21st National 9th International Congress on Biology

Conservation & Environmental Biology

Semnan University, Semnan, Iran

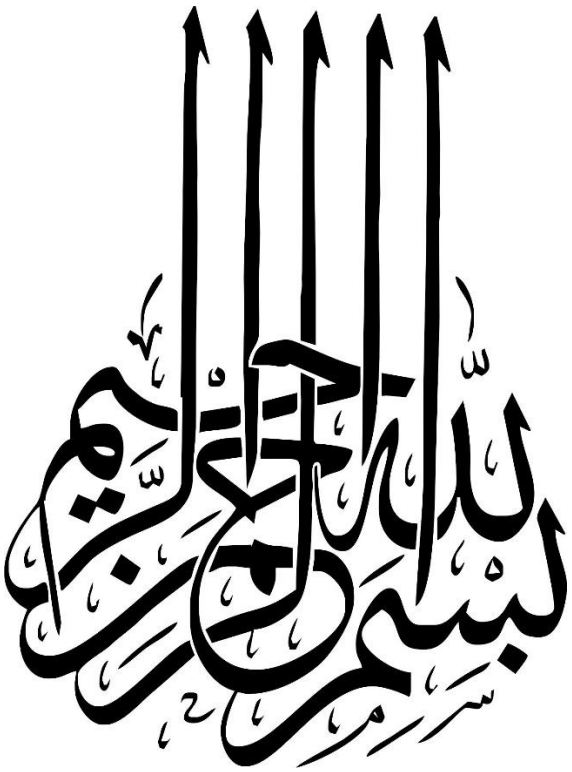
16-19 Feb. 2021

Welcome to IBS 2021

Conference On

Conservation & Environmental Biology

21st National & 9th International Congress On Biology


بسم الله الرحمن الرحيم

Abstracts

of

21st National & 9th International Congress on Biology

Conference on Conservation and Environmental Biology

16-19 Feb. 2021

Semnan

IRAN

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

Edit, Layout and Preparation by Darvishalipour A. Shakiba

Name Index

This congress was indexed by ISC (# 99200-22082) and CIVILICA (# BIOCONF21).

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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Table of content

Keynote Speakers

KN1 Why does the world need an integrative system approach to biology 3
KN2 Wisdom-based Outlook on Biological Sciences 5
KN3 The imperative to develop a sustainable solution to iron deficiency 6
KN4 Immune cell types in severe asthma 9
KN5 Multi omics approaches to improve none-domesticated Jatropha curcas: Challenges to counteract land degradation 11
KN6 Biological supertrends, futures studies and futures perspectives of human society and civilization 13

Invited Speakers

IS1 Pneumolysis in COVID-19: pathophysiology and high altitude implications 2
IS2 Applying behavioral insights to control COVID-19 epidemic in I.R. of Iran 2
IS3 Emission, effects and mitigation of greenhouse gases (GHGs) in agriculture 3
IS4 Characterization of the complete chloroplast genome sequence of the IRLC species and its phylogenetic implications 4
IS5 DNA Barcoding: An Effective Molecular Tool to Identify Gene Expression Host Organisms 4
IS6 The fate of silver nanoparticles in *Lycopersicon esculentu* 4
IS7 Plant life on gypsum: living at the edge 5
IS8 Using Protected Areas to Secure Forest Tree Genetic Diversity in Hyrcanian forest (Application to the endemic and endangered *Populus caspica* 5
IS9 Molecular Biophysics of SARS-CoV-2 virus and its susesepibiliy 6
IS10 ole of hmgb1 and decorin in preeclampsia 6
IS11 Oxygen sensing and Lead (Pb) toxicities: Molecular interactions, cell signaling & antioxidant defense 7
IS12 Proteomic dissection of signaling pathways in cancer cells 7
IS13 Integrated Biorefineries 7
IS14 Antimicrobial resistance (AMR) and Role of the laboratory in AMR control 8
IS15 Survey of Microorganisms' World in Kerman Desert 8
IS16 The resulting experience of wildlife management and biodiversity conservation to maintain quality habitat in Semnan province 8
IS17 Regulatory mechanisms of sperm motility initiation in fishes – a review 9
IS18 Making Meaningful Decisions for Life: Epigenetic Monoallelic Gene Expression in Mammals 9
IS19 Consequences of Simulated Microgravity in Biosystems: Structural Effects and Cellular morphology 10
IS20 Bone Tissue Engineering; Advances and Challenges 10
IS21 The importance of Bioinformatics and Computational Biology in Systems Biology 11

IS22 Development of artificial enzymes with biomedical and industrial applications; Perspectives and future challenges 11
IS23 Biophysical understanding and control of living systems 12
IS24 Signaling pathway modeling for systematic study of diseases 12
IS25 Design of antimicrobial and anticancer peptides based on membrane and peptide biophysical properties 13
IS26 Pan-cancer analysis of microRNA expression profiles highlights microRNAs enriched in normal body cells as effective suppressors of multiple tumor types 13
IS27 From Birth to Birth 14
IS28 Scale-up Production of Liver Organoids 14
IS29 Structure function relationship in active and inactive Apaf-1 in apoptosome formation 15
IS30 Applications of integrative biology to address global challenges 15
IS31 Ecological Responses of Algal Community to Hydrological Changes in the MacKenzie River, Australia: Implications for River Basin Management 15
IS32 Identification of Medicinal Plants Value Chain, Challenges and Opportunities (Case Study of Thyme) 16
IS33 15 years of taxonomic study on the genus *Silene* (Caryophyllaceae) in Iran a pattern for taxonomic studying of species rich genus in Iran 16
IS34 The Value of Micromorphological Studies in Poaceae 17
IS35 The phylogeny of Rosoideae (Rosaceae) in Iran, based on cpDNA and nrDNA sequenced data 17
IS36 Inhibitory effects of some mosses extracts on phytopathogenic fungi *in vitro* and *in vivo* 17
IS37 A Survey of Moss flora of Zagros Mountains in Khouzestan Province 18
IS38 OMICS approaches towards deeper insight into cellular processes: genome projects and decoding the genomic and transcriptomic data 18
IS39 SARS-CoV-2: genome evolution, possible causes of divergenve and expansion of somelinage, and the pathogenic importance of different variants 19
IS40 Prefrontal cortical-hippocampal-amygdala functional loop in memory formation 19
IS41 Wnt signaling in dopaminergic neuron development and degeneration 19
IS42 Role of non-coding RNAs in morphine function 20
IS43 Selection of competent oocytes for assisted reproductive technologies 20
IS44 A review on the role and importance of oribatid mites, taxonomy and status of species reported from Iran 21
IS45 An overview of assisted reproductive technology procedures 22
IS46 Exosome application in cancer diagnosis and therapy 22
IS47 The effect of green nanoparticles on the aggregation of protein 22
IS48 Herbal research: Important forgottens 23
IS49 Drug Delivery Using Nanoparticles 23
IS50 A review on history and taxonomic status of bats in Iran 24
IS51 Animal models in physiological studies: Challenges and prospects 24

IS52 Royan Kidney Group (RKG): Cells Therapy and Tissue Engineering in Renal and Urinary Tract Diseases: Stem cells as a new trend 25

IS53 Novel Cellular Strategies for Generation of Human Cardiomyocytes in Vitro 26

IS54 Wnt signaling in development and stem cell control 26

IS55 Wolbachia in scale insects: A unique pattern of infection prevalence, high genetic diversity, and host shifts 26

IS56 Molecular data proves successful in resolving taxonomy, phylogeny and biogeography of Pompilidae (hymenoptera) 27

IS57 Mass production of live food and their by-products in semi-arid areas 27

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 cell……..…….27

IS59 The effect of Mouse Embryonic Stem Cells (mESCs) transplantation on ischemic tolerance in animal stroke model……28

IS60 Cerebral folate and cerebrospinal fluid: essential components of normal brain development……...…….....28

IS61 Novel strategy for reduction of morphine dose in pain relief: the underlying mechanisms…….…….....29

IS62 Investigation of the effect of point mutations on human transthyretin protein structure and aggregation……..…29

Oral Presentations

EO1 Identification of Environmental Impacts Affected by Exploiting Gravel and Sand from Karun Riverbed by Checklist Method and Analytic Hierarchy Process 2

EO2 Is NDVI the best index for vegetation studies? 2

EO3 Heliotrine extraction and detoxification by bacterial derived FAD-dependent oxidoreductase 3

EO4 Environmental assessment of Amirkelayeh Wildlife refuge using SWOT management analysis model based on ecosystem integrated management plan 3

EO5 The most contributung biovariables in geographical distribution of tulips based on ecological niche modelling (ENM) 4

EO6 Ecological assessment of Bushehr coasts (OuLi to Kangan) using Macrobenthos as biomarkers 4

EO7 Feasibility study of Kavir National Park habitat in order to re-introduce the *Equus hemionus onager* 5

EO8 The first report of microplastic observation in waterfowl of southern Caspian sea 5

Poster Presentations

EP1 Investigating the possibility of formation of cyanobacterial biocrust in desert soil model 7

EP3 Habitat preference modeling of Iranobuthus krali (Scorpiones: Buthidae) in Iran 7

EP4 Evaluation of nanoparticles movement in soil and their environmental impact 8

EP5 Hormonal responses of wild and cultivated barley genotypes to cadmium stress 8

EP6 Threat problemology by Tree analysis Technique in The ecosystem integrated management plan(Case Study: Amirkelayeh refuge) 8

EP8 Evaluating the predictive performance of habitat models for Yarrow (*Achillea millefolium)* 9

EP10 Effect of Ammonium Nitrate on the Development and Survival of Marsh frog (*Pelophylax* sp.), (Amphibian: Anura) 9

EP11 Sensitivity to Urea Fertilization in the Marsh frog (*Pelophylax* sp.): Survey of Development and Survival 10

EP12 Water quality assessment in the Sufi-Chay river (NW-Iran) using diatoms as bio-indicators 10

EP15 Investigation of Basal Area, Volume and Carbon Sequestration Allometric Models according to independent variable of Age *in Populus deltoides* Plantation 11

EP16 The seasonal distribution of Ilyoplax frater in mudflat ecosystems of Hara Biosphere Reserve, Persian Gulf 11

EP17 Study of some quantitative and qualitative characteristics of fruit and seed cones to identify two species of *Juniper* (*Juniperus excelsa* and *J. polycarpos*) in Goinik Jargalan habitat of North Khorasan province 12

EP18 Pollen study of two *Juniperus* L. species in Goinik Jargalan habitat of North Khorasan province 12

EP19 Survey the toxic effect of Abamektin in *Artemia franciscana* by using Response Surface Methodology 13

EP20 Survey some poly aromatic hydrocarbons (PAHs) accumulation in tissues of wild pigeon from Tehran megacity 13

EP21 Evaluation of Surface morphology and erosion in marine microplastics 14

EP22 Distribution patterns for Liliaceae in order to determine the priorities of conservation management in Iran 14

EP25 Modeling of climate change effects on distribution of *Aegilops* L. (*Poaceae*) toward biodiversity conservation in Iran 15

EP26 Climate change modeling of wheat wild relative (GP1) in Iran: Conservation aspect 15

EP27 Ecological assessment of tidal zone in Chabahar Gulf coastal zone using IUCN ecological criteria 16

EP28 Reliability of benthic indices in health assessment of coral reefs subjected to oil pollution 16

EP30 Characterization of Lepidopteran- specific *Cry* genes in Iranian strains of *Bacillus thuringiensis*. 16

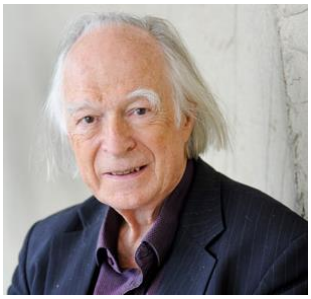
EP31 Investigation of the effect of native isolates of the bacterium, *Bacillus thuringiensis* on mortality of Mediterranean flour moth 17

EP32 Flora, life form and chorology of plants in *Pallas's* cat habitat (case study: Jashloobar, Semnan). 17

EP33 Variation in expression of thermal stress genes in massive *Porites harrisoni* corals in the Persian Gulf 18

EP34 Investigating the conflicts between local communities and the natural environment in relation to the protection of biodiversity in Haraaz protected catchment area- Case study: Ab-Ask village.. 19

KEYNOTE SPEAKERS



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

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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
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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
Faculty of Medicine, National Heart & Lung Institute
https://www.imperial.ac.uk/people/ian.adcockMobasheriwolkenhauer

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

Ian M Adcock, Angelica Tsitiou, Nazanin Zounemat Kermani, Yusef Badi & Ying Shi -*National Heart & Lung Institute Imperial College London. E.mail: ian.adcock@imperial.ac.uk*

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

Professor of Plant Functional Genomics
University of Natural Resources and Life Sciences Vienna,Vienna, Austria
https://forschung.boku.ac.at/fis/suchen.person_uebersicht?id_in=5595&menue_id_in=101&sprache_in=en

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

Fatemeh Maghuly, Ph.D. - *Department of Biotechnology, University of Natural Resources and Life Sciences, BOKU, Vienna, Austria. E-mail: fatemeh.maghuly@boku.ac.at*

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

Professor,Senior Lecturer(MSc, MSPH, PhD, Fellowship)
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Educational records & qualification: Fellowship in Bio-Medical Ethics. Medical Ethics & Law Research Center. Shahid Beheshti Uni. of Med. Sci., Tehran. Iran (2008-2009). Ph.D in Molecular Biology. School of Biological Sciences. The Uni. Of Manchester. Manchester. UK (1999-2002). M.Sc in Molecular Biology. School of Biological Sciences. The Uni. Of Manchester. Manchester. UK (1998-1999). M.S.P.H. in Medical Mycology. Tarbiat Modarres Uni. Faculty of Medical Sciences. Tehran. Iran. (1986-1991).
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

Elham Taghipour[1], Fateme Frootan[1]*, Ali Hatef Salmanian[1], Jafar Amani[2] -*National Institute of Genetic Engineering & Biotechnology (NIGEB), Department of Plant Biotechnology, Tehran, Iran, [2]Applied Microbiology Research Center, Baqiyatallh University of Medical Sciences, Tehran, Iran. E-mail: f_frootan@nigeb.ac.ir*

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

EO1 Identification of Environmental Impacts Affected by Exploiting Gravel and Sand from Karun Riverbed by Checklist Method and Analytic Hierarchy Process

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In this study, the destructive effects of over-harvesting gravel and sand resources from the Karun River bed are investigated in order to prevent and minimize the negative effects and adverse effects. The study area is a part of the Karun river located in Khuzestan province, from Bandghir in Shushtar to the intersection of Karun river with Arvand river.Research Method: This research is a combination of statistical, documentary, descriptive-analytical, and library methods. Considering the available information and the extent of the study area, the purpose of this study was to use statistical analysis and matching as well as the use of checklist method and hierarchical process.Results: Prioritization of effects using a checklist and analytic hierarchy process (AHP) method shows that the most effects in the physicochemical environment (land shape, soil characteristics) is in the construction phase weighing 0.64, and in the economic and social environment (public and local trade), it is in the operation phase with a weight of 0.750. After that, most effects will be imposed on biological environments (protected areas) in the construction phase and physicochemical environment (on topography and land shape, soil resources) in the exploitation phase.Conclusion: The results of this study showed that harvesting from the riverbed is much more than permissible harvesting from the river and it is recommended that the amount of harvesting be reduced; the effects are weaker than modern methods. Therefore, it is suggested that due to the low environmental potential in developing countries, including Iran, modern methods replace traditional methods.

Keyword: Regional Environment, Khuzestan Province

EO2 Is NDVI the best index for vegetation studies?

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The vegetative percentage is one of the determinant parameters for energy equations at ground surface and have special importance in various issues such as hydrology, agriculture, and natural resources. There are several methods for decryption vegetation changes, with their own advantages and limitations. One method to study vegetation coverage changes is using plant indices. A review of previous studies shows that the NDVI index is the most widely used plant index in remote sensing which is widely used to study the presence, absence and percentage of vegetation in areas with different climatic, coverage, and topographic characteristics. This index may have completely different performance in different regions. This study tested 21 plant indices statistically (18 true indices, two soil line indices, and one atmospheric impact modifier) to compare other index's performance with the NDVI index. All indicators were obtained using IRS-1D satellite imagery data. This satellite produces spectral data in four bands (green, blue, red, and near-infrared). This study was conducted in the Gharkhoad protected area of North Khorasan province. Classified random sampling methods were used to harvest canopy percent. Then, the relationship between numerical values in plant indices and the harvested canopy percentage on the ground was tested and the correlation between them was calculated. The results showed that the TSAVI index from the category of soil line indices shows the best correlation with vegetation percentage (R = 0.54), and NDVI showed the seventh rank in terms of correlation (R = 0.42) among the 21 studied indices. Based on obtained results, the NDVI index cannot be considered as the best index for studying vegetation by default and the best one should be determined through statistical tests.

Keywords: Satellite imagery, Gharkhoad, coverage percentage, correlation analysis

EO3 Heliotrine extraction and detoxification by bacterial derived FAD-dependent oxidoreductase

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Alkaloids are plant secondary metabolites or toxins produced by plants. Pyrrolizidine alkaloids (PA), with toxic effects on human, are widely distributed in plants. Hepatoxic pyrrolizidine alkaloids are one of the most important causes of human disease in the prevalence of liver poisoning. To remove PA from feed, enzymatic biotransformation currently is concerned. Here, heliotrine a dominant PA in Gole Gav-Zaban herbal tea, from *Echium amoenum* was investigated. The petals were extracted with methanol at 60°C by soxhlet extractor. The impurities were removed applying diethyl-ether and ethyl-acetate, the resin debris pelleted by NaCl. The method ended by adding chloroform to collect heliotrine. The purification of heliotrine was done by silica gel column and a concentration gradient in chloroform-methanol. FAD-dependent oxidoordoxase derived from Pseudomonas aeruginosa 27853 ATCC Structurally similar to human-specific FMO3, effective on the metabolism of toxins in the liver was used to oxidize heliotrine as a pyrrolizidine alkaloid precursor. Enzyme activity of Fmo5p was assayed photometrically. reaction was set up in a total volume of 200 µl, 0.1-1 µm the final concentration of the recombinant enzyme (periplasmic proteins, 50 mM Tris-HCl buffer pH=8 and 100 µM NADPH at 25°C in Quartz covet. The reaction was followed by the decrease of NADPH absorption at 340 nm with an UV/Visible Spectrophotometer in 30 second steps until the change stops. Control experiments without enzymes were prepared. The difference in light absorption at 340 nm for the test sample was 0.404 and for the control reaction was 0.027 over 5 minutes, which was a confirmation of the oxidative activity of Fmo5p enzyme to be used to detoxify heliotrine. This enzyme is introduced as a drug design candidate. Detoxification effects of this oxidoreductase on other types of pyrrolizidine alkaloids is suggested in the continuation of present study.

Keywords: *Echium amoenum,* FAD-dependent oxidoreductase, Heliotrine, Pyrrolizidine

EO4 Environmental assessment of Amirkelayeh Wildlife refuge using SWOT management analysis model based on ecosystem integrated management plan

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Environmental assessment of ecosystems to understand the situation, develop appropriate environmental management strategies, monitor and evaluate is essential. The purpose of this study was a comprehensive evaluation of the capabilities and problems of Amirkelayeh wetland based on the results of an ecosystem integrated management plan for protection and optimal management using the SWOT model. In this study, the strengths and weaknesses as well as the opportunities and threats of wetland have been identified and ranked to formulate more accurate strategies in ecosystem integrated management plan. Internal factors included the components of strength and weakness, external factors included the components of opportunity and threat. To form the matrix, the components of internal and external factors were extracted from the ecosystem integrated management plan and weighed. The results showed rich habitat, high species diversity, bird watching ability, and water supply of agricultural lands with the most score were the main components of strength. Wetland pollution to fertilizers and pesticides, hunting and trapping, land occupation and land-use change, interference guide plan of two villages with wetland area and low income in the local community were the main components of weakness.The opportunities components consisted of international importance, receiving of the international fund, laws, and plans in ecosystem integrated management and environmental flow requirements. Non-implementation ecosystem integrated management plan and environmental flow requirements, eutrophication, growth of wetland plants and reduction of wetland water area, and dissociation (lack of interaction between stakeholders and local community) were the main threats components. Finally, the matrix total score showed 3.31 2.98 score respectively for internal and external components. These indicated strength-opportunities strategies can more suitable in implementation of Amirkelayeh integrated management plan.

Keywords: Amirkelayeh Wetland, SWOT**,** The ecosystem integrated management plan

EO5 The most contributung biovariables in geographical distribution of tulips based on ecological niche modelling (ENM)

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The genus *Tulipa* L. (Liliaceae) comprises ca. 100 species worldwide and 12 in Iran, and naturally restricted to central Asia, Africa, Europe, and Middle East. Tulips have beautiful and eye-cattching flowers and have special importance in terms of agriculture, economy, and ornamentation. Climate change can have considerable effects on biodiversity, phenological shifts, and geographical distribution of its species. The main aim of this work is to predict the most important climatic factors in distribution of *Tulipa* species under the present climatic scenario. Ninetheen bioclimate variables were obtained from WorldClim ver. 2.1, and altitudinal layers' dataset of collected tulips were extracted from our current project. Analysis were implemented in Maxent ver. 3.4.1 with 5000 iterations and Crossvalidate model. Models and area under the receiver operating characteristic (ROC) curve (AUC) was assessed to exhibit the capability of the model against actual observations. Graphical outputs were displayed using QGIS ver. 2.18.15. The test AUC showed acceptable results in all studied specimens, and colorful maps revealed the geographical distribution of each species very well. In addition, Jackknife tests introduced temperature as the most important contribution factor among all studied samples. Indeed, the current study highlight the significance of climate ranges, especially temperature, in plant geographical occurrence. Here we suggest a future and historical ecological niche modelling in order to track changes in the geographical distribution of *Tulipa* species through time.

Keywords: AUC, Climate, Jackknife, Maxent, *Tulipa*

EO6 Ecological assessment of Bushehr coasts (OuLi to Kangan) using Macrobenthos as biomarkers

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The destructive impact of unsustainable and uncontrolled exploitation of beaches has increased the harmful effects on coastal ecosystems and their destruction. In this study, in order to evaluate the health of coastal ecosystems in Ouli, Dayer and Kangan in the Persian Gulf coasts, IUCN ecological criteria was used to ranking, evaluating and determining the degree of ecological protection. Biodiversity, naturalness, dependence, representativeness, uniqueness, productivity, vulnerability and integration were the studied indicators. The information about industries and other environmental activities recorded in the studied area along sampling of macro benthic community and measuring environmental variables including temperature, salinity, pH, turbidity, and grain size, total organic matter in supratidal, midtidal, infratidal and sub tidal region. The gathered data from studied area was scoring based on IUCN criteria. Consequently, the Bushehr beaches (Ouli to Kangan) was classified in the second level of protection category of International Union for Conservation of Nature (IUCN). Therefore, the traditional activities, diving and tourism activities could be allowed in the region, but aquaculture, mining activities, discharge of untreated wastewater, mining in the bed and the creation of artificial rocks are among the prohibited items on these beaches.

Keywords: Ecological protection, IUCN, National park

EO7 Feasibility study of Kavir National Park habitat in order to re-introduce the *Equus hemionus onager*

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The *Equus hemionus* is distributed in the steppe habitats of desert areas. *Equus hemionus onager* is one of the five subspecies of *E.h. onager* that has the lowest population compared to other taxon. Their habits are fragmented and this species are listed as highly endangered in the IUCN Red List. Reintroduction and release of animals to their native and historical areas is an important issue in wildlife management. Kavir National Park has a high habitat similarity to Turan Protected Complex. In the present article, based on the presence data of the of the *E.h. onager* in the Turan protected area and environmental variables (physiography, land cover and climate), modeling, feasibility and habitat suitability of *E.h. onager* in Kavir National Park were performed. Population presence data were obtained during the annual census of Turan area between 2011- 2018 (195 points). The distribution pattern of *E.h. onager* showed that the most suitable habitats for this species are located in the east of Kavir National Park. The habitat areas of high and medium suitability of *E.h. onager* in Kavir National Park were estimated at 29440 and 56797 hectares, respectively (6.58% and 12.68%). The results of sensitization and determining the importance of each of the variables in the model showed that precipitation in the wettest season of the year is the most influential parameter in the development of the feasibility model of *E.h. onager* distribution probability in the study area. Distance to poor rangeland cover (≤ 25%), distance to barren areas, distance to saline lands, total annual rainfall, altitude, Variety of roughness and average annual temperature were other important variables in the development of *E.h. onager* distribution model, respectively. According to the modeling results, the eastern part of the Kavir National Park near the watering place of Talhe spring is one of the favorable habitats of *E.h. onager* and has a suitable habitat connection with Dom Dozdan spring and Shoorab Tak area.

Keywords: Species management, Large herbivores, Persian zebra, Turan protected area, Kavir National Park

EO8 The first report of microplastic observation in waterfowl of southern Caspian sea

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The term microplastic was first used in 2004 to describe very small plastic particles (50 micrometers) in a column of water and sediment. In 2009, researchers suggested that microplastics should include all parts less than 5 mm. However, there is currently no universal definition of the size range for microplastics. Microplastics are present in the aquatic ecosystem as a pollutant and pose a threat to the marine environment. In addition to occupying marine environments, these microplastics are also easily eaten by marine organisms. In many types of research, ingestion of microplastic particles by seabirds, especially from the Procellariiformes, has been reported. Ingested parts due to being indigestible can have destructive effects on birds, including: obstruction of the animal's stomach due to its occupation with microplastic particles, deformation, the volume of the gizzard or stomach of the bird, as well as direct death for the animal. For the purposes of this study, in the present study, a total of 95 bird carcasses of Anatidae, Scolopacidae, Rallidae, Podicipedidae, Laridae and Phoenicopteridae were collected. The stomach contents of all birds were described using a scalpel. After this step, their contents were washed with a 1 mm sieve and then placed in a petri dish. The remaining material was taken under a stereomicroscope and examined for plastic parts. Microplastic was found in 86% of birds. At the species level, 94% of birds ingested at least one type of microplastic. Fragments, fibers and films were the most common type of microplastic observed among birds.

Keywords: Fragment, Fiber, Film, Stomach contents, Aquatic ecosystem

POSTER PRESENTATIONS

EP1 Investigating the possibility of formation of cyanobacterial biocrust in desert soil model

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Nowadays, the problem of desertification is the most important global issue after global warming and water scarcity. Several methods including biological and non-biological for desertification have attracted the attention of many environmental researchers. Among the important biological methods in desertification is to strengthen biocrusts. Biocrusts include various organisms such as mosses, algae, lichens, fungi, archaea, and different photosynthetic and heterotrophic bacteria. The key organisms that make up the biocrusts are cyanobacteria .Studies have shown that cyanobacteria are very effective in increasing organic matter, soil enrichment, strengthening of the soil structure and fixing the dust. So, we decided to do some scientific research on cyanobacteria and their roles in desert soils. For this purpose, 19 cyanobacteria which was isolated from different soil of the country selected, subcultured on medium BG-11, and incubated at 25°C for 3 weeks. Then, the released carbohydrate production was determined by the phenolic sulfuric acid method. The amount of carbohydrate was 86.66 µg/ml for *Anabaena sphaerica*, 64.19 µg/ml, for *Nostoc pruniforme* and 55.91 µg/ml for *Geitlerinema*.sp. The selected strains that produce the highest amount of the released carbohydrate were inoculated to the pots, which was filled by the desert soil. The results of the scanning electron microscope (SEM) showed that three of these strains can form biocrusts on the laboratory model soil. More studies are necessary to solve the problem of desertification and cyanobacteria can be used with more extensive applied research.

Keywords: Cyanobacteria, Biocrust, Desertification, Scanning electron microscope, Carbohydrate

EP3 Habitat preference modeling of Iranobuthus krali (Scorpiones: Buthidae) in Iran

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Today, ecological niche models (ENMs) are one of the main components of ecological, conservation, and biogeography studies. The ENMs using presence records and environmental variables estimate the presence probability of different species in the desired geographical area. In this study, using MaxEnt software, 19 bioclimatic variables, and 13 occurrence points recorded in previous studies from the provinces of Isfahan (Kashan), Qom, Markazi, Hormozgan, Fars, Tehran, and Alborz, the *habitat preference* of Kral Iranian scorpion (*Iranobuthus krali*) was modeled in Iran. The AUC value for training dataset was equal to 0.991 which indicates high discriminative performance of the model. Three bioclimatic variables including precipitation of coldest quarter (Bio19), precipitation of driest quarter (Bio17), and minimum temperature of coldest month (Bio6) collectively had the highest percentage of contribution (47.5%) in building the model. Based on the Jackknife test, the Bio17 contained the most information than other variables and annual precipitation (Bio12) contained the most useful information in building the model. Based on the response curves, *I. krali* preferred some parts of Iran with precipitation of coldest quarter more than 80mm, precipitation of driest quarter between 1-10 mm, and annual precipitation more than 100 mm. Also, the potential distribution range of the species included some parts of Khorasan Razavi, South Khorasan, Semnan, Kerman, and Yazd provinces. The results of this study which predicts some ecological features of the Kral scorpion can be used in conservation programs as one of the valuable biological resources of Iran.

Keywords: Kral Iranian Scorpion, *Habitat preference*, Maxent, Climate variables, Iran

EP4 Evaluation of nanoparticles movement in soil and their environmental impact

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The entry of pollutants to surface and groundwater has been of recent public of environmental. The application of efficient solid materials and nanoparticles (NPs) as adsorbent has been investigated in recent years. Nanoparticles are remarkable due to their transport capacity in soil, effective surface area, high adsorption capacity, low solubility. NPs transported in the environment may have posed potential risks to organisms. Therefore, it is essential to understand the release of the NPs from soil column. In this study, the tested adsorbents were NPs (TiO_2, Al_2O_3 and Fe_3O_4) and modified NPs with chitosan applied at rate 3% for soil amendment in leaching experiments. The soil columns were leached with 250 mg P/L solution. The concentration of Al, Fe and Ti in the leached was measured. The amount of Ti and Fe leached in the control soil (1.89 and 0.11 mg kg^{-1}), with Ti and Fe leached from amended soil with TiO_2 and Fe_3O_4 (1.64 and 0.15 mg kg^{-1}) and amended soil with modified TiO_2 and Fe_3O_4 with chitosan (1.47 and 0.09 mg kg^{-1}) was not significant, while Al leaching in control soil (0.51 mg kg^{-1}) with amended soil with Al_2O_3 (1.06 mg kg^{-1}) significantly different. This study demonstrated Ti and Fe were stable in soil column. Studies have shown that the environmental toxicity of Al causes different diseases, include of Alzheimer and Lung-Kidney disease in human body. Therefore, more studies on evaluation of the ecological toxicity of NPs for living organisms and the bioavailability and bioaccumulation of these substances through food chains are recommended.

Keywords: Pollutant, Adsorbent, Soil columns, Leaching, Environment

EP5 Hormonal responses of wild and cultivated barley genotypes to cadmium stress

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Contamination of agricultural soils with heavy metals, including cadmium, has been increasing in recent years and has caused serious problems for the production and safety of agricultural products in these contaminated areas. The objective of present study was to evaluate and contrast the effects of cadmium (Cd) toxicity on growth and hormonal response of wild and cultivated (Zehak) barley genotypes. Plants were subjected to different levels of Cd concentrations including 0 (control) and 1.5 mg g^{-1} in soil. Cd treatment led to accumulation of Cd in shoot and reduction of dry weight in both genotypes. Content of stress related hormones including abscisic acid, jasmonic acid and ethylene significantly increased as compared with control group. Under Cd stress, ethylene content of cultivated genotype was significantly higher than wild genotype. The content of kinetin hormone significantly decreased in response to Cd stress in both genotypes. Significant decrease in auxin content under Cd toxicity was only observed in cultivated barley genotype. In both genotypes, gibberellic acid content did not affect by Cd stress. Based on these results, during cadmium stress, changes in stress-related hormones can induce appropriate stress responses in barley genotypes. On the other hand, the decrease in growth hormones such as kinetin can contribute in growth retardation observed under cadmium stress.

Keywords: Abscisic acid, Auxin, Cytokinin, Ethylene, Heavy metals, Jasmonic acid

EP6 Threat problemology by Tree analysis Technique in The ecosystem integrated management plan(Case Study: Amirkelayeh refuge)

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The necessity of wetland management and conservation based on a comprehensive and integrated approach by attracting cooperation and participation of individuals, organizations, and groups in the community (stakeholders) is inevitable. The ecological approach is a strategy for the integrated management of water, land, and livelihood resources that promotes sustainable conservation and sustainable use in a balanced way .In this article, the problems of the wetland were investigated using the tree analysis Technique (facilitation technique) resulting from holding participatory workshops in the Amirkelayeh ecosystem

integrated management plan. The results of drawing problem trees in working groups showed biodiversity problems consist of insufficient manpower and protective equipment, illegal hunting and fishing, the entry of invasive and non-native species, wildlife diseases, increasing of sediments caused by the decomposition of plants. These problems have created impacts including eutrophication, reduction of species diversity, and population of species, especially the population of native and migratory birds. In the socio-economic field, problems such as lack of awareness of managers and local communities about the functions of the wetland, lack of inter-organizational interaction, occupation land, and change of land use, intentional and unintentional fire, interference of the guide plan of Hassan-Bakandeh, and Amirabad village With the area of the wetland, and livelihood and economic problems causes habitat destruction. The Water- soil problems section consists of the entry of agricultural wastewater (fertilizers and pesticides), water withdrawal by unauthorized pumping, non-dredging of drains entering the wetland have caused consequences such as soil and water pollution, reduced surface area, and depth of water area. The sum of the results showed cannot be prevented from irreparable and progressive destruction also loss of its values and function if the Amirkelayeh ecosystem integrated management plan was not implemented.

Keywords: Amirkelayeh Wetland, Tree analysis Technique, The ecosystem integrated management plan

EP8 Evaluating the predictive performance of habitat models for Yarrow (*Achillea millefolium)*

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Predicting geographical species distributions has become essential in several aspects of the biogeographical, environmental, and biological sciences. One of its most important applications is related to conservation and control of species, especially endangered species. A variety of statistical techniques has been used in species distribution modeling that attempt to predict occurrence of a given species in respect to environmental conditions. The objective of this study is to compare the performance of some of the most common methods of presence-absence models to mapping geographic distribution of a non-woody species, Yarrow *(Achillea millefolium),* in central Germany. This study compared the performance of three machine-learning algorithms, i.e., Random Forest (RF), Artificial neural network (ANN), and Gradient Boosting Machine (GBM). Accordingly, eight topography-climate predictors, i.e., slope, aspect, elevation, topographic wetness index, mean summer temperature, sum summer precipitation, summer solar radiation, and soil moisture index were selected and prepared by GIS techniques for model calibration. Also, 102 occurrences of Yarrow were selected as species-presence data. The predictive maps were developed for the target species after calibration of the models. Finally, model accuracy was evaluated using the area under Receiver Operating Characteristics curve (AUC) and true skill statistics (TSS). The results show that the mean summer temperature followed by the sum summer precipitation and the slope are most important predictors for modeling the distribution of Yarrow, and soil moisture index was the least important predictor for this plant species. Also, the results show that the mean AUC values of the three models is 0.74 (ANN), 0.84 (RF), 0.89 (GBM), and 0.61 (ANN), 0.69 (RF), 0.72 (GBM) for TSS index. Both indices illustrate that the GBM model has better performance than the other two models, and the produced distribution map by that way has higher accuracy.

Keywords: Random Forest, Artificial neural network, Gradient Boosting Machine

EP10 Effect of Ammonium Nitrate on the Development and Survival of Marsh frog (*Pelophylax* sp.), (Amphibian: Anura)

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Amphibians are sensitive to nitrogen-based fertilizers such as ammonium nitrate, which are used in agriculture and enter aquatic ecosystems through runoff. However, data on the responses of Marsh frog (*Pelophylax* sp.) in north and northeast of Iran to this chemical pollution are lacking. In this study, to evaluate the toxicity of ammonium nitrate on the embryonic period (Gosner≤25) and early larval period (Gosner 26-31), we investigated the survival rate, hatching time and hatching rate. For this purpose, 780 eggs of Marsh frog with a density of 20 and a water volume of 1500 ml per container, in three replications

at concentrations of 0 (control), 10, 20, 30, 50, 70, 90, 120, 150, 180, 220, 220, 260, 300 mg/l, with an average temperature of 14.50 °C, conducted for 56 days. The larvae hatched in the control treatment and concentrations of 10, 20 and 30 on day of 6±0.00, in concentrations of 50, 70, 90 and 120 on days of 7±0.00, 9.66±4.61, 12.66±4.04 and 13.66±1.15, respectively. The hatching rate in concentrations above 120 was 0%, but in the control treatment and concentrations of 10, 20 and 30 were 100%, in concentrations of 50 was 95%±8.66, in concentrations of 70 was 96.66%±5.77, in concentrations 90 was 88.33%±10.40 and in concentrations of 120 was 43.33%±28.86. The survival rate 48h after hatching period (hatching period 16 days) in the control treatment and concentrations of 10 to 30, 50 and 70 to 120 recorded 100%, 16.66%±3.33 and 0%, respectively. Survival rates at 56 days in the control treatment and concentrations of 10, 20, 30 recorded 100%, 95%±8.66, 95%±8.66 and 93.33%±7.63, respectively. The results of this experiment showed that concentrations above 30 mg/l of ammonium nitrate greatly affected the survival of Marsh frog larvae and may play an important role in the global amphibians decline.

Keywords: Global amphibians decline, Nitrogen pollution, Embryonic period, Larval period

EP11 Sensitivity to Urea Fertilization in the Marsh frog (*Pelophylax* sp.): Survey of Development and Survival

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A large proportion of the amphibian life cycle occurs in ponds, streams, and temporary pools that are often associated with agricultural areas receiving fertilizers. Therefore, some anuran species inhabiting such environments may be exposed to the toxic effects of fertilizers. Urea is one of the most widely used fertilizers in agricultural lands, but little data is known about its impact on the development and survival of amphibians. For this purpose, to evaluate the impact of urea fertilization on the eggs of Marsh frog (*Pelophylax* sp.) which distributed in north and northeast of Iran, we investigated survival rate, hatching time and hatching rate during embryonic period (Gosner≥25). In this study, 720 eggs of Marsh frog with a density of 20 and a water volume of 1500 ml per container, in three replications at concentrations of 0 (control), 50, 100, 150, 200, 300, 500, 700, 1000, 1500, 2000 and 3000 mg/l, with an average temperature of 24°C, conducted for 24 days. The larvae hatched in the control and concentrations of 50 to 500 on day of 6. The hatching rate in concentrations above 500 was 0%, but in the control and concentrations of 50 to 300 were 100%, in concentration of 500 was 11.66%±20.20. The survival rate 72h after hatching period (hatching period 10 days) in the control and concentrations of 50 to 150, 200, 300 and 500 recorded 100%, 96.66%±2.88, 70.33%±22.91 and 1.66%±2.88, respectively. Survival rates on the 24 days in the control and concentrations of 50, 100, 150, 200, 300 and 500 recorded 100%, 100%, 95%±5.00, 90%±5.00, 91.66±5.77, 61.66±14.43 and 0%, respectively. According to the results, concentrations above 300 mg/l of urea fertilization greatly affected the survival of Marsh frog eggs. Therefore, these effects are important to consider in light of possible threats to the conservation status of many amphibian species.

Keywords: Global amphibians decline, Anuran, Embryonic period

EP12 Water quality assessment in the Sufi-Chay river (NW-Iran) using diatoms as bio-indicators

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This study can be considered as the first case study on the rivers of Azerbaijan, Iran, which tries to analyze the Sufi-Chay river using diatoms, water chemistry and biological factors. The Sufi-Chay river is located in the region of Azerbaijan (northwestern Iran). In order to study of diatoms, a number of rocks from different areas of the riverbed were collected and then rubbed in some river water. After that, the solution transferred to the bottles and then tansferred to laboratory. In the next step, the solutions were digested with hydrogen peroxide and put it on the heater for one and a half hours and boil it (Hot H2O2 method). Then pick up the solutions from the heater and place at room temperature to cool. Then add some HCl to the solution and put it again on the heater and boil for fifteen minutes. After this time, add the residual solution

of distilled water to wash the acids in the solution, this wash continues for three days and every 24 hours. After washing, put a few drops of the solution on the cover slip to dry completely. In the next step, after drying, we fix the cover slip on the slide using Naphrax glue. Then, we start studying the slides under microscope. The study showed that *Nitzschia palea, Nizschia amphibia, Diatoma vulgaris* were dominant during spring, summer and winter whilst *Navicula tripunctata, Gomphonema parvulum* were dominant in autumn. Ecological evaluation of the river by using diatom community showed that the upstream of the river had high quality of water whilst downstream had low quality.
Keywords: Rivers, Sufi-Chay, Diatoms, Water quality.

EP15 Investigation of Basal Area, Volume and Carbon Sequestration Allometric Models according to independent variable of Age *in Populus deltoides* Plantation

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Populus deltuides is one of the most important economically (wood production), environmentally (biomass production and carbon sequestration) and fast growing species in plantations. Therefore, the purpose of this study was to investigate basal arae, volume and carbon sequestration allometric models according to the age using stem analysis method in 9 parcel of poplar plantations in Shaft County, Guilan province. Measurement features included diameter at breast height and total height of all trees in two 1-hectare plots area. Then, 30 trees were randomly selected in different diameter classes, fell down and the discs were obtained in order to stem analysis. The annual rings of discs counted, age at different tree heights obtained, and the annual rings diameter were measured to determine annual diameter and volume growth. Carbon measurement, volume measurement of wood, volume conversion to weight ratio were calculated. Finally, regression analysis performed by the relationship between volume and basal area by age based on the highest coefficient of determination and minimum standard error. The results showed that the highest stands volume occurred in 29 years, the highest annual volume increment at 9 years and the highest carbon storage at 29 years in the stand with 145 trees per hectare, respectively. The model of basal area was $BA = ab^t X^c$ with adjusted coefficient of determination of 0.99 (R2=0.99) and SD= 0.17, the model of volume was $V = \frac{a+bt}{1+ct+dt^2}$, (R2=0.99) and SD= 4.06 and carbon sequestration model was $C = ab^t t^c$ with adjusted coefficient of determination of 0.99 and SD= 0.54. The nonlinear models were able to show the highest coefficient of determination (R2≥0.99) and the least standard error of the relationship between these characteristics.
Keywords: Allometric models, Carbon storage, Plantation, *Populus deltoides* , Stem analysis

EP16 The seasonal distribution of Ilyoplax frater in mudflat ecosystems of Hara Biosphere Reserve, Persian Gulf

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The aim of this study was to identify the density of crab *Ilyoplax frater* in mudflats adjacent to mangrove forests in Hara Biosphere Reserves, Persian Gulf. *I. frater* is a key species conserving a large amount of the organic matter in ecosystem through its nutritional activities, which help shaping structure and functioning of the mangrove ecosystem. Due to its small size and palatability, *I. frater* is an important food source for many fish species living in mangrove ecosystems. Temperature fluctuation in intertidal zone in summer and winter could impact the distribution and density of invertebrates. Accordingly, sampling was conducted seasonally during February 2018 and June 2019 in six sampling sites in Bandar Khamir and Qeshm. The results showed that, the mean crab density was 77±122.77 (±SE) ind. m^{-2} and 16± 32.71 ind. m^{-2} in summer and winter, respectively. In addition, the mean density was significantly higher in Qeshm 74.66 ± 126.78 ind. m^{-2} than Khamir 18.66 ± 20.27 ind. m^{-2}. Also, a significant difference in density was observed between Khamir and Qeshm regions and also between summer and winter seasons.
Key words: Density, Mangrove, Invertebrates, Persian Gulf

EP17 Study of some quantitative and qualitative characteristics of fruit and seed cones to identify two species of *Juniper* (*Juniperus excelsa* and *J. polycarpos*) in Goinik Jargalan habitat of North Khorasan province

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Vegetation is high value in different ecosystems, specially trees, that they destruction is faster than reproduction and rehabilitation in nature. Then, it is necessary to pay attention to resistant species to harsh climates with the ability to adapt to natural and unnatural destructive factors, such as *Juniperus excelsa* M. Beib and *J. polycarspos* K. Koch. *Juniper* habitat in Goinik Jargalan protected area in North Khorasan province, currently has sparse and endangered *juniper* forests. These two species are difficult to identify and distinguish from each other difference only in the index of being monopod or bipedal. This study evaluates the quantitative and qualitative characteristics of fruit and seed cones with the aim of helping to identify two species of *Juniper* in the Goinik Jargalan region. In this area, systematic random sampling of natural habitat was performed. a total of 26 plots, drawn in 3 transects, 20 native base of each species were selected and their geographical information was located and recorded by GPS. A maximum of 200 cones were collected from each base, and the traits of cone and its seeds were measured and recorded. Quantitative characteristics of female cones, such as the number of cones per unit area of crown, length, width and mass of fruit, are significantly higher in *J. polycarpos* than *J. excelsa*. Analysis of seed data including length, width, mass, Volume and density shows that the two species are differ in the mentioned traits, at the level of the 1% to 5%. The mentioned morphological properties can distinguish two species of *Juniperus*; Therefore, it is advised to have scientific assessment of the status of these species, especially *J. excelsa*, and finally carry out a special resuscitation program for *J. excelsa* before the complete removal of such species from the natural habitats of *Juniperus*.

Keywords: Goynik (Goinek), Archa, Seed, *Juniper*, Protected area

EP18 Pollen study of two *Juniperus* L. species in Goinik Jargalan habitat of North Khorasan province

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Vegetation has undeniable environmental and economic benefits. sustainable management of natural plant ecosystems requires knowledge of species and their habitats, therefore, one of the important priorities of researchers and executives active in the fields of environment and natural resources, is paying attention to plant species capable of adapting to harsh climatic conditions; *Juniperus* L. species are important in habitats. Goinik Jargalan region in North Khorasan is one of the important habitats of two *Juniper* species, including *J. excelsa* and *J. polycarpos*. This study investigates the pollen characteristics of these two species. this study was conducted, from February 2018 to April 2019, the cones of the studied species were collected from the habitat area and the pollens were separated from the cones and studied. Pollen was examined by light microscope (LM) and electron microscope (SEM). Analysis of 10 pollen grains data from each of the studied species were observed that most of the pollen grains contain granular elements. In the LM, the general design of the pollens is circular but in the SEM they are irregular. According to the ratio (P/E); the pollens of both species are Prolatespheroidal in both study habitats. In all samples, the pollens are in the group of small pollens (10-25 microns) in terms of size. In the study of pollens, Exin layer thickness was measured in LM images in *J. excelsa*, 0.99 microns and in *J. polycarpos*, 1.41 microns. according to the data, it was found that *J. polycarpos* has a better establishment than another species, which may be due to the thickness of the exin and the resistance of the pollen to natural factors; however, there is a risk of extinction for *J. excelsa* in this area and it needs special attention.

Keywords: Conifera, Archa, Pollination, Exin, Pollen grain

EP19 Survey the toxic effect of Abamektin in *Artemia franciscana* by using Response Surface Methodology

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Abamektin is a pesticide which is worldwide application against insect pests in agriculture and livestock activities. But, extensive use of Abamektin and enhanced release into environment can be harmful for aquatic organisms due to their toxic and bioaccumulation properties. This study was carried out as the lethal endpoint bioassay of Abamektin on adult stage of *Artemia franciscana* (due to their important roles in aquatic ecosystems food chain) in various environmental conditions (variation of pH and salinity) and their interaction by using the response surface methodology. The analysis of central composite design applied for study of three factors including Abamektin concentration (0.05-0.5 µg/l), salinity (10-255 g/l) and pH (4-11) at five levels. The experiment process was conducted in 20 runs in laboratory in 24h. Results showed that the test salinity itself has significant influence on the lethal effect of Abamektin. Dependent on the values obtained by RSM, the model was significant ($p<0.05$) with the coefficient of $R^2 = 0.78$, Adj $R^2 = 0.597$, Pred $R^2 = 0.37$ and press = 1834.06. Thus the Abamektin has toxic stress on the *A. franciscana* in high concentration (>130 g/l) and low concentration (<30 g/l) of salinities at the concentration rather than 0.145 µg/l of Abamektin. Overall, the *Artemia* has the capacity to tolerate a wide range of salinities, because of balance between the flows of ions from ambient water with their hemolymph through osmoregulation mechanisms which allow them to survival. It is assumed that the lethal effect of Abamektin in low (<30 g/l) and high (130< g/l) concentration of salinities, can be due to alteration in osmoregulate mechanisms in *A. franciscana* rather than optimum condition.

Keywords: Pesticide, Bioaccumulation, Central Composite Design, Osmoregulation

EP20 Survey some poly aromatic hydrocarbons (PAHs) accumulation in tissues of wild pigeon from Tehran megacity

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Megacities like Tehran are polluted with some air pollutants including poly aromatic hydrocarbons (PAHS) released from fossil foil burning, which can influence on human and organism's health. The wild pigeon *Columba livia* is widely distributed in megacities and can be used as sentinel species, because of high metabolic rate, inhaling environmental pollutants as well as swallowing pollutants particles and their bioaccumulation. The PAH_S with 5 and 6 rings like Benzo a pyrene and Benzo a anthracene are well recognized as toxic pollutants for genotoxicity, carcinogenicity and motagenicity. This study is aims to survey the level of some PAHs with 5 and 6 rings (BghiP, dAHa, IcdP, B(k)F, B(b)F) in rock pigeon (*Columba livia*) from Tehran megacity. The muscle, liver, kidney and skin were collected for PAHs analysis. Sample preparation and PAHs analysis were conducted with standard procedures. The concentrations of pollutants were carried out using Gas-chromatography mass-spectrometry (GC-MS). Data were subjected to one-way analysis of variance (ANOVA) and Tukey post-hoc and were employed to survey whether concentration varied significantly between tissues. The mean concentrations of PAH_S were obtained 13.19, 3.79, 4.30 and 3.07 $ng.g^{-1}$ dw in muscle, liver, kidney and skin respectively. According to the finding, significant different were found between tissues and muscle had more concentration ($p<0.05$). Also, the same accumulation pattern (kidney≤liver<skin<muscle) were determined for all studied samples ($p<0.05$). In conclusion, based on the overall results and comparing with available studies, the *C. livia* could serve as a suitable indicator for survey of PAHs in Tehran megacity.

Keywords: Benzene ring, Bioaccumulation, Pollutant, Indicator, Sentinel species

EP21 Evaluation of Surface morphology and erosion in marine microplastics

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Microplastics (MP: 1mμ-5mm) have received particular attention due to their number and wide range of their distribution in all water, soil, and air sources. These particles have physical and chemical damage risks because of the carcinogenic plasticizer chemicals and pollutants absorbed into the plastic surface so breathing and eating them can cause disturbances even at cell and tissue level. As a piece of a macro-plastic or a primary one, marine MPs are exposed to mechanical, biological, and chemical surface erosions as soon as entering the marine environment. Over time, the erosion changes their surface properties and effectively degrade them into smaller MPs and even nanoplastics. Researches on MPs' surface morphology are dependent on the expert's skills and the high resolution and accurate images captured by the electron microscope. In the central laboratory of Shahid Beheshti University, after visual separation by an Olympus SZ40 stereomicroscope, and plastic polymer approval by EDAX method (Energy Dispersive X-ray Spectroscopy), the Hitachi SU3500 electron microscope (Hitachi, Japan) was used to capture high-resolution images of surface detail, possible erosion, and sedimentation on the MP's surface. SEM images showed some diverse morphologies including deposited or adhered biological or non-biological particles; indentation and protruding; shallow surface cracks and deep grooves; pits; breakages; and scaly appearances. The results showed that the intensity and type of surface erosion varied depend on the type and shape of the MPs i.e. irregular fragments, beads, and fibers. The highest deformation was observed in the surface of fragments. However, the minor erosion in fibers and beads indicate their slow degradation process and durability in the environment. It may lead to their higher stability and transfer rate in the food chain, make them available to a wide range of marine biota, and put human health in danger due to the consumption of seafood products.

Keywords: Pollution, Plastics, SEM, Surface erosion

EP22 Distribution patterns for Liliaceae in order to determine the priorities of conservation management in Iran

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Due to the existence of numerous plant species and their vast habitats, time and budget limitation, facility deficit, as well as a low number of experts, it is impossible to evaluate and conserve all habitats. Iran, located in the southwest of Asia, is one of the principal cores for diverse and endemic species that belong to Liliaceae family, which are endangered due to some threatening factors. So far, no study has been conducted on their distribution patterns and the protection necessities for this family in Iran. Therefore, this study tries to act on the conservation and management of the Liliaceae family members in this country. The distribution dataset for Liliaceae includes 1327 points, which were collected from field-work, Shahid Beheshti University's herbarium, Wien's virtual herbarium, University of Wien, Geneva, and Kyoto's herbarium images, Iranica and Iranian floristic dataset, and published articles for different regions of Iran. The information in regards to the exact species names was obtained from IPNI and plant-list sites. The latitude, longitude, and altitude of the species occurrences were entered in ArcGIS, and the distribution maps of the genus and its species were prepared. The results of this study showed that Liliaceae family in Iran includes 73 species, 27% of which are endemic. The principle distribution cores of the species are mostly in Alborz and Zagros regions. The critical, vulnerable, endangered, and threatened categories comprise 30%, 10%, 71.5%, and 1.42% of the whole species investigated in this study. The use of domestication methods based on people's participation (especially people living in areas with a high

diversity of these species) while reducing the pressure of exploitation and damage by creating sustainable livelihoods and economic prosperity leads to a better protection of those species. In addition, the number of endangered species in this family, a wide range of which is located outside protected areas, emphasize the importance of planning for regular and accurate ecological and genetic monitoring in areas with high diversity and endemism rate, in order to provide sustainable management for these species.
Keywords: species richness**,** conservation, distribution map, IUCN red list of species

EP25 Modeling of climate change effects on distribution of *Aegilops* L. (*Poaceae*) toward biodiversity conservation in Iran

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The demand for food resources is increasing quickly because of growth in human populations; therefore, food security may become one of the largest human challenges for this century. Due to the low genetic diversity of the most crop plants, they have the low tolerance against the climatic changes challenge. Crop wild relatives (CWRs) are the most valuable plant genetic resources (PGR) for the conservation of genetic diversity in crops. However, climate change is an added pressure on biodiversity, particularly on this valuable group of plants. Some of the wild relative of crop plants including *Aegilops* species are growing in Iran and the country has the special importance in view of their conservation. The important CWR *Aegilops* genus has been investigated for climate change effects. MaxEnt modeling method was applied to predict the spatial distribution of four *Aegilops* species under different climatic scenarios (RCP 2.6 and RCP 8.5) of 2050 and 2080. According to the findings mean annual temperature and annual precipitation were identified as most important factors on the species distribution. According to our finding all species showed reduction and expansion responses under all future climatic scenarios. However, the range change was negative for some species (i.e. *A. cylindrica* Host, *A. speltoides* Tausch , *A. tauschii* Coss.) and positive for *A. crassa* Boiss. ex Hohen. The results of this study emphasize, except *A.crassa* the in-situ and ex-situ conservation of studied species as gene bank, regular population monitoring and ecological assessment.
Keywords: Conservation, Crop wild relative, MaxEnt modeling, South west Asia

EP26 Climate change modeling of wheat wild relative (GP1) in Iran: Conservation aspect

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Climate changes have severe negative effects on biodiversity, extinction as well as population decline. In addition, climate change affects a global threat to food security by creating tensions and reducing agricultural yields. A wide range of wild relatives of crops have been endangered due to negative effects of climate changes, and their protection is essential. Many of first-degree wild relatives (GP1) of bread wheat (*Triticum aestivum* L.) distributed in Iran. Therefore, predicting their future distribution based on climate modeling is very important for conservation planning. Based on field floristic and herbarium data, the distribution points of these species were prepared and geo-referenced. MaxEnt modeling was used to investigate the distribution status of the mentioned species in Iran in 2050 and 2080 under two scenarios of optimism (RCP2.6) and pessimism (RCP8.5) (Phillips et al., 2006). The results of this study showing that the most important factors affecting distribution patterns of mentioned species are the average temperature of the coldest month of the year, precipitation in the driest month, precipitation in the driest season, average temperature of the wettest season, annual precipitation, altitude, soil organic carbon and the cation exchange capacity of the soil. Among the mentioned species, *T. spelta* Koern. has the highest distribution increase (96%) under the optimistic scenario of 2080 and the highest decrease (-98%) is related to *T. dicoccoides* L. in both optimistic and pessimistic scenarios by 2050 and 2080. The two following species *T. momococcum*

L. and *T. urartu* Thumanjan ex Gandilyan will have a decrease of -18% and -13%, respectively, under a pessimistic scenario. Accordingly *T.spelta* has not any particular problem in the future. However, *T. dicoccoides* should be protected through ex-situ conservation. In addition, the other species should be protected in protected areas by in-situ conservation method.
Keywords: Food security, South west Asia, In-situ conservation, Ex-situ conservation, *Poaceae*

EP27 Ecological assessment of tidal zone in Chabahar Gulf coastal zone using IUCN ecological criteria

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Coastal areas have an important role in the health and conservation of marine ecosystems. These ecosystems contain a variety of habitats and They are spowning, nuersering or feeding ground, for aquatics. Chabahar Bay coast due to its special geopolitical position, special biological features **and** its proximity to the open ocean waters is of interest to national and international bodies and institutions. In this region, infrastructure, development, and productivity programs are growing rapidly Therefore, the coefficient of vulnerability is very high on these beaches and the likelihood of irreparable biological damage has increased. In this study, the viability of Chabahar Bay coasts was evaluated using IUCN indicators. After determining its degree of protection, effective management solutions, maintain sustainable In order to development in the area of the mentioned beaches.

Keywords: Chabahar Gulf, IUCN, Assessment, protection, effective management

EP28 Reliability of benthic indices in health assessment of coral reefs subjected to oil pollution

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Coral reefs provide humans with numerous ecosystem services and therefore the need for sustainable use of their resources is evident. Oil pollution introduces numerous hazardous pollutants into the marine environment, which could easily influence the viability, assemblage structure, and species composition of benthic organisms. Consequently, any alteration in benthic communities can provide a warning of stress and ecosystem decline. Using powerful statistical tools, the main objective of the present study was to evaluate the reliability of benthic indices to detect possible impacts of oil pollution on coral reefs across an oil pollution gradient in Kharg Island. In this regard, multiple indices including the bioaccumulation of polycyclic aromatic hydrocarbons (PAHs) in coral tissues, live coral cover, alpha and beta diversity of macroinvertebrates, as well as a new index called "Sediment Constituent Index" (SEDCON) were investigated. Live coral cover was estimated by video transects. Five cm of surface sediment was collected and immediately fixed with ethanol and Rose Bengal solution for macrobenthic communities and SEDCON measurements. The reliability of each index was assessed using estimations of the effect size (using omega-squared), and decision trees (Classification and Regression Tree (CART)). The findings suggest that PAHs concentration more than 136 $ng.g^{-1}$ in massive corals, live coral cover less than 29%, and the SEDCON values below 4.25 may reflect the adverse effect of oil contamination and provide warning of degradation in a coral reef area. This encourages decision-makers to execute routine monitoring and mitigation practices to maintain healthy reefs in the study areas.

Keywords: Persian Gulf, Polycyclic aromatic hydrocarbons, Bioaccumulation, Hard coral, Benthic communities

EP30 Characterization of Lepidopteran- specific *Cry* genes in Iranian strains of *Bacillus thuringiensis*

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Bacillus thuringiensis (*Bt*) is a gram-positive and soil-dwelling bacterium commonly used as a biological toxin. After sporulation, the bacterium forms crystal proteins that are encoded by *Cry* genes located on the

plasmid. This study aimed to identify active *Cry* genes against Lepidopteran in *Bt* bacteria isolated from soil in Eastern and Central Iran. These strains, along with two bacteria including *Bt thuringiensis* and *Bt kurstaki* as positive controls, were examined by Polymerase Chain Reaction (PCR) technique with specific primers including SPCry1Aa, Cry2Aa1, Cry, Lep2, Cry1D, Cry1C, Cry2Ab2 and Spe-Cry8B. However, no gene was detected by the SPCry1Aa, Cry2Aa1, Cry and Spe-Cry8B primers. The results showed that the plasmid extracted from 90.9% of the isolates contained lethal genes of Lepidopteran including *Cry1A* (90.9%), *Cry1D* (90.9%), *Cry1C* (72.72%) and *Cry2Ab2* (63%). The shape of crystal proteins in two native strains including 1053 and 1068, with the highest pathogenicity against Mediterranean flour moth *Ephestia kuehniella* (Lep.: Pyralidae), was examined by electron microscopy. The spherical and ovoid crystals for 1053 and diamond, bipyramidal, ovoid and cuboidal crystals for 1068 were identified. The native strains containing these genes can be used as commercialized biological control agents against Lepidopteran pest and to manage resistance.

Keywords: Plasmid, *Cry* genes, Biological toxins , Polymerase Chain Reaction

EP31 Investigation of the effect of native isolates of the bacterium, *Bacillus thuringiensis* on mortality of Mediterranean flour moth

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Today, microbial pest control, including the use of *Bacillus thuringiensis (Bt)*, has become important because of its adaptability to the environment and the provision of healthy food. In this study, native isolates of *Bt* were isolated and selected from the soil of different regions with sodium acetate selective method. The isolates were initially identified with Coomassie brilliant blue staining which were divided into 13 groups according to the shape of the crystal proteins. The spherical and irregular shapes were observed the most frequently. To determine the pathogenicity of the isolates, after purification of spore-crystals, a 2000 µg -suspension of each isolate in 1 ml distilled water was prepared. The mentioned suspensions were mixed with one gram flour and 15 larvae of *Ephestia kuehniella* were treated with the mixtures in three replicates. Two bacteria included *Bt thuringiensis* (*Btt*) and *Bt kurstaki* (*Btk*)were used as the positive controls. The test was done as a completely random design and the averages were compared by the Tukey's test at the probability level of 5%. The isolate (1053) collected from Chenaran- Khorasan Razavi had the highest percent mortality (77.14±6.44%). *Btt* along with the two native isolates (1080 and 1084) showed the lowest mortality (4.60±1.08, 11.26±2.06 and 21.27±2.82 %), respectively. The two other native isolates including 1090 and 1087 as well as *Btk* mostly had around 50% mortality. However, there is no significant difference among the rest of nine isolates, which had up to 50% mortality. The most pathogenic isolate (1053), had ovoid , spherical and irregular shape of crystals and was isolated from the soil under the pear trees. These isolates could be a source of new genes with high lethality and used in integrated pest management to control farm and stored product pests.

Keywords: Biological control, Pathogenicity, Coomassie blue, Spore-crystal

EP32 Flora, life form and chorology of plants in *Pallas's* cat habitat (case study: Jashloobar, Semnan)

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The *Otocolobus manul* is a small cat of Felidae family and Felinae subfamily. The Pallas cat is protected in many countries in its range. According to the laws of Iran's Department of Environment, it is classified as a protected species. Although this species is found in a wide range of habitats including steppes, dry mountains to grasslands and mountainous and rocky areas, but now the suitable habitats of this species are fragmented and reduced due to habitat destruction. In the conservation of the fauna habitats, correct and scientific knowledge of their habitat as basic studies is essential. Therefore, considering the role of plants as hiding spot, den and food source for its preys, the present study was conducted to identify plant flora in

Jashloobar habitat of Semnan province. 72 species was identified based on plant samples collected in 2019, which belong to 22 families. The largest plant families are Asteraceae ،Poaceae ، Fabaceae و Apiaceae with 18%, 18%, 11% and 8% of species frequency, respectively and the largest genus is Astragalus of Fabaceae. The diagram of plant life formed by the Raunkiaer method showed that the dominant life forms of the area were hemicryptophytes with 54%, therophyte with 9.7% and geophytes (Cryptophytes) with 8.33%, whose high percentage demonstrate the cold climate and mountainous region. The chorotypes of plants species showed that about 60% of the plant species belong to Irano-Touranian zone. In addition, forbs, grasses and bushes have the most vegetative forms in this region, respectively. The dominance of these plants in the region provides a favorable environment for the presence of rodents, both in terms of nutrition, den and shelter, which are the main prey of Pallas cat, and creates a suitable habitat for this species.
Keywords: Raunkiaer, Life form, Chorotype, Flora, Semnan.

EP33 Variation in expression of thermal stress genes in massive *Porites harrisoni* corals in the Persian Gulf

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Coral reefs cover only a small fraction of the ocean's surface but have more biodiversity than any other marine habitats. These ecosystems are highly vulnerable to small changes in the physical and chemical properties of the water column. Increasing ocean temperatures sometimes exceed their physiological tolerance and leads to loss of symbiotic algae, reduced fitness for the coral host, and decreases in coral cover. In this study, the expression changes of heat shock proteins and apoptosis genes in scleractinian coral *Porites harrisoni*, which were collected in August during low tide conditions concurrent with peak daily temperature from Hengam Island, were investigated. To evaluate the potential for acclimation, healthy fragments were taken from the deep and relatively cold site and transplanted to the shallow site. Gene expression levels were analyzed using Quantitative real-time PCR. A significant upregulation of heat shock proteins in response to heat stress was identified as the most important defense mechanism in response to heat stress. Significant downregulation of the apoptotic gene expression was observed in acclimation experiment samples, which indicates the compatibility of the deep corals to thermal changes. The results suggest that the studied corals are thermal tolerant compared with similar species in other tropical and subtropical regions. Therefore, they can be classified as a super-coral. The use of this coral in regions where native corals have been subjected to extinction, might be a key strategy to maintain the coral community.
Keywords: Global warming, Gene expression, Heat shock proteins, Apoptosis, Acclimation

EP34 Investigating the conflicts between local communities and the natural environment in relation to the protection of biodiversity in Haraaz protected catchment area- Case study: Ab-Ask village.

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Reducing "Brown trout" as one of the critical endangered (CR) species in Iran inland rivers, especially the Haraz Protected River, is a common concern among environmentalists and indigenous people. With increasing competitiveness of societies to access natural resources, and also human-made changes, pollution and human manipulation in nature and the possibility of conflicts between Locals, nature and professionals, it was assumed that "overfishing" and "water pollution" were the main reasons for this decrease. This study was designed in public participation method (PRA) to find out the answer to this assumption and also to find possible conflicts between locals and specialists. In this study we tried to examine the reasons of reduction of Brown trout by means of the knowledge of specialists and also the PRA method during 15 field visits to the region and conduct semi-structured interviews with 50 villagers. Data collection was performed by means of problem tree, effectiveness plant, historical course, Transverse cutting map and social map. Due to locals Observation Sand extraction from the riverbed, reduce water

discharge and Contaminants enter the water was the main cause of water pollution and declining salmon. Finally, the people ask for Follow the rules for the restaurant waste, construction the septic tank for domestic sewage, observe river area for fish breeding pound and organizing environment workshops for Locals to improve biological and habitat conditions.

Keywords: Participation, Public participation appraisal, Biodiversity, Locals, Brown trout

INDEX

Keynote Speakers
(Page IBS2020-K 1-13)

Adcock Ian M, 9
Kazemi Abdolhasan, 13
Maghuly Fatemeh, 11
Mosavi-Movahedi Ali, 5
Noble Denis, 3
Summerlee Alastair JS, 7

Invited Speakers and their co-authors
(Page IBS2020-I 1-27)

Abdoos Amir, 8
Ahmadi Shamseddin, 20
Akmali Vahid, 24
Akrami Mohammad Ali, 21
Alam Iqbal Md., 6
Alavi Sayyed Mohammad Hadi, 9
Alipour Shirin,
Alijanpour Sakineh, 29
Amani Jafar, 4
Asadboland Roghaieh, 18
Asadi Farhad, 5
Ashraf Jafari Ali, 16
Atazadeh Ehsan, 15
Attari Farnoosh, 22
Azin Mehrdad, 7
Badehian Ziaedin,
Bahadori Farzanr, 16
Bakhshandeh Behnaz, 10
Beygom Faghir Marzieh, 17
Bigdeli Mohammad Reza, 28
Chavoshi Mahin, 27
Dalman Azam, 21
Das Kusal K., 7
Dehghan Gholamreza, 11
Dering Monika, 5
Elahi Elahe, 19
Eslahch Changiz, 11
Eslahi Mohammad Reza, 18
Espahbodi Kambiz, 5
Ewing Robert, 7
Farazmand Ali, 9
Feizabadi Mohammad Mehdi, 8
Frootan Fateme, 4
Ghadami Seyyed Abolghasem, 29
Ghahghaei Arezou, 22
Gholipour Abbas, 16
Hassani Fatemeh, 22
Hekmat Azadeh, 10
Hosseinkhani Saman, 15
Houshmand Massoud, 14
Inanloo Kolsoume, 19
Iranbakhsh Ali Reza, 18
Javed Arshad, 3
Karami Manizheh, 24
Kashanian Soheila, 23
Kavousi Kaveh, 12
Kazempour Osaloo Shahrokh, 4
Keshavarzi Maryam, 17
Mirza Mehdi, 16
Miyan Jaleel, 28
Mobasheri Hamid, 6, 12
Moghadasali Reza, 25
Moghaddam Mahtab, 4
Mohammadi Parisa, 8
Moradi Sharif, 13
Motevalian Seyed Abbas, 2
Nikkhah Maryam, 15
Noori Ali-Reza, 15
Noori Azam, 4
Palacio Sara, 5
Parvaneh Tafreshi Azita, 19
Rafipour Ronak, 23
Ramdan Mahmoud, 28
Ranjbar Massoud, 15
Rashtbari Samaneh, 11
Rezaei Arezou, 23
Rezayof Ameneh, 19
Ridha Abbas Amer, 23
Safari Iman, 19
Salami Seyed Alireza, 18
Salmanian Ali Hatef, 4
Sanaei Ehsan, 26
Sari Alireza, 27
Sepehri Houri, 27
Sharifi Ashorabadi Ebrahim, 16
Shirzadian Saeed, 18
Taghipour Elham, 4
Talkhabi Mahmood, 26
Vosough Massoud, 14
Walas Łukasz, 5
Yousefzadeh Hamed, 5
Zahmatkesh Ensieh, 14
Zarrabi Mahboobeh, 13
Zeynali Bahman, 26
Zubieta-Calleja Gustavo R., 2

Conservation & Environmental Biology
(Pages IBS2020-E1-20)

Abdoli Asghar, 19
Abdoos Amir, 5,18
Abedi Roya, 11
Abedi Tooba, 11
Abedinzadeh Niloofar, 3
Abolmaali Shamsozoha, 3
Abtahi Behrooz, 14
Adibi Mohammad Ali, 5,18
Amini Elham, 12, 12
Amirjan Mohammad, 18
Atazadeh Ehsan,10
Babakhanzadeh Esmail, 3
Badi Yusef, 9 (IBS2020_K 9)
Bhehvendy Firooz, 2
Broumand-Foomani Behnam, 9, 10
Charandabi Saeed, 10
Daneshvar Abolfazl, 12, 12
Doustshensa Babak, 4
Ebadzadeh Haniyeh, 11
Eslami-Farouji Atena, 4
Fathian Hossein, 2
Ghadam Parinaz, 7
Ghasempouri Seyed Mahmoud, 5
Ghassemi-Khademi Taghi, 7
Ghodrati Shojaei Mehdi, 11
Ghotbi-Ravandi Ali Akbar, 8
Haerinasab Maryam, 4
Haghighi Maryam,3
Hosseini Marzieh, 7
Hosseini Naser, 15, 15
Jalali Mohsen, 8
Javadi Anaghizi Saeed, 14
Javanbakht Hossein, 9, 10
Karami Nader, 5
Keshtkar Hamidreza, 2, 9
Khaledi Hoda, 4,16
Khaleghizadeh Abolghasem, 5
Khosravi Rasoul, 7
Kiadaliri Hadi, 14
Kordezangeneh Bahareh, 5
Lahordi Mahdi, 5
Mehrabian Ahmadreza, 14, 15, 15
Merhkhou Fariba, 17, 17
Moghaddam Sanaz, 18
Mohammadasgari Hosein, 4
Mohammadi Parisa, 7
Mohammadkhani Maliheh, 3
Moharami Somayeh, 8
Mostafavi Hossein, 14,15,15
Mozafari Moslem, 18
Naseri Somayeh, 5, 18
Nazemi Ardakani Shahrzad, 14
Neyshaboori Fatemeh Alzahra, 8
Oladi Mahshid, 16
Pakniyat Davood, 5
Pakzad Toochaei Sahel, 13, 13
Radman Ahmad, 5
Rahimi Razieh, 14
Rakhshan Mojdeh, 19
Rashki Maryam, 17, 17
Ravanbakhsh Mokarram, 3, 8
Rezaei Azadeh, 4
Saboora Azra, 7
Sattarian Ali, 12, 12
Savari Ahmad, 4
Sayadi Sadaf, 15
Sehat Parseh Mohammad, 12, 12
Seyfabadi Seyed Jafar, 11
Shah Hosseini Mighadam Reza, 5
Shariatmadari Zeinab, 7
Shi Ying, 9 (IBS2020_K 9)
Shirazi Mohammad Reza, 5
Shokri Mohammad Reza, 16, 18
Siahpoor Godratollah, 2
Soltani Nezhad Pariya, 17, 17
Taghizadeh Rahmat Abadi Zahra, 14
Tohidfar Masoud, 18
Tsitiou Angelica, 9 (IBS2020_K 9)
Vaissi Somaye, 9, 10
Yaravesh Sajedeh, 3
Zaker Mohamadi, 5
Zounemat Kermani Nazanin, 9 (IBS2020_K 9)

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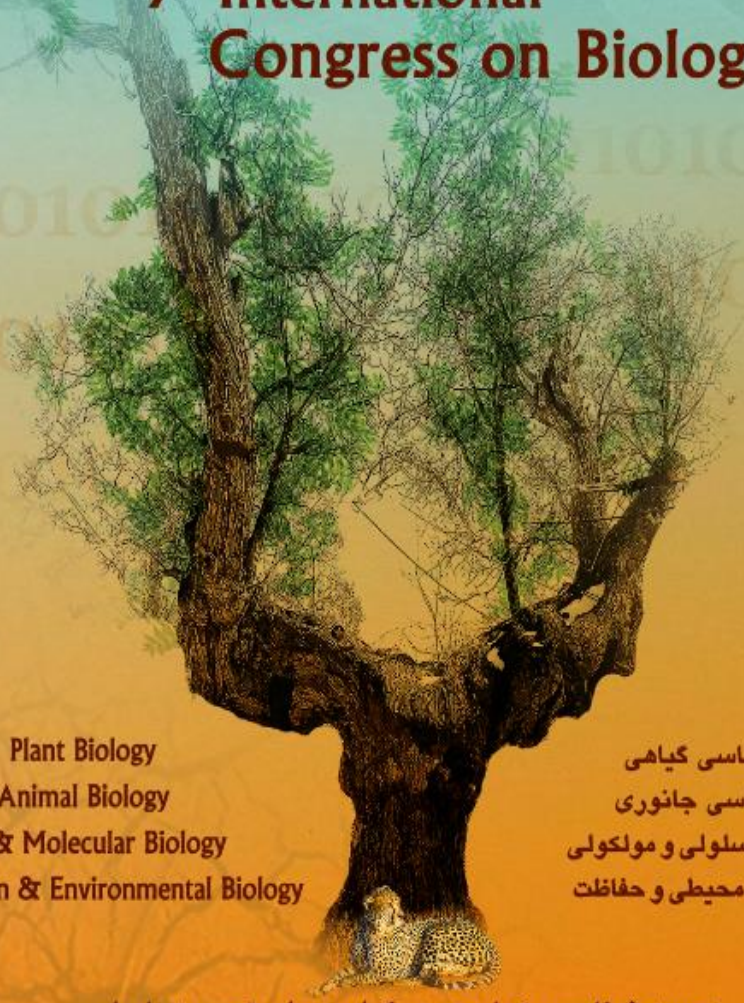

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