed mutagenesis. To evaluate protein structure and aggregation, some techniques such as turbidity, mass spectrometry, dynamic light scattering (DLS), fluorescence, circular dichroism (CD), and X-ray crystallography have been widely used. Results show that a W41F protein mutation in transthyretin leads to intense instability and amyloid fibril accelerated formation. In contrast, W79F protein mutation shows no sensible structure or stability alternation. Changes in protein sequence and structure can affect properties such as hydrophobicity, secondary structure propensity, and charge. These changes in the way of increasing the hydrophobicity or polypeptide propensity to convert from alpha-helix to beta-sheet and decreasing the total surface net charge of protein can increase the aggregation propensity.

Keywords: Amyloid-β, Protein folding, Neurodegenerative diseases, Transthyretin, Intrinsic disorders

ORAL PRESENTATIONS

CO1 The effect of niosome nanoparticles encapsulating stevia extract on the expression of TNF- a and IL-6 genes in type2 diabetic model induced by intravenous injection of streptozotocin in male rats

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Today, diabetes has spread and the drugs used so far have not been completely effective. Therefore, although natural compounds have fewer side effects than chemical compounds, the treatment of diabetes has advanced towards these methods. Therefore, the aim of this research project is to use Stevia Newsome to increase drug efficacy in male diabetic rat models. The purpose of this study was to the effect of niosome nanoparticles encapsulating stevia extract on the expression of TNF- a and IL-6 genes in type2 diabetic model induced by intravenous injection of streptozotocin in male rats. In this study, 40 Wistar rats with an average weight of 200-250 g were used. They were divided into 4 groups including healthy control, diabetic control (sham), stevia, and niosome stevia. Mice received daily stevia and niosome stevia at a dose of 500 mg / kg by gavage for 30 days after diabetes. Forty-eight hours after the last treatment time, the rats in each group were anesthetized and their liver tissue was removed and real-time PCR was performed to examine the TNf- a and IL-6 genes. Streptozotocin injection significantly increases blood sugar compared to the control group. Injection of stevia with nanoniosome also reduced blood sugar to the control group ($p < 0.001$). Decreased expression of inflammatory factors (TNF- a and IL-6) ($P < 0.01$). It can be stated that one of the effects of stevia is the effect on gene expression and the improvement of diabetes, and during this study, the groups that received the drug in the form of niosome further improved this and reduced the expression of the gene. Niosome also produces a better and more effective effect.

Keywords: Diabetes - Stevia – TNF-a gene – IL-6 gene –Stevia

CO2 The effect of tobacco extract as a biological elicitor on the growth and production of terpenoids of the medicinal fungus *Ganoderma lucidum*

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The medicinal fungus *Ganoderma lucidum* has been used in traditional East Asian medicine for thousands of years to treat diseases. Studies show that terpenoids inhibit the growth of SW620, 95-D, and MCF-7 cancer cells. Despite the many properties of terpenoids, their use limited due to low production and difficult extraction. One way to increase the production of fungal secondary metabolites is to use elicitors in fungal culture media. The addition of tobacco extract as an inducer of apoptosis and p450 can increase the production of terpenoids. This study aimed to evaluate and optimize tobacco extract effects on the growth and terpenoid production of *Ganoderma lucidum* CCGMC 5.616. After five days of culturing in YPD medium, terpenoids extracted using chloroform from dried mycelium. The tobacco extract was prepared from the dried leaves of *Nicotiana tabacum*. Tobacco extract in three concentrations (0.1, 0.4, 0.7 mg/L) was added to the fungus culture medium on the seventh day, and the mycelium was isolated after 14 days. The effect of two variables of concentration and addition time of tobacco extract on growth and production of terpenoids optimized by the response surface method. The results show that the addition of tobacco extract to the fungal culture medium inhibits cell growth. Production of terpenoids increases by 60% with the addition of 0.1 mg/L of tobacco extract. The response surface method analysis showed that both variables had significant effects ($p \leq 0.05$) on growth and terpenoid production. Most terpenoids are produced when cells are exposed to 0.2 mg/L of tobacco extract on the fourth day. In all samples treated with tobacco extract, the dry weight of mycelium increased compared to the control.

The optimal amount of terpenoid production was 260.5 mg/g dry mycelium. The results of this study can be used to increase the production and effectiveness of terpenoids.
Keywords: Elicitor, *Ganoderma lucidum*, Tobacco, Triterpenoids

CO3 Evaluation of oral administration of probiotic isolated from dairy products in mice

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Consumption of probiotic microorganisms in the effective doses shows positive impacts on the health. In this study, resistance to papain and lysozyme and the effect of oral administration of 4 probiotic isolates from dairy product were evaluated on mice. The tested-isolates were SUBC2; *Enterococcus faecium*, SUBC4; *Lactobacillus plantarum*, SUBC5; *Enterococcus faecalis*, SUBC57; *Lactobacillus plantarum.* To detect the resistance to papain, the isolates, were washed twice after overnight incubation, then treated in PBS with 0.3% papain for 3h. The samples were plated by dilution method in MRS agar, incubated for 18h at 37 °C, and then the number of colonies compared to the control plates. Using the same method in lysozyme resistance test, the isolates suspended in PBS containing 0.5% lysozyme, and inoculated in medium MRS Agar. Every group of five female mice(30-35gr) was orally fed by gavage with 10^8 CFU from fresh culture- washed with PBS buffer for 14 days. PBS was used for five mice of control group. After removing diet for 12h, blood sampling was performed and the sera collected. In the sera, changes in the liver enzymes were compared to controls. Finally, the immunization level was evaluated by indirect ELISA method. Sera of the BSA-immunized mice were used as the positive control. Isolates SUBC2 and SUBC57 showed the highest and the lowest survival rates as 10.65 and 0.41% respectively. Using the isolate SUBC57 the highest resistance to lysozyme with 91.66% and in the isolate SUBC4 the lowest resistance with 65.49% were detected. 14 days orally administration of probiotic revealed no immunogenicity. The study of the alteration in the liver enzymes is under progression. These preliminary results indicated that dairy products show the potential to be used as probiotic for fermentation industry.
Keywords: *Enterococcus* (sp), Immunogenicity, *Lactobacillus* (sp), Mice, Probiotic

CO4 A Phylogenetic study of canine parvovirus in Alborz province

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Canine parvovirus-2 (CPV-2) causes severe and highly contagious disease in dog, particularly puppies, with worldwide distribution. The viral agent is small, nonenveloped, single stranded DNA virus and belongs to the *Parvoviridae* family. The virus possesses two major open reading frames (ORF) encoding nonstructural and structural (Capsid) proteins. VP1 and VP2 proteins construct the viral capsid, in that VP2 is the major and outer capsid protein, comprises epitopic antigenic sites and plays critical role in determining viral host range and tissue tropism. Mutation in the VP2 protein is frequent, which may lead to the emergence of new CPV strains and variants. In order to identify the molecular characterization of circulating CPV in Iran, the full length of the VP2 sequence of two CPV-2 isolates from Alborz Province was characterized. The viral genomes were extracted from the feces of two diarrheic puppies and the DNA fragments including VP2 gene were amplified by using PCR and specific primers. The amplified DNA fragments were sequenced in both directions by using external and internal primers, and the obtained sequence were assembled to produce a 1752 bp sequence including the full length of the VP2 gene. Comparison of the VP2 gene from the Iranian CPV-2 isolates with those available in the GeneBank revealed that the both CPV-2 isolates were 2a type of the virus. The Iranian CPV-2a isolates shared 95.8% nucleotide sequence identity and they were both found to be most identical to

the available sequences originated from China since 2008. These results again emphasize that CPV-2 is a highly variable pathogen which can be spread over the countries and the world. To better understanding the molecular epidemiology of the circulating canine parvoviruses in Iran, molecular characterization of more viruses across the country is recommended.
Keywords: CPV-2, VP2, Molecular epidemiology

CO5 Green Synthesis of silver nanoparticles using *spirulina* algae extract and induction of apoptosis and autophagy in colon cancer cell line

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Green synthesis is a simple and inexpensive way to produce silver nanoparticles using plant extracts. In addition, finding new therapeutic and diagnostic effects for silver nanoparticles is an interesting area in cancer research. Use of algae extract is one of the ways of green synthesis. However it does not have an adverse effect on human cells, *Spirulina* is rich in biologically active compounds and has antiviral, anti-cancer and immune-boosting properties. The aim of this study was to fabricate silver nanoparticles using *spirulina* algae extract to evaluate the anti-cancer properties on the clone cancer cell line (CaCo2). In order to carry out this project, silver nanoparticles were synthesized by green method and evaluated by FT-IR, TEM, SEM, DLS and XRD methods. The biological properties of these nanoparticles were evaluated by MTT method (at 24, 48 and 72 hours with concentrations of 32, 16, 8, 4 and 2 µg / ml) and the effect of cellular apoptosis and cell cycle inhibition was examined. Annexin V/PI staining method was used to induce programmed cell death. In addition, cell cycle inhibition was assessed by flow cytometry. Also, genes expression responsible for apoptosis (BAX and BCL2) and genes expression responsible for autophagy (Beclin1 and ATG5) was evaluated in the molecular phase by Real Time PCR method. The results showed that silver nanoparticles synthesized from *Spirulina* at a concentration of 4 µg / ml leads to a 50% reduction in cell viability. In treated cells, increased BAX gene expression and decreased BCL2 gene expression indicate induction of cell death by silver nanoparticles. In addition, increased expression of autophagic genes indicates the induction of this type of cell death in clone cancer cells. In addition, flow cytometry results show 68% of apoptosis in cells treated with silver nanoparticles compared to cells treated with the extract. Also, the presence of 35% Sub-G1 indicates the optimal inhibition of the cell cycle in cells. According to the results, it can be said that nanoparticles synthesized with *spirulina* algae extract can exert their cytotoxic effect on caco2 cells by inducing apoptosis and autophagy.
Keywords: Clone Cancer, Green Synthesis, Silver Nanoparticles, Apoptosis, Autophag

CO6 Screening of bacteriophage effective on *Pseudomonas aeruginosa*

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Bacteriophage has been used as strategy for developing new drugs to reduce the incidence of bacterial infections. Here, the bacteriophages were isolated from the sewage water from Semnan University followed by filtering (0.45µm). The plaques formed using the double-layer agar method. The host range was determined by Spot test. The eclipse period and plaque formation were estimated using the data from the growth curve. Stability at different temperatures and pH values and the optimal MOI was obtained. The plaques were approximately 1 mm in diameter to infect *Pseudomonas aeruginosa*. The phage belongs to the family Siphoviridae. Gram-positive strains, *Bacillus cereus*, and *Staphylococcus aureus* and gram-negative strains, *Pseudomonas aeruginosa* were susceptible to the phage. The titer was 10^9 PFU/ml and the eclipse period was 20 minutes, which released 100 phage particles from each bacterium. The optimal MOI 100 showed the highest stability at 4 °C and pH 7. Phage therapy using DDPCC10 phage inhibited *Pseudomonas aeruginosa* infection.
Keywords: Bacteriophage, *Pseudomonas aeruginosa*, Sewage

CO7 Structural bioinformatics study of new synthesized chromene derivatives bind to β-amyloid fibrils

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Amyloid is associated with the pathology of a type of disease known as amyloidosis. One of these diseases is Alzheimer's disease, in which β-amyloid peptides bind to each other outside the brain cells to form β-amyloid fibrils. Thioflavin T (ThT) is a common detector of amyloid fibrils that shows an increase in fluorescence emission by binding to β-amyloid. The use of thioflavin T is limited due to disadvantages such as fluorescence quenching at high concentrations, its positive charge that lead to failure in crossing the blood-brain barrier. In order to identify new probes for amyloid fibrils detection, chromene derivatives were examined. To conduct bioinformatics studies, two-dimensional and three-dimensional structures of compounds were first prepared in ChemDraw software and Chem Office package ver. 14. The final optimization and energy minimization of the compounds was performed in Avogadro software. The coordinate file of β-Amyloid fibrils was obtained from the RCSB protein data center with 2beg code. β-amyloid fibrils were considered as acceptors and compounds as ligands. The MGL package ver. 1.5.6 was used to prepare coordinate files containing information about charges and active torsions. All available protein surface was selected as the search space to match the ligand. Energy maps of ligand atoms in the search space were prepared using Auto Grid 4 software. Finally, using Auto Dock 4.2 software, the structure of the most probable protein-ligand interaction due to lower energy with a total of 100 runs of the search was obtained from Lamarck's genetic algorithm. Bioinformatics studies show the binding site of new compounds to β-amyloid fibrils similar to the binding site of thioflavin T to them, which is the channel region of fibrils. Regarding the mechanism of thioflavin T probe to detect amyloid, the similarity between compounds and thioflavin T binding site to amyloid and also the fact that compounds have a better binding coefficient than the reference dye, they may be promising with more specificity and better performance than the reference dye.

Keywords: Amyloid detection, Beta amyloid, Fluorescent probe, Thioflavin t

CO8 Impact of vitamin D on TGF-β Expression in peripheral Blood Mononuclear Cells of asthmatic patients

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Considering the importance of the immune system in increasing the pathogenesis of asthma through the expression of TGF-β gene, the regulatory effect of vitamin D on the expression of this gene in the culture medium of mononuclear cells of patients with asthma was investigated. For this purpose, 2 groups of 20 of both sexes were selected as the case group (asthmatic patients) with a mean age of 27/64±5/12 and the control group (healthy people) with a mean age of 28/17±4/64 in Jahrom city. 5 cc of blood was taken from both groups, and after heparinization and dilution one by one with PBS, it was added to the follicle solution and centrifuged for 20 minutes. The isolated peripheral mononuclear cells were cultured in medium (RPMI + FBS). The cells were divided in control group (without treatment), the two treatment with vitamin D at concentrations of 10^{-6} and 10^{-7}M and the group treated with dexamethasone (as positive control). After RNA extraction, their cDNA was made and the expression of TGF-β gene was measured and compared in case and control groups using real-time PCR technique. Obtained data were analyzed with Graph pad statistical software (20) at $P < 0.05$. The results showed a significant decrease in TGF-β gene expression in cells treated with vitamin D and dexamethasone in the control group compared with the case group. There was no significant difference between the vitamin D-treated groups together and with the dexamethasone-treated group. Obtained findings indicate a positive effect of vitamin D in reducing asthma symptoms. So, with more research on the mechanism of this vitamin, it can be suggested as a potential factor in the prevention and management of asthma.

Keywords: Antigen stimulation, Cytokine, peripheral blood

CO9 Studying the presence of SARS-CoV-2 in wastewater

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from the beginning of the outbreak of Covid-19 in the country, the officials of the water and wastewater company decided to monitor the SARS-CoV-2 virus in the aqueous environment (water and wastewater). At first, the latest methods and instructions from WHO and EPA for identifying coronavirus and other enveloped viruses were reviewed. Due to the lack of a standard test method for the detection of this virus in water and wastewater, a method for SARS-CoV-2 identification was developed by a combination of the 2017 standard method and the EPA1615 standard. Then, the required equipments and materials were prepared and the test methods were implemented for the first time on 2020/06/22. Sampling was performed according to the standard method of 2017 from the incoming raw wastewater and the effluent of twenty municipal wastewater treatment plants located in Tehran province. Raw wastewater and effluent of wastewater treatment plants were monitored by RT-PCR method from July to the end of December. Because of the nature of raw wastewater, concentration-time lasts between 8 to 13 hours for each test. Enterovirus test was used as positive control to validate the method. Also, comparative tests were performed in three rounds between the laboratories of Tehran and Alborz Provinces. Results showed 60% of the raw wastewater samples were contaminated with SARS-CoV-2, while the virus genome was not observed in the effluent. Due to the presence of the virus from several days before the onset of symptoms in infected people and its excretion until long after the end of the acute period of infection, according to wastewater-based epidemiology, monitoring the virus genome in raw wastewater in addition to monitoring the efficiency of wastewater treatment plants, also can alert the country's health net about any outbreak in different places.

Keywords: Coronavirus, Treated effluent, RT-PCR Method

CO10 Inhibition of CTLA-4 receptor on the surface of T cells using a recombinant protein for cancer immunotherapy

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Immune checkpoints are molecules with the inhibitory role to prevent an immune response to destroy healthy cells in the body. In cancer immunotherapy with blocking these inhibitory receptors, the immune system is activated and as a result the cancer cells are killed .One of the inhibitory receptors in the surface of T cells that is the target of many cancer immunotherapy methods is CTLA-4. So far, many monoclonal antibodies have been produced to block CTLA-4; by inhibiting this receptor, the T cell remains active. Due to the costly production of antibodies and the side effects reported in their usage, in this study we tried to design and produce a recombinant protein with high affinity for CTLA-4 by using the natural ligands of this receptor.CD80 is a transmembrane protein in the surface of B cells and monocytes and binds naturally to CTLA-4. In this study an extracellular domain of this protein was extracted from PDB data bank and amino acids 29, 31 and 33 were mutated by using R software. After calculating the binding energy of each mutant with foldX software, the best variant was selected and its gene was cloned in pET22b vector. Finally, corresponding protein was expressed in *E. coli*. The results showed that the variants with point mutations R29Y, Y31R and Q33K and the binding energy of -21.43 kcal/mol is the best protein for binding to CTLA-4. Also, recombinant protein produced in *E. coli* was purified and subsequently its secondary structure was determined by CD spectroscopy. The results showed that produced protein has a secondary structure with acceptable similarity to native CD80; so, it can be considered as a drug candidate for CTLA-4 inhibition and cancer immunotherapy.

Keywords: CD80, checkpoint inhibitors, *E. coli*

CO11 Immobilization of urate oxidase enzyme on the surface of graphene oxide and evaluation of its stability

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Enzymes are used as biocatalysts in diagnostic and large-scale industrial processes. Urate oxidase or uricase (UOX) is a medicinal enzyme that is used in the treatments of patients with hyperuricemia and belongs to the family of oxidoreductases (EC 1.7.3.3). UOX converts the uric acid to 5-hydroxyisourate and H_2O_2 and reduces the amount of uric acid in the blood. Enzyme immobilization using nanomaterials, as a novel approach, can improve the half-life, stability, catalytic activity, and reusability of enzymes. In this work, the immobilization of UOX on the surface of graphene oxide was examined. For this purpose, the gene encoding uricase was cloned in E. coli and purified after expression. Then, 1 ml enzyme solution (0.4 mg/ml) was mixed with GO in the buffer and mixture was shaken at 5°C for 2 h at 150 rpm. The GO-enzyme suspensions are centrifuged at 13,000 rpm and the supernatant is removed. The residue is washed with buffer 6 times to ensure the thorough removal of free enzyme. The enzyme concentration in the supernatant after immobilization was measured, using Bradford method to determine the enzyme bound to the GO surface .The specific activity of free and immobilized states of UOX was measured. Furthermore, the kinetic and thermodynamic parameters, optimum temperature and pH, and the intrinsic fluorescence of free and immobilized enzymes were examined. The obtained results showed that the immobilized enzyme retained 48% of its activity after one hour at 37°C while, free enzyme had only 28% of its original activity at this temperature. Furthermore, immobilization of UOX on the surface of GO increased the half-life of the enzyme at 45°C from 13 minutes (free enzyme) to about 21 minutes (immobilized enzyme).

Keywords: Uricase, Thermal stabilization, Enzyme immobilization, Graphene oxide nanosheets

CO12 HTERT-driven immortalization of human sertoli cells down-regulates P53 expression

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Telomere is a structure composed of DNA and proteins made by the telomerase enzyme. This enzyme is present in high levels in cancer, stem and embryonic cells, but its expression is reduced in normal somatic cells. Transcription factor P53 is a tumor suppressor expressed in more than 50% of cancer cells. In recent years, the correlation between P53 expression and HTERT has been recognized and in this study this relationship was clearly observed. Telomere sequence shortens during the cell cycle and by reaching a critical level the threshold leads to cell cycle arrest. Telomerase has two main subunits, HTERT and HTERC, the former of which is the catalytic subunit and the latter is the template strand. Telomerase has been considered as an anti-apoptotic factor through inhibiting apoptotic signals and circumvent aging. Therefore, inhibition of HTERT is considered as a tumor suppressor. The relationship between p53 and HTERT is both direct and indirect. Direct binding of p53 to sub-telomeric area will alter the transcription and chromatin conformation. HTERT promoter has binding sites for c-myc, SP1, and P53. In this study; sertoli cells - which naturally exhibit degree of resemblance to the metabolic state of cancer cells - were transduced and immortalized by a lentivirus containing HTERT. For both non-immortal and immortal sertoli cells, RT-PCR was performed with two pairs of HTERT and P53 primers, which showed high expression of HTERT in immortal Sertoli cells and decreased expression of P53 in them. Previous studies such as p53 knock-down have shown an increase in HTERT expression. In some studies, overexpression of HTERT led to decreased expression of p53. In this study, an increased HTERT expression ectopically, reduced P53 expression significantly. Although more studies are needed in this area, such results are a bright horizon for future HTERT-based anticancer therapies.

Key word: Apoptosis, Cancer, Immortality, RT-PCR

CO13 Benzodiazepine Toxicity Treatment: A Comparative Molecular Docking study of flumazenil and diazepam

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Epilepsy is a set of chronic or long-term neurological disorders characterized by an epileptic seizure. Epilepsy is one of the most common neurological diseases in Iran and its prevalence is higher than the world standard. Scientific studies show that about one to one and a half percent of Iranians have epilepsy, which indicates that epileptic patients in Iran are about three times more than in Europe. Flumazenil is a benzodiazepine antidote and is used to treat benzodiazepine poisoning, but studies show that people who take the drug have an increased risk of seizures, a symptom of epilepsy. Different concentrations of diazepam and flumazenil were injected into mice at different intervals to obtain the effective dose and effective time of action of each drug. In this study, it is demonstrated that a concentration of 0.75 mg / kg of flumazenil can decrease the threshold of induced seizures with PTZ to control value. But concentrations higher than this value reduce the threshold for induction of seizures more than control group and therefore reduce the dose of PTZ.The molecular docking studies identify the binding site of these two drugs on the GABA receptor and show that flumazenil can act as an inhibitor at a site close to the diazepam binding site and neutralize its action.

Keywords: Seizure, Pentylenetetrazol, Auto dock Vina

CO14 Synthesis and evaluation of Chitosan Chloride/plasmid nanoparticles and evaluation of plasmid release from nanoparticles by electrophoresis and PCR

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Chitosan chloride is a derivative of chitosan and, like chitosan, is a biodegradable polymer with no toxicity. Because of the weaker interaction with DNA, DNA release from chitosan chloride/DNA nanoparticles is more easily performed, today, chitosan chloride/DNA nanoparticles are of great interest to researchers and have been studied in this study. After adsorption of plasmid DNA (size 3633 bp) on the surface of chitosan chloride nanoparticles by simple complex method, the size and morphology of nanoparticles were examined by scanning electron microscopy (SEM). Agarose gel and UV rays were used to confirm the adsorption of plasmid on the surface of nanoparticles. The release of plasmid by treatment with the enzyme lysozyme and soluble phosphate-buffered saline (PBS) was investigated. PCR was also used to further evaluate the release. The results showed that the average size of nanoparticles is less than 150 nm and the morphology of nanoparticles is spherical. Examination of agarose gel revealed that plasmid DNA was adsorbed on the surface of nanoparticles and after treatment, plasmid DNA was released, the results were confirmed by PCR. Because chitosan chloride/plasmid nanoparticles are easily synthesized, despite the protection of DNA, DNA release from them also occurs easily, they are cost-effective and suitable for therapeutic purposes.

Keywords: Simple complex, release, adsorption, lysozyme, biodegradable

CO15 The Protein Encapsulation in the Modified Chitosan Self-Aggregated Nanoparticles

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Pharmaceutical drugs, such as proteins and peptides are well known as a new generation of drugs. However, the delivery of proteins and peptides in the body is limited by their specific physicochemical properties such as complex structure and high molecular weight. Encapsulation is an excellent method to the efficiently delivery of the proteins and peptides. Chitosan nanoparticles, with the ability to trap proteins in a hydrated polymer-network and minimize the protein fluctuations, are widely used as a drug delivery substance. In this study, we have evaluated the mechanisms of interactions between cholesterol-modified chitosan self-aggregated nanoparticles and human growth hormone (hGH) and follicle stimulating hormone (FSH) by using circular dichroism (CD), fluorescence, UV–vis absorption spectroscopy and molecular dynamics (MD) simulation. The

fluorescence intensity of the proteins has indicated that the emission intensity increased with increasing of the nanoparticles concentration. The CD data have also revealed that the secondary structure of the proteins have not changed so much in the presence and absence of nanoparticles. The MD results have confirmed that the hormones backbone remained practically unchanged along MD simulations. According to previous studies and our results, the number of the cholesterol molecules per chitosan is critical for efficient performance. Our results have demonstrated that the protein molecules can be loaded on the cholesterol-modified chitosan self-aggregated nanoparticles and the mechanisms have been suggested to be regulated by several factors such as hydrogen bonding, hydrophobic, and electrostatic interactions. This study suggests that the cholesterol-modified chitosan self-aggregated nanoparticles can be useful as a carrier for protein drugs in the fields of nanomedicine and nanobiotechnology sciences.

Keywords: Human growth hormone, Follicle stimulating hormone, Drug delivery, Nanobiotechnology, Interactions

CO16 Investigation the protective effect of catechin nanosystems against aluminum chloride-induced oxidative stress

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Catechins is a polyphenol with antioxidant properties, and nanoencapsulation can preserve its antioxidant properties and increase its bioavailability.This study aimed to investigate the protective effect of the catechin nanosystems against aluminum chloride-induced oxidative stress compared with catechin. For this purpose, catechin-loaded chitosan/alginate nanosystem was synthesized . Then, male Wistar rats aged range12-14 weeks were feded with catechin nanoparticles at a dose of 10 mg/kg and catechin at a dose of 50 mg/kg by gavage. At the end of the treatment period, the activity of antioxidant enzymes catalase (U/ml), glutathione peroxidase(U/ml), and glutathione redoctase(U/L) was measured in the serum sample. Catalase activity in the control , catechin, aluminum chloride , catechin nanosystem , aluminum plus catechin nanosystem and aluminum chloride plus catechin groups were 39.11±2.40, 38.68±2.94, 19.54±2.07,39.78±5.32, 29.35±4.65, and 29.07±2.57, respectively.The activity of glutathione peroxidase in control, catechin, aluminum chloride, nanosystem catechin, aluminum chloride plus catechin nanosystem, and aluminum chloride plus catechin groups were 1.69±0.15, 1.57±0.19, 0.78±0.13, 1.52±0.21, 1.29±0.24 and1.27±0.34, respectively.The activity of glutathione reductase enzyme in the control, catechin,aluminum chloride, catechin nanosystem,aluminum plus catechin nanosystem, aluminum chloride plus catechin were 40.92±6.41, 39.55±2.90, 24.90±2.47, 38.77±2.42, 35.23±8.92 and 38.66±6.06, respectively. As the results show, the activity of antioxidant enzymes in rate treated with aluminum chloride showed a significant decrease ($p<0.001$) in the control group, while the use of catechin or its nanoparticle prevents the reduction of enzyme activity. Since the lower dose of the catechin nanosystem was used, it is predicted that catechin encapsulation, caused the increased antioxidant property and reduced possible side effects of catechin.

Keywords: Catalase, Glutathione peroxide, Glutathione reductase, Antioxidant

CO17 Investigation of Aloin effects on hen egg-white lysozyme fibril formation

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Amyloid fibrils are extracellular aggregates found in organs and tissues which are composed of beta plates**.** The mechanism of fibril formation is the spontaneous accumulation of proteins and peptides due to misfolding. Amyloid fibrils have been found in many diseases, such as type 2 diabetes, Alzheimer's, and Parkinson's. These beta-sheet deposits cause cell damage and death. Since proteins can form amyloid fibrils at different biophysical conditions, hen egg-white lysozyme (HEWL) was applied as a model protein for in vitro fibril formation in the presence and absence of Aloin. Aloin is extracted from the leaves of the Aloe Vera plant. Aloe Vera gel is used in the food and cosmetics industry. Aloin has low stability as a solution and should be kept away from light and in a cool place. Aloin has anti-oxidation, and anti-tumor properties, and no molecular level studies were done about its' anti fibrillation effects on HEWL. Experiments were done using UV-vis (concentration

determination) spectroscopy, fluorescence spectroscopy and atomic force microscopy (AFM). The increase in fluorescence intensity in the presence of thioflavin T showed that HEWL could form amyloid fibrils at pH 2 and 57°C over time. Fibrils were also observed by AFM. Therefore, as a next step, fibril formation was detected in the presence of different Aloin concentrations over time. Fluorescence intensity of HEWL decreased in the presence of Aloin. It means that Aloin has inhibitory effect on HEWL fibril formation. However, more studies are needed to know the general inhibitory effect of Aloin on protein fibril formation.
Keywords: Thioflavin T, Amyloid fibrils, Atomic force microscopy

CO19 Effect of D226N point mutation on the structure of the enzyme IMPDH1 in comparison with the wild type

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IMPDH is one of the protected enzymes in prokaryotes and eukaryotes. The function of this enzyme is in de novo biosynthesis of purine nucleotides. Mammals have two homologues of the IMPDH gene, named IMPDH1 and IMPDH2. Retinal isoforms of the enzyme IMPDH1 were detected in the retina of humans and mice. Mutations associated with retinitis pigmentosa (RP) have been discovered in the IMPDH1 gene and new functions have been demonstrated for it. IMPDH1 enzyme function in the retina is disrupted by R224P and D226N point mutations and RP disease develops. Based on the description given, we decided to study this enzyme structurally. Therefore, after cloning the wild type IMPDH1, expression and purification of both isoforms 514 and 546 and cloning of mutant type D226N, expression and purification of mutant isoform 514, we studied the structural properties of this enzyme by using Gel Filtration Chromatography technique. According to the chromatographic results, the mutant isoforms form extremely large structures compared to the wild type. The wild type of enzyme in the presence of ATP / GTP causes octameric structures with enhanced enzyme activity. While the presence of a mycophenolic acid inhibitor causes the formation of extremely large inactive macromolecules. It seems that the presence of C-terminal sequence in the retinal isoform has increased the sensitivity of this isoform to conditions. This structural adjustment directly affects or inhibits enzyme activity. To better understand this issue, it is necessary to conduct more studies on retinal and canonical isoforms of this enzyme.
Keywords: retinitis pigmentosa, Chromatography, Retinal isoforms

CO20 Identification and evaluation of regulators in esophageal squamous cell carcinoma using comprehensive transcriptome analysis

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Esophageal cancer is the second and third most common cancers in Iranian men and women after gastric cancer, respectively. Esophageal squamous cell carcinoma (ESCC) is the most common type of cancer. Understanding the cellular and molecular mechanisms involved in this type of cancer will help identify, control and treat this lethal cancer. The aim of this study was to identify key genes and their role in this type of cancer. The expression data for this study containing 17 samples of ESCC and 17 samples of healthy esophageal tissue with access number GSE20347 were selected from the GEO database and further analyzed by R script. Using the GEOquery package to get expression matrix (GSEMatrix) as well as their Annotation GPL were extracted and normalized. Then, via Limma package, statistical parameters adj.P.vlaue<0.05 and |LogFC|≥1.5 were applied to determine genes with significant difference in expression (DEGs) that 221 and 321 genes showed increase and decrease in expression of cancer samples, respectively. In the first stage of analysis, cellular and molecular mechanisms and signaling pathways related to DEGs were identified by GO and KEGG databases. In the next step, the list of transcription factors (TFs) and protein kinases (PKs) in the list of DEGs were determined by a review study and X2K database to identify these types of proteins in the list of DEGs, respectively. The interaction between the three protein groups in the list, including three sets of intermediated proteins, TFs, PKs, was determined by the STRING database and plotted in Cytoscape. Also, the module networks present in the list of DEGs and their

role were clearly defined. CDK1, FN1, and AURKA as well as FLG, SPRR1B and IVL were identified as key genes (hub-genes) in cancerous tissue and healthy tissue, respectively. Finally, DEGs-related metabolites such as ursodeoxycholic acid and superior microRNAs that targeting cancer genes such as has-mir-29b-3p were obtained by HMDB and miRTarbase, respectively. Comparison of the obtained results with other studies confirmed our present results.

Keywords: Bioinformatics, Signaling pathway, Transcription factors, Protein kinase, Metabolite

CO21 The study of *Oct4* gene expression of mouse blastocysts influenced by embryo splitting

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Embryo splitting is widely utilized as a novel technique in reproduction biotechnology. After splitting embryo at the two-, four- or eight-cell stages, each single blastomere can be developed to a separate embryo that is similar to other blastomere genetically. In the present study, the effects of the mouse embryo splitting on the *Oct4*, as one of the pluripotent genes, expression were evaluated. After stimulating ovulation in female mice and isolating two-cell embryos, they were grouped as split and non-split, then washed and transferred to M16 medium. When zona pellucida was removed, the blastomeres of the split group were dispersed then, as well as non-split and normal blastomeres, transferred into embryonic fibroblasts to develop. About 72 hours later, normal blastocysts from each group were separately isolated for molecular evaluation. Changes in *Oct4* expression were analyzed by Real-time PCR. The results showed that the pluripotent gene (*Oct4*) expression were similar between split and non-split groups. In another words, there was no significant changes in *Oct4* expression, among all the study groups.

Keywords: Embryo Splitting, Mouse Blastocyst, Two-cell Embryo, *Oct4* gene

CO22 Bioengineered nanoemulsions-chitosan nanoparticles for rapid brain intranasal delivery of hybrid medicinal compounds

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The bioengineering of nanoemulsions for the transportation of various therapeutic agents such as quercetin and eugenol to the brain have sparked a growing interest among researchers. These compounds are known to have great medicinal value and modulatory effects on cell apoptosis and alzheimer via various signaling pathways, but their application are limited. Problems like poor aqueous solubility, rapid metabolism and blood brain barrier make them unreliable for therapeutic purposes. To overcome these issues, development of sustained release and rapid delivery for these compounds is proposed which can be administered directly from nose to brain utilizing olfactory nerve channels. In this study, quercetin-loaded eugenol nanoemulsions (Q-ENEs) were synthesized and coated with chitosan, which induces mucous adhesion. The synthesized Q-ENEs yielded a size of 16.7 nm ± 5 nm, PDI of 0.204 ± 0.08 and zeta-potential of −8.8 ± 1.4 mV (mean ± SD, for n = 3 batches) and were larger in size compared to empty ENEs with a size of 14.1 ± 3.7 nm, PDI of 0.266 ± 0.02, and zeta potential of −4.2 ± 1.4 mV. Size of chitosan surface-modified Q-ENEs yielded a size of 17.7 nm ± 5 nm, PDI of 0.266 ± 0.06 and zeta-potential of +29.7 ± 1.3 mV. SEM showed spherical shape for these particles. Next, these formulations were analyzed for quercetin release by using the dialysis bag method which showed that Q-ENEs caused a release of 56.7% of drug within 12 h. Furthermore, The encapsulation efficiency of quercetin (95.1% ± 2.0) showed optimal conditions. The results of the analyzes show that the Q-ENEs along with successful surface modification and good drug penetration, are an appropriate choice for increasing the retention time of hybrid compounds in the nasal cavity and opens the way for further research on the nasal pathway.

Keywords: Quercetin, Eugenol, Alzheimer, Surface modification, Nasal

CO23 *De novo* design of Antibacterial peptides by ensemble machine learning methods

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Antibiotic resistance is a great challenge. Since Antimicrobial peptides directly act on the microbial membrane and normally didn't have any specific protein targets, it is less likely, bacteria arise resistance against these molecules. Recently statistical analysis and machine learning algorithms have been considered. Ensemble learning techniques, in machine learning, are a combination of several models that are used to provide an optimal model for predicting or classifying data. The most widely used algorithms are Bagging, Adaboost and RandomForest with several estimators. In this study, to predict peptides with specific antibacterial effects, the data has been gathered from the DRAMP2.0, EDA were performed with the Seaborn, Numpy, and Pandas packages in Python. 554 peptides with antibacterial function and 626 without it were provided. Descriptors have been defined based on biophysical features like length, Molecular weight, Charge, Charge density, pI, Instability index, Aromaticity, Aliphatic index, Boman index, and Hydrophobic ratio. Modeling was performed using an SVM algorithm with linear, polynomial (degree=5) and RDF (gamma=3) kernel functons, RandomForest algorithm, Bagging classifier and Adaboost with 100 and 1000 estimators. The accuracy and precision of the model made using the RandomForest algorithm with 1000 estimators was 87% and 90% and this model was the most optimal compared to other methods. The average of accuracy and precision for SVM method with mentioned kernels,Bagging and Adaboost was 78%,87% and 86%, respectively. For the data and features of this study, the ensemble technique had better results than the SVM method due to the way the train data is used, the data is randomly segmented and used several times to learn the model. Despite the advancement of computational methods in drug design and therapeutic peptides, there is still a need for laboratory methods for more accurate evaluations, which is one of the next steps in this research.

Keywords: Antibiotic resistance, EDA, SVM algorithms, Random Forest, Peptide

CO24 Evaluation of the antibacterial effects of diffrenet fractions from iranian scorpion venom Buthotus schach (BS), in – virto condition

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Nowadays, the development of drug resistance in pathogenic bacteria to many antibiotics has an important and fundamental role in the lack of control and treatment of bacterial infections and is a major concern in human societies. Scorpion venom is rich in biologically active compounds and components that may be used in the development and discovery of new antibacterial drugs. So far, many compounds such as neurotoxins, salts, proteins and peptides with therapeutic properties have been identified in them that can quickly kill a wide range of bacteria. The aim of this study was to investigate the antibacterial properties of *Hottentotta (Buthotus) schach.* Scorpion venom was obtained by electrical stimulation and its peptides were purified by gel filtration chromatography. Then, the protein concentration was calculated with nanodrop and the quality of the poison was evaluated by SDS-PAGE electrophoresis. Dilutions 1/1 - 10/1 - 100.1 µg / ml Fractions were prepared from the initial concentration of 1 ml / mg for plate well diffusion method and MIC based on CLSI 2019 protocol to determine the antimicrobial effect of the venom on bacteria. Gram-negative *Escherichia coli* ATCC 25922 and *Pseudomonas aeruginosa* ATCC 9027 and Gram-positive bacteria *Staphylococcus aureus* ATCC 25923. The results showed that F1 and F2 fractions of *B. schach* scorpion venom had a significant inhibitory effect on Gram-positive bacterium *S. aureus* and Gram-negative *E. coli*. This antimicrobial effect on *Ps .aeruginosa* was much weaker. The results of the hemolysis test also showed that at concentrations similar to MIC, the toxin had no hemolytic effect on fresh human blood. Therefore, suitable therapeutic indicators can be found in natural AMP of scorpion venom. They themselves are good candidates for the production of antimicrobials.

Keywords: *schach* scporpion**,** Chromatography, *E. coli*, *S. aureus*, *Ps. Aeruginosa*

CO25 Wnt5A orchestrates multiple epithelial to mesenchymal-associated signaling pathways through up-regulation of integrin alpha v in epithelial ovarian cancer

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Wnt5A is a non-canonical signaling member of the Wnt family which is involved in epithelial to mesenchymal transition (EMT) in embryonic development and cancer. However, the molecular mechanism of Wnt5A-induced EMT in epithelial ovarian cancer (EOC) remains largely unknown. Here we investigated whether Wnt5A crosstalk with TGFβ1/Smad and YAP/TAZ pathways in epithelial ovarian cancer-associated EMT. For this, we used human ovarian cancer cell lines SKOV-3, OVCAR-3, CAOV-4, and human serous ovarian cancer specimens. We show here significantly higher expression levels of TGFβ1 signaling components, Wnt5A/ROR1/ROR2, and YAP/TAZ in human high grade serous ovarian cancer (HGSOC) specimens related to other histological serous subtypes and normal ovary. Moreover, Wnt5A showed a positive correlation with TAZ and TGFβ1 in metastatic serous subtypes specimens. Next, we demonstrated that the silencing of Wnt5A in ovarian cancer cells in 2D and 3D cultures led to significantly decreased levels of Smad2/3 activation, and Wnt5A was required for TGFβ1-induced migration and invasion of ovarian cancer cells. Moreover, we found that inhibition of YAP transcriptional activity by Verteporfin (VP) alters ovarian cancer cell migration and invasion by two mechanisms: 1) through suppression of Wnt5A expression, and 2) via the inhibition of Smad2/3 activation which was reverted upon recombinant human Wnt5A addition. Moreover, we found that Wnt5A induce up-regulation of integrin alpha v expression and activity which was involved in the activation of the TGFb1 pathway and YAP/TAZ transcriptional activity. Together, our work showed that Wnt5A orchestrates the EMT-associated signaling pathway through the up-regulation of integrin alpha v in epithelial ovarian cancer.

Keywords: EMT , Wnt5A, TGFβ1/Smad signaling, YAP/TAZ signaling, integrin alpha V

CO26 Different effects of bacterial host strains and inducers on expressing of two recombinant antibacterial protein

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Selecting suitable bacterial host strain and using of proper inducer also is one of the most imporatnt challenges in soluble recombinant proteins production. One of the main strains used for recombinant protein expression is *E.coli* BL21(DE3) since it lacks OmpT and Lon genes. Also *E.coli* BL21(DE3)pLysS has T7 lysozyme gene and is used for expressing of recombinant protein with toxicity effect on host. Therefore, in this study an engineered recombinant fusion protein with peptidoglycan hydrolysis effect (P-R) and a not engineered protein (P) as control were expressed in *E. coli* BL21(DE3) and BL21(DE3)pLysS using pET expression system in presence of IPTG or lactose as inducer. First, BL21(DE3) harboring P-R and P were separately cultured in Luria Bertani broth medium and both hosts at OD~0.5 were induced with IPTG 1 mM and incubated overnight at 37 ^{o}C and 220 rpm. In addition, to investigate the effect of lactose as inducer, both bacteria were cultured first in a non-inducing lactose-free media as a preculture and then in an auto-inducing media containing glucose, lactose and glycerol as previous conditions. The expression of normalized samples was analyzed using SDS-PAGE and compared with ImageJ program. The expression amount of P-R engineered protein in auto-inducing media was 1.146 mg/ml, which was more than twice of when IPTG was used as inducer. However, P protein, showed better expression in LB medium. In addition, expression of P gene in BL21(DE3)pLysS was 34 times more than BL21(DE3). Due to higher expression of engineered protein in BL21 (DE3) with lactose as inducer, IPTG was replaced with lactose as expression inducer. This issue is more important in industrial scale. Besides cost, using of lactose as inducer allows to easier producing process because of it is not required to monitor of optical density. However, different proteins show dissimilar behavior in equal conditions.

Keywords: Fusion protein, Auto-inducing media, IPTG, Lactose, *E. coli*

CO27 The effect of calcium nanofluoride on breast cancer cell MDA-MB-231 migration

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Cancer is abnormal cell proliferation. When cancer cells develop in the breast tissue, it is called breast cancer. Nanotechnology began at the suggestion of renowned physicist Richard Feynman. Nanotechnology has many advantages over conventional methods of cancer diagnosis, treatment and prevention. In this study, MDA-MB-231 cancer cell migration was prevented by using calcium nanofluoride. Calcium nanofluoride was formed from the combination of calcium carbonate with synthesized hydrogen fluoride by sonication as nanoparticles. Verification of fabricated nanoparticles was performed using (TEM) and (DLS). Breast cancer cells were cultured in DMEM medium and by MTT assay on MDA-MB-231 cell lines, cell viability was assessed and LC50 calcium nanofluoride was obtained. Then, according to the obtained LC50, cell migration test was performed on breast cancer cells. Finally, it was found that calcium nanofluoride reduced the migration of cancer cells by 30%. Calcium fluoride nanoparticles have anti-cancer properties. More research is needed to confirm it as an anti-cancer agent.

Keywords: Lymph nodes, Richard Feynman, MTT test, cell death, LC_{50}

CO28 CRISPR-Cpf1 mediated targeting of TRAC locus in T cell line

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Genetically engineered T cell therapy is employed for various types of cancer and it has shown considerable therapeutic potential, both for solid tumors and blood cancers. However, endogenous TCRs at the surface of the engineered T cells, have faced these treatments with the challenge of GVHD (graft versus host disease) for allogeneic approach, where these endogenous TCRs reacts against the recipient tissue. Whereas, TCRαβ at the surface of engineered T cells causes this allogeneic reaction, prevent the expression of functional TCRαβ at the surface of engineered T cells can solve this challenge. In this study, we have assessed the application of CRISPER/Cpf1 gene editing system to knock out TCRα chain in a Jurkat T cell line. To target the *TRAC* locus that encodes the constant region of TCRα, three crRNAs was designed and constructed. The efficiency of this gene editing system was assessed in two levels, genome sequence and protein expression, respectively, was examined by using DNA sequence analysis and flowcytometry. The results showed that two of three designed crRNAs against *TRAC* locus, introduced indel mutations in the constant region of TCRα and prevented the functional TCR expression at cell surface. These findings show that CRISPER/Cpf1 is appropriate gene editing system in order to remove endogenous TCR from the surface of Jurkat T cell line. Using two crRNAs designed in this study, CRISPER/Cpf1 gene editing system can be applied to remove endogenous TCR from the surface of primary T cells for manufacture of allogeneic engineered T cell therapy.

Keywords: CRISPER/Cpf1, *TRAC* locus knockout, endogenous TCR depletion

CO29 Cyclophosphamide chemotherapy may reduce the repairing capacity of oocyte in confronting sperm dna fragmentation

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In recent years, sperm DNA fragmentation have been considered as a factor in the diagnosis of male infertility and assisted reproductive techniques(ART). It is believed that oocytes play a crucial role in repairing sperm DNA fragmentation after fertilization and in the embryonic stage. In this study, the ability of mouse Oocytes

after chemotherapy to repair sperm DNA fragmentations was investigated. Animal models of DNA fragmentation creates by inducing oxidative stress in sperm and damage to oocytes was makde by chemotherapy drugagent, we aimed to investigate the role of oocytes in repairing fragmentation by examining the expression of DNA repair genes of Rad51, Brca1, Mre11a and Xrcc4 in the resulting embryos at two stages (Zygote and blastocyst).DNA breakage was induced in male FVB/N mice by injection of TBHP (Tert-Butyl hydroperoxide) that causes oxidative stress. Dosage of 0.1-0.2 LD50 of TBHP were considered to induce DNA fragmentation in adult male mice (6-8 weeks of age) for two weeks. In modeling female mice with cyclophosphamide chemotherapy, after injection of different doses and histological survey of ovarian tissue and follicular count, dose 60mg/kg of cyclophosphamide was selected. After a single dose injection of cyclophosphamide and two weeks recovery and the first estrous cycle observation, mating was performed between male and female mice in different groups. Finally, zygote and blastocyst collection was performed 12 hours and 4 days respectively after observing the vaginal plaque. The expression of double-stranded DNA breaks genes including Brca1, Mre11a, Xrcc4 and Rad51 was evaluated by Real time PCR. Data from the study of DNA repair double-strand break genes showed increased expression in the zygote embryos derived from mating of mice with DNA fragmented sperm and female mouse treated with chemotherapy agent, whereas in the blastocyst stage we observed decreased expression of the mentioned genes. Damaged sperm in the groups greatly increased the repair activity Whether the oocyte is healthy or damaged. The maternal transcriptome of oocytes seems to play an effective role in repairing sperm DNA fragmentation, but oocytes after chemotherapy may lose not only their capacity to repair damages to themselves but also damages to sperms.

Keywords: Oxidative stress, Reactive oxygen species, ROS, Repair gene, Cyclophosphamide

CO30 Evaluation of the effect of *Helicobacter pylori* virulence factors on macrophage cells Times

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Helicobacter pylori bacilli Gram-negative is one of the prominent features of this bacterium important pathogens such as urease, flagell, CagA, VacA, BabA, SabA, AlpA / AlpB, IceA, DupA, LPS and OipA. In addition, macrophages can and do initiate a central mediator between the innate and acquired immune systems, and the immune response to *Helicobacter pylori* is predominantly by these cells. The aim of this study was to investigate the effect of 2FlgE protein present in the flagellum pod if electricity is present, and the immune system response and cells of this system, if not using the knowledge used in this study, to design a vaccine candidate and evaluate the mechanism of action. This factor is from bacteria .Culture of standard *Helicobacter pylori* strain and purification of bacterial genome, study of genome banks and obtaining FlgE2 related sequences. cloning, expression and purification of recombinant FlgE2 protein. FlgE2 protein is purified and crystallized, the structure of which is determined by SAD method. The second third is *H.pylori*. FlgE2 crystal surface projector and Cap protein FlgD regulatory protein represent complementary function between FlgE1 & FlgE2 proteins in bacterial flagella. The presence of two different proteins at the hook site indicates that your *H.pylori* structure is different. This study was performed for the first time in the world by recombinant FlgE2 protein, the details of which are *Helicobacter pylori* flagellum, introduced as a candidate for vaccine and immune response against *Helicobacter pylori*. This study suggests that this protein may play a role in maintaining the necessary conditions under stress. But more studies are needed to confirm this hypothesis.

Keywords: Flagel ,FlgE2 protein,vaccine, Macrophage,cytokines

CO31 Application of bioinformatics in discrimination of pathogenic and non-pathogenic strains of bacteria

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Xanthomonas campestris is considered in the industry due to its xanthan production ability. However, some strains are pathogenic for Brassicaceae plants and can cause significant economic losses. In present

bioinformatics study, the genomes of five *X. campestris* strains including three pathogenic and two non-pathogenic bacteria were retrieved from NCBI database. After genome annotation with RAST, the gene clusters and proteins related to pathogenesis in *Xanthomonas* were identified by BLASTP and then compared. Gene clusters related to production of two virulence factors, secretion system type II (*xps* and *xcs* genes) and xanthan exopolysaccharide (*gum* genes) were present in all of the strains. Pathogenic strains showed the complete gene cluster associated with virulence factor secretion system type 3 (*hrp* genes) but the non-pathogenic strains lacked them. The effector type III profile analysis of the *X. campestris* strains genomes showed that pathogenic strains have the ability to encode a significant number of effector proteins but there are a few encoding genes for these proteins in the genome of non-pathogenic strains. After the examination of the gene cluster related to production of LPS virulence factor, it was found that the content of this gene cluster was different in pathogenic and non-pathogenic strains. The investigation of the presence of secretory system type III gene cluster and the content analysis of LPS encoding genes can help identifying pathogenic strains of *X. campestris*. The genome comparison of pathogenic and non-pathogenic strains of a bacterium using bioinformatics analysis leads to the identification and development of gene markers which can be useful and efficient in identifying pathogenic strains as well as early diagnosis of the disease.

Keywords: Comparative genomics, *Xanthomonas campestris*, Secretion system type III, Xanthan

CO32 Evaluation of synergistic effects of cisplatin and methotrexate on proliferation and death of colorectal cancer cells

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Cisplatin (CDDP) is one of the most frequently used chemotherapy drugs, displays a strong therapeutic effect against cancer. Predominantly, CDDP binds to the DNA, prevents transcription and replication, and induces programmed cell death. Nevertheless, some types of cancer, like colorectal cancer, are very resistant to cisplatin. It leads to a large number of side effects and tumor relapse in treated patients. To overcome these problems, combination chemotherapy is a superior treatment strategy. The present study aimed to evaluate the therapeutic efficacy and safety of the combination of CDDP and methotrexate (MTX) against colon cancer. So, the effect of cytotoxicity and induction of apoptosis of a single drug (CDDP or MTX) or combination of CDDP plus MTX on CT26 colorectal cancer were studied, by MTT assay and Ao/EtBr staining. The results were revealed an intense synergistically cytotoxic effect in CT26 colorectal cancer when they were co-treated with CDDP and MTX. Also, staining of samples with Ao/EtBr showed an increase in induction of apoptosis, as programmed death, in CDDP and MTX-treated cells, compared with that in single drug-treated cells.

Keywords: Cancer, Combination therapy, Cisplatin, Methotrexate, CT26 cells

CO33 Sequence analysis of Newcastle disease virus isolates in the Middle East from 2010 to 2020

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Newcastle disease (ND) is caused by a virulent strain of Newcastle disease virus (NDV). The viral disease has a high number of mortality and morbidity in birds. Due to this, there is no effective treatment for this infectious disease and options are mostly vaccination and following the sanitary protocols. The circulating NDVs in a specific region shows specifications related to that place. So, a comparative study may help to understand the features of viruses in that region. For this purpose, we designed a study to evaluate the NDVs circulating in the Middle East during 2010 and 2020. For this purpose, Sequences were obtained through a database of isolates stored in GenBank® (National Center for Biotechnology Information, USA). The used isolates were all obtained from Middle Eastern countries. This study has investigated the homology, pathotype, genetic distance, and molecular phylogenetic analysis of circulating NDVs in Middle Eastern countries by In Silico approaches.

Our result showed that six countries didn't participate in nucleotide sequence submission in GenBank®. Iran and Egypt were the countries with the most contribution in GenBank® for submitting new sequences of NDVs. By far, the Fusion gene (F gene) was the most studied gene of NDVs. Sequence analysis showed that there is 99-97 percent coverage between complete genome sequences. In a pairwise comparison, sequences collection showed similarity in hotspots which could show differentiation. This indicates an endemic spread of the virus in this area. The phylogenetic analysis also supported these results and showed no to little variation between sequences. The results of this study illustrate that NDV strains that are present in Middle Eastern countries and have been submitted in GenBank® are very similar. Therefore, these strains may have a common ancestor. This study suggests a wider range of sequence analysis based on bird migration patterns from other countries with Middle East destinations.

Keywords: NDV, Bioinformatics, Fusion Gene, Phylogenic analysis, Pathotyping

CO34 The effect of niosome nanoparticles encapsulating stevia extract on the expression of Glut2 and Glut9 genes in type 2 diabetic model induced by intravenous injection of streptozotocin in male rats

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Diabetes is on the rise in communities. So far, no drug has been identified that can completely cure the disease. Because natural compounds have fewer side effects than chemical compounds, treatment with these methods .Therefore, the aim of this study was to treat diabetes using niosome stevia in a model of male diabetic rats.The purpose of this study was to evaluate the effect of niosome nanoparticles encapsulating stevia extract on the expression of Glut2 and Glut9 genes in type 2 diabetic model induced by intravenous injection of streptozotocin in male rats.In this study, 40 Wistar rats with an average weight of 200-250 g were used. They were divided into 5 groups of 8, including healthy control, diabetic control (sham), stevia, niosome stevia, niosome. After becoming diabetic, mice received daily stevia and stevia niosome and niosome at a dose of 500 mg / kg by gavage for 30 days. Forty-eight hours after the last treatment, rats were anesthetized and liver tissue was removed from their bodies, and real-time PCR was performed to examine the glut 2 and glut 9 genes.Streptozotocin injection caused a significant increase in blood sugar compared to the control group ($p < 0.001$). Glut2 gene expression was increased in the stevia and stevia nanoniosome groups compared to the control and sham groups. ($p < 0.001$) The expression of glut9 gene was increased in stevia and stevia nanoniosome groups ($p < 0.001$).Due to the fact that in this study, the expression of glut 2 and glut 9 genes had increased compared to the diabetic group due to treatment, and this increase was more in the niosome group. It can be said that one of the effects of stevia in improving diabetes is the effect on the expression of genes involved in glucose transfer. So we can say that by updating the drug, we can increase its stability and efficiency in the treatment of diabetes.

Keywords: Diabetes , Stevia , GLUT2 gene , GLUT9 gene ,Niosome.

CO35 Expression and Diagnostic Values of Long Non-Coding RNAs, *MIAT*, *H19*, and *NRON*, in Multiple Sclerosis Patients

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Multiple sclerosis (MS) is a chronic complex autoimmune disease of the CNS. The specific criteria for MS are axonal degeneration and demyelination. Long non-coding RNAs (lncRNAs) appear to have an important role in the development and progression of MS. This study aimed to compare the lncRNAs, *MIAT*, *H19*, and *NRON* in peripheral blood samples of MS cases to a healthy control group. We collected blood samples of MS cases and controls. We focused on the expression of *MIAT*, *H19*, and *NRON* lncRNAs in peripheral blood samples of 76 relapsing-remitting (RR) and 19 secondary progressive (SP) MS cases and compared them with controls

using quantitative real-time PCR. Results indicated that *MIAT*, *H19*, and *NRON* expression levels were significantly increased in the RRMS and SPMS subgroups compared to the controls. A positive correlation was found between MS type and the expression levels of *MIAT* and *NRON* lncRNAs. Also, the expression level of *H19* was correlated with sex in MS patients. Based on the area under curve (AUC) values, *NRON* had the best performance in the differentiation of MS patients from controls (AUC = 0.94, $P < 0.0001$). A combination of *MIAT*, *H19*, and *NRON* expression levels could be useful in differentiating MS patients with 91.77% sensitivity, 73.35% specificity, and a diagnostic power of 0.91 ($P < 0.0001$). In conclusion, the levels of *MIAT*, *H19*, and *NRON* in peripheral blood could be important biomarkers for MS diagnosis.

Keywords: Multiple Sclerosis, LncRNA, Biomarkers, Real-Time PCR

CO36 Investigation of the influence of vitamin C against oxaliplatin-resistant HCT116 colorectal cancer cells

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Oxaliplatin (Oxa) is used as first-line chemotherapy in colorectal cancer (CRC), one of the most incidental and mortal types of cancer in worldwide. Acquired resistance to Oxa is an inevitable problem and the major reason for the failure of CRC therapy. Vitamin C, as a glycolysis inhibitor, selectively uptakes by KRAS and BRAF mutant CRC cells and induces cytotoxic effects by impairing cellular energy metabolism. We aimed to evaluate the cytotoxic activity of vitamin C on Oxa-resistant HCT116 colorectal cancer cells. Oxa-resistant HCT116 colorectal cancer cells were established by the exposure of HCT116 cells to increasing concentrations (0.5-4.3 μM) of Oxa. The cells which had grown exponentially in the presence of 4.3 μM Oxa were considered as Oxa-resistant HCT116 cells (HCT116/Oxa4.3). The viability of HCT116 and HCT116/Oxa4.3 cells at 48 h after a 2 h-treatment with vitamin C was assessed using MTT assay. The IC_{50} values of vitamin C against HCT116 and HCT116/Oxa4.3 cells were 0.6 ± 0.02 mM and 0.28 ± 0.08 mM, respectively, indicating that Oxa-resistant HCT116 cells were more sensitive to vitamin C compared to the parental cells. The results of colony formation indicated that vitamin C reduced the clonogenicity of both cells in a concentration-dependent manner with higher inhibitory potential against HCT116/Oxa4.3 cells. Wound healing assay results showed that the migration ability of HCT116/Oxa4.3 cells was lower than that of HCT116 cells and vitamin C had more anti-migratory activity against HCT116/Oxa4.3 cells compared to the control cells. In conclusion, HCT116/Oxa4.3 cells exhibited more sensitive than the parental cells to vitamin C, suggesting that vitamin C might be a promising candidate for further investigation for the treatment of oxaliplathin-resistant colorectal cancer cells.

Keywords: Colon cancer, Oxaliplathin, Drug resistant, Vitamin C

CO37 Isolation of actinobacteria with ability to degrade oil of wastewater from combined cycle power plants

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Increasing petroleum hydrocarbons pollution due to the continuous and increasing demand for oil and related products and the significant harmful effects of these pollutants on terrestrial and marine ecosystems, has caused much more attention and concern in recent years. Lubricating and cooling oils, which are used in industries such as combined cycle power plants to lubricate turbine bearings, generators and compressors, cause the wastewater of these industries to become oily. As regards these oily wastewaters can contain lethal and difficult degradable toxic substances, such as polyaromatic hydrocarbons, phenol, etc., if discharged to marine and terrestrial environments, they will have harmful effects on living organisms. The aim of the present study was to isolate and identify lubricating oil-degrading bacteria from oily wastewater of a combined cycle power plant. For this purpose, first, to enrich the oil-degrading bacteria, some wastewater of the combined cycle power plant was added to the bacterial liquid culture medium with equal volume. After incubation and growth, the bacteria were transferred to a culture medium containing lubricating oil and without any other carbon source. Then the

oil-degrading bacteria were purified using a solid culture medium and the effects of temperature and pH on their growth were investigated. PCR and sequencing of the 16S rRNA gene showed that the oil-degrading bacterium belonged to the *Actinobacteria*. In the culture medium containing oil as the only source of carbon, the temperature range of bacterial growth was 20 to 40 ° C and the pH range of growth was between 7 and 8. Optimal bacterial growth occurred at 35 ° C and pH 8. The results of this study indicate that the actinobacterial isolate obtained in this research can be used for bioremediation of oily wastewater of combined cycle power plants.

Keywords: Bioremediation, Hydrocarbon, Oily wastewater, Actinobacteria

CO38 The effect of citalopram as antidepressant drug on TM4 sertoli cells

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Depression, is a common chronic illness and crisis like the Coronavirus Disease 2019 (COVID-19) pandemic may increase the current prevalence of these illness. Citalopram is a antidepressants drug, which commonly is prescribed. Among the relatively neglected and less-studied potential side effects of psychotropic drugs are impairment of sperm parameters and fertility problems among male patient. The aim of this study was to evaluate the effect of citalopram on quantitative and qualitative parameters of sperm Which is important in fertility.In this study, the antiproliferative effect of citalopram on TM4 mouse sertoli cells at 24, 48 and 72 at concentrations of 0, 10, 50, 100, 120, 160 and 250 µM was investigated. These cells were cultured in DMEM/F12, HEPES containing 2.5% FBS, 5% HS and 1% of penicillin and streptomycin antibiotics. The morphology of the cells was examined using an electron microscope. MTT result was performed to determine toxic and non-toxic concentrations. Annexin-V expression was examined by flow cytometry to determine the type of induced death on cells. Microscopic observations of citalopram-treated cells and their comparison with each other at low concentrations showed little morphological changes; however, at concentrations of 120, 160, and 250 µM, certain morphological changes were observed in the treated cells. MTT results showed that increasing the concentration of citalopram significantly reduced (****p<0.0001) the proliferation of TM4 mouse sertoli cells. Also, analysis of Annexin-V expression by flow cytometry showed that the type of death induced by citalopram was apoptosis. The results of this study showed citalopram induced apoptosis in TM4 class sertoli mouse cells at high concentrations (120-250 µM) and it affected the natural morphology of sertoli cells. Therefore, the possibility of infertility disorders in the use of this drug should be considered.

Keywords: Fertility, Apoptosis, Depression, Flow cytometry, Cell proliferation

CO40 Investigating bacterial sources for vitamin K_2 production

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Vitamin K_2 is one of the three types of vitamin K, which produced by bacteria. It has an important role in bone and cardiovascular mineralization and prevents osteoporosis and cardiovascular disease that are of the major matters in public health concern. This vitamin is rare in dietary uptake. Thus, finding high vitamin production in bacterial strains can be valuable .Ten soil samples from different regions of Iran includes Golestan, Mazandaran, Markazi, and Tehran provinces were collected. These include forest, garden, farm, forest park, and red soil fields during April and May 2019. Bacillus strains were isolated and investigated for vitamin K_2 production through liquid state fermentation in specific media contain soy peptone, yeast extract, glycerol, and K_2HPO_4. The vitamin concentration measured in 248nm UV-spectroscopy following extraction by n-hexane: 2-propanol. High vitamin producing strains were biochemically characterized. From 97 isolated strains, 20 strains have higher absorbance value in comparison with a standard calibration curve. According to the biochemical characteristics, high vitamin producer isolates were *Bacillus subtilis*, *Bacillus cereus*, and closely

related bacteria. Isolating high vitamin K_2 producer strains is a global matter and soil is widely used as a major source of bacillus species that are candidates for high vitamin K2 producing strains.
Keywords Vitamin K, soil, *Bacillus*, fermentation, optical density

CO41 The effect of *Lactobacillus rhamnosus* on the concentration of liver enzymes in the serum of rats exposed to a toxic dose of acetaminophen

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High doses of non-steroidal anti-inflammatory drugs (NSAIDs) such as acetaminophen may cause oxidative stress and hepatotoxicity. Probiotic bacteria may have beneficial effects in preventing liver damage caused by oxidative stress. The present study aimed to investigate the effects of *Lactobacillus rhamnosus* on acetaminophen-induced hepatotoxicity. In this study, four groups (n = 6) of rats were used: negative control group, bacterial positive control group, acetaminophen positive control group, and the experimental group. The negative control group did not receive any treatment during the experimental period (21 days). The bacterial control group received 6×10^9 of the bacterial colony forming unit once daily for 21 days. The acetaminophen control group was given a high dose of acetaminophen (1 g/kg) on day 21 of the experiment. The experimental group received the bacterium for 21 days and received a high dose of acetaminophen (1 g/kg) on the last day of the experiment. On day 22, blood samples were taken from all the rats. Then, serum concentrations of alanine transaminase (ALT), aspartate transaminase (AST), and alkaline phosphatase (ALP) were measured. The results showed that on day 22 of the experiments, in the acetaminophen group, the concentrations of all the enzymes indicating the hepatotoxicity were higher than the other groups. Pretreatment of *Lactobacillus rhamnosus* for 21 days could significantly reduce the concentration of the enzymes that indicating acetaminophen toxicity. The administration of the bacterium alone had no significant effect on the serum concentrations of liver enzymes in the serum of rats. Therefore it can be concluded that, pretreatment of *lactobacillus rhamnosus* may reduce acetaminophen- induced hepatotoxicity.
Keywords: Alkaline phosphatase, Oxidative Stress, Probiotics

CO42 Electricity generation in a microbial fuel cell from dairy industrial wastewater using *Shewanella* ME-1

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Microbial fuel cell (MFC) is a new method for simultaneous wastewater treatment and electricity generation. In a microbial fuel cell, bacteria used a wide range of organic substrates to convert chemical energy into electrical energy. The aim of this study was to investigate the production of electricity by *Shewanella* ME-1from whey in a two-chamber MFC with aeration and non-aeration conditions at the cathode chamber. *Shewanella* was inoculated into LB broth and incubated for 24 hours at 30 °C. Then 1% of the fresh culture of *Shewanella* was inoculated into the anode chamber containing whey. The cathode chamber containing the phosphate buffer was continuously aerated 100 $mL.min^{-1}$ but the anode chamber was kept under anaerobic condition. The MFC was incubated at 30 °C for 48 hours and the maximum open circuit voltage was measured. The results of electricity measurement was showed a maximum voltage,maximum power densitie , current densitie in MFC containing whey with aeration at the cathode chamber were511.2 mV, 48.9 $mW.m^{-2}$,218.99 $mA.m^{-2}$. The COD of initial and final in MFC were measured 33188 and 26808 $mg.L^{-1}$, respectively. In addition, the maximum voltage,maximum power densitie ،current densitie in anaerobic MFC containing whey were measured 473 mV, 18.09 $mW.m^{-2}$,133.19$mA.m^{-2}$, respectively. The COD in MFC was measured 33188 and 29036 $mg.L^{-1}$, respectively. Also, the electricity generation in artificial wastewater containing 1% glucose was investigated and the maximum voltage, maximum power densitie ,current densitie were 461.6mV, 15.1 $mW.m^{-2}$, 73$mA.m^{-2}$. The COD in MFC was measured at 17188and

14376 mg.L^{-1}, respectively. The results of the current study showed that the highest electricity was generated in the aerated MFC containing whey. In addition, the lowest electricity was generated in the aerated MFC containing glucose artificial wastewater.
Keywords: microbial fuel cell, electricity generation, dairy industrial wastewater, *Shewanella*

CO43 Study of the interaction between new triazole-derived agonists and GABAA receptors

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Gamma-aminobutyric acid (GABA) is the most important inhibitory neurotransmitter in the brain. GABA works by acting on GABA Receptors. GABAA receptors are ligand-gated ion channels that are activated by the GABA molecule and have other sites for the binding of allosteric modulators. One of the most important of these sites, is the Benzodiazepine Binding Site. Benzodiazepines act as a positive allosteric modulator of the GABAA receptor. According to role that the GABA receptor plays in the central nervous system as well as diseases related to the nervous system, the study of agonists that can play a role in modulating this receptor is very useful for pharmaceutical studies. In this study, using docking and molecular dynamic simulation method; The interaction of new triazole-based benzodiazepine agonists with GABAA receptor was investigated. To perform these steps, a PDB file with the code 6HUP containing the human GABAA receptor structure and diazepam as the leader agonist was used. After calculating the structural parameters (such as: hydrogen bonding, gyrate radius, RMSF, RMSD) and thermodynamic parameters (such as: Gibbs free energy changes) of agonists in complex with GABAA receptor, finally agonists with desirable properties were chosen. The results of structural and thermodynamic parameters analysis were in good agreement. Selected agonists were synthesized for investigation of in vitro effects and were examined by Radio ligand receptor binding assay. In binding studies, compounds 4c and 5a (with Ki = 0.41nM and Ki = 0.48nM, respectively) showed the highest affinity for GABA receptor compared to Diazepam.
Keywords: GABA, Allosteric modulator, Benzodiazepine, Docking, Molecular Dynamic Simulation

CO44 Cannabis sativa Extract suppresses the expression of iNOS in spinal cords of Experimental Autoimmune Encephalitis mice as a model of Human Multiple sclerosis

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Experimental autoimmune encephalomyelitis (EAE) is an animal model of human CNS demyelinating disease, multiple sclerosis (MS). EAE is a complex condition in which the interaction between a variety of immunopathological mechanisms leads to an approximation of the pathological features of MS: demyelination ,inflammation, , axonal loss and gliosis. Inducible nitric oxide synthase (iNOS) is an enzyme that produces nitric oxide (NO) during the brain inflammatory conditions and is thought to contribute to the pathogenesis of multiple sclerosis. Cannabis sativa have been shown to pose potential therapeutic effects in different models of oxidative stress-induced neurodegenerative disorders.Herein, the potential effects of Cannabis sativa Extract (100mg/kg/day i.p.), as an herbal antioxidant was evaluated on the mRNA expression iNOS using real-time RT-PCR, following the induction of EAE. Although the expression of iNOS was increased in EAE mice spinal cords, administration of Cannabis sativa Extract could significantly suppress its expression at day 9 after induction of EAE, resulting in alleviation of overall inflammatory responses This indicates a potential therapeutic value of Cannabis sativa in MS patients and defines a new pharmacological tool for reducing the neuroinflammation and oxidative injury occurs in brains and spinal cords of the MS patients.
Keywords: Multiple sclerosis, iNOS, Cannabis sativa,EAE

CO45 Auraptene inhibited migration of human colon cancer cells *in vitro*

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More than 90% of cancer mortality is due to metastasis of malignant cells, as local or distance migration of cells makes their eradication by surgery or conventional chemotherapy and/or radiation therapy very difficult. Regarding colorectal cancer, approximately 20% of patients have metastases at diagnosis, most often to the liver, lung or peritoneum. Auraptene, 7-geranyloxycoumarin, is a *monoterpene coumarin* with numerous pharmacological properties such as antibacterial, antigenotoxic and cancer preventive activities. The present study was designed to investigate effects of auraptene on migration of human colon cancer cells *in vitro*.

After auraptene was synthesized using 7-hydroxycoumarin and transgeranyl bromide, its purification was done by column chromatography and ^{1}H- and ^{13}C-NMR experiments were used to confirm its structure. For wound healing migration assay, LoVo and HT-29 cells were seeded in 24 well plates and after 24 h, a straight scratch was made by a sterile pipette tip to create a gap with constant width. After washing the cells with PBS, they were treated with 20 and 40 μM auraptene and incubated at 37˚C in the presence of 5% CO_2 for several days. To note, untreated cells and cells treated with 0.4% DMSO, as auraptene solvent, were considered as control. Finally, cells migrated to the gap were photographed and analyzed by Image J software. Obtained finding indicated that auraptene inhibited the migration of both cell lines in a dose dependent manner. For LoVo cells, 20 μM auraptene reduced the number of migrated cells after 48 h, while the optimum time point for 40 μM auraptene was 24 h. In case of HT-29 cells, which have lower migration ability, 20 and 40 μM auraptene inhibited cell migration upon 144 h and 72 h of incubation, respectively. Taken together, our results suggest auraptene as a potential anti-migratory agent in colon cancer cells, although its effect needs to be further investigated *in vivo*.

Keywords: auraptene, colon cancer, cell migration, *in vitro* assessment

CO47 Evaluation of the Nanoparticles Containing Tyrosol Effect on the Expression of GLUT2 and GLUT9 Genes in Diabetic Rats

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Diabetes, a metabolic disease with decreased insulin secretion or insulin insufficiency and high blood sugar, has three different types, and about 90 percent of type 2 diabetes. Given the destruction of the International Diabetes Association (IDF), which will increase the number of patients to 592 million by 2025, it is crucial to address the challenge of treating type 2 diabetes (1, 2, 3). High blood sugar is one of the aggravating factors of this disease, and so far, the conventional treatment strategies have not been effective in transferring glucose into the cell. GLUT2 and GLUT9 are facilitated membrane glucose transporter that facilitates blood glucose release through the kidney, liver, and placenta's plasma membrane. In addition to its anti-inflammatory and antioxidant properties, tyrosol has been shown to have insulin-like functional properties that face the challenge of targeted cell delivery. Niosome carriers; or nonionic surfactant vesicles can be valuable in the targeted delivery of tyrosol to the cell .In this study, Niosome carriers' function in targeted tyrosol transfer to rat hepatocytes was evaluated by measuring the expression of GLUT2 and GLUT9 genes. For this purpose, diabetic rats were divided into five groups: control, diabetic, nanoniosome, tyrosol and nanotyrosol and were treated for 45 days. After dissection and extraction of liver tissue, the expression of GLUT2 and GLUT9 genes was measured by real-time PCR. The nanotyrosol and tyrosol groups showed the highest gene expression, respectively.

Keywords: Type 2 diabetes, Thyrozol, Niosome, GLUT2, GLUT9

CO48 Synthesis and studying of Nano-Niosome formulation containing Thymus essential oil and its effectiveness in fungal infections

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In this study, we optimized the Nano-Niosome formulation containing Thymus essential oil(TEO). The effect of the dose of this drug for the treatment of fungal infections was investigated. We aim is to reduce the dose, cytotoxicity and prevent fungal infections in cell culture and a suitable alternative to chemical drugs .In this study, we prepared Nano-Niosomes based on surfactant for proper attachment to the fungal wall and using the thin-film hydration method. using the UV-Spectrophotometric (evaluate of encapsulation and drug release), DLS(determine the size), TEM (determine the morphology), FTIR spectroscopy(interaction between drugs and Nanocarrier) .The structure of Niosomes containing tween 60: cholesterol: DPPC: PEG (ratio 20:30:50:3), was designed and developed. In the proposed formula: Rate of entrapment efficiency 88.20%, Niosomes-Thymus 24h, 54 ٪, size 150 nm, dispersion index 0.22 and Zeta is (-20.56mv). FTIR spectral data showed that drugs and Nano-carriers did not react chemically with each other. Free drug molecules (Niosome and TEO) at a concentration of 100 µg/ml caused the toxicity of cells, and the survival rate of the cells is, 91.5%, 38% respectively. Whereas, the toxicity of encapsulated drugs at a concentration of 200 µg/ml, was lower compared to free drugs, and the cell survival rates were, 54.88%. We were able to optimize Nano-carrier drug-delivery compounds based on surfactant and proportional to the structure of fungal cells, which has the ability to bind to the fungal cell wall. As a result, we can with this method treat or prevent fungal-infected cells.

Keywords: Nano-Niosome, Encapsulation, Thymus essential oil, fungal cells

CO49 Design, Synthesis and Evaluation of 1,3,5 Triphenylbenzene Derivative Compounds as Effective Inhibitors of Amyloid Fibril Formation

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Inhibition of the amyloid aggregates as pathological hallmark of various neurodegenerative diseases are one of the therapeutic approaches which still attracts scientific research interest. One approach to the development of therapeutic agents in neurodegenerative diseases has been the use of small molecules that specifically and efficiently inhibit the aggregation process. In the present study, a series of small aromatic compounds with different substitutions of 1,3,5-triphenylbenzene have been synthesized and their possible effects on amyloid fibril formation by hen egg white lysozyme (HEWL), a model protein for amyloid formation, and of their resulting toxicity were examined. Acidic pH and high temperatures were used to drive hen lysozyme towards amyloid formation. The inhibitory effect of the compounds against HEWL amyloid formation was analyzed using thioflavin T and Congo red binding assays, atomic force microscopy, Fourier-transform infrared spectroscopy, and cytotoxicity assays, such as the 3-(4,5-Dimethylthiazol)-2,5-Diphenyltetrazolium Bromide (MTT) reduction assay(with SH-SY5Y human neuroblastoma cells) and caspase-3 activity measurements. We found that all compounds in our screen were efficient inhibitors of HEWL fibril formation and their associated toxicity. We showed that electron-withdrawing substituents such as –F and –NO2 potentiated the inhibitory potential of 1,3,5-triphenylbenzene, whereas electron-donating groups such as –OH, –OCH3, and –CH3 lowered it. These results may ultimately find applications in the development of potential inhibitors against amyloid fibril formation and its biologically adverse effects.

Keywords: lysozyme aggregation, thioflavin T, Cell cytotoxicity, small aromatic molecules

POSTER PRESENTATIONS

CP1 Control of microorganisms in drinking water using biocompatible and biodegradable composite nanofibers based on polyvinyl alcohol/cyclodextrin

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The removal procedure of pathogenic microorganisms from drinking water is of special importance. Conventional methods such as application of chemicals, ozonation, ultraviolet light and membrane processes have been used to disinfect drinking water. The purpose of this study is to improve the quality of drinking water by removing *Navicula* algae as an indicator of water pollution using new fibrous nanostructures in the adsorption process. Nanofibers as one-dimensional nanostructures have remarkable physicochemical properties such that not only they have a high surface area, but also suitable mechanical connections in them cause effective communication of various microorganisms with the components of the fibrous network. In this study, biocompatible and biodegradable composite nanofibers of polyvinyl alcohol/cyclodextrin were synthesized using fast, controllable and environmentally friendly electrospinning method. The final products were characterized by various techniques such as scanning electron microscopy, nitrogen adsorption/desorption technique, and thermal and phase stability analyses. Due to the nanometer range of the nanofibers (30 nm), desirable specific surface area (680 m^2/g), and considerable thermal stability (175 °C), these novel composite nanostructures are used to control the microorganisms in drinking water. After culturing *Navicula* algae, the results showed a significant reduction in the colony of microorganism species to 2 colonies. It seems that the favorable physicochemical properties of nanocomposite samples, as well as their high specific surface area have a significant effect on the performance of these nanostructures. Systematic process studies are recommended in order to achieve controllable properties of products and also to study synthetic parameters on the removal of microorganisms.

Keywords: composite nanostructures, physicochemical properties, polyvinyl alcohol compounds, microorganisms.

CP2 Optimizing the conditions for thiolation of magnetic chitosan- CNT

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Chitosan is a linear polysaccharide which deacetylated derivative of the biopolymer chitin for nanotechnology applications due to its unique characteristics such as the lake of nontoxicity, excellent biocompatibility, and biodegradability. Magnetic nanoparticles (MNPs) have a large specific surface area and provide rapid and easy recovery of the biocatalyst from the reaction. Carbon nanotubes (CNT) have a higher surface area for enzyme immobilization and the conjugation of enzymes with CNT can increase the stability and activity of the enzyme. This study aimed to optimize the conditions for thiolation of magnetic chitosan- CNT for enzyme immobilization. Fe3O4 nanoparticle was made by the CO-precipitation method in which chitosan was coated on the Fe3O4 during adding TPP. Then multiwalled CNT was functionalized with carboxyl groups (CNT-COOH) and cross-linking with amine groups of chitosan by glutaraldehyde. Thiolated chitosan was synthesized using different concentrations of 0.5, 0.75, 1 M TGA in the presence of 1-ethyl-3-3(3-dimethylaminopropyl) carbodiimide hydrochloride (EDC). Ellman's method was used to determine the amount of thiol groups. The composites characterized by Fourier transform infrared spectroscopy (FTIR). The result showed magnetite – chitosan and magnetite- thiolated chitosan-CNT were absorbed by external magnetite and that enzyme binding to the thiol functional group of chitosan was successful. The prepared TCS could be used for biomedical applications such as drug and gene delivery, enzyme application such as enzyme immobilization for removing heavy metals from wastewater, and preparation of biosensors.

Keywords: Thioglycolic acid, Glutaraldehyde, Enzyme immobilization, Biosensor

CP3 Isolation and Screening of Microbial Protease Enzymes from Soil

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Proteases are enzymes that hydrolyze peptide bonds of proteins due to their highly selective modality and high activity at very low concentrations. Recently, microbial protease have been widely used in various industrial fields such as (cosmetics, food, pharmaceuticals, leather, detergents, livestock and poultry feed, etc.). By studying various sources, researchers have obtained protease enzymes from plants, animals, and microorganisms. two-thirds of the world's commercial proteases produced by microorganisms. One of the methods of production and development of protease enzymes from microbial sources is the use of microbial waste and isolation of microorganisms growing on them. The aim of this study was to screen and isolate proteolytic bacteria from the soil of slaughterhouse areas. Soil is an ideal source of many microorganisms that produce extracellular enzymes. soil samples were collected from the area around the slaughterhouse located in Charmshahr, Isfahan. Bacteria were isolated by dilution series technique and selected from 10^{-8}dilutions. Selective isolates were screened for extracellular protease production. For qualitative analysis (hydrolysis region), all isolates were inoculated in gelatin agar and skim milk plates and incubated in $37C^0$. 2 isolates (D3 and G2) with the largest clear area were selected. By the growth optimization technique and drawing the standard diagram, the best growth temperature and time were obtained at 37 C^0 and 20 hours, respectively . Isolates after Gram stain test for more accurate, identified by 16S-rDNA ,The isolates were from the Bacillus family. By complementary techniques such as biochemical tests and by providing various protein sources such as blood and bone waste, selective isolates can be evaluated and used on an industrial scale.

Keywords: Microorganism, waste, protein, proteolytic

CP4 Cytotoxicity assay of some amide derivatives using luminescent *Vibrio* isolated from the Caspian Sea

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Today, given the extensive pollution of water, food, and environment by different pollutants, use of novel, fast, and efficient methods of detecting pollutants is being paid much attention. One of the methods of measuring the toxicity of the samples is to use luminescent bacteria for assessing toxicity based on bioluminescence inhibition. The unique characteristic of luminescent bacteria makes them suitable for measuring toxicity. The objective of this study was to measure the toxicity of amide compounds and their derivatives in foods by bioluminescence inhibition of luminescent *Vibrio* MM1. The luminescence of the luminescent bacteria were assessed by a luminometer. To do this, one ml of some amide derivatives including acrylamide, tio-urea, and bis-acrylamide at 10^{-1}-10^{-8} gL^{-1} was added to one ml of bacterial growth medium for 18-24 h. The toxicity of amide derivatives was measured based on the luminescence reduction of *Vibrio* by using luminometer. To assess the toxicity, EC_{50} parameter was measured. The results showed that the luminescence greatly decreased in the presence of amide derivatives. Bis-acrylamide at 10^{-1} gL^{-1} had the greatest effect on the luminescence reduction as the Vibrio luminescence decreased from 14×10^{-6} RLU to 3.5×10^{-6} RLU. Also, EC_{50} values for acrylamide, bis-acryl and tio-urea were 2.63×10^{-4}, 1.17×10^{-4}, and 2.18×10^{-4} gL^{-1}, respectively. Thus, bis-acrylamide showed more toxicity than acrylamide and tio-urea. The results revealed that the luminescent bacterium Vibrio MM1 was a good choice for examining the presence of amide compounds in food and wastewater.

Keywords: luminescent bacterium, toxicity assey, wastewater, pollution

CP5 Bovine Tendon-Derived Extracellular Matrix Enhances the Growth and Proliferation of Cerebral Microvascular Endothelial Cells

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The basement membrane surrounding the microvascular endothelial cells in the brain has an essential role in maintaining the integrity of the blood-brain barrier (BBB). To develop an *in vitro* BBB model, beyond having specific endothelial cells called cerebral microvascular endothelial cells and their junctions, recreating proper basement membrane using extracellular matrix (ECM) components is necessary. Accordingly, we attempted to extract the ECM of bovine tendon tissue. We used two decellularization methods: physical (lyophilization) and chemical (washing with triton x-100), followed by protein solubilization in urea. Protein pattern was analyzed by SDS PAGE and measuring protein concentration using BCA kit indicated higher protein extraction yield from physical decellularization. Pre-coating the culture plates with sterilized extracted ECM showed an increase in the proliferation of the human cerebral microvascular endothelial cells (hCMECs) in a dose-dependent manner. To verify the details of ECM mechanism of action on the BBB properties, more investigations on the BBB model's functions/structure such as its angiogenesis, tight junction structure, and permeability rate are needed.

Keywords: Basement membrane, Blood brain barrier, Decellularization

CP6 Structural study and sub-cloning of a type of endolysin

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Identification of new antibacterial compounds as a treatment is a way to solve the health care against antibiotic resistant infections. Lysines, are one of antibacterial agent against to remove antibiotic resistant infections.N-acetylmuramyl-L-alanine amidases, also known as Endolysins, which encode in phage's genome are ableto break down the amide bonds in the peptidoglycan wall of bacterial. The physicochemical properties and secondary and tertiary structure of this enzyme were studied by bioinformatics softwares and the predicted-tertiary structures evaluated by q-mean software (0.6% confidence). The synthetic gene encoding N-acetyl muramyl-L-alanine amidase of SPP1 phage was subcloned in pET28a vector. The clone was confirmed by enzymatic digestion.The exoression of the recombinant protein was induced by IPTG 100mM and purified by 100mM imidazole gradient using a Nickel column chromatography. Toremove salts and imidazole, recombinant enzyme was dialyzed against PBS buffer for 3 h. Bioinformatics studies showed that this protein has pI 9.6, molecular weight 30 kDa, alpha index 83.87 and a polarity index of -0.49. The secondary structure of this protein includes of 34.32% of alpha helix, 6.64% of beta sheets, 23% of extended strands, and 35% of random coils. The 33kDa band enzyme observed in SDS-PAGE 12%. Surveying the enzymatic reactions for the antibacterial effect on *E.coli* and *S. aureus* is under processing

Keyword: Endolysin,Phage SSP1, N-acetylmuramyl-L-alanine amidases, recombinant Gene

CP7 Evaluation of IL-23 Gene expression in cardiovascular patients and its comparison with coronary artery disease

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Atherosclerosis is a chronic inflammatory disease of the walls of blood vessels that involves both innate and acquired immune systems. The role of IL-23 in inflammatory diseases, autoimmunity and coronary artery disease has been considered in recent years.The aim of this study was to evaluate the expression of inflammatory cytokine IL-23 in peripheral blood lymphocytes (PBMCs) in patients with coronary artery disease .In this study, after collecting blood samples, patients with more than 50% coronary artery occlusion were classified as the study group and patients without coronary artery stenosis as the control group .Then RNA isolation as well as cDna fabrication was performed for all groups and finally the expression level of IL-23 gene was quantitatively

examined by Real Time PCR .The findings of this study showed that there was no statistically significant difference between IL-23 gene expression and coronary artery pathogenesis (CI = 0.39-0.3, P = 0.812) .It should be noted that the results in both tests were obtained from diabetic and non-diabetic people, people with high blood pressure and people without blood pressure at a value of $P_{value} > 0.05$ .Statistical data in this study show that the expression of IL-23 gene did not have a significant effect on the pathogenicity of people with coronary artery disease, while it was previously shown that the expression of IL-23 gene had a significant role in this disease .These results indicate that IL-23 can be used for therapeutic applications in such diseases.

Keywords: Atherosclerosis, Real time PCR, Diabetes, Blood pressure

CP8 Simple and Green Synthesis of Carbon Dots from the Fruit of the Pyracantha Plant

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Carbon Dots is the new class of fluorescent carbon nanoparticles with a particle size of less than 10 nm that have many applications in various fields including Bioimaging, Bioassays, and disease diagnosis. These particles have excellent biocompatibility, unique optical properties, high stability, low toxicity, and good solubility in water. In this study, Pyrolysis and Hydrothermal methods are used to make these Carbon Dots, which are cost-effective and easy methods. In the hydrothermal method, the precursor of the Pyracantha fruit, was prepared and placed in a 50 ml stainless steel autoclave then distilled water was added, afterward placed in the oven. By optimizing the plant precursor ratio, temperature, and reaction time ،carbon dots with high fluorescence property was obtained. In the Pyrolysis method،the precursor was subjected to high and direct oven temperature and carbon dots with optimal fluorescence was obtained. Subsequently, by comparing the fluorescence intensity of Carbon Dots obtained from both methods, the hydrothermal method was selected as a more appropriate method due to its higher fluorescence emission. In general, these prepared carbon dots have promising potential and many applications in nanotechnology.

Keywords: Carbon nanomaterials, Natural Precursor, Fluorescent material, Hydrothermal, Pyrolysis

CP9 Scrutiny the interaction of irinotecan with human serum albumin by multi-spectroscopic techniques: identification of possible binding site of the drug

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Irinotecan is considered to be one of the most effective anticancer drug for colorectal cancer therapy. In this study, the role of human serum albumin (HSA), as safe drug delivery systems, in binding of irinotecan were surveyed. The interactions between irinotecan and HSA have been studied by fluorimetry, circular dichroism (CD) and Fourier transform infrared (FT-IR) spectroscopy. By the analysis of fluorescence spectra, it was observed that irinotecan has an ability to quench the intrinsic fluorescence of HSA through a static quenching procedure. According to Stern–Volmer equation, the binding parameters between irinotecan and HSA were determined. The enthalpy change (ΔH°) and entropy change (ΔS°) were calculated to be -29.82kJ mol^{-1} and -22.15J mol^{-1} K^{-1}, indicating that the hydrogen bonds and van der Waals interactions played a dominant role in the binding. The distance, *r*, between donor (HSA) and acceptor (irinotecan) was obtained according to the forster's theory of non-radiation energy transfer. Changes in the CD spectra and FT-IR spectra were observed upon drug binding. The quantitative analysis of CD spectra represented that irinotecan induced alterations in the secondary structure of the protein via increasing in the content of α-helical structure of protein.

Keywords: Fluorescence quenching, Stern–Volmer, Circular Dichroism (CD), Fourier transform infrared (FT-IR)

CP10 Bacterial surface display of VEGF with the aim of the design of a whole-cell biosensor

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Cell surface display technology has recently gained much attention as a powerful tool for biotechnology and biomedical applications. Here, we used the bacterial surface display system for VEGF expression on the surface of *E. coli* fusing it with the InaK anchoring motif from an ice nucleation protein. Vascular endothelial growth factor (VEGF) is a key regulator of both physiological and pathological angiogenesis. To create the desired construct, after digestion of the amplified VEGF gene and pET21a vector containing the encoding gene of truncated INP (InaK) using the identical restriction enzymes (HindIII/XhoI), the VEGF gene was ligated into the vector. The construct was transformed into *E. coli*, BL21 (DE3), followed by the screening of positive colonies and induction of the recombinant bacterial cells with IPTG at 27 °C for 6 h. After harvesting and lysis of the cells, the bacterial cell wall was analyzed by SDS-PAGE to evaluate VEGF display on the cell surface. The results confirmed the over-expression of VEGF on the surface of bacteria. Such a cell surface display system could be considered as a good platform for the design of whole-cell biosensors.

Keywords: Cell Surface Display, VEGF, Whole-cell Biosensor

CP11 Optimization of the synthesis chitosan fluorescent carbon dots for cellular imaging

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Recently, carbon dots with indicative characteristics, such as adjustable fluorescence, high optical stability, water solubility, biocompatibility, and easy and simple synthesis have been used in cell imaging. During the recent years, synthesizing carbon dots from the green sources have been absorbed more attention. In this research, this natural biopolymer is used to synthesize green carbon dots during two different methods of hydrothermal synthesis at 180 °C for 10 hours. Then, physical measurements, quantum efficiency, and photoluminescence characterizations of carbon dots were investigated. In one method, a combination of chitosan and citric acid was used, and in the second one, a combination of chitosan and ethanol was used. The results confirmed that synthesized carbon-dots had both specified properties. In another hand, a comparison of these two methods stated that the quantum efficiency in the first synthesis is better than that of in second synthesis. Also, luminescence properties of both syntheses at 390 nm wavelength showed that the first synthesis had more ideal luminescence rather than the second one. Herein, the first synthesis is preferred to cellular studies.

Keywords: Quantum efficiency, Ethanol, Citric acid

CP12 Evaluation of antibacterial properties and wound healing ointment based on curcumin and honey

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Wounds from various burns can severely impair the life quality of patients. The use of natural compounds in the treatment of various diseases has long been considered. Curcumin and honey have been used as traditional wound-healing medicines in some ancient civilizations. The study aimed to investigate the synergistic healing properties of these substances as a novel burn ointment in secondary burn wounds. In this study, MIC_{50} and MIC_{99} use of curcumin and honey on 200 clinical isolates of *Pseudomonas aeruginosa* were compared with imipenem *in vitro*. Their killing time and cytotoxicity were also studied using standard *P. aeroginosa* isolates, fibroblast stem cells, and mouse embryonic fibroblasts, respectively. Then, 150 male Wistar rats weighing between 280 and 300 gr were divided into four experimental groups receiving a newly prepared burn ointment

containing honey and curcumin, ointment base, zinc oxide ointment, and no treatment as the control for 3 weeks on the experimentally induced burn wounds. Histopathological and histomorphological assessments were then conducted on the injured area to evaluate the efficiency of the prepared burn ointment MIC_{50} and MIC_{99} against *P. aeruginosa* were at least 64 and 128 μg mL^{-1} for imipenem, 16 and 32 μg mL^{-1} for curcumin, and 8 and 16 μg mL^{-1} for honey. Histopathological results showed wound re-epithelialization According to the results, it can be claimed that burn ointment containing honey and curcumin has a significant effect on accelerating the healing of burn wounds.

Keywords: Wounds, Second-degree burns, Medicinal plants, Burn healing

CP13 Simulation of erythrocyte membrane disruption by the anticancer peptide tritrpticin

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According to the World Health Organization in 2020, the annual incidence of cancer has exceeded 18 million patients. Cancer is predicted to be the number one cause of death in the world in the future. Efforts are made to discover an effective treatment with the aim of overcoming the drug resistance. The membrane disruptive peptides have been introduced as a new generation of receptor-independent drugs in the treatment of cancer. They are less likely to cause resistance, but they are toxic to normal cells and their structural properties should be modified. An essential prerequisite in this process is to understand the structure-function mechanism by simulating the molecular dynamics of a peptide–membrane system. Therefore, in this project, the role of the anti-cancer peptide, Tritrpticin, in disrupting the erythrocyte membrane was analyzed by molecular dynamics simulations. In this regard, both erythrocyte membrane with realistic lipids content and Tritrpticin (1D6X), were simulated for 100ns with charmm36 force field in a isothermal-isobaric ensemble (NPT) and target temperature of 310.15K°. For analyzing peptide-membrane interactions, the peptide structure was prepared at a distance of 3 nm from the surface of the RBC membrane. Then the peptide-bilayer system, simulated for 100ns in same NPT conditions. Analyzing kinetic and potential energy surfaces, charge density and roughness of bilayer surface and changes in peptide RMSD and RMSF contents, indicates tritrpticin affinity for disrupting erythrocyte membrane. These results are consistent with experimental studies of Arias et al. It is suggested to perform steered molecular dynamics simulations to evaluate the free energy between two components.

Keywords: Molecular dynamics, Gromacs

CP14 Comparison of bioinformatics algorithms and tools related to RNA-Protein interactions

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Proteins and nucleic acids play an important role in the biological diversity of living organisms, and each has its structural and functional characteristics. Therefore, RPI (RNA-Protein Interaction) prediction is of significant importance. Protein-RNA interactions (RPI) play a key role in most cellular processes such as transcription, reverse transcription, post-transcription processing, replication, RNA transmission, translation, and regulation of RNA values in the cell. Various high-power laboratory methods are used to identify RPIs that generate valuable data, but these tests are costly, and time-consuming. Therefore, various computational methods have been developed to study, analyze, and build RPI networks. In this regard eight important algorithms (PRINTR, PLPIHS, XGBPRH, LPI-IBNRA, Xpred RBR, Struct-NB, SRC PRED, and RPiRLS) were investigated. Assessment of accuracy indices using LooCV and 10-fold-cross validation showed that LPI-IBNRA algorithm, with accuracy (88%) and percision (87%) in the 4796 data set known protein-lncRNA interaction from NPInter V2.0 database is more powerful than other comparable algorithms.Finally, it should be noted that some important and unsolved biological problems in this field are related to the specific binding of a protein to its target RNA. Therefore, creating algorithms for the role of RPI monitoring in diseases,

identifying RPI in viruses, introducing more suitable features for use in RPI prediction algorithms, determining RPI patterns in mitochondria, and chloroplasts of plants and using combination methods and deep machine learning, and has been proposed to produce more powerful bioinformatics tools to predict RPI.
Keywords: Algorithms, accuracy indicators, software, computational methods, machine learning

CP16 Synthesis of carbon quantum dots from natural precursors of Vitaseae using bottom-up Methods

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In recent years, carbon quantum dots have been considered due to their suitable properties and have found many applications. Optimal properties of carbon quantum dots include low toxicity, long life, good optical properties, high stability and good solubility in water. Different methods and precursors have been introduced for the synthesis of carbon quantum dots. Among these, the use of natural precursors have an important place due to their low price, availability and environmental friendliness. In this study, the natural precursor Vitaseae was used to synthesize carbon quantum dots. There are two general methods of top-down synthesis and bottom-up synthesis for the synthesis of carbon quantum dots. In this study, two bottom-up synthesis methods (pyrolysis and hydrothermal) have been used. The most important advantages of the methods used are the ability to control the size of the product, the ability to mass produce and the ability to better control the chemical structure of synthesized carbon dots. First, the natural precursor of Vitaseae was prepared. Then synthesis was performed using two methods of pyrolysis and hydrothermal. Then the time and temperature required for the synthesis of carbon quantum dots from the Vitaseae precursor was optimized. Finally, the fluorescence intensity of the synthesized carbon quantum dots was measured. According to the obtained results, the carbon dots synthesized from Vitaseae natural precursor by pyrolysis and hydrothermal methods had high fluorescence intensity. Also, the synthesized carbon dots had high stability and good aqueous solubility. The desirable properties of synthesized carbon quantum dots make it possible to use these materials in a variety of biological applications.
Keywords: Carbon nanomaterials, Green synthesis, Pyrolysis, Hydrothermal, Fluorescent material

CP17 Utilization of reducing potential of *Kalanchoe daigremontiana* extract in production of gold nanoparticles

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The rapid and wonderful development of nanotechnology, both in the field of making nanoparticles and nanostructures and in the field of widespread applications, has made it one of the requirements of human life. Of the various nanoparticles, metal nanoparticles and especially gold nanoparticles have attracted more attention due to their many and increasing properties and applications. Among the three physical, biological and chemical methods for the production of nanoparticles, the biological method has the most advantages due to its cheapness, high speed, ease of production and safety and compatibility for living organisms and the environment. The aim of this study was to biosynthesis of gold nanoparticles using the extract of *Kalanchoe daigremontiana*. The leaf extract of plant was exposed to a solution of gold salt ($HAuCl_4.3H_2O$) at a concentration of 1 mM. The change color from pale yellow to purple red was the first sign of the production of gold nanoparticles. Subsequent spectrophotometric analysis showed a specific adsorption peak of nanoparticles (about 550 nm). Transmission Electron Microscope (TEM), Sscanning Electron Microscope (SEM), particle size analysis (PSA) and X-ray diffraction (XRD) were used to analyze the size and shape of the nanoparticles. They showed that produced nanoparticles were spherical with an average size of 35 nm. The results of infrared spectroscopy (FTIR) analysis also showed that heterocyclic compounds such as alkaloids and flavonoids in plant extracts reduce metal ions and produce gold nanoparticles.
Keywords: Reducing potential, Plant, *Kalanchoe daigremontiana*, Gold nanoparticles

CP18 The effect of a tumor targeting peptide on the proliferation and migration of breast tumor cell line

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Vascular endothelial growth factor (VEGF) family members and their receptors (VEGFR) are essential in the formation of new blood vessels by angiogenesis. Recent studies aimed at inhibiting angiogenesis have focused specifically on inhibiting the VEGF-R2 receptor, and significant advances have been made in clinical trials of antagonists designed as antiangiogenic agents. In the present study, based on the VEGF-A/VEGF-R2 structure, a cyclic peptide (VGB-A1) was designed from the L1 loop region containing residues 33-51 of VEGF-A. The ability of VGB-A1 bound to both VEGF-R1 and VEGF-R2 receptors was evaluated and the bioactivity and efficacy of the peptide were evaluated in vitro. Based on immunocytochemical studies, VGB-A1 bound to VEGF-R2 and blocked their homo- and heterodimerization in 4T1 mammary carcinoma tumor cells. Peptide blocked cell migration and metastasis by inhibiting phosphorylation and thus inhibiting the activation of ERK1/2, AKT and further inhibiting the FAK/Paxillin, MMP and E-Cad signaling pathways in 4T1. VGB-A1 can be a strong candidate for therapeutics in various angiogenesis therapies, especially cancer.

Keywords: VEGF-A, KDR, Angiogenesis, Peptide Design

CP19 Ginkgobiloba plant extract decreases cell proliferation by induction of apoptosis in KG1-a , acute promyelocytic leukemia cells.

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Recently, scientists have reported that Ginkgobiloba inhibited the growth of HCT116 human colorectal cancer cells. In the present study, we evaluated cytotoxic effects of Ginkgobiloba that inhibited the proliferation of the KG1-a acute promyelocytic leukemia cells through induction of apoptosis. The KG1-a cells were cultured in the presence of various concentrations (100-1000 μM) of the compound for 3 days and cell viability was determined by MTT assay. Induction of apoptosis was qualitatively assayed by Hoechst 33342 staining. Ginkgobiloba decreases cell proliferation of the KG1-a cells in a dose- and time-dependent manner. The IC50 value following 72 h exposure was found to be 350 μM for the cells. The results of fluorescence microscopy indicated that the Ginkgobiloba induced apoptosis in KG1-a cells. Taken together, these results suggest that this compound with significant anticancer activity can be proposed as effective agents for further investigation in the future.

Keywords: Cytotoxity, Fluorescence, Anti tumoric compound

CP20 Study of the anti-cancer effects of Grandivittin on A549 lung cancer cell line

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Lung cancer is one of the most common cancers and the leading cause of cancer death. It is estimated that there are approximately 1.5 million deaths from lung cancer worldwide each year. Therefore, identifying new diagnostic markers and treatment goals for lung cancer is very important. Because common drugs cause cell resistance and have many side effects. Therefore, finding a plant-based agent to control cancer can be very promising. In this study, we investigated the toxicity of coumarin derivatives (Grandivittin) extracted from the native plant of Iran through MTT, flow cytometry methods, and its effect on the expression of apoptotic pathway genes through Real-time PCR on A549 cell line. We have observed that this substance at a concentration of 0.7 μM has a toxic effect and can induce apoptosis in treated cancer cells.

Keywords: cell line treatment, coumarin, gene expression, apoptosis, IC50

CP21 The study of genotoxic and cytotoxic effects of the gum of *Ferula gummosa* on A-375 cells

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Melanoma is a malignant skin cancer with a high potential for metastasis that arises from melanin-producing cells. A-375 cells, are proper model for the study of cancer drugs and inhibitors. *Ferula gummosa* grows in different parts of Iran. In the past, it used to reduce abdominal pain, to treat Rheumatism and diabetes, and also is used as laxative. *F. gummosa* has a milky white gum obtained from its root and bark. In this study, we investigated the cytotoxic effect of *F. gummosa* on A-375 cells. After preparation of the gum of *F.gummosa*, A-375 cells were treated with different concentrations of the gum for 48 hours. The IC_{50} value of the gum for A-375 cells was calculated to be 8 µg/ml. The DNA fragmentation assay showed that treatment of cells with lower concentrations of the gum also led to cell death and genomic DNA fragmentation. The results of wound healing assay showed that the gum inhibited the invasion of treated cells in concentration-dependent manner. The results of Micronucleus experiments showed that the gum of F. gummosa induced the formation of micronucleus and inhibited the cell proliferation in treated cells. Our results showed that, due to having different chemical compounds, the gum of *F. gummosa* can inhibit cancer cells proliferation.

Keywords: *Ferula gummosa*, Cytotoxicity, Genotoxicity, Melanoma

CP22 Improving the Stability of Anterior Gradient 2 Protein Using Rational Design

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Despite major advances in wound healing, healing remains one of the major challenges ahead. One of the effective factors in improving the wound healing process is AGR2 protein and can be effective as a local factor in the healing process. Therefore, increasing thermodynamic stability and ensuring the effectiveness of this protein as a drug is important. To date, no studies have been performed to increase the thermodynamic stability of this protein using point mutations. The aim of this study was to improve the thermodynamic stability of a protein using targeted point mutations in its amino acid sequence. For this purpose, the structure of AGR2 protein in the PDB database was first systematically analyzed using Dezyme software and the parts of the structure that are most likely to be stable after mutation were identified. By comparing these data with information from previous structural studies on protected and unprotected areas, a total of 3 unprotected points were selected to create point mutations. Using the DynaMut server, we first predicted changes in protein stability due to Y150K, N163F, and S65L point mutations individually. Then, in a study, the effect of all 3 mutations together on the stability of the protein by the mentioned server was studied. The results of these studies showed that the stabilizing effect of Y150K, N163F and S65L mutations were 0.374, 0.533 and 2.165 kcal/mol, respectively. Also, the stabilizing effect of these three mutations together on the stability of the protein was approximately 1Kcal / mol. Therefore, applying all three of these mutations together has a better effect on increasing the thermodynamic stability of the protein by reducing energy. Experimental confirmation of the effect of these mutations on protein stability and their in vitro studies could offer new perspectives in this field.

Keywords: Site-directed muttion, Wound healing, Dezyme Software, DynaMut server

CP23 Downregulates the expression of Toll-Like Receptors in Experimental Autoimmune Encephalitis mice by Picrocrocin

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Multiple sclerosis is a neurodegenerative disease of CNS in which, inflammation causes the myelin to disappear, ensuing disturbances in vision, speech, walking and memory. This overwhelming inflammatory pattern is accompanied by a progressive increase in free-radicals generation resulting to oxidative stress. Toll-like receptors (TLRs) are a class of proteins that play a key role in the innate immune system. TLR-mediated activation of innate immunity is involved not only in host defense against pathogens but also in immune

disorders such as MS. The aim of this study was potential therapeutic effects of Picrocrocin in different models of oxidative stress-induced neurodegenerative disorders. Following the induction of Experimental Autoimmune, the potential effects of Picrocrocin (200mg/kg/day i.p.), as an herbal antioxidant on the mRNA expression different members of TLR family using real-time RT-PCR was evaluted. Encephalitis (EAE) is an animal model of Multiple Sclerosis.Although the expression of TLR-2, TLR-3 and TLR-4 were increased in EAE animals spinal cords, injecting Picrocrocin could significantly downregulate the TLR-2 and TLR-4 expression at day 5 after induction of EAE, resulting in alleviation of overall inflammatory responses. These observations reveal that saffron extract may be valuable in the treatment of MS on several fronts as well as the disturbances in oxidative stress parameters in the hippocampus of experimental models of MS.
Keywords: Multiple sclerosis, TLR-2, PCR_RT

CP24 Comparison of morphological characteristics of gall and branches of species salix alba

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The willow tree is a deformed tissue that is formed at the same time as the feeding or spawning activity of eriophid ticks. With the aim of investigating and comparing the morphological characteristics of gall and healthy branches, in the spring of 1399, healthy and gall branches from Najvan Park in Isfahan were collected completely randomly with 6 replications. Relative water contents, length and width of leaves, and the length of the petioles, internodes, weight, and area were of leaves measured. The results showed that length, width, leaf area and weight in gall branches were significantly lower than those without gall branches. There was an increase in the relative water content of the leaves in the gallbladder branches compared to the gall-free branches, but this increase was not significant. The results of this study indicate that the changes observed in the leaves in trees with the presence of galls cause the tree to react to ticks, which weakens the environmental conditions of the habitat. Therefore, due to the absorption of nutrients in the gall, it is considered a kind of danger and threat to the plant.
Keywords: Eriophyte mite, Leaf length, Leaf weight, Relative water content

CP25 Identification of extracted antimicrobial peptide from hemolymph of *Tenebrio molitor*

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Insect antimicrobial peptides are belonged to the innate immune system, which are produced in their fat mass and secreted into the hemolymph. The aim of this study was to isolate and purify the antimicrobial peptide from hemolymph of this insect and to determine the range of activity of the peptide. To increase the activity of insect immunity for the inducible expression of antimicrobial peptides, the suspension of *Escherichia coli* (ATCC25922) of 10^8 cfu/ml was boiled for 20 minutes, and washed twice with PBS buffer, then 10^5 cfu/ml was inoculated to 30 larvae of *T. molitor* and to 10 larvae as control with the same volume of PBS buffer by G30 syringe. At the time of injection and during hemolymph extraction, the larvae were inactivated by cold stress and ether. Then, 18 and 32 hours after injection, hemolymph was extracted in cold tubes containing anticoagulant buffer, then centrifuged at 10000 rpm (3 to 4 times), 4 ° C, 30 minutes. After extraction of hemolymph from other cell components, the proteins pattern in hemolymph of infected insects was compared with control using 12% SDS-PAGE. To study the antibacterial nature of hemolymph, 50µl of control and infected insect's hemolymph was loaded on a well with 5 mm diameter made on nutrient agar which were previously inoculated with 10^5 cfu/ml of *E. coli* and *Staphylococcus aureus* (ATCC25923), and the zones of inhibition was measured by agar diffusion method after 14 hours. Differences in 30 kDa band width were observed compared to controls after 32 h. The diameter of the inhibition zone for both bacteria increased about

14 mm compared to the control (PBS). The steps of purification and separation of each protein from each set of proteins are underway to make a comparison with the same from local insects in Semnan.
Keywords: Antimicrobial peptides, *Tenebrio molitor*, Hemolymph, Infection

CP26 Antibacterial Activity of Shilajit

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Pseudomonas aeruginosa and *Staphylococcus aureus* are the most important causes of nosocomial infections in a wide range of immunocompromised patients, including malignancies, cystic fibrosis, and others. Shilajit is a blackish-brown substance that forms next to boulders adjacent to underground oil reserves and is traditionally used to treat bone fractures. The aim of this study is investigating the effect of Shillajit on the growth of *Staphylococcus aureus* and *Pseudomonas aeruginosa* bacteria. Shilajit is prepared from Sardoyeh area of Jiroft city, Iran. Then the aqueous solution was prepared at the concentration used by the natives to heal the wound. The amount of 100 cc of solution was dried completely at 70 ° C for 30 hours. 30 mg of powder was dissolved in 3 ml of sterile distilled water to prepare a stock solution. Concentrations of 100%, 75%, 50% and 25% of this solution were prepared and the antibacterial effects were assayed. The antibacterial activity was studied by disk diffusion method and measurement of the diameter of inhibition zone. The disk containing the extract was used as the sample and the disk containing the solvent was used as the negative control and the disk containing the antibiotic ampicillin as the positive control were placed on the culture medium containing the bacteria. The plates were placed in the incubator at37 degrees temperature, for 24 to 48 hours. Then the growth inhibition zone diameter was measured by a millimeter ruler. The results showed that there was a significant difference between the diameter of the growth inhibition zone of the samples containing the extract with positive and negative controls ($p < 0.05$). This study showed that shilajit had an inhibitory effect on the growth of these bacteria and could be a suitable alternative to antibacterial drugs of chemical origin.
Keywords: Shilajit, Antibacterial activity *Staphylococcus aureus*, *Pseudomonas aeruginosa*

CP27 Investigation on feasibility of blood grouping kit Producing by gel microcolumn technique

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Nowadays the determination of blood type (ABO & Rh) plays a very important role in the blood transfusion process, and every year some patients who receive blood transfusion die due to the false results of blood group typing. In old methods, technician errors and false reading of the results may cause change of the results. In this study we determined the kind of gel chromatography component and buffer which was suitable for micro-columns blood grouping test and we also found suitable and stable conditions such as anti-body concentration, PH, etc. for better agglutination reaction in gel technique. In the second part of this study, micro-columns were prepared and compared with tube blood group typing method, 200 blood samples were used for performance evaluation and it was found that the sensitivity and specificity of micro-column method are consistent with the tube method, but the measurement of agglutination grade was slightly better in the micro-column method than tube method. According to the functional tests, the micro-columns made in this study can be produced at industrial scale and this method can be used to standardize the blood group test instead of tube method. Moreover, gel method can be accomplished by automated sampling and image processing system in order to reduce human errors while administrating blood group typing test and reading the results.
Keywords: agglutination, blood group, gel chromatography, gel technique, micro-column

CP28 Evaluation of NLRP3 gene expression level in patients with coronary artery disease and its comparison with healthy Persons

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NLRP3 is one of the most important inflammatory flames, which is a set of multi-protein signaling. The NLRP3 gene is known to be associated with many human autoimmune and inflammatory diseases.Therefore, the aim of this study was to evaluate the expression of NLRP3 gene in patients with coronary artery disease and compare it with healthy individuals .In this study, sampling was performed on all individuals who had referred to Shariati Hospital in Tehran for diagnostic angiography of coronary artery disease within 5 months .Patients were divided based on normality and coronary artery occlusion and evaluated for NLRP3 expression after RNA extraction from peripheral blood and cDna fabrication by Real time PCR .All patients with and without diabetes and hypertension were also evaluated .According to the results, there was no significant difference in the expression of NLRP3 gene in patients with coronary artery stenosis compared to patients without coronary artery stenosis and also in the presence or absence of diabetes and hypertension .However, various studies have previously reported the association of the NLRP3 gene with the disease.

Keywords: Inflammasome, Real time PCR, Diabetes, Blood pressure, Lupus

CP29 Functionalized nano-magnetic hydrotalcite particles with tannic acid: A targeted drug delivery platform for oxaliplatin-resistant HCT116 cells

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Magnetic hydrotalcite (HT)-based nanoparticles are unique carriers for anticancer drug delivery due to their two-dimensional layered structure, high biocompatibility, and their ability to respond to an external magnetic. Tannic acid (TA), a natural polyphenol, is a ligand for estrogen receptor (ER). Acquired resistance to oxaliplatin (Oxa) is an inevitable problem and one of the reasons for the failure of colorectal cancer (CRC) therapy. We aimed to explore the ability of functionalized nano-magnetic MgAl HT particles with TA (TA@HT@Fe_3O_4) as a doxorubicin (DOX) delivery carrier to Oxa-resistant ER-expressing colorectal cancer HCT116 cells. The synthesized TA@HT@Fe_3O_4 nanoparticles and loaded particles with DOX (DOX/TA@HT@Fe_3O_4) were characterized by various analytical techniques. The entrapment efficiency (EE%), loading content (LC%), and *in vitro* release of DOX was measured at various pH values using UV-Vis spectrophotometer. The reduced negative value of the potential zeta of TA@HT@Fe_3O_4 nanoparticles after DOX loading and FT-IR spectra of DOX/TA@HT@Fe_3O_4 particles confirmed the successful DOX loading. The EE% and LC% values of TA@HT@Fe_3O_4 nanoparticles were about 51% and 8%, respectively. The release of DOX from TA@HT@Fe_3O_4 nanoparticles was pH-dependent with an initial rapid release (within 16 h) followed by a sustained release for 120 h. Hemolysis results revealed the highly biocompatible behavior of TA@HT@Fe_3O_4 nanoparticles. Oxa-resistant HCT116 colorectal cancer cells were established by the exposure of HCT116 cells to increasing concentrations (0.5-4.3 μM) of Oxa. The exponentially-growing cells in the presence of 4.3 μM Oxa were considered as Oxa-resistant HCT116 cells (HCT116/Oxa4.3). Fluorescence microscopy images and flow cytometry data confirmed the uptake of DOX/TA@HT@Fe_3O_4 particles by HCT116/Oxa4.3 cells. MTT results showed that the anti-proliferation activity of DOX/TA@HT@Fe_3O_4 nanoparticles against HCT116/Oxa4.3 cells was in a concentration dependent manner. Conclusion: TA@HT@Fe_3O_4 nanoparticles is a pH-responsive release system and offers promise as a safe and an effective system for targeted drug delivery to ER-expressing cells.

Keywords: Hydrotalcite MgAl nanoparticles, Oxaliplatin, Drug resistance, Colorectal cancer, Tannic acid, Targeted drug delivery

CP30 Comparison the effect of cytoplasmic chaperones co-expression on cytoplasmic and periplasmic production of activin A protein in *E. coli*

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Activin A, a member of transforming growth factor β superfamily (TGF-β), is a dimmer of two inhibin βA subunits. This protein plays many important roles in the body, such as cell growth and differentiation, maintenance and survival of the neurons, anti-inflammatory role, wound healing, and hematopoiesis; so it can be used as a therapeutic agent in the treatment of related diseases. The goal of this study is recombinant production of soluble activin A with correct structure in the cytoplasmic and periplasmic space of *E. coli*. For this purpose, cytoplasmic chaperones GroEL/GroES, DnaK/DnaJ and TF (Trigger factor) were expressed in order to help protein folding and prevent the formation of protein aggregates (inclusion body) as well as increase the production of soluble protein. It is worth noting that the co-expression of cytoplasmic chaperones not only affects the protein folding but also increases the production of recombinant proteins. After cytoplasmic and periplasmic expression of activin A individually and simultaneously with cytoplasmic chaperones, soluble proteins were extracted and the level of protein expression in each case was evaluated with western blotting technique and Image J software. The results showed that GroEl/GroES chaperones increased the cytoplasmic expression of soluble activin A due to assisting in protein folding; but in the periplasmic expression, TF was the best chaperone because it is the first chaperone bound to a synthesizing protein. As in the Sec secretory pathway, the protein is translocated to the periplasmic space with unfolded structure, TF can increase the amount of protein secreted from this pathway. Also, the results of structural analysis using CD spectroscopy showed the correct secondary structure of the protein produced in both cases.

Keywords: soluble protein, Sec secretory pathway, TF chaperone

CP31 lncRNAs with specific tissue expression involved in the diagnosis and prognosis of various cancers

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lncRNAs have been shown to be involved in cellular processes. One of their prominent features is the special and specific expression of tissue. In present study, using RNAseq data from the TCGA database for 19 most common cancers, we identified lncRNAs with specific expression for each cancer as good candidates for diagnosis and prognosis for respective cancer. Therefore, RNAseq data for all 19 common cancers were downloaded as raw data (HTSeq-count) and initial preprocessing and data normalization were performed with limma, edgeR and NOIseq packages. A CPM criterion of less than 0.5 was chosen to filter out genes with zero expression(Abbas-Aghababazadeh F et al, 2018). A list of all lncRNAs was obtained from the HGNC database and all the lncRNAs expressed in each cancer were extracted. The expression network showed that there are a large number of lncRNAs that have specific expression only in specific cancer, such as: breast, cervix, kidney, liver, lung, prostate, and thyroid. Also, the expression level differences between them compared to counterpart normal samples. Many of them had high diagnostic potency in distinguishing cancer samples from normal ones. Such as breast, colon, kidney, liver, lung (AUC> 0.9 and P <0.001). Also, some of them were related to the survival of patients in terms of expression, such as breast, neck and neck, kidney, liver, lung, prostate and thyroid (HR> 1, HR <1, P <0.001). Taken together, these lncRNAs could be used as a diagnostic and prognostic biomarkers. They can also be good candidates for identifying specific and common pathways in cancers and can be a good therapeutic target in cancer treatment.

Keywords: Bioinformatics, R software, cytoscape, Prism, Long non coding RNA

CP32 Molecular docking study of anti-breast cancer drugs and Tyrosine kinase receptors with focus on reducing hair loss

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Tyrosine kinase inhibitors are one of the most effective treatments for breast cancer. Chemotherapy-induced alopecia is a common and unavoidable side effect of breast cancer protocols. The unpleasantness of this condition causes impairment in quality of life, with a lot of psychological burdens and negative impact on self-image as some patients refuse chemotherapy. This study evaluated interactions between tyrosine kinase receptors, anti-breast cancer compounds, and hair follicles. The end goal is to identify drugs with lesser hair loss side effects. Docking was performed between ligands of 52 drugs (FDA-approved) against 80 tyrosine kinase receptors. Auto Dock Vina and Auto Dock tools were utilized for docking. After analyzing results of molecular docking, we selected 10 compounds. After docking between the selected compounds against 48 follicular targets, results were evaluated with Ligplot++ and Discovery Studio software. Fostamatinib and Regorafenib were selected with promising high binding energies against all 80 tyrosine kinase proteins and low binding energy against 48 hair follicle targets. Analysis of the results showed that reduction of Hydrogen bonds leads to minimum energy of drugs and reduces hair loss. It seems that the design and optimization of these two compounds could lead to discovery of a new generation of breast cancer drugs with reduced hair loss in the future.

Keywords: Drug design, Hair Follicle, Cancer, Molecular modelling

CP33 Evaluation of Anti-oxidant and Anti-cancer properties of the new derivative of 1, 3, 4-oxadiazole containing methoxyphenyl ring against MCF-7 cell line

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Nowadays, drug resistance has become a serious issue in the treatment of cancers. 1, 3, 4-Oxadiazole is a compound containing one oxygen atom and two nitrogen atoms in a five-membered ring, which is a major component of the development of new alternative therapies among oxadiazoles compounds. Therefore, the aim of this study was to investigate the antioxidant and anti-cancer properties of two methotrexate derivatives of 1, 3, 4-oxadiazole against MCF-7 breast cancer cells. In this study, new derivatives were first synthesized and then purified from the reaction between N-iso-cyanoimino triphenylphosphoran and carboxylic acid derivatives and then 2-pyridine carbaldehyde in acetonitrile solvent. Antioxidant effects of the product were evaluated using ABTS and DPPH assays. The cytotoxicity effects of the compounds were evaluated by MTT assay towards breast cancer cells. The obtained results showed that the synthesized compounds had a significant effect on scavenging free radicals. Also, these compounds had cytotoxicity property towards MCF-7 cells and reduced the survival of cancer cells in a dose-dependent manner. Based on our results, new derivatives of oxadiazoles that have methoxyphenyl in their original structure, have cytotoxicity as well as antioxidant properties towards MCF-7 cancer cells and can be proposed as a suitable Structure in the field of pharmacy and medicine.

Keywords: Drug resistance, oxadiazoles, free radicals, breast cancer cells

CP34 Biosynthesis and characterization of silver nanoparticles synthetized using extract of *Haplophyllum obtusifolium* and evaluation of the anti-cancer properties of synthesized nanoparticles

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Silver nanoparticles exhibit unusual physicochemical properties and biological activity. With extensive research activities, the use of silver nanoparticles, especially in the field of health, has become widespread. Scientists are using biological methods (green methods) as environmentally friendly and cost-effective ways to

synthesize nanoparticles and nanomaterials. In this study, the biological approach was aimed at producing nanoparticles from *Haplophyllum obtusifolium* watery extract. The biochemical nature of the plant extract was investigated and analyzed to determine the total amount of phenolic and flavonoid compounds with spectrophotometry. Several methods have been used to identify synthesized nanoparticles, the most important of which are: transverse electron microscopy (TEM), Ultraviolet–visible spectroscopy, Fourier-transform infrared spectroscopy (FTIR) and X-ray diffraction spectroscopy (XRD) which indicates the shape and structure of the nanoparticle. In this study, the toxicity of silver nanoparticles synthesized against the two major categories of Mcf7 and HepG2 cancer cells was extensively investigated by using MTT assay method, which strongly confirms the toxicity of nanoparticles against cancer cells. New advances in nanobiotechnology are a clear indication of the potential for cancer treatment.

Keywords: Green method, Morphology, Metastasis, Apoptosis, Angiogenesis

CP35 Studying the Cytotoxic and Genotoxic effects of *Teucrium persicum* on A375 Melanoma Cancer Cells

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Melanomas are malignant skin tumors originate from the transformation of the melanocytes. *Teucrium* genus belongs to the Lamiaceae family and the Ajugoideae subfamily, which its species are used to treat a diversity of diseases including diabetes, inflammation, hyperlipidemia, rheumatism and cancer. *Teucrium persicum* is an endemic plant of Iran, which is used in traditional medicine for relieve headache and abdominal pains. The purpose of this study is to investigate the cytotoxicity and genotoxicity effects of methanolic extract of *T. persicum* on A-375 cells. In this study, the efficacy of different concentrations of *T. persicum* plant extract on A-375 and HEK-293 cell lines was evaluated by using MTT assay and the genotoxicity effect of *T. persicum* extract was studied using the micronucleus assay. The results of MTT assay showed that *T. persicum* extract significantly reduced viability of A-375 cells (IC_{50} = 36.13 and 13*μg/ml for 24 and 48 hours respectively*) and HEK-293 cells (IC_{50} = *49.94μg/ml for 48 hours*). In addition, the treatment of A-375 cells with different concentrations of *T. persicum* extract significantly led to micronucleus production. These results suggest that *T. persicum* is a plant with very potent anticancer activity.

Keywords: Melanoma, *T. persicum*, A-375 cells

CP36 Study of human Interleukin-10 -1082(A/G) Gene Promoter Polymorphism in patients with Psoriasis using ARMS-PCR technique

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Psoriasis is a chronic inflammatory skin disease that is prevalent among ethnic groups. IL-10 is a cytokine produced primarily by monocytes and to be a lesser extent by lymphocytes. This gene is located on the long arms of chromosome number one (1q32.1). Gene promoter Zone of it is very polymorphic and has three point mutations; also, rs1800896 is considered in position of A/G (-1082). In general, this study compares the frequency of gene polymorphism rs1800896 (01082) A/G IL-10 in people with Psoriasis and healthy persons. This case-control study was a performed on 50 patients and 35 health individuals in west Mazandaran and east Guilan. After extracting DNA of blood samples, (-1082) A/G (rs1800896) IL-10 gene polymorphisms was studied using ARMS PCR method. The results were validated using DNA sequencing method. Data analysis were performed with SPSS22 software. A frequency percentage of genotypes AG, GG and AG in the control group are 0, 18 and 82 percent; and also 56, 32 and 12 percent in the patient group, respectively. However, this difference in level 0.05 (p=0.014) is significant. Also, the frequency of alleles A and G in the control group are 9 and 91 percent; but in the patient group are 72 and 28 percent, respectively. So, this difference is significant in level 0.05 (p=0.002). Based on the results, it can be said that IL-10A/G gene polymorphism is likely to play an important role in causing psoriasis.

Keywords: IL -10, Cytokine, Genotype, Allel

CP37 Study of human TNF-α -308 (G/A) Gene Promoter Polymorphism in patients with Psoriasis using ARMS-PCR technique

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Psoriasis is a common and reversible chronic immune disease of the skin and joints. genetic factors play an important role in the inflammatory and immune effects of psoriasis. One of the candidate genes involved in this disease is the TNF-α gene located on chromosome 6 (6p21.3) and encodes a multifunctional proinflammatory cytokine that is dependent on the tumor necrosis factor superfamily and is usually secreted by macrophages. There are several single nucleotide polymorphisms (SNPs) in this gene, the two most commonly polymorphisms being the conversion of G to A at the -308- and 238-position promoters, which are both functional and important. The aim of this study was to compare the frequency of rs1800629 (-308) G/A TNF-α gene polymorphism in psoriasis patients and healthy controls. This study was a case-control study performed on 50 patients and 30 healthy individuals in west Mazandaran and east Guilan. After extracting DNA of blood samples, (-308) G/A TNF-α gene polymorphisms was studied using ARMS PCR method. The results were validated using DNA sequencing method. Data analysis were performed with SPSS22 software. GG genotype and G allele were evaluated in patients with psoriasis. The frequency and percentage of GG genotype in control and patient groups were 30 (100%) and 50 (100%), respectively. The frequency and percentage of G allele in control and patient groups were 60 (100%) and 100 (100%), respectively ($P < 0.047$). According to the results of TNF-α G/A polymorphism frequency in this study, there is no relationship between this polymorphism and susceptibility to psoriasis.

Keywords: Tumor Necrosis Factor alpha, cytokine, genotype, allele

CP38 Investigation of the cytotoxic effects of the gum of Barijeh on SW480 cell line

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Colon cancer is one of the most common types of cancer worldwide, and the fourth leading cause of cancer death. Recent studies have shown that herbal remedies play an important role in the treatment of various cancers. *Ferula gummosa* is one of the plants that has many pharmacological effects. In traditional medicine, the gum of this plant is used to treat various diseases including abdominal pains, cholera, diarrhea, epilepsy, swelling and inflammation, and also in the treatment of neurological and cardiovascular diseases, liver disorders, diabetes, and rheumatism. Also, its antioxidant and anticoagulant activities have also been reported. This study aimed to investigate the anti-cancer effects of the plant on the SW480 cell line. After preparing the gum of *Ferula gummosa*, SW480 cells were cultured and treated with different concentrations of the gum for 24 and 48 hours. The cytotoxic effects of the gum on the SW480 cell line were evaluated by using the MTT method. The results obtained for the SW480 cell line show that at the lowest concentration of the gum which is used in this study (2µg/ml), the extract of this plant has an inhibitory effect on cell growth, and the IC50 value of the gum for this cell line was calculated to be 0.6346 µg/ml. It seems that more studies are needed to evaluate its applications in treatment of colorectal cancer.

Keywords: Colon cancer, *Ferula gummosa*, Cytotoxic effect

CP39 Interaction between Berberine alkaloid and some synthetic oligonucleotides

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Cancer is one of the leading causes of death among the communities. The use of cancer drugs that could specifically interact with particular forms of DNA has been more popular due to its lower toxicity. Among them, DNA quadruplex structures that found in telomere of eukaryotic chromosomes and promoter of some oncogenes have been more inspiring. Aiming these structures in promoter of oncogenes can be described as a

potential treatment strategy for cancer control by transcription prevention. The theory of presenting G-quadruplex structures in regulatory regions of some key genes, led to use synthetic oligonucleotides for Kit and Ceb. The formation and stabilization of four-strand structure with berberine in sodium cacodylate buffer was investigated by FRET method. Comparing main factors such as melting point showed that berberine binds and stabilizes Kit G-quadruplex structures concentration dependently. In comparison, the effect on Ceb oligonucleotide is even stronger. In conclusion targeting such structures in promoters of key oncogenes can be considered as a novel therapeutic strategy against cancer.

Keywords: G-quadruplex DNA, FRET and method, promoter, cancer

CP40 Investigation of human interleukin 6(174) gene rs1800795 polymorphism in patients with Psoriasis using ARMS-PCR technique

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Psoriasis is a chronic inflammatory skin disease that is prevalent among ethnic groups. IL-6 is a multifunctional cytokine that is involved in host defense, immune responses and inflammatory responses. The IL6 gene with rs1800795 is located on the short arm of chromosome 7. In the IL6 promoter region there are four polymorphisms located at positions (G/A) -597, (G/C) -572, (A / G) -373, (G/C) -174. In this study, rs1800795 was evaluated at (-174) G/C. The aim of this study was to compare the frequency of IL-6, rs 1800795 (-174) G/C gene polymorphism in patients with psoriasis and healthy individuals. This case-control study was performed on 50 patients and 23 healthy individuals in west Mazandaran and east Guilan. After extracting DNA of blood samples, (-174) G/C IL-6 gene polymorphisms was studied using ARMS PCR method. The results were validated using DNA sequencing method. Data analysis were performed with SPSS22 software. The frequency of CC, CG and GG genotypes in the control group were 44%, 39% and 17%, respectively, and in the patient group were 22%, 26% and 52%, respectively. So this difference is significant at the 0.05 level ($p = 0.018$). Also the frequency of G and C alleles in the control group were 63% and 37% and in the patient group 35% and 65%, respectively, Therefore, this difference is significant at the 0.05 level ($p = 0.002$). Based on the results, it can be said that IL-6 G/C gene polymorphism is likely to play an important role in causing psoriasis.

Keywords: Interleukin 6, Cytokine, Genotype, Allele

CP41 Comparison of bioinformatics tools to detect the copy number variation (CNV) based on the *whole-exome sequencing*

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Copy number variation (CNV) is a kind of structural variation, which leads to an increase and decrease in DNA sequence length of 1kb to several pairs of megabase. This type of variation can lead to changes in gene dose, coding sequences, gene expression regulation, and biomarkers that are important predictors of cancer. Comparative *Genomic Hybridization methods, SNP arrays, and various forms of next-generation sequencing (NGS), such as* whole-genome sequencing (WGS) and *whole-exome sequencing* (WES), have been used to identify CNA in the laboratory. The use of WES data has been found to be useful in clinical trials because it includes only protein-coding regions in the genome, due to high coverage, and relatively low cost. *Unwanted signals associated with WES data that result from the detection of exons and contaminants generated by the target tissues complicate CNA estimation.* Using bioinformatics tools to accurately estimate CNA data related to WES can be helpful. In this study, the seven bioinformatics tools (ExomeCNV, CoNIFER, VarScan2, CODEX, ngCGH, saasCNV, and falcon) were used to identify CNV using data from the total eczema sequence of 419 pairs of breast cancer tumor samples obtained from the Cancer Genome Atlas. SaasCNV showed the highest increase and decrease (0.65%), sensitivity (49.6%) and specificity (89.1%) to estimate the increase or

decrease in the number of copies. Finally, to improve the identification of CNV, it is recommended to create software to identify CNV in higher plants and bacteria, software that has a high level of sensitivity, accuracy, and precision. Creating an algorithm for predicting and identifying CNV without the need for a control sample, using combination machine learning methods to produce stronger software for accurate CNV identification can also be helpful, also it is recommended to create software that combines both the sequences of the whole-genome sequencing (WGS) and the *whole-exome sequencing* (WES).
Keywords: Chromosomal structure variation, whole-genome sequencing, *whole-exome sequencing*, Bioinformatics tools

CP42 Application of plant growth promoting microorganisms to combat oak decline

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The oak decline is a world and progressive phenomenon causing death and decrease of oak forest area whole world. This phenomenon is also spreading rapidly in Iran and it is necessary to replace dead trees and reclamation of affected habitats. It has been proved that plant growth promoting microorganisms increase resistance of seedling against adverse environmental condition which are possible causes of oak decline. The aim of this study was to determine and compare the effect of plant growth promoting rhizobacteria on growth parameters of *Quercus brantii* and *Q. libanii* in greenhouse condition. Seeds of Q. brantii and *Q. libanii* were inoculated by phosphate solubilizing bacteria which isolated from their natural habitat in Garaan Research station, Kurdistan, Iran. The experiment was conducted in a factorial design based on randomized complete block design with two main factors including species (two levels) and bacteria (five levels). At the end of the growing season, parameters of seedling growth like shoot length, collar diameter, dry mass of different organs and nutrient status including phosphorous, iron, magnesium, manganese and zinc concentration were determined. Oak seedling growth increased by bacteria depending on oak species as *Q. libanii* had better response in compared to *Q. brantii*. Inoculated bacteria increase seedling shoot length, collar diameter and dry matter. There was increase in phosphorous and other microelements concentration in inoculated seedling in compared to un-inoculated one. The bacteria acted differently as *Pseudomonas putida* and *Bacillus subtilis* had better efficiency. It seems inoculated *Q. libanii* with *P. putida* and *B. subtilis* have more growth and nutrient status making them suitable candidates in reclamation programs in order to combat oak decline.
Keywords: Reclamation, Inoculation, Growth, Phosphorous, Micronutrient

CP43 Microbial diversity in semiarid area determined by next generation sequencing

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Our information on the soil microbial diversity especially in arid and semiarid areas, which cover 40% of the earth area and more than 70% of Iran area, is very limited. This study aimed to determine the impact of climate and grazing on the soil bacterial composition in two semiarid areas by next generation sequencing. Soil samples were taken from four zones which were either cold or warm and either grazed by cattle or not grazed in Khabr National Park and Ruchun Wildlife Refuge, Kerman province, Iran. Sequencing was done by Illumina Miseq platform after DNA amplification by 27f-518r primers. Data were analyzed by Qiime to determine bacterial community composition, diversity (Chao1) and evenness (Shannon's H). The abundance of Proteobacteria (28.3%±1.0) and Actinobacteria (44.6%±1.1) was highest at the cold-grazed and warm-grazed zones, respectively, which account for ~70% of all OTUs. Greater richness and less evenness of bacteria at the cold areas, compared to the warm areas, was also observed and is attributed to more vegetation cover and soil nutrient and organic matter availability and moisture improving bacterial growth. The significant differences were observed in the bacterial diversity between the grazed and not grazed sites due to the change in organic matter compounds resulting from animal waste. According to the Chao1 and Shannon's H, the least richness and the highest evenness belonged to the warm-grazed zone, indicating grazing had a greater impact because of their

fragile condition. Then warm areas need more scientific management as well as more attention to prevent sever damage.

Keywords: Climate, Bacteria, Grazing, V1-V3 region, Evenness

CP44 Evaluation the performance of polysaccharide base hydrogels in drug delivery of Gemcitabine hydrochloride in the treatment of breast cancer

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Gemcitabine (2', 2'-difluoro-2'-deoxycytidine) is a chemotherapeutic agent against human cancers. However, the therapeutic efficacy of gemcitabine is limited by its hydrophilicity and low plasma half-life. To improve the maintaining and efficacy of gemcitabine, we developed a pH sensitive hydrogel drug delivery system based on natural polysaccharides including chitosan and alginate. To optimize the hydrogel preparation procedure, the effect of critical parameters on the physicochemical characteristics of nanoparticles was investigated through the Box-Benkehen design. Finally, optimized formulation resulted in stable NPs around 14.96 nm by polydispersity index 0.225 and a maximum entrapment efficiency of 34.11%. The in vitro release studies have shown that in the presence of the alginate layer, the burst release is reduced under different pH conditions and ~80% of gemcitabine hydrochloride was released within 4h. Based on the results of the cell cytotoxicity the drug-loaded NPs showed increased toxicity over human breast cancer cells (MCF-7). The flow cytometry results suggest that the prepared NP can induce apoptosis more effectively than free gemcitabine hydrochloride. Moreover, cell-cycle analysis indicated that G2/M arrest, also the results of cell uptake studies represented the time-dependent increasing behavior which can be evidence for the developing pH-responsive and time-dependent drug delivery systems based on CS-AL polyelectrolyte complex. So to sum up, the assembled nature polymeric core-shell system not only provides the pH sensitivity and improved biocompatibility hydrogel but also enables protecting Gemcitabine hydrochloride from enzymatic degradation.

Keywords: Chitosan, Alginate, drug delivery, pH-sensitive system

CP45 Inhibitory properties of enzymes involved in the Quorum Sensing process in *Pseudomonas aeruginosa* by molecular modeling

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Quorum Sensing (QS) is a bacterial communication mechanism that regulates the production of many pathogenic factors, including the formation of pigments and the ability to form biofilms that are essential for chronic infections .Biofilm formation is crucial in the survival and continuation of bacterial infection and antibiotic resistance in most bacteria. *Pseudomonas aeruginosa* is a Gram negative bacterium and opportunistic hospital pathogens cause a lot of death. In this study, the enzyme inhibitory activity of selected compounds against Triphenyl-LasR and AHL Synthesis Lasl involved in the QS system and biofilm formation of *P . aeruginosa* were investigated by molecular modeling approach. The molecular docking was done using the Glide software in the Schrödinger drug discovery suite. More than 700 drugs downloaded from PubChem were prepared with Ligprep software; proteins were obtained from a protein data bank (PDB). The Qikprop application was used to find the Lipinski formula for the compounds; also QSAR studies were done. The results of molecular modeling showed that compounds with PubChem ID 118732850 and 122187653 showed the highest docking score -12.019 and -8.009 $Kcal.mol^{-1}$ had the highest inhibitory activity on triphenyl-LasR complex receptor and AHL synthase protein, respectively. As a suggestion for experimental study of anti Quorum sensing properties of compounds that have given the best answer and if they have a suitable and similar solution, making other derivatives of these compounds

Keywords: Molecular docking, QSAR, biofilm, enzyme inhibition

CP46 Evaluation of the presence of *Campylobacter Jejuni* and *Listeria Monocytogenes* in water sources of Kermanshah city before chlorination based on comparison of culture and PCR

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Despite abundant advances in water and wastewater treatment, waterborne diseases still threaten the health of the people of the world. *Listeria Monocytogenes* bacterium is a pathogen that causes listeriosis. This pathogen can also cause meningitis, poisonous sepsis and abortion in humans. One way of transmitting this microorganism is water and Food. Quick and accurate identification plays an important role in preventing infections. Also, due to the importance of *Campylobacter Jejuni* in water and food industries and causing infection, toxication and digestive problems in humans .identification of this bacterium can be an effective step in preventing water contamination with *Campylobacter Jejuni*. The aim present study was to identify *Listeria Monocytogenes* and *Campylobacter Jejuni* through culture and PCR and compare them in water supply of Kermanshah city. 18 samples before chlorination, 2 liters for PCR and 2 liters for culture were collected from different water supplies in Kermanshah. DNA was extracted from standard Campylobacter Jejuni *and Listeria Monocytogenes* using DNG-Plus kit. PCR reaction was optimized using specific primers . After determining the specificity and PCR limit of detection, the collected water samples were examined and at the same time the samples were cultured and examined. From 18 samples of water supply sources in Kermanshah by PCR, *Campylobacter jejuni* were isolated from all samples, and *Lysteria Monocytogenes* were isolated from17 samples, and also 4 cases of *Campylobacter Jejuni* and 2 cases of *Listeria Monocytogenes* were isolated by culture method. The results show that PCR has a better performance than culture for detecting *Listeria Monocytogenes* and *Campylobacter Jejuni*.

Keywords: Meningitis, Digestive problems, Septicemia, listeriosis

CP47 Evaluation of sequence, structural, peptide and amino acid diversity of bacteriocin Nisin

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Nisin is a bacteriocin from the group of lantibiotics and consists of 34 amino acids that are mainly produced by different strains of *Lactococcus lactis*. Pathogen inhibition of nisin has been observed in bacteria such as *Listeria monocytogenes*, *Staphylococcus aureus* and *Escherichia coli*. Nisin contains the unusual amino acids lanthionine, methylanthionine, dihydrolanin, and dehydroaminobutyric acid. The antimicrobial mechanism of action of nisin is through two binding to lipid II as a precursor of bacterial cell wall peptidoglycan and inhibition of wall biosynthesis and the formation of pores in cell membranes and the release of essential ions. Because in the design of nisin peptide analogues, accurate knowledge of the sequence, structural, peptide and amino acid diversity of nisin is necessary, so in this study, the mentioned variations were performed using related databases including Bactibase, NCBI-Genome, Ensemble Bacteria, MBGD, BAGEL4. The results showed that there are 9 different variants of nisin including A, Z, Q, F, U, U2, P, H, O. The diversity of nisins is due to substitution at amino acid positions of 9, 10, 15, 18, 21, 27, and 30. Structurally, nisins are linear peptides with 5 rings formed by disulfide bonds. The rings are necessary for maintenance and insensitivity to proteolytic degradation and resistance to thermal inactivation. Ring A in nisin is vital for biological activity. The results of this study can be used to explain the relationships between structure and function, stability, antimicrobial properties and directional mutagenesis in order to be used as a bioactive inhibitor of pathogens.

Keywords: Bacteriocin, Nisin, Sequence variability, Structure variability

CP48 Detection of Potato Virus Y (PVY) from *Solanum alatum* weed in the Potato Fields of Hamedan Province

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Viral diseases are among the factors limiting potato production in the world. *Potato virus Y* (PVY) from the family *Potyviridae* is one of the most important plant pathogens in the world, which reduces the quality and yield of *Solanaceae* family products such as tobacco, potatoes, tomatoes, peppers and weeds of this family and its worldwide spread is an ongoing challenge. PVY has a positive single- stranded RNA and its molecular weight is about 9.8 kb. The virus is transmitted mechanically as well as by the green peach aphid *Myzus persicae*. In order to detect the virus, 30 samples of *Solanum alatum* that showed suspected signs such as mosaic, wavy leaf margin, chlorotic spots and leaf deformation were collected from Bahar city of Hamedan. Suspicious plant extracts were inoculated on indicator plants including *Nicotiana occidentalis* and *N. glutinosa*. After one week, signs of necrosis, vein clearing and mosaic were systematically observed in inoculated plants. Total RNA was extracted from symptomatic indicator plants and PVY contamination of samples was confirmed using RT-PCR test and specific primers of PVY coat protein gene. This is the first report of *Solanum alatum* infection to PVY in Hamedan province. This virus was reported in 2008 by Shamseddin Saeed *et al.* from *Solanum alatum*, *Chenopodium urbicum*, *Emex spinosus* and *Physalis divaricata* in Jiroft, and from *Geranium pusillum* and *Lactuca serriola* weeds in 2010 by Pourrahim *et al*. Because weeds are winter hosts of plant viruses, early detection of virus-infected weeds plays an important role in disease control and epidemiology.

Key words: Identification, Molecular Method, *Solanum alatum*

CP49 Detection of *Tomato spot wilt virus* (TSWV) from *Pelargonium hortorum* in Hamedan city

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Tomato spotted wilt virus (TSWV) is an *Orthotospovirus* of the family *Tospoviridae*, first reported in Australia in 1919 and causing extensive damage to vegetables, legumes and ornamental species. This virus has the worldwide spread and is one of the ten most harmful plant viruses in the world. TSWV is transmitted by thrips in a circulatory and propagative manner in nature. The virion of the virus is isometric and has a three-part genome in the form of single-stranded RNA. In order to detect the virus, 35 samples of *Pelargonium*, *chrysanthemum* and *Dahlia* flowers were collected from Hamedan city, which showed symptoms of suspected infection such as yellowness, chlorosis and necrosis spots, deformation and wilting. The extract of suspicious plants was mechanically inoculated on indicator plants including beans, cucumbers and *Chenopodium quinoa*. After about two weeks, in indicator plants which inoculated with *Pelargonium* extract, symptoms such as necrosis and deformation appeared in bean leaves, as well as chlorotic spots in cucumber and *Chenopodium* leaves. Then, total RNA was extracted from symptomatic indicator plants and the contamination of the samples was confirmed using RT-PCR test and specific primers of TSWV coat protein gene. This is the first report of TSWV infection of *Pelargonium* flowers in Hamedan city. The virus was reported in 2000 by Moeini and Izadpanah from a *Pelargonium* in Tehran. Also in the same year, it was separated and reported from the city of Mahallat in Markazi province by Hassani Mehraban and Shahraein from *Pelargonium*. The best way to control viral diseases is to prevent the occurrence and spread of infection. Therefore, considering that the method of propagation of most ornamental plants is through vegetation, creating virus-free and safe seedlings, onions and vegetative parts is one of the effective ways to prevent the spread of viral diseases in ornamental plants.

Keywords: Identification, Molecular Method, *Pelargonium*

CP50 Investigating the Association between *Col2a1* Gene Variants with Mandibular Prognathism

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Class III malocclusion is one of the most common dentofacial malformations which Mandibular protrusion (overgrowth of the mandible) may lead to this phenotype. Genetic, environmental, or a combination of these factors can cause this protrusion. The *Col2A1* gene, which effects on chondrocyte differentiation and cartilage formation, has been reported in association with this phenotype. The aim of this study is investigating the association between genetic polymorphisms of *Col2A1* gene loci and mandibular prognathism by *in silico* method. In this research, NCBI database was used for gene analysis and selection of single nucleotide polymorphisms, and online servers PolyPhen-2, PROVEAN, SIFT and Mutation assessor were used to investigate the effect of these SNPs on pathogenicity and protein damaging. The results of our studies showed that between two missense polymorphisms rs3803183 and rs2070739, the rs2070739 can be deleterious and damaging. Also analyzing by KEGG server (To study cell-signaling pathways) showed rs2070739 may cause abnormal growth in mandibular condyle (The rounded protuberance on the back of the mandible) by involving in signaling pathways such as CD44-casscade and effect on chondrocyte differentiation. Therefore, it seems that the rs2070739 of *Col2A1* gene can play an important role in the formation of mandibular prognathism.

Keywords: Mandibular protrusion; Missense polymorphisms; *Col2A1* gene; Chondrocyte; CD44 pathway; Dentofacial malformation

CP51 COVID-19 Correlation with Diabetes Mellitus Presents Ascending Rate Throughout the Pandemic Peaks

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Coronavirus disease (COVID-19) is an infectious disease with a high rate of mortality. Recent studies suggest that severity of COVID-19 is amplified in patients diagnosed with Diabetes Mellitus. In order to study the relationship between the prevalence of COVID-19 and Diabetes Mellitus (DM), correlation coefficient between the two variables was calculated using WHO and International Diabetes Federation (IDF) Diabetes Atlas data sets. The data was assorted into ten regions including; Central Asia, Middles east and western Asia, Africa, North America and the Caribbean, South east Asia, East Asia, Europe, South and Central America, South Asia and Oceania. Locally in the Middle East and Western Asia and also on a global accumulative scale when testing a total of 190 countries, a moderate positive correlation was observed. Furthermore, a strongly positive correlation coefficient of 0.693 in the 15 most affected countries by COVID-19 was achieved. The data was analyzed in five windows of 45 days since the emergence of the pandemic. Results indicate that there is an increasing pattern of the correlation coefficient in the last three windows. Since the spread of COVID-19 was uneven and the pandemic peaks happened at different times in the countries, this pattern was not observed in the first and the second windows. This study proves that if the prevalence of Diabetes Mellitus increases, the prevalence of COVID-19 cases may also increase.

Keywords: COVID-19 pandemic, Diabetes Mellitus prevalence, local and accumulative correlation

CP52 Comparative study of the effect of catechins and catechin nanosystems on preventing oxidative stress with aluminum chloride

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Aluminum is one of the most abundant metals on earth, which can cause oxidative damage if it enters the body. This study pH-sensitive nanosystem on the prevention of oxidative induced with stress aluminum chloride. For this purpose, 36 male Wistar rats in the weight range of 200 to 250 g were randomly divided into 6 groups, and

treatments were performed. At the end of the treatment period, blood samples were taken from aimed to compare the effect of catechins and catechin loaded the mice, and serum was isolated. Then the level of total antioxidants was measured by the FRAP method and the rate of lipid peroxidation was measured by measuring the level of malondialdehyde. The level of total antioxidants in the control, catechin, aluminum chloride, catechin nanosystem, aluminum chloride plus Nanosystems and aluminum chloride plus catechin groups were 800.13±74.19, 703.46± 79.28, 473.80± 22.29, 699.13± 99.15, 595.80±53.34 and 578.13 ±84.70, respectively. Malondialdehyde level in control, catechin, aluminum chloride, catechin nanosystem, aluminum chloride plus catechin Nanosystem and aluminum chloride plus catechin groups were 1.90 ±0.16, 1.96±0.28, 4.37±0.33, 1.90±0.22, 2.38 ±0.55 and 2.28±0.42, respectively. According to these results, total antioxidants in the group treated with aluminum chloride showed a significant decrease compared to the control group. Malondialdehyde level in aluminum chloride treated group showed a significant increase compared to the control group, while the use of catechin or catechin nanosystem prevents the rise of malondialdehyde level. According to our study, it can be inferred that pH-sensitive nanosystem was effectively released catechin in the intestine and caused efficient antioxidant effects compared with catechin.

Keywords: FRAP, MDA, Nanoparticle, Rat

CP53 (A DNA vaccine against Vibrio cholera based on recombinant construct consisting OMPW, TCPA, CTB genes and evaluation of its immunogenicity)

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Vibrio cholera is one of the major causes of mortality in children under 5 years particularly in developing countries. Therefore, it is very important to improve preventive measurements and treatment strategies. The three most important pathogenic factors in *Vibrio cholerae* that are able to stimulate the immune system are: a) B subunit of CtxB *Cholera* enterotoxin, responsible for toxin binding to eukaryotic cells ,b) TcpA, an essential factor for bacterial colonization, and c) OmpW, the highly conserved extracellular protein ,as an stabilizing agent against environmental shock. DNA vaccines, due to their advantages such as ease of production and durable antibody production, have become the focus of researchers. In the present work, a then DNA consisting the aforementioned genes was clone on pEGFP-N1 harbouring fluorescent tags and expressed in HT 29 cell line. After conforming the expression under fluorescent microscope, the chimer was sub cloned on pcDNA3 vector. BalbC mice were administered with100 µg of the new construct for 3 times along with freunds adjuvant. Antibody titers against DNA vaccine was estimated by indirect ELISA using recombinant proteins and whole cells of bacteria as a target. The minimum amount of IgG inhibiting the effect of CT toxin on Y1cell line was evaluated. After determining the bacterial lethal dose, the viability of neonatal mice from immunized mothers were challenged. Our data indicated that the antibody titers was increased more than 3 folds in immunized mice compared to control group. Animal challenge showed 100% survival rate against one LD of bacteria for pups from immunized mothers whereas pups of unimmunized mothers were totally died. Results from ELISA and animal challenge indicates that the new DNA construct have a significant productivity and can be as a DNA vaccine candidate.

Keywords: DNA vaccine, pcDNA3, Protectivity, Diarrhea Enterotoxin, *Vibrio cholera*

CP54 Isolation and Identification of Cadmium Resistant Bacteria from Steel Factory Wastewater as biosorbents and their Ability

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During the recent years, with the expansion of industrialization of the modern world, new methods of agriculture, and changes in climate conditions such as weathering, heavy metal pollution in the environment has increased. The accumulation of heavy metals in the ecosystem is extremely dangerous to the health human beings. For instance, Cadmium (Cd) is a heavy metal element and it is found to be exceedingly poisonous and

carcinogenic. New techniques have been developed to rectify heavy metal contaminated sites. Among these methods, biosorption is proved to be more effective on a large scale. This study was performed to isolate the local bacteria, capable of biosorption of Cadmium, from the heavy metal contaminated sites. Based on the Minimum Inhibition Concentration (MIC) test, the bacteria most resistant to Cadmium (up to 5000 mg/l) was isolated from the strains in the Steel Factory wastewater was selected. This isolate was identified based on the morphological, physiological, phylogenetic, biochemical, and antibiotic resistance test characteristics as *Pseudomonas sp.* The effect of important parameters such as pH, temperature , and concentration bacteial biomass on the biosorption of Cadmium was studied. The optimum temperature and concentration of bacterial biomass for biosorption of cadmium were 45 ° C and 1.5 g /l, respectively. The adsorption percentage was up to 85%, with the highest adsorption rate seen at pH=7. *Pseudomonas sp.* adsorption rate results were compared to other bacteria and their studies. It was concluded that the bacteria isolated from heavy metals contaminated had the high adsorption rate of Cadmium and and changing the pH parameter is more effective than other parameters. *Pseudomonas sp.* biomass can be a promising, efficient, cost effective, and ecofriendly way in the removal of Cadmium from the polluted environments.

Keywords: Local bacteria, Minimum Inhibition Concentration test, *Pseudomonas*, pH

CP55 Confirmation of effective immunotoxin constructs in breast cancer

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Immunotoxins often referred to as "targeted therapies," are a combination protein consisting of a toxic moiety that is targeted to a specific deletion of target cells. The targeting part is generally a monoclonal antibody or genetically engineered antibody fragments. Antibody-based biologics are one of the well-known treatment strategies in cancer therapy. After modeling and simulating the desired immunotoxin in an aqueous medium and evaluating its binding affinity to the EGFR antigen, the immunotoxin was synthesized. In order to amplify and confirm the synthesized immunotoxin, the following steps were performed in vitro. The bacterial strain E.coli DH5α is used to amplify plasmid DNA. Therefore, before starting the experimental steps, it is necessary to confirm the absence of any foreign plasmids in this bacterium. For this purpose, the linear culture of this strain was performed in the environment with and without antibiotics, which showed that the bacteria in the environment without antibiotics have very good growth, while in the environment with it, there is no growth, so it lacks The gene is resistance. Thus, new methods based on genes, cells, hormones, and bacteria have made it possible to understand the difference between normal and deformed cancer cells at the molecular level. Then, after determining and selecting the best structure, its synthesis, cloning, and approval were performed in laboratory conditions

Keywords: Cancer, Targeted Therapy, Cloning, Combined Protein

CP56 Effect of simulated microgravity condition on mouse myoblast (C2C12) cells growth

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This study aimed to investigate the effect of simulated microgravity on the growth of mouse myoblast (C2C12) cell line. It has been believed that microgravity directly can modify the structure, function, and morphology of biosystems and numerous research have been performed to recognize these alterations. As a direct consequence of exposure to microgravity astronauts experience several physiological alterations, which can have serious medical implications when they return to Earth. The C2C12 cell line was purchased. The 2D clinostat was applied for the simulation of the microgravity. Then, the morphological studies, acridine orange/propidium iodide (AO/PI) staining, and MTT cytotoxicity assay were utilized to determine any alternation in cells after 48 h simulation microgravity exposure. However, after 72 h exposure about 40% of cell death occurred (P<0.05). The Acridine orange/PI staining confirmed this observation too. This finding could help astrobiologists to

realize major health risks for astronaut crews and space travelers and reduce these harmful effects. Furthermore, our observations can open fascinating research lines in astrobiology, biophysics, and exobiology.
Keywords: Astrobiology, Atrophy, Mouse myoblast, Microgravity, Cell viability assay

CP57 Synthesis of Silver Nanoparticles Using Green Method of Plant Extract (*Campsis radicans*) an their Antibacterial Effects

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There are many different methods for production of silver nanoparticles (Ag-NPs). But using of plants in the synthesis of nanoparticles due to a cost effective and ecofriendly approach has been extensively noticed. In this research study, the synthesis of green silver nanoparticles using the extract of Campsis radicans and the study of antimicrobial properties as well as the study of secondary metabolites of this plant have been reported for the first time. After extraction and synthesis to evaluate the properties and confirm the synthesis of UV-noticeable spectroscopy (UV-Vis), Fourier change infrared spectroscopy (FT-IR), X-beam diffraction (XRD), transmission electron microscopy (TEM). The antibacterial properties of nanoparticles synthesized on Staphylococcus aureus (ATCC25923) and Escherichia coli (ATCC25922) were also evaluated to measure MIC (minimum inhibitory concentration) and MBC (minimum lethal concentration). Finally, aluminum chloride (TFC) and fulline save cultive (TPC) were used to measure flavonoids and total phenols, respectively. FT-IR spectroscopy uncovered that AgNPs were functionalized with biomolecules that have essences amine gathered, carbonyl gathering, OH gatherings, and other settling useful gatherings. An assimilation band with a 450 nm pivot was watching, which is identified with the Surface Plasmon Resonance (SPR) of the silver nanoparticles. The structure and synthesis of silver nanoparticles were dissected by XRD which indicated that the AgNPs are crystalline in nature and have face-focused cubic (FCC) geometry. The morphological investigation of silver nanoparticles utilizing TEM proposes that the nanoparticles are circular with a distance across of around 75 nm. Our information demonstrated absolute phenol substance in aqueous extracts of flowers of *Campsis radicans* was 5.31 ± 0.1 mg GAE/g dry plant materials. Additionally, all out flavonoid substance in aqueous extracts of flowers of *Campsis radicans* were 2.38 ± 0.4 QE/g dry plant materials The synthesized nanoparticles also showed good antibacterial potential against gram-positive and gram- negative bacterial strains. Due to the presence of phenol and flavoonoides as antioxidant compounds in the extract of this plant. Its anticancer properties are recommended.
Keywords: *Campsis radicans*, Silver nanoparticles, Flavonoids, Antibacterial activity, Green nanoparticles.

CP58 In vitro antifungal effect of *Artemisia austriacea* extract on *Candida albicans*

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Today, fungal diseases caused by opportunistic fungi have increased significantly, and antifungal drugs have side effects, so the replacement with natural drugs is an important issue. Plants, which are a rich source of natural metabolites, are of great interest. In this study, the antifungal activity of *Artemisia austriacea* leaf extract on *Candida albicans* was investigated. Thirty samples of *C. albicans* were obtained from Microorganisms Bank at Razi hospital of Tehran. Tube mass testing and biochemical tests were performed to confirm *C. albicans*. Antibiogram was performed to determine antibiotic resistance against Clotrimazole and Ketoconazole. Ethanolic extract of *A. austriacea* leaves was prepared using the Soxhlet method. The antifungal effects of the plant extract against *Candida albicans* were investigated in vitro using diffusion test (well) at different concentrations. The minimum inhibitory concentration was determined by the microdilution method and the minimum lethal concentration of fungi was determined. The results displayed that *A. austriacea* extract has very good antifungal activity and can inhibit the growth of *C. albicans*. The minimum inhibitory concentration of ethanolic extract of *A. austriacea* leaves with a concentration of 80 ± 0.5 mg/ml has an antifungal effect on the growth of *C. albicans* and with a concentration of 160 ± 1 mg/ml had a growth inhibitory effect. The mean diameter of the growth inhibition zone was 12 ± 0.57 mm which had acceptable results in comparison with

Ketoconazole and Clotrimazole (p≤0.05). Today, medicinal plants are very popular in pharmacy and medicine due to the antimicrobial metabolites they produce. Given the high prevalence of this fungal disease and the side effects of chemical drugs, plants such as *Artemisia austriacea* can be processed for further drug researches.
Keywords: opportunistic fungi, medicinal plants, minimum inhibitory concentration

CP59 The Effect of Aluminum Containers on Cell Proliferation and Interphase and Mitotic Phase Aberrations in Meristematic Cells of the *Allium Cepa* Root

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Aluminum is a toxic metal that humans are exposed to in their daily lives at an increasing rate. Aluminum is also widely used in the manufacture of various types of household utensils. The aim of this study was to investigate the effect of water boiled in aluminum containers on cell proliferation and interphase and mitotic phase aberrations in the meristematic cells of onion root using *Allium cepa* test. Three aluminum container from three different companies were tested. Then water boiled containing concentrations of 5 and 10 mg / l aluminum was prepared from each container and five onions were tested for each concentration in each container. In order to rooting, the onions are exposed to distilled water for one day and then exposed to the mentioned concentrations of aluminum for 42 to 43 h, and distilled water was used as a control. The results showed that the mitotic index mean at concentration 5 from container 1 (P<0/05) and concentrations 10 from containers 2 (P<0/001) increased significantly compared to the control. The mean of total aberrations in the mitotic phase, in each of the concentrations of all three container was significantly increased compared to the control (P<0/05). Also, in all three containers, there was a significant positive correlation between the concentration of aluminum and the total aberrations in the mitotic phase .The mean of total aberrations in interphase, at both concentrations from container 3, increased significantly compared to control (P<0/05). Also, in containers 1 and 3, there was a significant positive correlation between the concentration of aluminum and the total aberrations in interphase. Considering the potential toxicity of aluminum, these types of containers should be considered as a serious threat to public health.
Keywords: Aluminium, Mitotic index, Chromosome aberration, Interphase, Mitotic phase

CP60 Fecal carriage of carbapenem resistance genes bla OXA-48 and bla NDM-1 in members of Enterobacteriaceae among hospitalized immunosuppressed children in the oncology ward of Mofid Children's Hospital in Tehran, Iran

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In the last few years, the frequency of carbapenem resistance genes among *Enterobacteriaceae* have been increasing through the world, which most of them are the cause of hospital and society acquired infections and mortality especially in high risk infection patients such as immunosuppressed patients. This study investigates the colonization and frequency of bla_{OXA-48} and bla_{NDM-1} genes as main reasons of carbapenem resistance, in carbapenem resistance *Enterobacteriaceae* separated from the intestinal tract of immunosuppressed children admitted to the oncology ward of Mofid Children's Hospital in Tehran during 6 months.Stool samples are collected during the first 24 hours of hospital admission, then *Enterobacteriaceae* isolates recognized with standard microbiological laboratory methods, carbapenem resistance isolates identified by using antibiogram test and the intended resistance genes recognized buy PCR and electrophoresis gel. Frequency of isolates were like: 26 *Eschershia,* (57.7%); 10 *Klebsiella,* (22.2%); 5 *Enterobacter,* (11.1%); 2 *Citrobacter,* (4.4%) and 1 *Serrati* (2.2), based on antibiogram tests, 19.2% *Eschershia* (5/26), 40% *Klebsiella* (4/10), 20% *Enterobacter* (1/5) and 50% *Serrati* (1/2) had identified, which all 12 of them had bla_{OXA-48} and 5 of them had bla_{NDM-1}.The conclusion of this study showed the high existence of carbapenem resistance isolates in oncology ward. The

high existence of *bla*$_{OXA-48}$ in these isolates, especially in *Escherichia*, can raise therapeutic challenges and concerns in case of systemic infections in these patients.
Keywords: Enterobacteriaceae family. Antibiotic resistance. Carbapenemase. Hospital acquired infection (HAIs).

CP61 Association study of *TBX21* gene polymorphism rs41515744 with Alzheimer's Disease

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Alzheimer's disease (AD) is the most prevalent neurodegenerative cause of dementia and is responsible for significant individual mortality, and has economic impact on the health care system of populations. It is characterized by progressive cognitive and functional impairment and memory loss. Pathologically, there is formation of amyloid plaques and neurofibrillary tangles in the brain, as well as neuronal loss, synaptic loss, brain atrophy, and inflammation. Accumulation of the amyloid-β (Aβ) peptide, the major component of amyloid plaques, is hypothesized to initiate a pathogenic cascade that eventually leads to AD.T-box expressed in T cells (T-bet), a member of the T-box family of transcription factor genes, was first identified from a Th1-cell cDNA library as a Th1-specific transcription factor, and was also cloned as TBX21. The aim of this study is to explore whether TBX21 gene polymorphism rs41515744 are associated with Alzheimer's disease by T-ARMS-PCR and Graph pad Prism methods. Significant difference in genotype frequencies between patients and controls ($p=0.03$) was observed and the frequency of TT genotype was significantly increased in the patient group (2.01 ± 0.03) compared to the control group (1.08 ± 0.01). So results suggests that (C/T) of (rs41515744) of TBX21 gene polymorphism might be associated with AD occurrence.
Keywords: Neurodegenerative Disease, Single Nucleotide Polymorphism, Inflammation

CP62 Evaluation and comparison of Tamoxifen, Fostamatinib and Regorafenib inhibitors on tyrosine kinase receptors using molecular modeling

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Today, there are several treatments available for breast cancer. The current treatments including tyrosine kinase inhibitors and estrogen receptor positive drugs. In this study, we evaluated interactions between Fostamatinib and Regorafenib compounds as tyrosine kinase inhibitors and Tamoxifen as aromatize inhibitor and compared to identified effective interactions. Docking was performed between these compounds against 48 hair follicles targets and 80 tyrosine kinase receptors using Auto Dock Vina, Ligplot++ and discovery studio software. Analysis of the results showed that no hydrogen bond was observed in the interaction between Tamoxifen and tyrosine kinase receptors. However, adjacent amino acids have established bonds, like π-alkyl, Pi-Pi T-Shaped, Pi-Cation, and carbon-hydrogen. In interaction between Tamoxifen and hair follicle targets only π-alkyl bond was observed. The interaction between Fostamatinib and Regorafenib, with tyrosine kinase receptors and hair follicle targets Hydrogen and hydrophobic bonds were observed. It seems that the drug forming is as important as the linkage limits in the drug activity and should be considered in the breast cancer drug design.
Keywords: Drug design, aromatize, hair follicles, cancer

CP63 Identification of potential key genes and pathways in Triple-negative breast cancer using bioinformatics analysis

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Triple-negative breast cancer(TNBC) refers to breast cancer that does not express estrogen receptor (ER), progesterone receptor (PR), or human epidermal growth factor receptor 2 (Her2). Due to the lack of these receptors, no targeted agents have shown broad effectiveness against TNBC, therefore, there is a critical need for more active therapeutic strategies. This study aimed to identify differentially expressed genes (DEGs) for

TNBC and elucidate the potential interactions among them. Microarray dataset GSE62931 was selected from GEO database, which composed of gene expression data from 100 samples, including 53 non-TNBC and 47 TNBC. The differentially expressed genes (DEGs) with adj P.value <0.01 and |LogFC|≥1.5 were identified using GEO2R. The GO and KEGG analyses were conducted through Enrichr. The protein-protein interaction (PPI) network of the DEGs was established through STRING website, visualized by Cytoscape and further analyzed by MCODE. CytoHubba was used to identify hub genes. 176 up-regulated and 217 down-regulated DEGs were identified. These significantly changed genes are mainly involved in the biological process termed response to estradiol, cellular response to estradiol stimulus and nervous system development. Protein digestion and absorption and regulation of lipolysis in adipocytes were the major enriched pathways for the up-regulated and down-regulated genes, respectively. FOXM1, EGR1 and RNF2 were the top transcription factors controlling the expression of up regulated genes. Hub genes selected, included KIF2C, KIF20A, CCNA2, NDC80, AURKB and BUB1. These pathways and genes identified could help to understand the mechanism of development of TNBC and might be promising targets for the TNBC treatment.

Keywords: Transcription factors (TFs), Signaling pathway, Biological process, Hub genes

CP64 Investigating the Effect of Methotrexate on Expression Changes of LncRNA CASC15 in Acute lymphoblastic leukemia (Jurkat E.6.1)

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Acute lymphoblastic leukemia (ALL) is the most common cancer in children. Methotrexate is produced and used for chemotherapy, either alone or in combination with other chemotherapy drugs. It is effective for the treatment of some cancers, including breast, head and neck, leukemia, lymphoma, lung, osteosarcoma, and bladder cancer. CASC15 is one of the important LncRNAs that expresses changes in most cancers. The aim of this study was to evaluate the effect of MTX drug on the expression of LncRNA CASC15 in acute lymphoblastic leukemia in the Jurkat E6.1 cell line. first, MTX drug was prepared as a drug. Different doses of MTX were examined with the MTT test. Then, the MTX was provided at 1 and 10 doses as optimal concentrations. Then, the Jurkat E6.1 was cultured in two doses at 72 hours with MTX. then RNA extraction and cDNA synthesis were down, and the expression of LncRNA CASC15 and GAPDH gene was evaluated as housekeeping gene by Real Time PCR. Finally, the results of Real Time PCR were analyzed by Rest 2002 Software. The Results of the research showed that the expression of LncRNA CASC15 significantly decreased after treatment with MTX at 1 and 10 doses in 72 with (p-value < 0.001) compared to non-MTX samples . According to the results, it has been found that doses of 1 and 10 MTX in 72 hours are the optimal doses and time of the effect of this drug. The expression of LncRNA CASC15 at the indicated concentrations and time were 0.417 and 0.652. Therefore, considering the oncogenic role of CASC15 in leukemia and reduced gene expression after drug treatment compared to the control group, it can be concluded that MTX can be an effective drug in controlling the expression and inhibition of oncogene genes in cancer.

Keywords: GAPDH, housekeeping, cDNA

CP65 Investigation of submerged fermentation of slaughterhouse wastes by proteolytic microbial isolates

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The meat industry (livestock, poultry, and fish) produces several tons of waste annually, sometimes with environmental problems. Different parts of these lesions have different types and amounts of protein. One of the current trends in biotechnology is the application of microbial-mediated processes in the valorization of the food industry by-products, including livestock slaughterhouse wastes. The exploitation of keratin proteins from livestock slaughterhouse wastes through microbial processes has been widely discussed in terms of prospects and economic conditions, where proteolytic microorganisms often play a crucial role. Peptides obtained from protein hydrolysates have received special attention from researchers due to their inherent bioactivities. This method is based on some bacteria or yeast species that secrete enzymes (including proteases) in the extracellular

growth medium. Therefore, inoculation of protein material with this type of bacterial cell can lead to proteolysis and peptide production. In this study, first, to isolate proteolytic isolates, blood powder, meat powder, a mixture of meat and blood powder, and bone of slaughterhouse waste were screened. Then proteolytic isolates were identified by culturing the isolates obtained in skim milk agar1% medium and isolates with strong protease properties were selected and used to ferment the wastes. Fermentation was performed by immersion for 5 days at a temperature of 30°C and 150 rpm by two isolates, B4, A5 with strong protease properties. Then the degree of hydrolysis of the hydrolyzed product was estimated based on the OPA method. 13 strains with the ability to grow on wastes powder were identified as carbon sources. A total of 6 bacterial isolates showed significant proteolytic potential. The results show that the degree of protein hydrolysis by fermentation with A5 bacteria is significantly increased ($P<0.05$) compared to fermentation with B4 bacteria.

Keywords: Protein hydrolysis, blood powder, meat powder,Screening, Fermentation

CP66 Identification and purification of a new milk-clotting protease from *Onopordum leptolepis*

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Milk coagulation is the basic step in cheese making. Milk clotting enzymes show the main role in cheese manufacturing ,which their activity leads to the enzyme-mediated cleavage of kappa-casein, rendering the casein micelles unstable and eventually aggregation that yields a clot and a gel afterwards. Chymosin (EC 3.4.23.4) from the calf rennet has been considered as the most widely used milk-clotting enzyme. Increasing world cheese production and consumption along with a reduced supply of calf rennet, has led to a systematic investigation for new rennet substitutes. The results of research conducted in recent years have shown the possibility of using plant proteases as a suitable, low-cost and safe alternative to others rennet. Accordingly, some plant milk-clotting proteases have been isolated from *Withania coagulans*, *Cynara scolymus*, *Silybum marianum* ,*Centaurea calcitrapa*, *Solanum dubium* and *Asparagus officinalis*. Here, a new milk-clotting protease from *Onopordum leptolepis* was identified and purified. The enzyme was extracted by grinding the flower of the plant in liquid nitrogen, then homogenized using sodium citrate buffer (pH 3.0). The plant extract was filtered and the enzyme was purified using ammonium sulfate precipitation. The homogeneity of the enzyme was assessed by SDS-PAGE. The crude enzyme showed the milk clotting activity about 62.85 ± 3 U/ml when assayed against bovine milk. The highest caseinolytic activity was detected at pH 3 and 45 °C temperature. The simple purification procedure together with the availability of the plants, as the enzyme-producing source, is cost effective in biotechnology. This approach could be used for large-scale production of the enzyme, allowing a broad study of its various probable applications. Moreover, high milk-clotting ability of the protease, could therefore pave the way for its uses in the cheese industry as well as other food and biotechnological industries.

Keywords: Plant rennet, *Onopordum leptolepis*, Milk-clotting activity

CP67 Inhibition of human neuroblastoma cell line SH-SY5Y growth due to the modulation of oxidative stress by retinoic acid

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Neuroblastoma is a type of malignancy with an embryonic origin of the autonomic nervous system. Tumors usually form in the chest or abdomen of children. The cause of the neuroblastoma is not exactly known. Environmental and/or genetic factors can play a role in the development of the disease. Success in treatment depends a lot on the age at which chemotherapy is started; with higher chance of success, and more possibility of reversing the progression of the disease at the age of less than eighteen months. Vitamin A derivative, all-trans retinoic acid (ATRA), with the ability to differentiate cells has antioxidant properties. Therefore, at the present study, the human neuroblastoma cell line SH-SY5Y was treated with a concentration of 1 μM ATRA.

After 7 days, by examining different cellular parameters, it was found that the rate of reactive oxygen species and lipid peroxidation was decreased by 20% and 50%, respectively, and the amount of glutathione (GSH), which is the most important natural antioxidant in cells, was increased by 50%. There was also a 40% reduction in cell viability. After treatment with 1 μM ATRA, SH-SY5Y cells were morphologically elongated, with longer and fused neurites and in the form of a network. According to the results of the present study, ATRA can be used as a growth inhibitor and viability reducer of neuroblastoma cells, effectively in chemotherapy.
Keywords: Reactive Oxygen Species, ATRA, Cancer, SH-SY5Y, Chemotherapy

CP68 Identification of homozygous splice site mutation of *SURF1* gene in a leigh syndrome affected patient

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Leigh syndrome or subacute necrotizing encephalomyelopathy in children is a severe progressive neurological disorder that affects the central nervous system. In normal population, the incidence this syndrome is 1 of 40,000 births. In this study, the patient was a 2.5-year-old girl born at consanguineous parents with symptoms including developmental delay, difficulty swallowing, motor Impairment, and progressive mental loss referred to genetic counseling center. Next Generation Illumina Sequencing was performed to enrich all exons of more than 22000 genes as well as some other important genomic regions in the patient studied. Subsequently, Sanger sequencing was used to confirm the mutation in the patient and her parents. The results showed a novel homozygous 3' splice site mutation NM_003172.3:c.516-1G>A in the *SURF1* gene of affected patient. Additionally, her parents were heterozygote for this mutation. In silico analyses using mutation taster, SIFT and mutation accessor software were confirmed the pathogenicity of a novel splice site mutation found in the *SURF1* gene. The product of this gene is involved in the biogenesis of the cytochrome c oxidase complex (COX), which plays a key role in electron transfer in oxidative phosphorylation and ATP production. Mutation in *SURF1* gene disrupts the encoded protein function and decreases COX complex formation, as a result leading to leigh syndrome. In conclusion, the present study revealed a novel pathogenic mutation in the *SURF1* gene in the studied family. These kinds of studies could be a blueprint for genetic counseling and prenatal diagnosis.
Keywords: Leigh syndrome, *SURF1* gene, NGS, Splice site mutation, mitochondrial disease

CP69 Study of expression profile of miRNA 397a in *Thymus vulgaris* under drought stress

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Thyme, *Thymus vulgaris,* is one of the most important plants from the *Lamiaceae* family which has medicinal and antimicrobial effects. thymol and carvacrol, two phenolic compounds with antioxidant property, are the main compounds of thyme extract . Drought stress is one of the most common abiotic stresses that limits the main function of the plant and is a challenge for agricultural scientists to produce plants with high productivity. miRNAs are a class of small non-coding RNAs with a length of 21 to 24 nucleotides that are involved in almost all plant biological processes during biotic and abiotic stresses. The evolutionary superiority of miRNAs for silencing transcription factors has made these small molecules the main key in plant growth and adaptive responses. In this study, thyme plants were exposed to concentrations of 0%, 10%, 25% and 50% of PEG 8000 during 2 and 5 hours.Then the changes in miRNA 397a expression in response to drought stress were investigated. After RNA extraction and cDNA synthesis, the expression pattern of miRNA 397a was examined by Real Time PCR. The highest level of expression was observed at the level of 25% of drought in 2 hours and The lowest was observed at the level of 50% drought in 5 hours. Efficient and reliable detection of miRNAs is an essential step in understanding the role of miRNAs in specific response of plant cells to stress.

Keywords: Thyme, gene expression, abiotic stress, miRNA

CP70 Biosynthesis of magnetic iron nanoparticles by Lactobacillus plantarum

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Magnetic nanoparticles have been very popular among researchers due to their wide application in information storage, sensors, catalysts, and in medicine as carriers of drugs and this has been the impetus for further research on their synthesis method and benefits. Lactobacillus plantarum PTCC: 14917 was obtained from Iran Scientific and Industrial Research Organization and inoculated in MRS broth, incubated for 72 h at 37 ° C and 5% CO2 concentration. The samples were centrifuged at 5000 rpm and their supernatant were collected. Aqueous solution (3.10 M) of Fe_2O_3 was prepared and added to the supernatant under ambient condition. The production of iron nanoparticles was demonstrated by changing the color of the solution, UV-vis spectroscopy, XRD, FTIR and TEM techniques. The change in color of the solution from Indian red to dark brown indicated that the nanoparticles were produced. The reduction of Fe^{2+}ions and the formation of nanoparticles were monitored by UV_visible spectroscopy and they were showed a peak during 400-500 nm. FTIR results in this reaction of hydroxyl groups (peak 3333.48cm-1) and carbonyl (peak 1661.00 cm- 1) showed. The formation of nanoparticles was prepared using XRD technique with irradiation $\lambda = 54.3$ Å for Fe_3O_4 and $\lambda = 33.2$ 2 for Fe_2O_3. Dispersions at angles 30.5, 35.9, 43.5, 54.5 showed the presence of Fe_3O_4 magnetic nanoparticles and the presence of peaks at angle 33.5 to produce Fe_2O_3 nanoparticles . TEM results, indicate dimensions 35-45 ±1 nm and in spherical shape. According to the results, iron nanoparticles were produced extracellularly by Lactobacillus plantarum. The nanoparticles produced in this way are very small and since Lactobacillus is the major group of probiotics, they are safe and non-pathogenic and can be used for medical and pharmaceutical purposes. This method is simple, cost-effective and eco_friendly.

Keywords: Green synthesis, Probiotic ,Nanoparticles

CP71 Evaluation of Ultraviolet-C on the Induction of Antibiotic Resistance in environmental Bacteria gamma resistance in Laboratory Conditions

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Recently, bacterial infections have increased due to overuse of antibiotics and that has created problems. One of the most influential factors in bacteria is ultraviolet radiation, which can cause different behaviors and may eventually lead to mutation. In this study, 3 bacteria of *Bacillus cereus*, *Bacillus subtilis* and *micrococci* that were sampled were exposed to ultraviolet light in two times of 10 minutes and 20 minutes. The antibiotic susceptibility of these three bacteria was assessed by measuring the inhibition zone diameter. The aim of this study was to evaluate ultraviolet radiation on the induction of antibiotic resistance in gamma-resistant environmental bacteria after exposure to ultraviolet radiation. Laboratory sampling was performed from a predetermined area in front of Gamma source. These three strains were exposed to ultraviolet light at two different times, cultured on Muller-Hinton agar and incubated at 37 ° C. The inhibition zone diameter of these three bacteria was measured before and after UV-C irradiation. Finally, antibiotic susceptibility of these three species of bacteria was measured. The results of this study showed that ultraviolet radiation completely killed the test bacteria for 20 minutes and test bacteria were reduced for 10 minutes, compared to the control group. It also increased the resistance of *Bacillus cereus* to Azithromycin and Piperacillin and *micrococci* against AZM, PRL and Oxacillin This in turn leads to the spread and resistance to antibiotics. radiation resistance can indirectly transmit resistance to antibiotics and the strain can spread and expand the resistance due to its spread in the environment.

Keywords: micrococci, *Bacillus cereus*, *Bacillus subtilis*, radiation

CP72 Study of association between Circular RNA000284, miR-506 and SNAIL -2 expression in breast cancer

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Breast cancer is the most common malignancy among women and along with lung and colon cancer is one of the most common cancers in the world. Therefore, finding solutions such as early diagnosis of the disease or targeted treatment can reduce the death rate. Today, biomarkers have received considerable attention for the diagnosis, prognosis and treatment of breast cancer. One of this Biomarkers is non-coding RNAs. In this study, the expression of non-coding RNAs including miR-506 and Circular RNA 000284 and their target gene SNAIL-2 was examined, also the relationship between their expression in breast tumor tissue was assessed, to nominate a possible biomarker for prognosis or a therapeutic goal. Initially, total RNAs were extracted from 30 breast tumor tissue samples and their adjacent normal tissue. Then relevant cDNAs were synthesized and finally, the expression of each was examined with the using of Real-time PCR technique. According to the studies, circular RNA000284 expression has increased in breast tumor tissue compared to the adjacent normal tissue and decreased expression of miR-506 was seen, also the expression of the SNAIL-2 gene in the tissues of patients has increased compared to the adjacent normal tissue. In this study, the expression of circular RNA000284, miR-506, and SNAIL-2 depicted that, circular RNA 000284 sponged the miR-506 in the tumor tissue of patients with breast cancer. the target mRNA of miR-506, which is SNALI-2, has increased. the SNAIL-2 is an EMT factor that leads to the epithelial to mesenchymal transition (EMT), consequently will cause to malignancy of tumor tissue in patients. Hence circular RNA000284 and miR-506 can be nominated as prognostic biomarkers in breast cancer.

Keywords: Cancer, Non-Coding RNA, Biomarker

CP73 Synthesis and Characterization of 5-Fluorouracil-loaded Calcium Carbonate Nanoparticles and their Cytotoxicity on Colorectal Cancer Cells

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Colorectal cancer (CRC), as the third most prevalent cancer and fourth principal cause of cancer death worldwide, is in urgent need of effective treatments. Though chemotherapy is still one of the powerful tools available for cancer therapy, it suffers from some limitations including the lack of selectivity, aggregation, and low biocompatibility. Therefore, the application of targeted drug delivery systems (DDS) is of greatest importance, among which nanoparticles have attracted considerable attention as carriers. In this study, after Calcium Carbonate ($CaCO_3$) nanoparticles were synthesized via spontaneous precipitation method, the synthesized nanoparticles were characterized by X-ray Diffraction (XRD), Fourier transform infrared (FT-IR), and Field Emission Scanning Electron Microscope (FE-SEM). 5-fluorouracil (5-FU), a common anti CRC therapeutic drug, was loaded on $CaCO_3$ nanoparticles. Then, the cytotoxicity of 5-FU alone and together with $CaCO_3$ nanoparticles were evaluated on the murine colorectal cell line, CT-26, by MTT assay. The successful synthesis of $CaCO_3$ nanoparticles was concluded owing to the crystallinity, purity of $CaCO_3$ nanoparticles and the appearance of the characteristic vibrational bands attributed to the bending and stretching vibrations of CO_3^{2-} in XRD pattern and FTIR spectrum respectively. Furthermore, after 5-FU loading on $CaCO_3$ nanoparticles, absorption bands which belongs to this drug emerged in its FTIR spectrum. Additionally, FE-SEM observations revealed the synthesis of oval-shaped $CaCO_3$ nanoparticles. The examination of the cytotoxicity of the drug-loaded nanoparticles on cancer cells showed that although free 5-FU has inhibitory effects on cancer cells with the IC_{50} value of 1.9±0.1 μg ml^{-1}, the chemotherapeutic drug efficacy is improved when loaded on $CaCO_3$ nanoparticles (IC_{50} = 0.9±0.16 μg ml^{-1}). Based on the findings of this study, 5-FU-loaded $CaCO_3$ nanoparticles could be considered as a promising candidate for colorectal cancer therapy.

Keywords: chemotherapy, biocompatibility, drug delivery system

CP74 Association of *ACE2* and *TMPRSS2* genes polymorphisms in altering host susceptibility to SARS-COV-2 virus

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The Covid 19 pandemic caused by SARS_COV_2 (Acute Respiratory Coronavirus 2 Syndrome) was first reported by the WHO in March 2020. The spike protein (S protein), a protein encoded by the virus, binds to ACE2 (the enzyme angiotensin 2), which acts as a receptor for the virus to enter the host. Then, the S protein causes the virus to enter the host cell through membrane processes, encoded by *TMPRSS2*. *ACE2* and *TMPRSS2* genes are expressed in many human tissues, but the individual expression of these genes varies in different societies. Examination of *ACE2* and *TMPRSS2* gene polymorphisms in different populations has shown that these polymorphisms can increase the host susceptibility to SARS_COV_2 or cause the host to become resistant to coronavirus infection. Extensive epidemiological studies have also been performed to investigate susceptibility to infection, severity of pathogenicity, and lethality of the virus in terms of gender and age differences. The obtained results showed that certain types of unique but common polymorphisms in *TMPRSS2*, such as rs12329760 and p.val160.met, can alter the susceptibility of individuals and their lung tissue to SARS_COV_2 virus infection. On the other hand, *ACE2* polymorphisms are significantly associated with the severity of SARS_COV_2 virus infection. Based on studies, 13 polymorphisms (including rs2097723, rs142017934 and rs4646140) have been observed in the coding and non-coding sites of the *ACE2* gene, all of which alter the expression of the *ACE2* gene. Also, the study of gender factor in studies of *ACE2* gene polymorphisms has shown the association of some polymorphisms with higher rates of infection and infectivity in one sex than the other sex. Further studies on these polymorphisms in different communities can be an effective guide in finding a cure, discovering effective drugs, and designing effective vaccines against SARS-COV-2.

Keywords: Covid-19, s-protein, Genetic polymorphisms, ACE2 genetic polymorphisms, Angiotensin receptor

CP75 Effect of Secretome secreted from mesenchymal stem cells cultured with colorectal cancer cells By analyzing the expression of *Bax* and Bcl_2 genes

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Colorectal cancer is the third most common cancer and the second leading cause of cancer mortality worldwide due to the fact that mesenchymal stem cells are very similar to cancer cells in terms of speed of proliferation, studies have shown that due to the anti-cancer properties of mesenchymal stem cells, the interaction between cancer cells and mesenchymal stem cells can help treat many cancers. The aim of this study was to investigate the expression of *Bax* and Bcl_2 apoptotic genes. In this study, we are looking for the role of apoptosis in the development and treatment of cancer and focus on the mitochondrial pathway of apoptosis, the most common regulator of cell death in cancer. Studies have shown that the two *Bax* and Bcl_2 genes contribute to programmed cell death or apoptosis. The association and ratio of *Bax* to Bcl_2 also determines cell survival or death after an apoptotic stimulus. In this study, we used co-cell culture for cancer cells and stem cells at different times using a 6-cell two-story plate with a diameter of 0.4 μm (Transwell) and Using qRT-PCR, we measured the expression of *Bax* and Bcl_2 apoptotic genes to find that the effects of mesenchymal stem cell scrotum on colorectal cancer cells inhibited or stimulated *Bax* and Bcl_2 apoptotic genes. The results showed that there was an inverse correlation between *Bax* and Bcl_2 expression in individual tumors and significant Bcl_2 inversion. The highest expression level Bcl_2 and the ratio Bcl_2.*Bax* were associated with *p53* mutant immunophenotype. Therefore, we conclude that aggressiveness in colorectal tumors could be linked, in addition to proliferation, to apoptosis-related factors.

Keyword: Colon cancer, Stem cells, Gene expression, *Bax*, Bcl_2

CP77 Investigation of multicolor carbon dots stability for cellular applications

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Recently, carbon dots (CDs) have received much attention owing to their advantages such as low toxicity, the ability of surface functionalization, high stability, and simple and cost-effective synthesis. Another feature of CDs is the ability of CDs synthesis from some natural or green sources such as fruits, vegetables, and etc. that this feature of CDs makes them biodegradable particles with low toxicity. Another interesting property of CDs is ability of multicolor CDs synthesis with concentration variation or surface functionalization that this property of CDs, recently receives much focus in cellular studies. In this research, we synthesized multicolor CDs from a green source by hydrothermal method. Then, after characterization, the optical properties of the appropriate concentration of prepared CDs were investigated. The fluorescence intensity spectra of multicolor CDs were measured during four different periods of time, including 0, 3, 6, and 12 months. It should be mentioned that, by decreasing CDs concentrations, the color of CDs changed from green to blue that these results were confirmed by fluorescence spectrophotometer. Besides, fluorescence spectroscopy and the quantum yield of synthesized multicolor CDs can indicate the high stability after a year and this photostability feature of nano particles is of crucial importance in different fields of cellular studies such as drug delivery, biomarkers, imaging in targeted cell lines or tissues.

Keywords: nanoparticles, cell imaging, fluorescence particles, biodegradable

CP78 Study the effect of oil extraced *Pseodomonas aeruginosa* to stimulate immune system in *Arabidopsis thaliana*

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In this research, the *Pseudomonas aeruginosa* which was isolated from oil, initially was grown in MS medium for 24 hours. The bacterium was harvested and inoculated to *Arabidopsis thaliana* seedling in 0. 002 optical density. It is observed that inoculated plants have lower growth compared to control plants. In order to determine whether the dead *Pseudomonas aeruginosa* can stimulate defense system of *A. thaliana*, the dead bacterium was inoculated to Arabidopsis plants. To the control plants only inoculation buffer without any bacterium was added. One hour after inoculation, it was seen that the dead bacterium can enhance the transcription of (*PR-1*) *PATHOGENESIS-RELATED GENE 1*. Furthermore, it is observed that the dead bacterium can enhance the transcription of *BRI1-ASSOCIATED RECEPTOR KINASE* 24 hours after inoculation. Transcription of *PR-1* and *BAK-1* genes is regarded as the most importnat factors that their transcription induce the immune system in *A. thaliana*. It is observed that compared to AtPep3 nano peptide, the dead *P. aeruginosa* could higher enhance the transcription of *PR-1* and *BAK-1* genes. The resutls of this study for the first time showed that the dead *P. aeruginosa* can enhance the defence systen in model plant *A. thaliana* and induce the priming effect. The application of priming effect to induce resistance againt plant diseases has great value to control important plant pathogen. It is suggested to apply this finding in important crop plants and control important plant pathogens.

Keywords: Innate immunity, Pattern triggered immunity, AtPep3, priming effect, defence

CP79 Study the effect of NaCl stress on the expression of the AtPropep family in *Arabidopsis thaliana*

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The protein product of the recently discovered AtPropeps family has very important role in the immune system in *Arabidopsis thaliana*. The final product of this family is eight small peptides named AtPropep1 to AtPropep8 and perceived by AtPEPR1 and AtPEPR2 receptors which are resident in the plasma membrane. It is identified that the immune system in *Arabidopsis thaliana* is fine-tuned through the cell to cell movement of these signaling peptides. So far, there is a very limited research about AtPropep family and their corresponding

receptors was done in response to NaCl treatment. In the current research, four weeks old *A. thaliana* was treated with 300mM NaCl in three time course including one, six and 24 hours. Distilled water was added to the control plants. The gene analysis showed that the response of this gene family is totally different from each other. It is identified that *AtPropep1* and *AtPropep3* were highly induced in response to NaCl treatment. The rate of gene induction was the highest six hours after treatment. *Atpropep3* gene induction was more than *AtPropep1*. In addition, compared to the control plants, we observed that 24 hours after treatment, *AtPEPR1* is induced in response to NaCl treatment. Furthermore, *AtPEPR2* was not induced in response to NaCl treatment. The result of this study showed that other members of this family were not induced in response to NaCl treatment, indicating that each member of this family has specific role. In conclusion, the result of this study showed that it is possible to apply members of this family against salt stress.

Keywords: Salt treatment, Receptor, peptide, gene expression, signal

CP80 Engineering of SARS-CoV-2 Virus Neutralizing Drug Using *In Silico* Analyses

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COVID-19 infectious disease has rapidly become a global epidemic with high mortality rates. SARS-CoV-2 virus is the causative agent of this disease. Binding between the viral spike surface protein (receptor binding domain-RBD) and a special cellular receptor called ACE2, which is present on the surface of cells, enables the virus to enter the cells. Thus, a foreign recombinant ACE2 (frACE) protein can act as an inhibitory agent and also a competitive antagonist for virus entry. To design a mutated ACE2, Molegro software was used to substitute the amino acids with central roles in enzymatic activity of the ACE2 with neutral amino acids. The saturation mutagenesis at the interaction surface of ACE2-RBD was performed by mCSM–PPI2 server to increase the affinity of frACE against RBD. Using the Chimera software, the amino acids with highest B factors were mutated to increase the thermal and structural stability of the frACE .The obtained results demonstrated that the Arg273Gln and Thr445Gly mutations have reduced the binding ability of the ACE2 ligand into the active site and consequently the enzymatic activity. The Thr27Arg was determined to be the most potent mutation to increase the binding affinity. The Asp427Arg mutation was shown to decrease the flexibility (CABSflex server) and ultimately promote of the B factor. The Pro451Met along with the Gly448Trp mutations were predicted to increase the thermo–dynamic stability and thermo–stability according to the results of the GROMACS software and molecular dynamics (MD) analysis. Bioinformatics design could lead to reduced laboratory costs and offer an effective recombinant protein drug for COVID-19 treatment. The frACE is advantageous over its natural homologous protein; it has no enzymatic activity (does not cause degradation in the patient's body), more stability, and more affinity against the RBD. This protein could potentially neutralize the virus and prevent it from entering lung cells.

Keywords: COVID-19 disease, Spike protein, Angiotensin Converting Enzyme 2

CP81 A simple and inexpensive in vitro enrichment of ovarian cancer stem cells for the identification of effective anti-cancer stem cell drugs

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Subpopulations of ovarian cancer cells in ascites exhibit cancer stem-like phenotypes that possess an enhanced resistance to chemotherapeutic drugs and have the potential for distant metastatic spread and recurrent disease. The isolation of cancer stem cells (CSCs) from ovarian cancer cell culture required a defined culture medium with different growth factors which in the long term is not cost-effective. Here, we describe for the first time a cost-effective method for the isolation of ascites-derived CSCs without using a cocktail of growth factors. In this study, ascites fluid samples were collected from patients (n=3) with high grade serous ovarian cancer

(HGSOC) and cultured with MCDB105/M199 (50:50) media supplemented with 10% fetal bovine serum (FBS) to reach a monolayer. For CSCs enrichment, EOC cells were cultured in 10% patient-derived ascites fluid and 80% of MCDB105/M199 without FBS using 3D spheroid culture. We found that ascites-derived EOC cells expressed high levels of epithelial markers: CK-7, CK-18, and EpCAM. Our results showed remarkably and significantly increased expression levels of CD133, CD44, Oct-4, Nestin, Nanog, and ALDH1 in secondary and tertiary spheroids cultured with 10% ascites fluid compared to monolayer cell culture. Moreover, we found a higher Paclitaxel (PTX)-resistance spheroids obtained from culture condition with ascites fluid compared to the monolayer. Treatment of tertiary spheroids with Galunisertib as a TGFBR1 inhibitor and Verteporfin an inhibitor of YAP1/TAZ signaling showed a significant and strong decrease of CSCs markers. This method could be a simple and cost-effective cell culture method for ovarian CSCs enrichment for the identification and targeting of key signaling pathways and molecules for ovarian CSCs maintenance.
Keywords: epithelial ovarian cancer, cancer stem cells, ascites fluid, chemoresistance, signaling pathways

CP83 Comparing the cytotoxic effects of ellagic acid derivatives on HT-29 Cells

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Ellagic acid, a natural phenol with valuable pharmacological activities, is frequently found in fruits, vegetables and nuts. Urolithins are main ellagic acid metabolites that induce chemopreventive and anticancer effects *in vitro* and *in vivo*. Colon cancer is among the five most common malignancies in the world. Great efforts have been undertaken to introduce novel and more effective compounds against aggressive colon cancer cells. In the present study, we evaluated and compared the effects of urolithins A, B, and the methylated form of urolithin A (UA,UB, mUA, respectively) on human colon cancer cells. After UA, UB and mUA were synthesized, HT-29 cells, a human colon cancer cell line, were treated with increasing concentrations of these three agents for four consecutive days. To note, 0.4% DMSO was used as control treatment. For viability assessment of cells, alamar blue was used and optical density of cells was detected at 600 nm. Determination of cell viability 96 h after administration of 10 µM UA, UB and mUA indicated that 69%, 91%, and 100% of cells were alive, respectively. Regarding 20 µM concentration, viability of cells was calculated as 72%, 85% and 98% for UA, UB and mUA, respectively. In addition, upon 96 h treatment with 40 µM of UA, UB and mUA, cell viability was as 72%, 60% and 96%, respectively. The highest cytotoxic effects were observed 4 days after treatment with 80 µM UA, UB and mUA, as cell viability was dramatically decreased down to 56%, 50% and 67%, respectively. To sum up, the current findings revealed that in concentrations < 80 µM, UA induced more toxic effects in comparison with other ellagic acid derivatives. Although, more research is required to confirm our results on other colon cancer cell lines.
Keywords: ellagic acid, urolithin, colon cancer, cytotoxicity

CP85 Prevalence of *Vibrio parahaemolyticus* species and frequency of *tdh* pathogenic gene in strains isolated from Persian Gulf fish and shrimp

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Vibrio are gram-negative, curved bacilli, halotolerant bacteria that live in sea waters. The present study was performed to determine the prevalence of *Vibrio parahaemolyticus* species and the frequency of tdh pathogenic gene in *Vibrio parahaemolyticus* isolated from fresh fish and shrimp samples and salt.

In this descriptive cross-sectional study, 118 samples consisting of fresh and salted fish and shrimp were collected from different regions of the Persian Gulf and immediately transferred to the lab. They were enriched and 1 g of the samples were poured into tubes containing alkaline peptone water and transferred for 6 hours at 37 ° C. After this incubation period, the samples were occulated on TCBS and incubated for 24 hours at 37 °

C. Initial identification of *Vibrio parahaemolyticus* based on the observation of green colonies that are not capable of consuming sucrose sugar and were Gram negative curved bacteria. In *Vibrio parahaemolyticus*, tdh gene was also identified on isolates using PCR. The results of the present study indicate the high prevalence of *Vibrio parahaemolyticus* in samples of fresh shrimp and salted fish. The results of biochemical tests showed that 36 out of 118 samples (30.5%) were infected with *Vibrio parahaemolyticus*. Therefore, it is suggested to use PCR method as a safe, accurate and fast test for detecting Vibrio species in seafood, in order to control the health of seafood in terms of the presence of Vibrio species.

Keywords: *Vibrio parahaemolyticus*, Seafood, Shrimp and fish, PCR, Pathogenic bacteria

CP86 Study of the effect of hemicellulose on flavonoid production from *Arthrospira*

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Flavonoids are polyphenolic secondary metabolites that have high nutritional and medicinal value due to their strong antioxidant properties and, consequently, have great economic value. Due to the limited natural resources of flavonoids and also the difficulty and high cost of their chemical synthesis, the use of various biotechnological methods, including culture of cyanobacteria, can be a good economic solution in the production of flavonoids. According to recent researches, the use of elicitors is one of the most important and effective economic strategies to improve cell growth and accumulation of secondary metabolites in the extensive culture of microorganisms. Therefore, the aim of this study was to investigate the potential of hemicellulose as an elicitor in increasing the production of flavonoids in *Arthrospira*. Therefore, *Arthrospira* was first cultured in optimized Zarok culture medium. The resulting biomass was harvested and dried. To investigate the effect of hemicellulose on flavonoid production, hemicellulose with different concentrations was added to the culture medium and at different times after treatment, biomass separation was performed by centrifugation. Extraction of total flavonoids was performed by extraction with alcohol solvent at high temperature and this extraction was confirmed by thin layer chromatography. The total flavonoid content was then measured by aluminum chloride colorimetric method with a spectrophotometer. The results showed that hemicellulose increased the wet and dry biomass, and also flavonoids of *Arthospira* compared to the control sample, so that the highest amount of wet biomass (19.9 g), dry biomass (0.61 g) and flavonoids of *Arthospira* (0.386 mg quercetin /mg extract) was achieved under treatment with 0.3 mg/ml of hemicellulose on the 8th day of culture. Taken together, these results indicate the positive effect of hemicellulose on increasing the growth and production of flavonoids in *Arthospira*.

Keywords: secondary metabolite, cyanobacteria, eliminator, biomass

CP87 Optimizing effective experimental parameters on the size of magnetic samarium nanoparticles

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Magnetic nanoparticles have received much attention in the biomedical research due to their unique magnetic properties and their ability in responding to external magnetic fields. Iron and samarium as the most abundant organic metal element and the rare earth element belonging to lanthanides, respectively, show magnetic properties. Considering the importance of size on the physical and chemical properties of materials, the present study was conducted to investigate the effect of laboratory factors on the size of magnetic nanoparticles containing samarium and iron. Green synthesis of magnetic samarium nanoparticles was performed by hydrothermal method using ginger extract. To this end, the effect of different parameters such as reactants ratio, solution pH, and hydrothermal process time on the size of synthesized nanoparticles was evaluated. To do this, samples were synthesized at pHs of 10 and 11 for 2, 4, 9, and 17 hours at 200 °C. The structure and size of the resulting nanoparticles were investigated by X-ray diffraction (XRD) and dynamic light scattering (DLS)

analyses. The size of the synthesized nanoparticles at a constant pH was about 11 and the different durations of 2, 4, and 9 hours were determined to be 178, 168 and 144 nm, respectively. Based on the laboratory data, it can be predicted that under optimal conditions (pH of 11, duration of more than 9 hours and deoxygenation of the reaction solution), nanoparticles with the size of less than 100 nm can be obtained which are useful for biomedical applications.

Keywords: Magnetic, nanoparticles, synthesis

CP88 Antiviral effect of Chlorhexidine-based antiseptics on enveloped virus's model

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Several investigations confirmed that chlorhexidine gluconat (CHG) has an antiviral activity against intraoral herpes simplex virus (HSV) infection (Brookes et al., 2020). The purpose of this work was to assess the in vitro antiviral effectiveness of CHG against type 1 HSV infection at the less concentrations regularly used in mouth rinse formula to recommend a nontoxic concentration for higher frequent usage during the pandemic. The cytotoxic effects of CHG concentrations at 0.001% to 0.12% was evaluated by MTT assay using ISO 10993-5 (Iso & STANDARD, 2009). In vitro antiviral activity of CHG was performed according to the DIN EN 14476 (DIN, 2011). For this purpose, the concentrations of 0.002%, 0.016% and 0.12% was examined on Vero cells infected by HSV-1 at the times of 30sec, 1, 2 and 3 min. CHG exhibits a dose-dependent toxicity effect for the cell tested and the viability of cells decreased to 50 % (IC50) at the concentration of 0.032%. The antiviral potency of CHG can be affected by both concentration and time factors. None of the CHG concentrations inhibited the HSV-1 cytopathic effect (CPE) in less than 3 min. But at concentration of 0.12%, CHG inhibited the CPE of HSV-1 up to 4 Log10 reduction in viral titter in comparison with untreated infected cells with 10^8 TCID50/ml viral load. According to *in vitro* studies, mouthwashes containing ≥0.2% CHG may be beneficial for the control of intraoral HSV-1 infection (Steinsapir & Woodward, 2017). These concentrations may causes different clinical symptoms because of high toxicity effect .It seems that reducing of the CHG concentration to 0.12% along with increasing the exposure time, in addition to preventing destructive effects, can also be effective in the viruses deactivation. Moreover, the range of nontoxic effective dose obtained in this study on HSV-1 can be selected in evaluation of CHG effect on SARS-CoV-2 as an enveloped virus.

Keywords: Mouthwash, Cell Toxicity, HSV-1, Antiviral Effect

CP89 Bioinformatics study of *Streptomyces* genome by antiSMASH web server

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Streptomyces produce two-thirds of the polyketide synthase antibiotics. The *Streptomyces* genome encodes three types of polyketide synthase (type I, type II, and type III). In this study, antiSMASH Web server was used to identify secondary metabolites, and evaluate the gene clusters of non-ribosomal polycystic syntheses and polyketide synthase. The 18 strains of *Streptomyces* genome sequence were obtained from the NCBI database in Gene Bank formate and analyzed by antiSMASH Web server for surveying the secondary metabolites production. *Streptomyces hygroscopicus* subsp. hygroscopicus had the most of PKS type I gene clusters and 5 of the strains had PKS type I gene clusters. Type I PKSs are multifunctional enzymes organized into modules, each of which has a set of distinct and non-repetitive activities responsible for catalyzing a cycle of increasing poly-chain. The cathode is synthesized by 6-dioxycyarithromycin B (DEBS) for the biosynthesis of reduced polypectides such as erythromycin. The PKSs type I gene cluster with a set of enzymes that are responsible for the biosynthesis of the base structure of polyketide synthase. Among the 18 strains of *Streptomyces*, *Streptomyces globisporus* and *Streptomyces libani* lacked PKS type II and PKS type III gene cluster respectively. Eleven strains had only PKS type III gene cluster. The results indicate that *Streptomyces* have a very high potential for the production of secondary metabolites and valuable for new metabolites.

Keywords: *Streptomyces*, polyketide synthase, *antiSMASH*, genome analysis

CP90 Isolation of carotenoid pigments from Staphylococcus aureus isolated from marine sponge

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Staphyloxanthine is a *Staphylococcus aureus* membrane-bound carotenoid with potential of antioxidant and anti-cancer. The genome sequence was obtained from the NCBI Genebank database and analyzed by antiSMASH software. *S. aureus* isolated from marine sponges were cultured in 100 cc of tryptose soy broth and incubated at 37 ° C for 24 hours. The bacterium was characterized by biochemical tests such as mannitol salt agar, catalase and oxidase, centrifuged, the precipitate was suspended in 15 cc of methanol and incubated at 55 ° C for 30 min, the suspension was centrifuged at 8000 rpm for 10 minutes.The supernatant was purified using a thin layer chromatographic and silica gel column (Merck 60 GF254) chromatography (13 cm height, a 1 cm width) by ethyl acetate and ethanol solvents (9:1). Evolution of the genome by antiSMASH software revealed that the genome of this bacterium contain genes encoding PKS type III enzymes, NRPS, terpene, siderophore and class I lentippeptide. The carotenoids shwed photo absorption in 460, 462, 437, 450, 373 and 275 nm. The yellow carotenoid band was observed in thin layer chromatography. Advance surveying is under progress.

Keywords: Staphyoxanthin, anticancer, antioxodant, antibacterial

CP91 Effect of cytotoxicity of silver nanoparticles synthesized with *Thymus vulgari*s extract on Nalm6 leukemia cell line

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Thymus vulgaris is a perennial plant with high antioxidant properties that grows in the Mediterranean regions. Today, with the help of nanotechnology, biocompatible metal nanoparticles can be synthesized from metals such as gold, silver and copper using compounds in plant extracts. Synthesis of silver nanoparticles by green method has various advantages that make these nanoparticles useful for interdisciplinary studies.The Nalm6 cell line belongs to acute lymphoid leukemia that are used for in vitro studies such as apoptosis induction in leukemia cells. In this study, we first synthesized silver nanoparticles with Thymus vulgaris extract by green synthesis method. Then, the nanoparticles were tested and approved by D.L.S technology. The synthesized nanoparticles along with the extract of *Thymus vulgaris* plant were exposed to Nalm6 cells at various hours and the amount of cytotoxicity of MTT test was examined. The obtained information indicates the successful synthesis of silver nanoparticles with the extract of Thymus vulgaris plant. The size of the synthesized nanoparticles is between 25 and 45 nanometers. The IC50 value for Nalm6 cells also decreased with increasing time. *Thymus vulgaris* extract and nanoparticles also induced necrotic apoptosis in Nalm6 cells. This study confirms the effect of nanoparticles and Thymus vulgaris plant on the induction of cell death in the studied cells and introduces a potential factor for the treatment of these diseases.

Keywords: *Thymus vulgaris* ،Nalm6 ،Green synthesis

CP92 Identification of a novel missense mutation of *RPE65* gene causing Leber congenital amaurosis 2

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Leber congenital amaurosis comprises a group of early-onset childhood retinal dystrophies characterized by vision loss, nystagmus, and severe retinal dysfunction. LCA is genetically heterogeneous. In this study, we investigated the genetic cause of vision loss in three consanguineous blind patients from Semnan. Therefore, Next Generation Illumina Sequencing was performed to enrich all exons of more than 22000 genes in the

proband. Subsequently, Sanger sequencing was used to confirm the mutation found in his parents and two other blind patients. The obtained results showed a novel homozygous missense mutation NM_000329:exon3:c.T170C:p.F57S in the *RPE65* gene of proband. In addition, his parents and the other two blind patients were heterozygote and mutated homozygous, respectively. On the other hands, *in silico* analyses using mutation taster, polyphen, SIFT, CADD_phred and REVEL software were confirmed the pathogenicity of a novel missense mutation found in the *RPE65* gene. The RPE65 protein encoded by *RPE65* gene is involved in a multi-step process called the visual cycle, which converts light entering the eye into electrical signals that are transmitted to the brain. In fact, the RPE65 protein then helps convert all-trans retinal back to 11-cis retinal so the visual cycle can begin again. Mutations in this gene are associated with early-onset severe blinding disorders called Leber congenital amaurosis 2 (LCA2) and retinitis pigmentosa 20. Altogether, such studies can be aid to conduct genetic counseling, prenatal diagnosis and clinical management of these types of inherited disorders.

Keywords: Vision loss, LCA2, *RPE65* gene, Next Generation Sequencing, Genetic counselling

CP93 Cloning, Expression and Purification of Carboxypeptidase Enzyme from *Bacillus halodurans*

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Microbial proteases have a large portion of the market of industrial enzymes, because of their wide application in detergents, drug enzymes and animal feed processing. *Bacillus* strains potentially produce, due to their physiological properties, a significant quantity of proteases. The kind of the protease which was cloned and expressed at the present study is Carboxypeptidase from *Bacillus halodurans*. The coding sequence of the gene from above mentioned strain was amplified with PCR using primer pair containing restriction sites NdeI and BamHI. After digestion of the PCR product, it was cloned into the appropriate site at PET28a$^+$ vector, then recombinant plasmids transformed into E. coli BL21 strain. After confirmation of the recombinant plasmids using colony PCR and Sanger sequencing, recombinant enzyme expression was optimized at different conditions, then purified with Nickel embedded Agarose affinity chromatography. IPTG concentration of 0.2 mM, expression temperature of 28 C^o and incubation time of 20 hours provided the maximum amount of enzyme expression. Molecular weight of the carboxypeptidase was estimated approx. 55 KDa using SDS-PAGE. With easily optimized expression and production of substantial amount of recombinant enzyme in E. coli system, it can be hoped that proteases originating from native bacterial strains of Iran, including carboxypeptidases derived from these strains, have a high potential to become suitable enzymes for industrial use. Following the steps of the present research in the second phase, which includes measuring the activity of the enzyme in different temperature conditions, salt concentration and pH, in case of competitive results with existing commercial enzymes, it is possible to introduce the obtained enzyme as a suitable candidate for industrial use.

Keywords: Recombinant, Protease, pET28a$^+$

CP94 Evaluation of the cytotoxic effects of cisplatin-loaded magnetic nanoparticles on CT26 cell line

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CDDP is one of the most potent antitumor agents; however, it is accompanied by severe side effects, including digestive tract reactions, renal toxicity, bone marrow suppression, and neurotoxicity. Furthermore, long-term use of CDDP can induce drug resistance. In recent years, much attention has been paid to developing targeted drug delivery systems, which are a promising strategy for increasing therapeutic drug accumulation in cancer cells, while reducing toxicity to normal tissues. Among these, magnetic nanoparticles are attracting more interest. Hence, in the present study, we employed Fe_3O_4 hydroxyapatite nanoparticles to improve the

therapeutic effect of cisplatin (CDDP) in colorectal cancer. So, magnetic hydroxyapatite nanoparticle (mHAP) was fabricated and CDDP was loaded in porous of hydroxyapatite. The synthesized nanocomposite was characterized by a UV–Visible spectrophotometer, FT-IR, and VSM. *In vitro,* biological experiments revealed that a high efficiency in the cytotoxic effect of Cs.CDDP:mHAP in CT26 colorectal cancer, using MTT assay and Ao/EtBr staining. The IC_{50} value of treated cells with CDDP (2.84±0.1 µg/ml) was decreased to be 2.34±0.092 µg/ml when the cells were treated with Cs.CDDP:mHAP. A pronounced increase in apoptosis was observed in the cells treated with the nanocomposite as compared with that in the cells treated with the CDDP, which is in accordance with the MTT assay results.

Keywords: Drug delivery system, Magnetic hydroxyapatite nanoparticles, Cisplatin, CT26 cells

CP95 Evaluation of different nitrogen sources in production of surfactant by *Pseudomonas putida KT-2440*

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Biosurfactants are used to increase the availability of nutrients in plant nutrition and bioremediation of contaminated soils. These compounds are biodegradable and can be produced from inexpensive renewable sources. In this study, aiming to find the optimal conditions of surfactant synthesis from *Pseudomonas putida KT-2440* in using sugarcane molasses as carbon source, the effect of different nitrogen sources (urea, sodium nitrate, ammonium chloride and ammonium nitrate), different carbon to nitrogen ratio (1:10, 1:20, 1:30 and 1:40) and incubation time (1, 4, 6 and 8 days) were investigated in separate experiments. The optimal treatment of each experiment was used in the next step .For this purpose, the pH of the culture medium, surface tension and dry weight of biosurfactant were measured. Among nitrogen sources, ammonium chloride showed the least surface tension at 55.93 $mN.m^{-1}$ compared to the control (74.55 $mN.m^{-1}$). While the highest dry weight of biosurfactant was obtained in the application of sodium nitrate (4.5 $g.L^{-1}$). The results showed that compared to the initial pH of the culture medium (7), the final pH of the solution decreased in application of ammonium chloride and increased in the other sources. By measuring the weight of biosurfactant at the pHs adjusted (7 and 2), it was found that the pH of the final solution affects the deposition of the biosurfactant in acetone method. In the application of sugarcane molasses and sodium nitrate, the lowest surface tension was measured in C:N ratio of 1:10 (39.92 $mN.m^{-1}$). Also, in this ratio, the highest dry weight of biosurfactant was obtained at neutral pH (2.73 $g.L^{-1}$). After the sixth day, time did not have a significant effect on the measured parameters in this treatment. The biosurfactant produced was investigated using Fourier-transform infrared (FTIR)spectroscopy. use of different nitrogen sources showed a significant effect on biosurfactant production, also the use of sugarcane molasses as an available and inexpensive raw material in the production of biosurfactants is recommended.

Keywords: biosurfactant, surface tention, sugarcane molasses

CP96 Study of the effect of hemicellulose on flavonoid production from *Arthrospira*

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Flavonoids are polyphenolic secondary metabolites that have high nutritional and medicinal value due to their strong antioxidant properties and, consequently, have great economic value. Due to the limited natural resources of flavonoids and also the difficulty and high cost of their chemical synthesis, the use of various biotechnological methods, including culture of cyanobacteria, can be a good economic solution in the production of flavonoids. According to recent researches, the use of elicitors is one of the most important and effective economic strategies to improve cell growth and accumulation of secondary metabolites in the extensive culture of microorganisms. Therefore, the aim of this study was to investigate the potential of hemicellulose as an elicitor in increasing the production of flavonoids in *Arthospira*. Therefore, *Arthrospira* was first cultured in optimized Zarok culture medium. The resulting biomass was harvested and dried.To investigate the effect of hemicellulose on flavonoid production, hemicellulose with different concentrations was added to the culture

medium and at different times after treatment, biomass separation was performed by centrifugation. Extraction of total flavonoids was performed by extraction with alcohol solvent at high temperature and this extraction was confirmed by thin layer chromatography. The total flavonoid content was then measured by aluminum chloride colorimetric method with a spectrophotometer. The results showed that hemicellulose increased the wet and dry biomass, and also flavonoids of *Arthospira* compared to the control sample, so that the highest amount of wet biomass (19.9 g), dry biomass (0.61 g) and flavonoids of *Arthospira* (0.386 mg quercetin /mg extract) was achieved under treatment with 0.3 mg/ml of hemicellulose on the 8th day of culture. Taken together, these results indicate the positive effect of hemicellulose on increasing the growth and production of flavonoids in *Arthospira*.

Keywords: Secondary metabolite, cyanobacteria, eliminator, biomass

CP97 Synthesis and Characterization of ZnO: MgO Nanocomposite and Evaluation of Cytotoxicity on Mesenchymal Stem Cells

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Mesenchymal stem cells (MSCs) are multipotent cells, using in regenerative medicine; However one of the challenges is to noninvasively monitor the delivery and biodistribution of administered cells during treatment without adverse effect on behavior of MSCs and targeted tissue. In this line, ZnO: MgO quantum dots were synthesized and cytotoxicity were evaluated on MSCs. ZnO: MgO nanocomposite were synthesized with Co-Precipitation method and then characterized by FT-IR, TEM and photoluminescence (PL) analyses. The cytotoxicity of nanocomposite was assessed by 3-(4,5-dimethylthiazol-2-yl)-2,5 diphenyl-tetrazolium bromide (MTT) assay. The FT-IR spectrum showed bands at 450 and 860 cm^{-1} which are related to the Zn-O and Mg-O groups, respectively. TEM images showed that the ZnO: MgO nanocomposite had a spherical shape with the mean dimeter of 6- 8 nm.PL analysis revealed a significant emission at 510 nm, favoring ZnO: MgO nanocomposite for stem cell labeling. based on the result of MTT assay, ZnO: MgO nanocomposite did not have any cytotoxic effect on the viability of the mesenchymal stem cells up to 0.8 mg/ mL Fluorescent properties and nontoxic effect of ZnO: MgO nanocomposite favor them for imaging and tracing of the MSCs as these cells are used in regenerative medicine.

Keywords: Nanocomposite, Photoluminescence, MTT, Cell Viability

CP98 Design of a Facile Glutathione Sensing Method on the Basis of Peroxidase-like activity of 2DTMD/MNP nanocomposite

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Due to the pivotal role of glutathione (GSH) in key biological processes, including intracellular signal transduction, detoxification, preservation of proteins structure, regulation of gene expression, and also the difference of its level between normal and cancer cells, development of a rapid, inexpensive and accurate sensing method is of great importance. Here, on the basis of the inhibition effect of GSH on the enzyme-like activity of peroxidase mimetic 2DTMD/MNP nanocamposite, a facile colorimetric method for glutathione sensing was established. After optimizing the assay condition, peroxidase-like activity of the nanozyme was detected in the presence of different concentrations of glutathione. In this sensing system, GSH can effectively inhibit the oxidation of TMB substrate in the presence of H_2O_2. The absorbance intensity at 652 nm was descended along with the increased concentration of GSH, as the reaction mixture turn from blue to colorless at 112.5 μM of GSH, detecting by naked eye. These findings offer an appropriate platform for colorimetric detection of GSH in a linear range of 0.02 μM to 0.175 μM. Regarding the interfering effect of some other biological molecules such as aminoacids and sugars in glutathione sensing system, the selectivity test is underway.

Keywords: Peroxidase mimetic, Nanozym, Colorimetric method

CP99 Partial purification of L.Asparaginase from *Cairana moschata*

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Asparaginase is an enzyme that catalyzes the hydrolysis of asparagine to aspartic acid. Asparaginase is naturally produced by microorganisms. Both the substrate and the product of this enzyme during the reaction play an important role in the metabolism of most organisms. Among the valuable physiological functions of this enzyme are control of expression and proper cellular activity in balancing the body with amino acids. In addition, the enzyme L-asparaginase plays an important role in the treatment of acute lymphoblastic leukemia. The aim of this study was to investigate the kinetic properties of Muscovy duck liver asparaginase enzyme and the effect of different parameters on the activity of this enzyme. In this study, asparaginase enzyme from Muscovy duck liver was partially purified using homogenization methods in Tris buffer pH 8.5, centrifugation, 20% and 60% ammonium sulfate precipitation and dialysis at 3 ° C. After extraction, enzyme activity was estimated according to wriston method with Nessler reagent. In this study, the specific activity of asparaginase enzyme isolated from duck liver was determined to be 40.35 U / mg. The optimum pH of the enzyme was 7 and its optimum temperature was 40 ° C. The Km and Vmax values of the enzyme were calculated to be 127.229 mM and 3.639 mM / min, respectively. Due to the side effects of asparaginase prepared from microbial sources, extraction and purification of this enzyme from other sources, including Muscovy duck liver for future studies was suggested.

Keywords: Partial Purification, Nessler Reagent, Kinetic Parameters

CP100 Inhibition of α-Amylase and α-Glucosidase from *Caucasotachea lencoranea* by flavonoids extract of *Arctium lapa* L.

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Citrus brown snail is one of the citrus pests in the north of Iran and the identification of digestive enzymes of this species can play an important role in controlling this pest. α-amylase and α-glucosidase enzymes were extracted from the gastrointestinal tract at 4 ° C after homogenization and centrifugation. The activity of α-amylase and α-glucosidase were 0.278 and 0.4 enzyme units per ml, respectively. Also, Km and Vmax values for amylase were calculated to be 0.13 mM and 0.062 mM / min, respectively, and for alpha glucosidase, 1.5 mM and 0.028 mM / min, respectively. *Arctium lapa* L. has been used in human medication due to its anti-inflammatory, liver protection, antimicrobial and antifungal effects. Flavonoid extract of this plant was prepared and activity of the enzymes were measured in its vicinity. The flavonoid content of the extract was measured by aluminum chloride method. This amount was equal to 2.1 mg equivalent to quercetin per ml of extract. Acarbose was used as a specific inhibitor. The α-amylase and α-glucosidase were inhibited by *Arctium lapa* flavonoids and the IC_{50} levels were determined: 0.16 mg / ml and 1.7 mg / ml, respectively. Due to the low value of IC_{50} and the results of our experiments, the flavonoid extract of this plant can be suggested as a suitable alternative for agricultural or therapeutic uses of chemical compounds.

Keywords: Kinetic Parameters, Partial Purification, Citrus Pest, Diabetes

CP101 Evaluation and comparison of Newcastle disease virus F protein to determine immunogenicity and pathogenicity of isolates in Eurasia

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Avian paramyxovirus serotype 1 (APMV-1) is the causative of Newcastle disease in birds. The disease has been reported in many organisms, including humans, but its acute form is found in birds. Newcastle virus has a single-stranded RNA genome that encodes proteins such as hemagglutinin-neuraminidase (HN), nucleocapsid protein (NP), phosphoprotein (P), and fusion protein (F). One of the most important factors in the pathogenicity of this virus is F protein. The precursor of this protein in the infected cell must be cleaved into two mature proteins by proteolytic cleavage. This protein also promotes high immunogenicity in infected organisms, which

is a target for the development of vaccines against the virus. In this study, the F protein of Newcastle disease virus isolates from different species such as camels, owls, pigeons, and chickens in the vast region of Eurasia, where many animal species migrate and interact, was examined. F protein sequences of different strains of Newcastle disease virus isolated from Eurasia were extracted from GenBank®. These sequences were then examined in the amino acid region of 112 to 117, which is the site of proteolytic cleavage. Immunogenicity and immunogenic epitopes of these sequences were examined by VaxiJen v2.0 tool and the IEDB website. The results showed that the cleavage site of the F protein precursor shows six diverse motifs. From these six motifs, four are specific to pathogenic strains and two are related to non-pathogenic strains. Twenty-six pathogenic samples and six non-pathogenic samples were identified from the studied sample pool. The immunization of the sequences was in the range of 0.49 to 0.56 with a threshold of 0.4 for viral proteins, indicating low immunogenicity of this protein alone. Also, high-scored common epitopes were identified among circulating F protein sequences of pathogenic and non-pathogenic strains. These epitopes will be used for further studies in vaccine design.

Keywords: Immunogenicity, Newcastle disease, epitope, F protein cleavage site

CP102 Optimization of effective factors in the expression of recombinant urate oxidase enzyme using response surface methodology

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The aim of the present study is to optimize the effective factors in the expressions and purifications process of uricase (urate oxidase) from E. coli. Urate oxidase is a class of oxidoreductase enzymes that lacks cofactor and converts the uric acid to allantoin. The purified uricase can be used for treating gout disease and hyperuricemia. Also, uricase is applied as a reagent in clinical diagnostic kits to specify the concentration of uric acid in the blood. Response surface methodology (RSM) has been widely applied as an effective technique to demonstrate the relationships and interactions among multiple variables by reducing the number of experimental trials due to the less laborious and time-consuming nature of the method. Based on the amount of IPTG concentration, temperature and incubation time that were the effective factors in expression process, the central composite design (CCD) was carried out and 17 runs were designed using the Design-Expert software version 11. In this study, recombinant urate oxidase enzyme from Escherichia coli BL21 was expressed in 17 runs. The protein was then purified using affinity chromatography and determined protein concentration by bradford method. The quadratic equation was used to describe the response of the system (UOX concentration). The optimized conditions were obtained, including the 0.55 mM concentration of IPTG and expression temperature 32.25 °C and 19 h incubation time. The results were corroborated by Bradford method that was showed 0.42 mg/ml uricase in the best condition and furthermore analysis of protein Gels (SDS-PAGE) by molecular mass of 34 kDa.

Keywords: Response surface methodology, Uricase, IPTG

CP103 Investigation of point mutations on the structure of human SOD1 enzyme by molecular dynamics simulation

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Superoxide dismutase 1 (SOD1) is an antioxidant enzyme. Mutation in superoxide dismutase 1 (SOD1) causes amyotrophic lateral sclerosis (ALS). Therefore, in this study, the conformational and dynamic changes of the mutant protein were investigated. The crystallographic structure of wild-type SOD1 code 2C9V was retrieved from the Protein Database (PDB). The G41D and L38R mutations were then created on the file. In this method, the interactions between atoms and molecules at the location and velocity of each atom at intervals of 5 nano seconds were calculated using GROMACS software. Using the root mean square deviation, the mean accuracy of the simulation was investigated and with the help of various other analyzes, including the study of changes

in the radius of gyration and the calculating of the number of hydrogen bonds, we observed that mutations have a significant effect on protein structure. The mean change curve of hydrogen bonds for G41D and L38R mutants are 106 and 103 versus 100 hydrogen bonds for wild-type protein, respectively. These changes, however small, are effective in reducing the flexibility of the G41D. For the L38R mutant, these changes are almost identical to the wild-type form. The results of the radius of gyration show that in the G41D mutant the protein structure is more compact than in the wild-type. The results of RMSF in G41D and L38R mutants in the 80-70 and 115-105 regions showed a decrease in the amount of RMSF compared to the wild-type enzyme, indicating that the mutants were less flexible than the wild-type protein. The results of molecular dynamics of this study show that the occurrence of mutations in loop 3 and β4 in SOD1 protein causes slight conformational changes in the mutated regions, so that according to these local changes, the G41D mutant is more stable and compact than the L38R mutant.

Keywords: G41D mutant enzyme, L38R mutant enzyme, RMSD, Radius of gyration

CP104 Investigating of structure and function of human superoxide dismutase enzyme by substitution of aspartate to glycine at position 41

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Superoxide dismutase 1 (SOD1) is an antioxidant enzyme. Mutation in the SOD1 enzyme cause ALS. So far, more than 170 mutations in the SOD1 enzyme with the inherited pattern of ALS have been reported, and the accumulation of this protein is associated with pathological features of the disease. In this study, by replacing aspartic acid with glycine (G41D), the activity and structure of the mutated enzyme and its comparison with the wild-type enzyme was investigated. In this study, plasmid pET28a (+), which contains superoxide dismutase gene, was used. Then, the primers were designed using Oligo7 software and the site directed mutagenesis (Quick-change PCR) method was used to create the mutation. The product was digested using Dpn1 enzyme and then transferred to E.coli DH5α strain by chemical method (heat shock). Induction of protein expression was influenced by IPTG and lactose and investigated SDS-PAGE electrophoresis gel. After purification of the protein by nickel-Sepharose column chromatography and dialysis, the activity of the enzyme was measured using pyrogallol at 420 nm by spectrophotometry method. Structural comparison of mutant and wild-type enzymes was performed by intrinsic and external fluorescence spectra at a concentration of 0.02 mg/ml. The highest specific activity of wild-type and G41D mutant were 7031 U/mg 5744 U/mg, respectively. Intrinsic fluorescence studies showed that the intensity of fluorescence in the mutant enzyme increased compared to the wild-type enzyme, indicating the location of the amino acid tryptophan in a more non-polar environment. External fluorescence studies showed that the intensity of mutant fluorescence was reduced compared to the wild-type enzyme, indicating a more compact structure and a reduction in hydrophobic pockets at the surface. As a result, it was found that this mutation caused local changes in the structure of the enzyme, which caused its compression.

Keywords: G41D mutant enzyme, Site directed mutagenesis, Specific activity, Fluorescence

CP105 Comparison of production of vitamin B_{12} under the influence of methionine and folic acid under aerobic and anaerobic conditions and different temperatures in *propionibacterium freudenreichii*

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Propionibacterium freudenreichii is a gram-positive bacterium that plays a key role in the production of vitamin B12.The aim of this study was to investigate the effect of folic acid and methionine in the aerobic and anaerobic phases on the optimal production of vitamin B12 and bacterial dry cell weight (DCW). The bacteria were inoculated into the fermentation medium containing corn. After incubation, methionine 0/05 ٪ (v / w) and four

different concentrations of folic acid (0.250, 750 and 1000 mg/l) were added to the culture media. The bacteria were then placed under anaerobic and aerobic conditions. Also, in order to study the thermal stress, bacteria were cultured at different temperatures (50 40 40, 40, 30, 25 º C) and their absorption was measured at 600 nm. Vitamin B_{12} production was assessed using HPLC under anaerobic and aerobic conditions. B_{12} production increased in the presence of methionine, in comparison with the absence of methionine (0.05 mg/l) and at a concentration of 750 mg/l of folic acid under anaerobic conditions (6.2 mg/l). Bacterial dry weight decreased with increasing folic acid concentration, which indicates the negative effect of folic acid on bacterial growth. It seems that the addition of folic acid in appropriate concentration (750 mg/l), in the presence of methionine and under aerobic conditions can lead to the highest production of vitamin B_{12} (6.9 mg/l). The optimum temperature for bacterial growth was 25-40 ° C, so that with increasing temperature to 50 ° C, bacterial mass growth decreased. The production of this vitamin using chemical methods is difficult and expensiveby adding folic acid at the right concentration, the aerobic phase and methionine to the bacterial culture medium can increase B_{12} production and achieve a way to economically and commercially produce this vitamin.

Keywords: Dry cell weight (DCW), High-performance liquid chromatography (HPLC)

CP106 Comparison of Pentose Phosphate Metabolism Pathway Genes Expression in Aerobic and Anaerobic Conditions in Wild Strain and Alcohol Deheydrogenase Negative *Escherichia coli*

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Escherichia coli is widely used in the biotechnology industry and in the production of various pharmaceutical products and has the ability to grow well in fermenters and other manufacturing devices under various aerobic and anaerobic conditions. Metabolic engineering is a new way to achieve mass production and high efficiency in Is the science of biotechnology.One of the methods of metabolic engineering is to pay attention to the expression of the desired bacterial gene in different growth conditions and to identify important genes that regulate the metabolic pathway. The metabolic pathway of pentose phosphate is an early and important pathway that has existed in prokaryotic and eukaryotic cells since the beginning of life. Evaluation of phosphate pathogen-producing genes in Escherichia coli under different aerobic and anaerobic conditions in mutant and natural species; The aim of this research is to achieve high product production in Fermentor. To conduct this research, all enzymes of the pentose phosphate pathway in the target bacterium have been identified through the KEGG database of enzymatic components and scientific characteristics (such as enzyme number, gene locus, homologous and orthological information). In the next step, GSE46455 and GSE1121 microarrays, which are related to the expression of the genes of this bacterium in aerobic and anaerobic conditions, were identified in both mutant and natural mutations on the NCBI website. Then, through the meta-analysis method in the GEO section of the NCBI website, we compared different microarrays in terms of the expression of the identified genes (the basis for comparing the two criteria logFC and Pvalue is the graph of each gene). Depending on aerobic, anaerobic, mutant and natural species; There are 4 modes for each microbial. The results of each microbial study showed that the gene mutation reduces the expression of pentose phosphate genes in aerobic and anaerobic conditions. The highest amount of gene expression is related to anaerobic conditions and the mutant species reduces the expression several times more than the normal species. Expression of glucose-6-phosphate dehydrogenase genes; increased 6-phosphogluconate dehydrogenase and gluconokinase genes; Transaldolase and deoxyribose-phosphate aldolase have shown a decrease in gene expression, so it can be concluded that the expression of genes in the metabolic pathway of pentose phosphate, especially oxidative genes, is highest in anaerobic conditions in the natural strain. It can be said that bacteria use this pathway to produce regenerative power and power generation to deal with stress and lack of oxygen**.**

Keywords: Meta-analysis, Microarray, GSE46455, GSE1121 GEO2R

CP107 Biogas production from sugarcane bagasse and marine algae using codigestion method

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The sharp increase in energy consumption and the production of waste are the important environmental challenges. Anaerobic digestion of waste with methane and fertilizer production is an eco-friendly method. The codigestion of suitable substrates with the adequate mixing ratio removes the difficulties to single digestion. The aim of this study was to investigate the effect of codigestion of sugarcane and algae collected from the Caspian Sea on biogas production. To measure the biogas production in anaerobic digester, various treatments including sugarcane, algae and their mixtures were prepared in two ways, untreated and treated with 1 M sodium hydroxide. In each digester, 20 ml of inoculum (cow manure) and 2 g of substrate were added and the final volume of digestion was increased to 80 ml with water. The digester was incubated at 37 °C for 30 days. The volume of biogas production was measured during 5 days intervals. The results was shown that the highest volume of daily gas production in the digester containing untreated sugarcane in the first 5 days was 22.57% (v/v). Also, the lowest amount of daily gas in this digester was produced 0.2% (v/v) volume during the last 5 days. The amount of biogas production in the digester containing sugarcane treated with 1 M sodium hydroxide was appropriate, so that the amount of gas produced per day was 5.36% (v/v) during the last 5 days. In addition, the results of daily biogas production in sugarcane and algae codigestion were average 3.184% (v/v), which in compare to the daily gas production during the 30 days was more than in both digesters containing untreated and treated sugarcane. The results of the present study demonstrated that the codigestion of sugarcane and algae increases the production of biogas. Increasing the efficiency of biogas production using codigestion method requires further studies.

Keywords: Biogas, codigestion, waste, sugarcane, marine algae

CP108 Investigation of Inhibitory and Anti-inflammatory Effect of New Imidazole Derivatives on Cox-2

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Cyclooxygenase enzyme is a transmembrane integral homodimer protein. COX-1 and COX-2 are two main isoforms that have been identified. Both isoforms are bifunctional enzymes. Each subunit consists of three domains: the epidermal growth factor domain, membrane binding domain and catalytic domain which contains active site of the enzyme. Concerning the involvement of COX-2 in inflammation the inhibition of COX-2 isoform is a pharmacological favorable target for investigators. This study is an attempt to investigate the inhibitory effect of five new imidazole derivatives on COX-2 enzyme. To better understand the efficiency of binding mode of interesting compounds, docking study was performed via AutodockVina software and the best docking conformations (energetically favorable according to their scoring function were selected for Molecular Dynamic (MD) simulation. The MD simulation was carried out using Gromacs 2018 and the obtained PDB entry 5ikr, for all compounds of interest. After equilibration of all compounds of interest through NPT ensemble, a production run was executed for 120 ns. The MM-PBSA method was applied to estimate binding free energy in the last 40 ns of the MD trajectories. Considering the utilized procedure, it was revealed that the main contribution values in $\Delta G_{binding}$ were van der Waals and electrostatic interactions. Since the $\Delta G_{binding}$ value of two enzyme-inhibitor complexes were less compared with others (-147.689 kcal/mol for 5e and -129.264 kcal/mol for 5c), selected compounds will be chosen for synthase process. In addition, the average of RMSD value (root mean square deviation) as a standard for stability evaluation of compounds, are as follow: 5c (0/1890 Å) and 5e (0/1821 Å), which suggest the less deviation relative to the starting structure. As a result, regarding performed analyses, compounds 5c and 5e were considered as the more potent inhibitors for COX-2 enzyme and were chosen for synthase process.

Keywords: Inflammation, Molecular Docking, Molecular Dynamic simulation, MM-PBSA

CP109 Investigation of water absorption properties of bio-concrete (self-healing concrete with bacteria)

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During different ages of concrete, due to various parameters, fine cracks appear inside and on the concrete surface. Several methods have been recommended to repair these cracks, one of the newest methods is bio-concrete, a type of self-healing concrete that is designed to repair cracks created with the help of bacteria. In this study, using two methods, *Bacillus pasteurii* were used to repair cracks and internal pores in concrete. In the first method (injection), when preparing concrete from 10, 20, 30 and 40% by weight of water, a combination of water suspension and bacteria was used as a water substitute. Also, in the second method (inoculated), the bacterial self-suspension was injected directly into the cracks. Then, in both methods, the amount of water absorption of concrete samples at the ages of 7, 28 and 90 days was tested and compared with bacteria-free samples (control). The results showed that no significant changes were observed in the injection method at all ages compared to the control. In inoculation method, at 7 and 28 days of age, water uptake of samples decreased compared to the control showed that the lowest water uptake was observed in 20% bacterial suspension, which is probably due to bacterial growth and calcite deposition in ITZ and IZ Calcium crystals fill the pores of the areas and prevent water infiltration, resulting in reduced water absorption.

Keywords: Bacteria, Bio-concrete, Crack repairing, Water absorption

CP110 Identification of a novel homozygous missense mutation in NDUFAF6 gene causing leigh syndrome

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Leigh syndrome is a clinically and genetically heterogeneous disorder resulting from defective mitochondrial energy generation.It most commonly presents as a progressive and severe neurodegenerative disorder with onset within the first months or years of life, and may result in early death. In normal population, the incidence this syndrome is 1 of 40,000 births. In this study, we investigated the possible genetic cause of 3 year old affected girl suspicious to leigh syndrome with symptoms including lactic acidosis, symmetrical involvement of the basal ganglia and subcortical white matter of the brain. Next Generation Illumina Sequencing was used to enrich all exons of more than 22000 protein coding genes in the affected patient. Subsequently, Sanger sequencing was used to confirm the mutation found in the patient and her parents. The obtained results showed a novel homozygous missense mutation NM_152416:c.719G>T:p.G240V in the *NDUFAF6* gene. Furthermore, her parents were heterozygote (carrier) for this mutation. *In silico* analyses using mutation taster, polyphen, CADD_phred, SIFT and mutation accessor software were confirmed the pathogenicity of a novel missense mutation found in the *NDUFAF6* gene. The *NDUFAF6* gene encodes a 38 KDa precursor protein which is located in mitochondria. The *NDUFAF6* protein contains a phytoene synthase domain and plays a key role in the assembly of complex I oxido reductase from the mitochondrial respiratory chain. Mutations in the *NDUFAF6* gene are associated with complex I enzyme deficiency leading to leigh syndrome. Altogether, this study depicted a novel pathogenic mutation in the *NDUFAF6* gene in the studied family which can be aid to conduct genetic counseling, prenatal diagnosis of leigh syndrome and clinical management of these types of inherited disorders.

Keywords: Leigh syndrome, *NDUFAF6* gene, Next Generation Sequencing, Pathogenic mutation, Genetic counselling

CP111 Derivative from Ciprofloxacins decreases cell proliferation by induction of apoptosis in KG1-a , acute promyelocytic leukemia cells

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Recently, scientists have reported that ciprofloxacin inhibited the growth of K562 human chronic myelogenous leukemia cells. In the present study, we evaluated cytotoxic effects of new derivative of ciprofloxacin (4-BHPCP) that inhibited the proliferation of the KG1-a acute promyelocytic leukemia cells through induction of apoptosis.The KG1-a cells were cultured in the presence of various concentrations (10-100 μM) of the compound for 3 days and cell viability was determined by MTT assay. Cell cycle analysis was determined by flowcytometry. (4-BHPCP) decreases cell proliferation of the KG1-a cells in a dose and time-dependent manner. The IC50 value following 72 h exposure was found to be 25 μM for the cells. The results of cell cycle showed a time-dependent increase in sub-G1 peak.Taken together, these results suggest that this compound with significant anticancer activity can be proposed as effective agents for further investigation in the future.

Keywords: Cytotoxity, Fluorescence, Anti tumoric compound

CP112 Evaluation of Kombucha extract on macrophage cell activity

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Immune-related diseases and inflammatory diseases of the body include a wide range of diseases in which both underlying and environmental factors are involved. Autoimmune diseases and allergies are examples of overactive immune systems. Diet and lifestyle play an important role in such disease .Kombucha, is produced by a symbiotic association of bacteria and yeasts forming a tea fungus. The aim of this study was to investigate the effect of Kombucha extract on the activity of macrophage cells. In this experimental study, the macrophage cell line MJ774 was bought from Pasteur institute of Iran. Kombucha mushroom was bough and after culturing MJ774 macrophage cells, they were incubated with Kombucha extract for 24, 48 and 72 hours. Interaction of macrophage cells with different dosage of Kombucha was studied. Cell viability was assessed by MTT assay. MTT results showed that kombucha extract resulting in decreased proliferation of macrophages by increasing its concentration. Our findings show that Kombucha extract reduces the proliferation of macrophages in a does dependent manner and thus leads to the immunomodulatory. Therefore, we suggest to use kombucha to modulate the immune system and inflammations.

Keywords: probiotic, immune system, inflammation, tea fungus, allergies

CP113 Comparative identification of GspA in the proteome and genome of probiotic and non-probiotic bacteria for the treatment of type 2 diabetes

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GLP-1 is one of the types of incretins or digestive hormones and one of the strongest stimulants of insulin release in response to glucose. Studies have shown that GLP-1 activity is reduced in patients with type 2 diabetes. Administration of GLP-1 to patients with type 2 diabetes leads to normalization of hyperglycemic conditions. Therefore, strategies based on increasing and inducing GLP-1 seem to be a good goal for the treatment of type 2 diabetes. GspA is a secretory peptide with the MAADIISTIGDLVKWIIDTVNKFKK sequence that has GLP-1 secretion stimulating activity. In this study, GspA comparisons in the proteome and genome of probiotic and non-probiotic bacteria were investigated using NCBI-Genome and UniProt-Proteome databases. The results showed that GspA sequence was present in *Staphylococcus epidermidis* Scl31 with high similarity in several other strains of Staphylococcus, but was not observed in any of the probiotics. Studies on

human L cells and intestinal enteroids have shown that GspA alone is sufficient to increase GLP-1 secretion. The results of administration of GspA-producing *Staphylococcus epidermidis* in high-fat-fed mice showed a significant reduction in markers associated with obesity and type 2 diabetes, including obesity and hyperinsulinemia. GspA stimulates GLP-1 through calcium signaling. GspA can help establish a microbial peptide-based treatment for obesity and type 2 diabetes by creating a host-microbial interaction. Finally, in the absence of GspA sequence in probiotics, gene construct was designed by inserting the gene sequence of this peptide with inducer and secretory signal in the probiotic bacterium *Lactobacillus plantarum* as a suitable treatment strategy for the treatment of type 2 diabetes.

Keywords: Probiotics, Type 2 diabetes, GspA, GLP-1

CP114 Site-directed mutagenesis in loop 6 of human superoxide dismutase 1 to investigate characterization of mutant enzyme

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Human superoxide dismutase 1 (hSOD1) is an antioxidant enzyme that converts superoxide radicals to hydrogen peroxide and oxygen. More than 100 mutations have been founded in this enzyme to cause amyotrophic lateral sclerosis (ALS). The aim of this study was to investigate the effect of L106V mutation, which is located in VI loop of superoxide dismutase on its structure and activity. The superoxide dismutase gene in plasmid pET-28a (+) was used as a template for targeted mutagenesis by Quick-change PCR. After confirmation of the mutation, the plasmid containing the mutation was transferred to the *E.*coli expression bacterium strain BL21 (DE3). IPTG and lactose inducers were used to express the protein. Purification of the protein was performed by nickel-sepharose affinity chromatography and SDS_PAGE gel, which was used to determine the purity of the protein. Specific activity of mutant and wild enzymes were determined using pyrogallol substrate at 420 nm by spectrophotometry. Structural studies were performed using intrinsic fluorescence and external fluorescence techniques with ANS marker. The results of this study show that the specific activity of wild type and mutant enzyme (L106V) were 7031.25 U / mg and 7238.65 mg, respectively. Structural studies with intrinsic fluorescence showed that the emission intensity of L106V mutant was slightly lower than wild type. Increased intensity of extrinsic fluorescence emission L106V mutant compared to the wild type indicates exposes more hydrophobic surfaces to ANS. Thus, the L106V mutation in the superoxide dismutase gene is a genetic factor associated with the inherited form of amyotrophic lateral sclerosis.

Keywords: L106V mutant enzyme, affinity chromatography, intrinsic and extrinsic Fluorescence, Amyotrophic lateral sclerosis

CP115 Effect of point mutation on the structure and dynamics of human superoxide dismutase 1 using molecular dynamics simulation

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SOD1 is an important antioxidant enzyme. This enzyme contains 153 amino acids and the occurrence of mutations in it will cause ALS disease, which can be evaluated by molecular simulation. To investigate the role of mutations in the structure and dynamic properties of the protein, the PDB file with the code 2C9V was first received from the protein database. Then the G16S and L106V mutations were generated on a 2C9V file. Gromacs software was used to create the input structure to simulate molecular dynamics for wild type and mutant enzymes. By analyzing the data during the simulation time (5 Nano Second), the structural changes in the protein were evaluated. Using the mean square root, the accuracy of the simulation was checked and also the RMSF study showed that in the mutations of G16S and L106V in the regions of 71 to 79 and 107 to 117, a decrease in the amount of RMSF is observed compared to the wild type that indicates a decrease in flexibility

and an increase in stability. Also, in regions 127 to 136 of the L106V mutant, there is a significant increase in the amount of RMSF compared to the wild type. The average number of hydrogen bonds for G16S and L106V mutants is 103 and 101 bonds versus 100 hydrogen bonds for wild type, respectively. These changes, albeit small, are effective in reducing the flexibility of the G16S. The study of gyration radius showed partial compactness in the G16S mutant and the local unfolding in the L106V mutant compared to the wild type. molecular dynamics simulation studies support formation of aggregation and prone to ALS for mutations.
Keywords: Point mutation, Mean square root, RMSF, gyration radius, G16S mutant

CP116 A novel approach to produce DNA molecular size marker

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Determining the length of nucleic acid in molecular laboratories is necessary. The DNA molecular ladder consists of DNA fragments with different lengths but known sizes to estimate the size of unknown DNA molecules on the agarose gel electrophoresis. Therefore, DNA size indicators are essential tools in molecular biology, genetics, biotechnology, and the related-laboratories. Producing DNA molecular ladders encounters some limitations due to inflexibility, complexity, time-consuming, and costly methods. In this study, using bioinformatics and the combination of PCR and restriction enzyme, a simple and cost-effective method for production of DNA ladders is introduced. A house-keeping gene from the *Saccharomyces cerevisiae* was considered as the template gene. 17 pairs of primers and 2 restriction enzymes *Eco*72I and *Bsp*68I were also used to design the DNA molecular ladder. Two bioinformatics software Snap gene (version 3.2.1) and Gene runner (version 6.5.46 x64 Beta) were used in the primer design and PCR reaction and other related processes. Finally, 26 fragments with different lengths were obtained in a wide range from 50 to 10,000 bp with high accuracy. The designed fragments include 50 bp, sizes ranging from100 to1000 in 100 bp increments, 1250-1750 in 250 bp, 2000-4000 with a distance of 1000 bp, 4500-6500 with a distance of 500 bp, 6500-9500 with a distance of 1000 bp and 10,000 bp.

Keywords: Bioinformatics, DNA molecular ladder, PCR simulation, Enzymatic digestion

CP117 Investigating effects of galbanic acid on the viability of LoVo colon carcinoma cells

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Colorectal cancer (CRC) ranks among the highest causes of cancer related deaths in both men and women worldwide. Due to poor prognosis of CRC and inefficiency of current treatments, the search for new and more effective therapies is ongoing. Galbanic acid, $C_{24}H_{30}O_5$, is a natural product belonging to the class sesquiterpene coumarins with a wide range of pharmaceutical activities such as antiviral, anticoagulant, anticancer and cancer chemopreventive effects. In present study, cytotoxic effects of galbanic acid was assessed on LoVo cells as a human colon cancer cell line. Materials and methods: Galbanic acid was isolated and characterized from the roots of *Ferula szowitsiana DC.*, a plant of Apiaceae family. LoVo cells, obtained from Pasteur Institute (Tehran, Iran), were grown in RPMI1640 supplemented with 10% fetal bovine serum and incubated at 37°C in the presence of 5% CO_2. For viability assessment, cells were seeded in 96 well plates and treated with increasing concentrations of galbanic acid (20, 40 and 80 µM) for 3 consecutive days. Afterwards, alamarBlue was added to each well and upon 2 h incubation in the dark at 37°C, optical density was measured by a plate reader at 600 nm. To calculate the percentage of cell viability, cells treated with 0.4% DMSO were considered as control. Assessment of cell viability indicated that 20 µM galbanic acid did not induce toxic effects even after 3 days. However, upon 24, 48 and 72 h treatment with 40 µM galbanic acid, viability of cells was as 98%, 89% and 95%, respectively. More considerably, cell viability was reduced down to 81%, 68% and 79% upon 24, 48 and 72 h treatment with 80 µM galbanic acid, respectively. In conclusion, our findings indicated that galbanic acid

induced its effects in a time and dose dependent manner, and that concentrations with low toxicity could be used in future to affect migration/metastasis ability of human CRC cells.
Keywords: Colorectal cancer, Galbanic acid, Viability assessment

CP118 Optical properties investigation of two synthesis methods and highlighting the optimal method for cellular assessments

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Carbon dots (CDs) can be extensively applied in diverse sciences, such as biology. To improve photophysical properties of these materials, nitrogenous groups are used. These materials can transfer electrons into CDs and surface modification is occurred. Also, it can improve the optical performance of particles and the efficiency of cell imaging. In this study, two methods for CDs synthesis were investigated for optical properties improvement. First, CDs were synthesized from a green source via hydrothermal method. Then, the arginine amino acid was used to functionalize the particles with nitrogenous groups. In the first method, 30 mL of the plant extraction and 0.5 g amino acid were mixed, while in the second method, a dry powder of plant extraction was prepared using a freeze-dryer. Then, 2 g of the resultant powder and 0.4 g arginine were dissolved in water. The resulting solutions from both methods were used for CDs synthesis by Teflon-lined autoclave at 120 °C for 5 hours. After physical properties confirmation of CDs, the fluorescence evaluation of both samples under the UV-light were done. These results indicate blue and green emissions of our particles. However, the sample obtained from the first method illustrated higher fluorescence intensity. The fluorescence spectroscopy analysis and UV-Vis spectroscopy were used for measurement of fluorescence intensity and the quantum yield calculation, respectively. Comparison of two syntheses showed that both methods could create the main properties of CDs; however, the quantum yield of the first method was significantly higher than the second one. The fluorometry results of particles at 393 and 398 nm wavelengths showed the higher fluorescence intensity of CDs in first method. Therefore, the first method has more efficient role in cell imaging.

Keywords: Carbon dots, Nitrogen, Luminescence, Cellular imaging

CP119 Reduction of HB-EGF expression in the uterus of female mice in contact with Chlorpyrifos

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Scientists believed that there are many factors involved in abortion, one of which could be environmental factors. On the other hand, evaluating of adherent molecules that play an important role in implantation, can help us understand how this bridge between fetus and mother is easily broken by some environmental contaminants. This study aimed to investigate the effects of Chlorpyrifos (CPF) as a pesticide before pregnancy, and its function on sex hormones and fetal adhesion molecules during pregnancy. In this study, CPF was injected into ten female NMRI mice, the equivalent number was considered for the control and sham groups. After six weeks of 3 mg/kg injection, female mice were mated then euthanized on day 5th of gestation. Estradiol (E2) and progesterone (P4) hormones level were assessed by the ELISA method. The expression of heparin-binding EGF-like growth factor (HB-EGF) as a molecular agent of fetal adhesion to the uterus was also analyzed by Western and real-time polymerase chain reaction (RT-PCR). The levels of estradiol E2 and progesterone P4 were significantly reduced ($P < 0.05$) and ($P < 0.01$) in the experimental group compared to the other groups, respectively. There was also a significant decrease in both RNA and HB-EGF protein levels in the experimental group compared to the other groups, ($P < 0.05$) and ($P < 0.001$), respectively. Based on this experimental model, mice that were injected with the toxin had no clinical presentation, but the levels of sex hormones as well as the expression of uterine adhesive proteins decreased. It is therefore recommended that to prevent abortion, the

mother's nutrition, as well as the environment in which she lives, should be free of any chemicals such as pesticides.

Keywords: Chlorpyrifos; HB-EGF; Estradiol; progesterone

CP120 A survey of contamination to *Campylobacter jejuni* in the eggs from retails markets in Ardabil, Iran

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Campylobacter jejuni is the most important pathogens causing gastroenteritis in human which is generally transmitted through the contaminated food with animal origin. Among foods with animal origin, the egg always has the potential ability to transfer foodborne pathogens which cause food poisoning. Therefore, the purpose of this study was to investigate contamination to *Campylobacter jejuni* in the eggs from retails markets in Ardabil, Iran. A total of 160 eggs (80 bulk eggs and 80 labeled industrial eggs) were collected randomly from retail markets in different parts of Ardabil a period of six months and transferred to the laboratory under sterile conditions. Shell and contents of the eggs were examined for contamination to Campylobacter jejuni by standard culture methods. There was no contamination by Campylobacter jejuni among the 160 eggs examined . The results of this study that *C. jejuni* contamination of eggs does not make up a serious health hazard in this area.

Key words: *Campylobacter jejuni*, Egg, Retails market, Ardabil

CP121 Investigation of some protein properties extracted from tuna waste

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Fish proteins have many applications due to their properties such as water holding capacity, fat absorption, emulsifying and foaming properties and can be used as a food additive. Amino acids, which have a high nutritional value and are often used as flavorings in the food industry, can be easily recovered from waste. In this study, protein from fish waste was extracted by alkaline dissolution and precipitation at an isoelectric point and some of its properties were investigated. These characteristics can determine its role. In this study, Thunnus tonggol, which is a widely used species in food industry and tuna factories, was used. After extracting the protein, some of its properties were examined .To evaluate some functional properties of the isolated protein, it was first placed in a freeze dryer for 48 hours .The studies performed included foaming stability, emulsifying properties, water adsorption and protein fat adsorption. Knowing the properties of the protein determines the type of application in different industries. According to the results, the ability to absorb water in the isolated protein was calculated to be 1.5 g / g and the ability to absorb fat was 0.41 g / g. The volume of foam formed in zero minutes was 18 ml, which decreased by 3 ml after 60 minutes. Foam stability was expressed as the volume of the remaining foam after 30 and 60 minutes. Foam stability was calculated to be 83.3%. Turbidity measurement method was used to measure emulsifying properties and casein protein was used as a standard protein for comparison. To calculate the emulsion stability, the absorption of protein solution was calculated at 0 min and at 10 min at 500 nm. The emulsion stability of the protein was calculated 86.54% .The emulsion stability of the isolated protein was higher than that of casein. Alkaline and acidic dissolution methods can be used to recover proteins from tuna factory waste. By optimizing, higher yields and better performing proteins can be extracted. Although the functional properties of the extracted protein make it suitable for use in a variety of industries, much research is needed to use the waste protein for food or pharmaceutical purposes or other purposes.

Keywords: alkaline dissolution, isoelectric point, freeze dryer

CP122 Extraction of protein from tuna waste by pH shift method

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Tuna fish is one of the most important species used in prepared seafood and its waste is also one of the most important components of coastal waste .Due to the large volume of waste from tuna processing, recovery of biological materials can be effective in reducing environmental pollution. Fish waste can be used for valuable products such as protein, fish oil, minerals, amino acids and enzymes. For this purpose, in this study, protein extraction from tuna waste was investigated using pH changes. The use of pH changes for extraction involves dissolving in acid or alkali and precipitating them at an isoelectric point. The highest solubility was observed at pH 2 and 12 and the lowest solubility at pH 5.5. The highest protein recovery was observed after the first centrifugation at pH 12 and the maximum protein recovery during the second centrifugation was observed at pH 5.5. Protein concentration was measured at all stages by Biuret method. The efficiency of protein extraction by this method without using pretreatment methods was estimated to be 35%. The pattern of protein distribution by sds page showed the presence of protein bands from 20 kDa to 100 kDa. Due to the appropriate extraction efficiency, acidic and alkaline solubility methods can be used to recover tuna proteins from tuna factories. It is also possible to apply some effective factors such as centrifuge speed, distilled water ratio and some pretreatment processes in the extraction steps to improve protein yield and increase recovery.

Keywords: alkaline dissolution, isoelectric point, Biuret method

CP123 Investigation of hydro alcohol extract of *Polygonum Bistorta* plant on coagulation tests

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Hemophilia is an inherited disease caused by a disorder of blood factors, which are proteins needed for blood to clot, in the absence of these proteins, the blood does not clot and bleeding will continue. The aim of this study was investigation of *Polygonum Bistorta* root extract on bleeding.in this method first, the hydro alcoholic extract of *Polygonum Bistorta* plant was prepared and the mice were randomly divided into 3 groups with three doses of 150,200 and 300 mg/kg and a control group. The extract was gavage to mice daily and on day 14, blood samples were taken from the mice and the collected blood was examined for PT (Prothrombin time) and aPTT (Activated partial Thromboplastin time) tests. This tests acutely show how blood clots in the coagulation pathway. The results of PT and APTT tests showed that coagulation time in *Polygonum Bistorta* treated mice was less than control mice in all three doses and the 300 mg/kg dose had the lowest value among the other two doses. Since PT and APTT study coagulation factors in the external and internal pathway of coagulation cascade, respectively, so this plant can affect both coagulation pathways.

Keyword: *Polygonum Bistorta*, Hemophilia, Medicine traditional, PT, APTT

CP124 Evaluation of antioxidant activity and toxicity of LFcin-11 peptide on gastric cancer cell biosynthesis (AGS)

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Oxidative stress is the result of increased production of reactive oxygen species, which causes various diseases, including cancer. Antioxidant enzymes, as the body's defense system, reduce reactive oxygen species. In this study, peptide fragment containing 11 amino acids (LFcin-11) derived from Lactoferricin, which has a functional Lactoferricin sequence, was chemically synthesized. Then, antioxidant activity, toxicity and anti-cancer effect on AGS cells were investigated. The effect of peptide toxicity on gastric cancer cells was investigated by MTT assay. The results of the MTT test show a direct relationship between the concentration of the synthesized peptide and its lethal effect on gastric cancer cells. Also, the results of measuring the

antioxidant activity of LFcin-11 peptide indicate the ability of the peptide to remove DPPH radicals. Due to its antioxidant activity and anti-cancer properties of LFcin-11 peptide, this peptide can be used in the treatment of cancer.

Keywords: Reactive oxygen species, Lactoferricin, Antioxidant, Cell Viability

CP126 Energy transfer to gold nanoparticles from firefly luciferase reaction

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Photinus pyralis Luciferase enzyme is a monomeric protein that emits bioluminescence light by substrate including D-luciferin, ATP my $MgSO_4$. The molecular weight of this enzyme is 62 kDa and the light emitted from it is green-yellow in the range between 550-570 nm. The ability to measure the light emitted by the enzyme has led to its use in various fields such as microbial contamination detection, ATP assay, biological assessments and reporter genes. This enzyme is very sensitive and changing environmental conditions cause a sharp and rapid decline in its activity, so the use of analytes to improve this issue is very useful. Gold is a stable metal and gold nanoparticles have valuable applications in the fields of biosensors, drug release and medical diagnosis, disease treatment and antimicrobial effects. In this study, we evaluate the effect of gold nanoparticles on luciferase enzyme. For this purpose, recombinant luciferase enzyme was expressed and then purification of the enzyme based on histidine tags of N-terminal head of the protein was performed using a chromatographic column. Then, the effect of gold nanoparticles on the third structure of luciferase protein, assuming no change in the intrinsic fluorescence emission of luciferase enzyme, was performed using a fluorescence device. The results showed that increasing the concentration of gold nanoparticles in the presence of luciferase enzyme reduces the emission of intrinsic fluorescence of protein, which is similar to the published study in which the effect of quantum dot cadmium tellurium on the emission of intrinsic fluorescence luciferase was reported. It is possible to change the structure of luciferase protein in the presence of gold nanoparticles.

Keywords: Luciferase enzyme, Gold nanoparticles, ATP assay, Bioluminescence, Intrinsic fluorescence

CP127 Study on the Interaction of zein and oleuropein by molecular docking

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Due to increasing consumers demand, food manufacturers tend to add bioactive compounds to food products . Oleuropein, the main phenolic compound of olive leaves, is one of these bioactive substances that is known for its numerous health benefits, including nutritional and medicinal properties. Zein is a plant protein from maize with unique hydrophobic and hydrophilic properties of a biopolymer for food applications; that make it suitable for encapsulation of bioactive compounds that cannot be added as pure compounds to beverages or foods. In this study, the three-dimensional structure of the zein predicted using the I-TASSER online server and the possible binding sites of oleuropein to zein with molecular docking were investigated using Autodac 4.2. The results showed that oleuropein can bind to three possible binding sites on the zein by hydrogen and hydrophobic interactions. The best site showed -5.5 kcal / mol free energy of binding, in which hydrogen bonding with Tyr 55 and Arg 56 and hydrophobic interaction with Ala 60, Ala 63, Gln 136, Gln 137, Leu 59, Pro 140 and Gln 144 was observed. Therefore, a complex of zein and oleuropein can be produced and it can be used to enrich food. This complex is probably less oxidizable than oleuropein and is not as bitter as it.

Keywords: Biopolymer, Olive, Molecular docking, Bioactive agents

CP128 Antibacterial activity of 2-pyridine-carboxaldehyde isonicotinoyl hydrazone against *Escherichia coli* and *Staphylococcus aureus*

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Newer derivatives of previous antibiotics may have good antibacterial activity. They may also have a much broader-spectrum antibacterial activity than the older antibiotics. Isoniazid (INH) is a well-known antibacterial drug in as a crucial drug in all multiple drug treatment of tuberculosis (TB) as approved by the WHO. Pyridine-2-Carboxaldehyde Isonicotinoyl Hydrazone (2-PINH) is one of the new isoniazid derivatives. The aim of current study was to evaluate the antibacterial activity of Pyridine-2- Carboxaldehyde Isonicotinoyl Hydrazone against *Escherichia coli* and *Staphylococcus aureus*. In this study, after preparing the solid form of Pyridine-2-carboxaldehyde Isonicotinoyl Hydrazon, 7.5 mg/ml, was completely dissolved in 50 ml of normal saline solution that containing 1 mg/ml NaOH. The solution was passed through a filter with pores of 0.2 µm under sterile conditions. Antibacterial activity of the filtered solution against *E. coli ATCC 8739* and *S. aureus ATCC 25923*, were determined by minimum inhibitory concentration (MIC) method. First, a constant amount of Mueller Hinton Agar culture medium (50 µl) was added to each well of a microplate. Then serial dilutions of 2-PINH were prepared by micro-titration method and were added to the wells. At last, 50 µl of bacterial suspension (0/5 McFarland turbidity) was added to each well. After the overnight culture, the microplate growth inhibition assay was conducted for monitoring any growth inhibition by 2-PINH. The results showed that the minimum inhibitory concentration against *E. coli* and *S. aureus* was 0.5 and 1 mg/ml, respectively. In conclusion, the aqueous solution of Pyridine-2-carboxaldehyde Isonicotinoyl Hydrazone had a good antibacterial effect on *E. coli* and *S. aureus*. These results suggest that 2-PINH may have antibacterial effects against other bacteria.

Keywords: Antibacterial, Isoniazid derivative, Minimum Inhibitory Concentration

CP129 Assessing the Synergistic Effects of Silver Nanoparticles and Nisin on *Staphylococcus Aureus* Genome

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Due to the increased resistance of microorganisms to antibiotics and the mutagenic effects of antimicrobials, researchers are looking for safer antimicrobial agents. Silver nanoparticles have received attention due to their high antimicrobial activity, but due to their free Ag^+ ions, they have mutagenic effect. The main purpose of this study was to investigate the effect of silver nanoparticles conjugated with nisin on the genome of *Staphylococcus aureus*. First, this bacterium is cultured in Nutrient Agar medium and after passage to Nutrient Broth, it is treated with silver nanoparticles, nisin and silver nanoparticle conjugated with nisin in 25, 50, 75, 100, 125, 150, 200, 300 µg/ml concentrations. Then the DNA of the control and treated samples with concentrations of 50 µg/ml of silver nanoparticles, nisin and silver nanoparticles conjugated with nisin were extracted and RAPD-PCR method is used to investigate the genomic effect. The results were analyzed in NTSYS-PC software based on Dice coefficient. The results show that the inhibitory effect of silver nanoparticles conjugated with nisin on the growth of microorganisms was more than silver nanoparticles and nisin, while the genomic effect was less than nisin and silver nanoparticles. silver nanoparticles conjugated with nisin can be used as a suitable and safer antimicrobial compound for other organisms.

Keywords: Antimicrobial, Mutagenicity, Inhibitor, RAPD-PCR, Genomic effect

CP130 The impact of umbilical cord's mesenchymal stem cells-derived secretome on the cerebral microvascular endothelial cells exposed to oxidative stress

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Disturbing the haemostasis of the blood-brain barrier (BBB) accompanies with losing the tight junctions, is increasing the pro-inflammatory factors and matrix metalloproteinase that directly implicates in various complex and cureless neuronal disorders such as Parkinson's disease (PD), Alzheimer's disease (AD), stroke, amyotrophic lateral sclerosis (ALS) and traumatic brain injury (TBI). In recent years, employing mesenchymal stem cells (MSCs) and their secretome converts to potential therapeutic approaches in regenerative medicine. MSCs secret neuroprotective factors such as chemokines, cytokines, and extracellular vehicles (EVs) in their culture medium collectively named secretome. In this study, we aimed to evaluate the effect of MSCs-conditioned medium (MSC-CM) on BBB toward oxidative stress. At first, with great efforts high pure MSCs was isolated from human umbilical cord (hUC-MSCs) tissue with the expanded method and the purity was confirmed by expression of positive cell surface markers (CD44, CD73, CD29), and lack expression of negative markers (CD34, CD14, CD45) using flow cytometry. The secretome was collected in sub-culture three from the serum-free medium after 24 hours of incubation and then added to a monolayer of hCMEC/D3 cell culture as a BBB model at different concentrations. The culture was treated with 100 µM of H_2O_2 to induce ROS and also NaOH for induction of cell death in different manners including: 4 hours pre-treatment, 4 hours post-treatment, or simultaneous treatment of the reagents and secretome. The results indicated that secretome-derived UC-MSCs modulated the ROS level in the presence of oxidative reagent and also cell degeneration in a dose-dependent manner. Accordingly, it seems that UC-MSCs secretome possibly has an antioxidant potential and a supportive role on the brain's endothelial cells.

Keywords: Blood brain barrier, Human umbilical cord, MSCs-conditioned medium, Neuroprotective, oxidative stress, reactive oxygen species

CP131 Evaluation of antibiotic susceptibility pattern and frequency of *bla*$_{TEM}$ and *bla*$_{SHV}$ genes in hospital isolates of *Klebsiella pneumoniae*

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Nowadays, one of the major problems in microbial infection treatments, is the antibiotic resistant bacteria. The *Klebsiella pneumoniae* is resistant against many of the antibiotics because of producing beta-lactamase enzymes. The aim of this study is to evaluate the resistance of *K. pneumoniae* against antibiotics and also to determine the frequency of beta-lactamase genes *bla*$_{TEM}$ and *bla*$_{SHV}$. 100 isolates of *K. pneumonia* from urine samples were collected and confirmed. Antibiotic resistance pattern was studied by disk diffusion method and *ESBL*producing isolates were identified in two stages including primary screening and phenotypic confirmatory tests. PCR method was used to study the frequency of *bla*$_{TEM}$ and *bla*$_{SHV}$ genes. Results showed that the lowest antibiotic resistance of isolates was to amikacin (32%) and the highest resistance was to amoxicillin, amoxicillin-clavulanic acid, cefalexin and cefalotin, so that all isolates were resistant to them. Finally from 23 samples of *ESBL* producing *K. pneumoniae*, 18 samples (78.27%) presented *bla*$_{TEM}$ and 21 samples (91.3%) presented *bla*$_{SHV}$ genes. Overall, the determination of the antibiotic susceptibility and identification of beta-lactamase genes in *ESBLs* producing bacteria would help to choose the appropriate antimicrobial agents for treatments.

Keywords: antibiotic resistant bacteria, betalactamase genes

CP132 The antimicrobial effect of *Rheum ribes* extract and Cu nanoparticles on *Klebsiella pneumoniae isolates*

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Klebsiella pneumoniae is one of the major effects of hospital acquired infections that is resistant to many antibiotics because of producing extended spectrum β-lactamases. Today using plant extracts and nanoparticles is one of the modern attitudes in microbial infection treatments. The aim of this study is to evaluate the synergistic effect of *Rheum ribes* extract and copper nanoparticles on *ESBL*- producing isolates of *K.*

pneumoniae. In this study, 100 isolates of *Klebsiella* were collected from urinary infections. After confirmation, the *ESBL*- producing isolates were identified with primary screening and phenotypic confirmatory tests. After preparation of *R. ribes* extract and Cu nanoparticles, different concentrations were prepared and the antimicrobial effects were studied with disk diffusion method and MIC and MBC were identified. From 100 isolates of *Klebsiella*, 86 isolates were *K. pneumoniae* that after confirmatory tests, 23 samples (26.74%) represented *ESBLs.* According to the results, the antimicrobial effect of extract and the synergistic effect of extract and nanoparticles were dependent to concentration in disk diffusion method. Minimum inhibitory concentration of *R. ribes* extract was 150±1 mg/ml. Cu NPS had no inhibitory effect at used concentration (10 mg/ml). Using *R. ribes* extract and Cu NPs together reduced MIC to 50±1 mg/ml. Overall, results showed that *R. ribes* extract had inhibitory effect on *ESBL*- producing *K. pneumoniae* but this isolate is resistant to increasing concentration of Cu NPs. On the other hand, simultaneous use of *R. ribes* extract and Cu NPs had synergistic effect and intensified their effects.

Keywords: antibiotic resistant bacteria, extended spectrum beta-lactamase, synergism

CP133 Synthesis of Fluorescent Carbon Dots from Urtica dioica as Precursor

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Carbon dots have been found as a fluorescent material for many applications in the field of biology due to their desirable properties such as high fluorescence, water solubility, low toxicity, good biocompatibility, excellent optical properties, and high chemical stability. These include drug delivery applications, bioimaging, and diagnostic sensors. So far, many methods have been introduced, including arc discharge, laser erosion, and microwave heating to synthesize carbon dots. In the present study, pyrolysis and hydrothermal methods have been used for the green synthesis of fluorescent carbon dots. Among the advantages of this method are simplicity, cost-effectiveness, and no need for advanced laboratory equipment. Urtica dioica has been used as a precursor. For the synthesis of fluorescent carbon dots prepared by the pyrolysis method, precursor was heated to a specific temperature and time and the product was obtained as a powder.To prepare fluorescent carbon dots by hydrothermal method, pre-prepared material was used as raw material and deionized water was used as a solvent, the resulting solution was transferred to autoclave; Then the heating process was performed inside the oven at a specific temperature and time. The synthesized carbon dots were characterized by fluorescence spectroscopy (PL), dynamic light scattering (DLS), and fourier transform infrared spectroscopy (FTIR) techniques. The synthesized fluorescent carbon dots had good biocompatibility, emitted intense ultraviolet blue light, and could be used as fluorescence probes in imaging.

Keywords: Carbon Nanomaterial, Green Synthesis, Natural Precursor, Pyrolysis, Hydrothermal

CP134 Association of the *MIAT* rs1894720 Polymorphism with Ischemic Stroke Risk and *MIAT* Expression Levels in Blood after an Ischemic Stroke

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Myocardial infarction associated transcript (MIAT) is a new disease-related lncRNA characterized by an improper expression in different ailments, such as ischemic stroke (IS), schizophrenia, diabetic complications, cancers, myocardial infarction, and cataracts. It is hypothesized that the MIAT rs1894720 polymorphism is correlated with ischemic stroke risk and MIAT expression rate. We studied 116 Iranian patients with clinically definite acute IS and 116 ethnicity-, age-, and sex-matched controls. The tetra-primer ARMS-PCR method was applied for DNA genotyping. The susceptibility of IS and MIAT rs1894720 polymorphism sites was analyzed. The MIAT expression in the blood was evaluated after RNA extraction, cDNA synthesis, and real-time PCR. We used the receiver operating characteristic (ROC) curve to evaluate the diagnosis and prognosis of IS. The mean age of IS patients was 65.90±14.44 years. The polymorphism of MIAT rs1894720 was related to IS susceptibility in the recessive model (OR=8.51, 95% CI=1.04-69.23, P=0.01). Furthermore, the co-dominant (OR=0.24, 95% CI=0.07-0.76, P=0.009 for GT genotype), dominant (OR=0.26, 95% CI=0.08-0.81, P=0.01),

and over-dominant (OR=0.19, 95% CI=0.07-0.52, P=0.0005) models of the rs1894720 were negatively associated with the risk of ischemic stroke. There was no correlation between rs1894720 polymorphism and MIAT expression levels. We, also, detected a significant up-regulation of MIAT gene expression in IS stroke patients in comparison to the control group. ROC curves showed that MIAT might serve as a biomarker for diagnosing IS patients. The rs1894720 polymorphism of the MIAT is correlated with the risk of IS but not with MIAT expression levels. In addition, the upregulation of blood-derived MIAT can be considered a diagnostic biomarker of IS.

Keywords: Stroke, Long Non-Coding RNA, Polymorphism, Biomarkers, Real-Time PCR.

CP135 Inhibitory effect of *Hyoscyamus senecionis* extract on non-enzymatic glycosylation of hemoglobin

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Diabetes is a metabolic disorder associated with hyperglycemia and caused by defect in insulin secretion or insensitivity of target organs to insulin. Non-enzymatic glycosylation of proteins and the formation of AGE is one of the factors involved in the pathogenesis of chronic complications of diabetes. Since glycation reactions combined with oxidation reactions disrupt the proper functioning of proteins, the use of plant-based antioxidant compounds can be used as a treatment to prevent these chronic side effects. One of the important genera of family Solanaceae is *Hyoscyamus* and its most important species *are H. niger* L., *H. muticus* L., *H. albus* L., *H. Aureus* L., *H. reticulates* L., *H. senecionis* Willd. and *H. pusillus* L. In this study, the effect of methanolic extract of *H. senecionis* seeds on inhibition of non-enzymatic glycosylation of hemoglobin was investigated in vitro. Then, in order to form AGE, hemoglobin was glycated by glucose in vitro and to evaluate the effect of methanolic extract of *H. senecionis* seeds on the glycosylation process, the fluorescence intensity of the samples was measured at 443 nm .In this experiment, the concentration of the extract required to inhibit 50% of the non-enzymatic glycosylation process of hemoglobin (IC50) was obtained and compared with the required amount of ascorbic acid as a positive control. Seed methanolic extract with IC50 = 253.84 µg / ml has anti-diabetic properties compared to ascorbic acid with IC50 = ۸۰,۹۲ µg / ml. According to the obtained IC50, the inhibitory effect of methanolic extract of plant seeds is low compared to ascorbic acid.

Keywords: Diabetes, Solanaceae

CP136 Inhibitory effect of *Hyoscyamus senecionis* extract on alpha-amylase enzyme

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Diabetes is a chronic disease that occurs when the pancreas does not produce enough insulin or the body cannot use the insulin it produces effectively. One of the most important issues in the treatment and control of type 2 diabetes is the reduction of hyperglycemia after consuming sugars, which is possible by inhibiting enzymes such as alpha-amylase and alpha-glucosidase. The use of plants has been common in the past for many disorders and diseases. Today, due to the side effects of chemical drugs and the high cost of these drugs, the use of herbal medicines in medicine and traditional medicine has increased significantly compared to the past. The Solanaceae is one of the most important latent genus in terms of medicine and nutrition because it contains important alkaloids such as hyoscyamine, atropine and scopolamine. *Hyoscamus senecionis* belongs to the genus Solanaceae. This family is mainly distributed in the tropics and the main origin of this plant is the United States. The aim of this study was to investigate the anti-diabetic effects of methanolic extract of H. senecionis leaf from Solanaceae genus. This experimental study investigates the anti-diabetic properties by measuring the inhibition of α-amylase. Alpha-amylase inhibition test was performed by measuring the reduction of oligosaccharide release power from starch solution and to evaluate the effect of methanolic extract of H. senecionis leaf on alpha-amylase inhibition process, the fluorescence intensity of the samples was measured. In this experiment, the concentration of the extract required to inhibit 50% of the enzyme activity (IC50) was

obtained and compared with the required amount of acarbose as a positive control. Leaf methanolic extract with IC50 = 811.62 µg / ml has anti-diabetic properties compared to acarbose with IC50 = 2.68 µg / ml.
Keywords: Diabetes, Alpha Glucosidase, Solanaceae

CP137 Study of the interaction of Aloin and its' light degradation products with hen egg-white lysozyme by spectroscopic methods

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Aloin is a major glycosyl anthraquinone found in Aloe vera and exists as A and B diastomers. Based on previous studies, Aloin has pharmacological effects like anti-oxidation, anti-inflammation, and anti-tumor properties. Aloin is a light sensitive component and can be degraded to other derivatives like aloe-emodin, which has apoptotic induction properties. Aloin is able to enter blood flow quickly and reach body organs. So the study of Aloin interaction with proteins helps us with molecular information. In this study, we examined the interaction of Aloin and its' derivatives with hen egg white lysozyme (HEWL). Lysozyme is an enzyme with anti-bacterial properties and is mostly found in all body fluids. It is used as a suitable model protein in molecular level detections. Unlike wide range cellular studies, no molecular level studies have been yet reported on the HEWL-Aloin interaction. We applied UV-vis and fluorescence spectroscopes in this study. In order to investigate the effects of Aloin and its' derivatives, different concentrations of these ligands were added to HEWL (0.3 mg/ml) and its' intrinsic absorbance and fluorescence were measured. Results showed absorbance intensity increase and fluorescence emission decrease of HEWL with increasing ligands concentration. Fluorescence quenching measurements were performed at different temperatures to find out the interaction mechanism. According to obtained Stern-Volmer constant, Aloin and its' derivatives bind to HEWL by a dynamic and static mechanism, respectively. The results indicated also conformational changes of HEWL. Therefore, Aloin or its' derivatives may be used as a drug by caution. However, further studies are needed to ensure Alion and its' derivatives effects on the conformation of biological macromolecules.
Keywords: Anthraquinone, Fluorescence quenching, Stern-Volmer constant

CP138 Evaluation of Cytomegalo, Epstein-Barr and Varicella-Zoster viruses in Leukemias by PCR

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Leukemia, as a complex disease, causes molecular changes in the cell by multiple variables. This disease interferes with the proliferation of bone marrow stem cells. It is classified in acute to chronic categories based on the invasion degree and its prevalence is increasing in our country. Therefore, identification of viral risk factors is very important, including CMV, EBV and VZV, all of which are the members of *Herpesviridae* family and have the potential for reactivation. For example, CMV is observed from prenatal to post-puberty, EBV with infection in B lymphocytes and VZV with dermal spread. Since the etiology of leukemia is unknown, we decided to evaluate these three viruses in types of leukemia and healthy controls using PCR. From 100 blood serum samples of leukemia patients and 100 healthy control samples prepared from Tehran laboratories, DNA was extracted from phenol-chloroform method from samples and All three optimal PCR tests and CMV, EBV and VZV amplicons with 257 bp, 129 bp and 216 bp respectively were observed by agarose gel electrophoresis method. In the feature test of all three tests, only the target viral patterns responded positively. The detection limit was 100 Copy / Reaction for CMV and 10 Copy / Reaction for EBV and VZV. All healthy controls were negative, 9% of the samples were infected with VZV, 33% were infected with CMV and 36% were infected with EBV.

Infectious agents in leukemias are controversial today, and these three viruses, can be possible causes of leukemias
Keywords: Specificity test، Etiology ،Amplicon

CP139 Bioinformatics identification of an effective peptide signal for the expression of periplasmic human growth factor in *E. coli*

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The human growth hormone is a single-chain polypeptide with a pivotal role in various biological processes. Although *E. coli* is considered a preferred host for producing human growth hormone, similar to many other eukaryotic proteins, the high expression of this protein in *E. coli* results in the accumulation of inclusion bodies. Periplasmic expression using signal peptides could be used to overcome the formation of inclusion body; still, the efficiency of each of the signal peptides in periplasmic transportation is varied and often protein specific. The present study aimed to use in silico analysis to identify an appropriate signal peptide for periplasmic expression of human growth hormone in *E. coli.* The amino acid sequences of 91prokaryotic and eukaryotic signal peptides were collected from the signal peptide database, and each signal's characteristics and efficiency in connection with the target protein were analyzed by signalP4.1 server. The prediction of the secretory pathway and the cleavage position was determined by the signalP5 server. Physicochemical properties, including molecular weight, instability index, Gravity and aliphatic index, were investigated by ProtParam software. The results of the present study showed that among all the signal peptides studied, five signal peptides ynfB, sfaS, lolA, glnH, and malE displayed high scores for periplasmic expression of Hgh in *E. coli*, respectively. In conclusion, the results indicated that in silico analysis could be used for the identification of suitable signal peptide for the periplasmic expression of proteins. Further laboratory studies can evaluate the accuracy of the results of the in silico analysis.

Keywords: Soluble expression, Growth hormone, In silico, Escherichia coli

CP140 CADD approach in the development of antibacterial molecules to inhibit Gyrase B in *Staphylococcus aureus*

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Given the growing number of drug-resistant bacteria, research into antibacterial agents is essential. As a pathogen, *S. aureus* is prone to rapidly acquire resistance genes. Bacterial DNA gyrase is one of the desirable targets for the development of antimicrobial agents. This enzyme catalyzes topological changes in DNA, and subunit B of this enzyme, GyrB, has ATPase activity. Therefore, if the activity of this subunit is inhibited, the necessary energy for replication and transcription of DNA is not provided. The proposed properties have made this enzyme a suitable new target for the identification of inhibitory molecules. Computer Aided Drug Design (CADD) approaches have played a very effective role in accelerating and optimizing the economic process of drug design and development. In this study, the pharmacophore modeling was used to identify potential inhibitors. In this regard, GyrB structure together with pyrazolethiazole (PDB code :3g75) was extracted from PDB database. Based on laboratory data, pharmacophore modeling was performed using Lipinski's five rules and Pharmit server. based on the pharmacophoric model, a search has been done in the ZINC database and 329 hits were found. Virtual screening was performed using Pyrx software and 20 molecules with the most favorable ΔG between -7 to -8.9, were selected. Finally, the ADMET properties prediction of these molecules was performed using ADMETlab.According to the results of previous researches on the factors affecting the optimal binding to the Gyrase and other features like, druglikines, logS and toxisity, ZINC000023430719, ZINC000072147459, ZINC000261365084, ZINC000005865328 and ZINC000001033944 were introduced as hit molecules. Based on this fact that search has been done on chemical molecules database and despite the development of computational systems and the high accuracy of these methods, it is suggested that selected molecules as drug hit compounds be evaluated by laboratory approaches.

Keywords: Drug resistance, Pharmacophore,ADMET, *S.aureus*, DNA gyrase

CP141 Molecular cloning and expression of coat protein gene of an Iranian isolate of sugarcane streak mosaic virus in *Escherichia coli*

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Sugarcane streak mosaic virus (SCSMV) is an important causal agent of sugarcane mosaic disease in Asian countries. It seems that the most appropriate way to control the virus is to use virus-free cuttings. ELISA is the most common laboratory test to detect viruses on a large-scale; therefore, antibody preparation against SCSMV to detect the presence of the virus in sugarcane cuttings is of importance. However, commercial antiserum to detect SCSMV is not available. To provide viral antigens for use in the polyclonal antibody production process, SCSMV-CP was amplified using specific primers for CP gene containing *Bam*HI and *Hind*III digestion sites at respective 5′ end of the forward and reverse primers, respectively. An 850 bp PCR product was amplified, purified, and ligated into a pTZ57R/T vector to generate pTZ57-SCSMV-CP. It was then transformed into *E. coli* strain DH5α. After culturing bacterial cells at 37 ºC overnight, the integrity of proper recombinant pTZ57-SCSMV-CP clones was confirmed by restriction enzyme analysis of extracted recombinant plasmid DNAs and PCR with specific-forward and reverse primers. The CP gene was released from pTZ57-SCSMV-CP by restriction enzymes and subcloned into the expression vector pET28a. The resultant recombinant plasmid, pET28-SCSMV-CP, was transformed into *E. coli* strain B21 (DE3) by the heat shock method. Transformed bacterial cells were grown on solid LB medium containing 25 μg/ml kanamycin overnight. The recombinant pE28a expression vector containing CP gene was confirmed by colony PCR, restriction analysis by *Bam*HI and *Hind*III, and sequencing of the insert DNA. Finally, expression of CP protein was induced by adding 1 mM IPTG to bacterial cultures containing the recombinant pET28-SCSMV-CP DNA. Sampling was done four hours after induction, and the bacterial protein was extracted. The extracted proteins from the harvested cells were separated by 12% SDS-PAGE, and a strong 35-KDa protein band was revealed in the gel.

Keywords: Antibody, Coat protein, Cloning, Restriction enzyme digestion, Expression vector

CP142 Study of antibacterial and photocatalytic properties of silver nanoparticles synthesized by *Haplophyllum obtusifolium* watery extract

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Silver has long been known for its antibacterial properties. In fact, silver nanoparticles, due to the release of silver ions, have such properties against aerobic and anaerobic bacteria. The binding of these particles to the sulfur-containing proteins at the surface of the bacterial membrane allows them to enter and modify the morphology and respiratory chain of the bacterium, eventually affecting the apoptosis process leading to the death of the foreign agent .Today, the unique properties of nanoparticles such as surface to volume ratio and quantum effects have increased the importance and photocatalytic role of these compounds in areas such as the environment, wastewater treatment and renewable energy. In this study, the antibacterial performance of synthesized nanoparticles against two gram-negative bacterias (E.coli, P.aeruginosa) and two gram-positive bacterias (*S.aureus, S. epidermidis*) was investigated by diffusion disc method. Antibacterial function was seen in all samples, but the study of districts of reticences howed a higher potential of nanoparticles in the removal of gram-positive bacteria. The photocatalytic ability of silver nanoparticles synthesized to remove industrial dye Methyl Orange, which is one of the most important elements of industrial wastewater, was performed using a spectrophotometer, which strongly confirms the photocatalytic nature of silver nanoparticles in methyl orange dye degradation in the visible region at 464 nm.. The achievements and findings of nanobiotechnology in the fields of health, treatment and the environment promise a bright future in this new science.

Keywords: Antibiotics, Apoptosis, Antibiogram, Methyl Orange, Industrial Sewage

CP143 Association of ACE2 genetic polymorphisms with susceptibility of catching COVID-19

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Human genetic factors are one of the most important factors in the high transmission of SARS-CoV-2. This virus infects the host cell by biding with angiotensin converting enzyme 2 (ACE2). Therefore, it is important to survey the virus-host cell interactions that occur during infection. The human ACE2 gene is located on chromosome Xp22. ACE2 is extendedly expressin the heart, liver, and other tissues. Respiratory complications are the major propellant to COVID-19 associated fatality rates because the alveolar epithelial type-II cells are rich with ACE-2 receptors. The aim of this study was to investigate the unique polymorphisms in ACE2 and their association with COVID-19 severity. In this view, novel data are collected from searching databases such as PubMed, ISI, and Scopus and are presented a purposeful survey on genetic susceptibility and unique polymorphisms in ACE2 and their association with COVID-19 severity. Accumulating evidence from RNA-seq data and single-nucleotide polymorphism studies now suggest that genetic polymorphisms in the ACE2 gene may modulate intermolecular interactions with the spike protein of SARS-CoV-2. Studies have shown a striking difference in allele frequency among populations for a polymorphism rs4646116 and rs4646116 that are likely to affect the severity of COVID-19. Recent studies done on ACE2 variants reported population-based frequency differences for two single nucleotide variants rs41303171 and rs4646116. The variable susceptibility to the SARS-CoV-2 infection may be associated with the certain genomic polymorphism within ACE2. Therefore, recognizing these polymorphisms could be helpful in identifying susceptible individuals.

Keywords: COVID-19**,** Angiotensin-converting enzyme 2 (ACE2), polymorphism, SARS-CoV-2

CP144 The evaluation of inhibitory effects of secretome from mesenchymal stem cells on invasion of pancreatic cancer cells by By analyzing the expression of *Vimentin* gene

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They can differentiate into specific cell types in vitro and in vivo and have a tendency to acquire tissue specific characteristics when co-cultured with specialized cell types like cancer cells Invasion is the first step in the metastatic cascade, when tumor cells acquire the ability to move, penetrate into the surrounding tissue and enter lymphatic and blood vessels in order to disseminate. The aim of this study was to determine the expression of *Vimentin* gene, a suppressor of cancer growth. Any dysfunction of this gene leads to cancer progression and metastasis. When the production of this protein decreases, cell-to-cell adhesion decreases and cell motility increases. This allows cancer cells to cross the basement membrane and invade nearby tissues. In this study, we used co-cell culture for cancer cells and stem cells at different times using a 6-cell two-story plate with a diameter of 0.4 μm (Transwell) and using qRT-PCR expression of *Vimentin* size gene to found that it inhibited metastasis or EMT by controlling *Vimentin*. The results showed that reducing the regulation of *vimentin* expression in pancreatic cancer cells by transfection with antisense-*Vimentin* resulted in a significant reduction in tumor cell motility and invasive activity. Furthermore, the expression of *E-cadherin* was inversely associated with expression of *Vimentin*. Our results suggest that *Vimentin* affects pancreatic cancer cells motility and invasiveness.

Keyword: Pancreatic cancer, gene expression, *Vimentin*

CP145 How SARS-CoV-2 (causative agent of COVID-19) outsmarts the host immune system

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Undoubtedly, the most succession of SARS-CoV-2 in creating a pandemic and persistent infection is related to how it outsmarts the host immune system. In the present study, the various strategies used by the virus to escape

the host's immune system have been reviewed. The ability to infect cells of various tissues and organs such as the lungs, small intestine, and liver is one of the successes of the virus in causing persistent infection, which ultimately leads to an increase in viral load in the host and challenging the immune system to combat with it. This ability is related to Furin, an enzyme that is involved in the activation of SARS-CoV-2 during entrance into the cells and expressed by cells of various organs. Like other coronaviruses, during SARS-CoV-2 infection, double-stranded RNAs from genome replication and RNA synthesis become inaccessible to cytosolic PRRs (pattern recognition receptors) of the immune system such as RIG-I, MDA5, and TLR3 by being placed inside the double-membrane vesicles. SARS-CoV-2, like other coronaviruses, can escape from the immune system by inhibiting or delaying the production of interferon. In persistent infection, successive mutations in the virus, especially in the spike protein, can protect the virus against humoral immunity. High genetic variability also leads to inefficiency of the immune system in recognizing and neutralizing the virus in subsequent encounters. Coinfection of the host with two different strains can lead to the emergence of a new strain with new capabilities by genomic recombination between these two strains. Ultimately, the virus's ability to infect different host species (humans and other animals) is most likely very effective in the wide range and stability of the outbreak. In conclusion, to combat the virus and design a vaccine, it is important to consider the significant ability of SARS-CoV-2 to cause infection and escape the immune system.

Keywords: Coronavirus, Escape, Immune system

CP146 Evaluation of Antibacterial and Antifungal Activity of New derivatives of two, three and four components of 1, 3, 4-oxadiazoles

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The emergence of antibiotic resistance in the treatment of diseases has become a serious problem; therefore, in the current situation, the discovery and presentation of alternative structures is very important. The aim of this study was to investigate the new 1, 3, 4-oxadiazole structures against bacteria and fungi resistant to treatment. Twelve new derivatives were obtained by single-step synthesis and their structure was evaluated by IR (Infrared), C-NMR (Carbon Nuclear Magnetic Resonance) and H-NMR (Hydrogen Proton Nuclear Magnetic Resonance).Then, to measure the antibacterial and antifungal activity of prepared derivatives agar well diffusion method was employed, and the minimum inhibitory concentration (MIC) and the minimum bactericidal concentration (MBC) were determined at a concentration of 0.1mg/mL with three replications on *Streptococcus Mutans*, *Enterococcus Faecalis*, *Klebsiella Pneumoniae*, *Escherichia Coli O157: H7, Candida Glabrata*, *Candida Krusei*. Statistical analysis of the data was performed using (IBM SPSS Statistics 22). The results showed that the best antibacterial activity among all compounds was related to the 4g compound against the E.faecalis (IZ= 45.33 ± 1.15 mm), (MIC: 250µg /ml), that showed inhibition zones greater than the control.The compound (4g) also showed acceptable activity on the S. mutans (IZ= 25.66 ± 0.57 mm) (MIC: 125 µg/ml), and other bacteria were affected too .In the case of fungal specimens, no acceptable results were obtained. Based on the results of this study, the compound 4g (with the chlorophenyl and morpholine functional groups) can be used as an alternative to the ability to inhibit gram-positive bacteria resistant to antibiotics.

Keywords: Antibiotic Resistance, *Enterococcus faecalis*, *Streptococcus mutans*, chlorophenyl, morpholine

CP147 Comparing toxic effects of auraptene and urolithin A in human colon adenocarcinoma cells

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Colon adenocarcinoma is a life threatening malignancy with high rate of incidence worldwide. Auraptene is an abundant natural monoterpene coumarin that possesses valuable pharmaceutical effects, and urolithin A is an ellagic acid metabolite produced by gut microbial flora with several biological effects. In the current study, we aimed to compare toxic effects of auraptene with urolithin A in colon adenocarcinoma cells.
Auraptene was synthesized by a reaction between 7-hydroxycoumarin and transgeranyl bromide, while 2-bromo-5-methoxy benzoic acid and resorcinol were used for urolithin A synthesis. After LoVo cells were treated with 10, 20, 40 and 80 µM auraptene or urolithin A, they were incubated for 24, 48 and 72 h. Finally, cell viability was assessed by resazurin as a colorimetric assay, and morphological alterations were recorded by an inverted microscope.Our finding indicated that auraptene toxicity increased during 3 consecutive days, as 97%, 89% and 69% of cells were alive upon 24, 48 and 72 h treatment with 40 µM auraptene, respectively. Meanwhile, viability of LoVo cells was calculated as 63%, 58% and 86% after 24, 48 and 72 h treatment with 40 µM urolithin A, respectively. Viability of cells decreased by the highest concentration of both agents; 80 µM auraptene reduced viability down to 63%, 33% and 26% after 24, 48 and 72 h treatment, respectively, and 43%, 31% and 41% of cells were alive upon 24, 48 and 72 h treatment with 80 µM urolithin A, respectively. To note, cell viability was $\geq 80\%$ and $\geq 70\%$ for lower concentrations of auraptene and urolithin A, respectively. Taken together, our findings revealed that auraptene and urolithin A induced their toxic effects in LoVo cells in a time- and dose-dependent manner. Moreover, cytotoxicity of urolithin A was more than that for auraptene in the same time and dose range, which make this agent a suitable option for further anticancer studies.
Keywords: Colon adenocarcinoma, Auraptene, Urolithin A, Cytotoxicity

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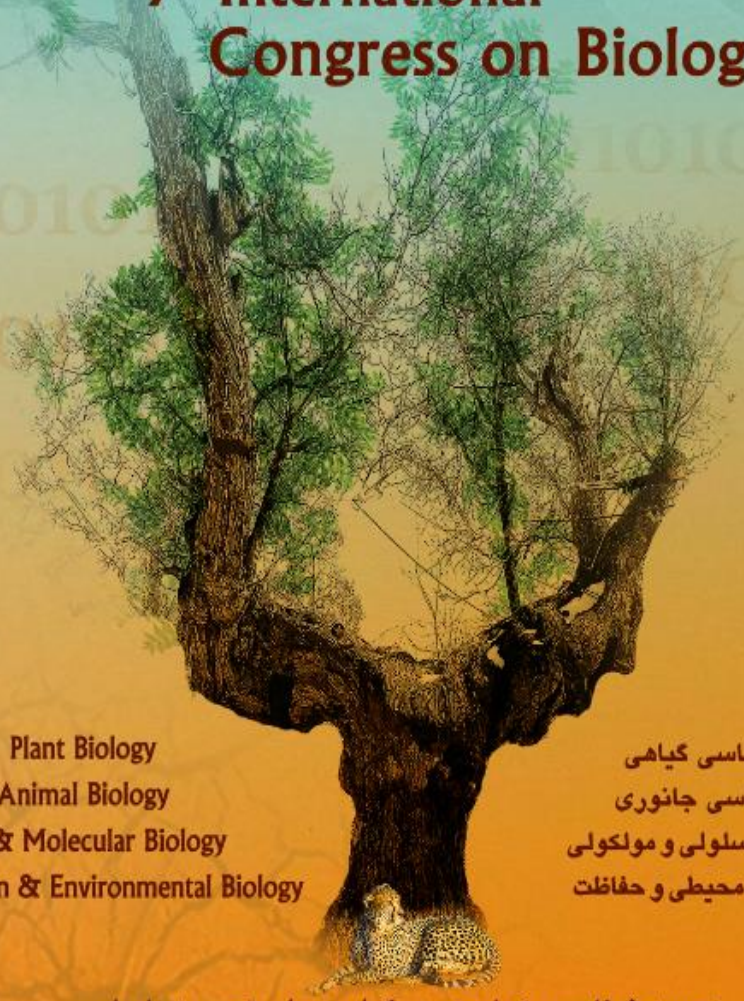

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