

**1st INTERNATIONAL CONGRESS ON
BIOTECH STUDIES**

SYMPOSIUM ABSTRACT E-BOOK

November 9-11, 2022



TAGEM
R&D AND INNOVATION

**BIOTECH
STUDIES**

1st International Congress on Biotech Studies

A Virtual Symposium

November 9-11, 2022

Hosted by
The Field Crops Central Research Institute Ankara,
TÜRKİYE

Symposium Abstract Proceedings

www.icbios.org

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

1st International Congress on Biotech Studies-2022

Honorary President

Metin Türker, Directorate General of Agricultural Research and Policy, Ankara, Türkiye

Congress Chair

Şerafettin Çakal, Directorate General of Agricultural Research and Policy, Ankara, Türkiye

Hümevra Yaman, Field Crops Central Research Institute, Ankara, Türkiye

Organising Committee

Asiye Seis Subaşı, Field Crops Central Research Institute, Türkiye

Buket Çetiner, Field Crops Central Research Institute, Türkiye

Burcu Gündüz Ergün, Field Crops Central Research Institute, Türkiye

Cuma Karaoğlu, Field Crops Central Research Institute, Türkiye

Elif Yetilmezer, Field Crops Central Research Institute, Türkiye

Emine Burcu Turgay, Field Crops Central Research Institute, Türkiye

Kutay Yılmaz, Field Crops Central Research Institute, Türkiye

Leyla Cüre, Field Crops Central Research Institute, Türkiye

Mehmet Doğan, Field Crops Central Research Institute, Türkiye

Melike Erol Demirbilek, Field Crops Central Research Institute, Türkiye

Merve Nur Ertuş Öz, Field Crops Central Research Institute, Türkiye

Mikail Çalışkan, Field Crops Central Research Institute, Türkiye

Nur Koyuncu, Field Crops Central Research Institute, Türkiye

Oğuz Acar, Field Crops Central Research Institute, Türkiye

Pervin Arı Akın, Field Crops Central Research Institute, Türkiye

Reyhan Bahtiyarca Bağdat, Field Crops Central Research Institute, Türkiye

Sevinç Karabak, Field Crops Central Research Institute, Türkiye

Sümevra Gültekin, Field Crops Central Research Institute, Türkiye

Şenay Boyraz Topaloğlu, Field Crops Central Research Institute, Türkiye

Ülkü Selcen Haydaroğlu, Field Crops Central Research Institute, Türkiye

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

1st International Congress on Biotech Studies-2022

Scientific Committee

Ana Sanches-Silva, National Institute for Agricultural and Veterinary Research, Portugal

Anake Kijjoa, Porto University, Portugal

Bahattin Tanyolaç, Ege University, Türkiye

Carlos Guzmán, Córdoba University, Spain

Davide Barreca, Messina University, Italy

Ebru Toksoy Öner, Marmara University, Türkiye

Fahriye Ceyda Dudak Şeker, Hacettepe University, Türkiye

Fatih İnci, Bilkent University, Türkiye

Fatih Ölmez, Sivas Science and Technology University, Türkiye

Fikretin Şahin, Yeditepe University, Türkiye

George Aggelis, University of Patras, Greece

Gökhan Hacısalihoğlu, Florida A&M university, USA

Gökhan Zengin, Selçuk University, Türkiye

Hakan Özkan, Çukurova University, Türkiye

Ibrahim M. Banat, Ulster University, UK

Ibrahim Demir, Ankara University, Türkiye

İlkay Erdoğan Orhan, Gazi University, Türkiye

İpek Süntar, Gazi University, Türkiye

İsmail Hakkı Boyacı, Hacettepe University, Türkiye

Jin-Xiong She, Augusta University, USA

Jutta Ludwig-Müller, Technical University Dresden, Germany

Kadriye Arzum Erdem Gürsan, Ege University, Türkiye

Kasim Bajrovic, University of Sarajevo, Bosnia-Herzegovina

Khalid Mahmood Khawar, Ankara University, Türkiye

Mahmut Tör, University of Worcester, UK

Mark A. Smedley, John Innes Centre, UK

Mehmet Cengiz Baloğlu, Kastamonu University, Türkiye

Mehmet İnan, İzmir Biomedicine and Genome Center, Türkiye

Muhammad Asyraf Md Hatta, University Putra Malaysia, Malaysia

Murat Elibol, Ege University, Türkiye

Naci Onus, Akdeniz University, Türkiye

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

1st International Congress on Biotech Studies-2022

Scientific Committee

Nedim Mutlu, Akdeniz University, Türkiye
Nuri Azbar, Ege University, Türkiye
Ömür Baysal, Muğla Sıtkı Koçman University, Türkiye
Pagona Papakonstantinou, Ulster University, UK
Pankaj Vadgama, Queen Mary University of London, UK
Patrick Fickers, Université de Liège, Belgium
Rasoul Moradi, Khazar University, Azerbaijan
Rasit Asiloglu, Niigata University, Japan
Ravishankar Rai, University of Mysore, India
Remziye Yılmaz, Hacettepe University, Türkiye
Sadiye Hayta-Smedley, John Innes Centre, UK
Seid Mahdi Jafari, Gorgan University, Iran
Serkan Uranbey, Ankara University, Türkiye
Yusuf Chisti, Massey University, New Zealand

1st International Congress on Biotech Studies-2022

Secretariat

Mine Tuncay, Edda Tourism & Organization, Türkiye
Hülya Dağıstan, , Edda Tourism & Organization, Türkiye

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

TABLE OF CONTENTS

PREFACE	1
INVITED SPEAKERS	2
The Importance Of Pharmaceutical Biotechnology In Health Sciences	3
Advancing Crop And Seed Dietary Nutrient Systems	4
Genetically-Modified Mammalian Cells As Biological Therapeutics	5
Pathogenomics-Assisted Plant Breeding For Disease Resistance	6
Food Biotechnology For The Future	7
<i>In-Situ</i> (Bio)Remediation As An Advanced Technology Of Sustainable Agriculture	8
Biochemicals, Feed And Food From Lignocellulose Hydrolysate By Oleaginous Yeasts.....	9
Blurring Disciplinary Boundaries To Offer Healthier, Safer Life To Individuals Through Nutritionally Enhanced, Safe Food Or Better Diagnostics	10
Environmental Biotechnology Application Areas And Recent Developments	11
Grape Pomace As A Source Of Bioactive Extracts	12
Harmonizing Nano-Scale Technologies With Extracellular Vesicles For Disease Diagnostics	13
The Era Of Multi-Omics Approaches In Crop Science	14
Exploiting Genome Editing Into Elite Wheat Cultivars By Deploying Morphological Gene	15
ORAL PRESENTATIONS	16
FOOD AND INDUSTRIAL BIOTECHNOLOGY - YELLOW/WHITE SESSIONS.....	16
The Effect of Microwave Treatment on Gene Expression Level of Argonaute (<i>AGO1a</i>) and Phosphoglycerate Kinase (P _{gk3}) Genes in Maize (<i>Zea mays</i>) L. Flours.....	17
Food Grade Biopigments Versus Synthetic Colorants	18
<i>In Silico</i> CRISPR-cas Based Screening of <i>Lactococcus Lactis</i> ASM2046375v1	19
Towards The Determination of Plant Species That Constitute Bingöl Honey Through Recent Meta Molecular Analysis.....	20
Approaches for Metagenomic Examination of Fermented Food Products.....	21
Role of Nanotechnology in Food And Biotechnology Sector	22
Analysis Of Protein Secretion By Baker's Yeast (<i>Saccharomyces cerevisiae</i>)	23
Use Of Real-Time PCR and High-Resolution Melting Analysis for the Identification and Discrimination of (<i>Saccharomyces boulardii</i>) Strains by (<i>AAD15</i>) and (<i>MAL11</i>) Genes	24
Effect of Bitter Melon Peel Powder on Functional Properties of Edible Films	25
Investigation Of Antibacterial Effects Of Some Safflower (<i>Carthamus L.</i> , Asteraceae) Flowers Against <i>Salmonella enteritidis</i> , <i>Escherichia coli</i> , <i>Staphylococcus aureus</i> and <i>Bacillus cereus</i>	26
Differences in Technological Properties Between <i>Saccharomyces cerevisiae</i> and non- <i>Saccharomyces</i> Yeast	27

BIONFORMATIC AND NANOBIO TECHNOLOGY - GOLD SESSION	28
RNAi Silencing By Prokaryotic Gene Sources	29
Liposomal Encapsulation of Green Synthesis Silver Nanoparticles Using Green Algae (Ulva lactuca) and Investigate of Antibacterial Effect	30
AGRICULTURAL BIOTECHNOLOGY - GREEN SESSION	31
The Mutant B-Type Response Regulator Hst1 Gene Regulates Transcriptomic Response To Provide Salinity Tolerance By Reprogramming Transcription Factors and Cytokinin Signaling Genes In Rice (<i>Oryza Sativa</i> L.)	32
Isolation of LEAFY- and TERMINAL FLOWER 1-like Genes from Two Tricyrtis spp. Showing Different Inflorescence Architectures	33
The Potential Biostimulant Effects of Macroalgae (<i>Cystoseira barbata</i>) Extracts on Broccoli Plant under Greenhouse Conditions	34
Marker-Assisted Selection (MAS) in Pepper Breeding	35
Comparison of Biochemical and Antioxidant Activities in Different Solvent Extracts Obtained from Olive Leaves	36
Cold Tolerance in Some Camelina (<i>Camelina Sativa</i> (L.) Crantz) Genotypes Under Controlled Conditions	37
Callus and Suspension Culture Techniques Optimized for Use in Carrot Breeding Studies (<i>Daucus carota</i> ssp. <i>sativus</i> var. <i>atrorubens</i> Alef and <i>D. carota</i>)	38
Comparative Response Of Coated And Commercial Urea On Lettuce Production And Nitrogen Contents	39
Seaweed Liquid Extracts (<i>Cystoseira barbata</i>) as a Biostimulant Agents for Wheat Plant	40
Optimization of Indole-3-Acetic Acid Biosynthesis in a Native <i>Bacillus Subtilis</i> Isolate	41
Drought Stress Induces Pattern-Triggered Immunity Highly Associated with Quantitative Disease Resistance in Brassica Oleracea	42
Development of IoT Based Hydroponic Smart Garden	43
Genetic Variation and Population Structure of <i>Medicago sativa</i> L. Using SSR Markers	44
Exploring The Potential of Psychrophilic Organisms For Crop Production Under Cold Conditions	45
Wheat (<i>Triticum aestivum</i>) is Protected by Arbuscular Mycorrhizae from the Combined Effects of Boron Toxicity and Salinity Stress under Low- and High-Phosphorus Conditions	46
Use of <i>Arthrobotrys</i> spp. in Biocontrol of the Root-Knot Nematode <i>Meloidogyne Incognita</i>	47
Phenotyping the Races of <i>Puccinia striiformis</i> fsp. <i>tritici</i> in Central Anatolia and Future Genotyping Studies	48
Screening of Stem Solidness Gene Content of Some Grain Varieties with SSR Markers	49
The Story of Constructing the First Barley Mapping Population in Turkey for Developing Molecular Markers Related to Some Foliar Diseases	50
The Effects of HighTemperature-time Stress Pretreatments on Callus Induction and Regeneration in Anther Culture of Some Bread Wheat Varieties (<i>Triticum Aestivum</i> L.)	51
The Effect of MS and Sucrose Doses on Direc Shoot Organogenesis of <i>Saintpaulia Ionantha</i> Wendl	52
Response of Some Turkish Rice (<i>Oryza Sativa</i> L.) Varieties to Anther Culture on Different Culture Medium	53

The First Studies of Adaptation, Spring Growth Behavior, Water Requirement and Temperature Response of Promising Multiple Developed Primary (Tcpt) And Secondary (Tcst), Tritipyrum, Under Three Different Irrigation Methods in Türkiye	54
The evaluation of Promising Trans Chromosomal lines of Primary (TCPT) and Secondary (TCST) Under Salinity of Na/CaCl ₂ for Seed Germination and Seedling Emergence Stages	55
The First Study of Photoperiod Sensitivity and Vernalization Genes in The Promising Primary and Secondary Lines of New Salt Tolerant Cereal, Tritipyrum	56
ENVIRONMENTAL BIOTECHNOLOGY - GREY SESSION	57
Predatory Protists Enhance Rice Plant Growth Through Regulating Rhizobacterial Community Composition	58
Impact of Water Pollution On Vital Organs of Fish Species (<i>Oreochromis Mossambicus</i>)	59
Evidences Showing Significant Alterations in Metabolic Processes in Selected Bacterium <i>Cellulosimicrobium Cellulans</i>	60
Diatoms and New Biotechnological Approaches	61
Prediction of the Bioremediation Potential of Microbial Diversity in Hypersaline Tuz Lake	62
HEALTH BIOTECHNOLOGY - RED SESSION	63
Neuroprotective Role of Chrysin Against Bupivacaine Induced Apoptosis and Oxidative Stress in SH-SY5Y Cell Line	64
Investigations of Antimicrobial Activities and DNA Interactions of Phosphazenes	65
Pyrogallol Prevents the Progress of Glioblastoma Multiforme Cells by Regulating Apoptotic Cell Death	66
An Investigation on the Protein Profile and Enzyme Activities of <i>Walterinnesia morgani</i> (Desert Black Cobra) Venom	67
In Vitro Effects of <i>Montivipera xanthina</i> (Ottoman Viper) Crude Venom and Its Fractions on Endothelial Tube Formation	68
Rhein Inhibits Cell Proliferation Through Induced Mrna Level of Apoptosis Related Genes and Supressed mRNA Level of TGF β Pathway and Metastasis Related Genes in Glioblastoma Multiforme Cells	69
The Response of Plant Secondary Metabolites on Climate Change	70
An Investigation on the Antifungal Effect of Some Benzimidazole Compounds	71
The Monetary Losses Due to Fasciolosis in Cattle in Muğla	72
Cytotoxicity Screening of the Skin and Parotoid Gland Secretions of { <i>Salamandra infraimmaculata</i> } ssp. { <i>semenovi</i> } from Anatolia	73
Guar Gum-Based Biofilms Containing <i>Momordica charantia</i> Fruit Extract and Biogenic Silver Nanoparticles (AgNP) for Medical Applications	74
Anti-Wood-Decay Fungal Activity of the Simultaneous hydrodistillation of <i>Salvia rosmarinus</i> Spenn and <i>Cedrus atlantica</i> Manetti	75
Effects of Corneal Alkaline Burns on Intraocular Pressure in Rabbits	76
POSTER PRESENTATIONS	77
Utilization of Food Wastes in Production of Bacterial Cellulose	78
An Attempt to Obtain Intracellular Melanins from the Biomass of <i>Aureobasidium Pullulans</i> A.P.-3	79
Phenolic Profile of “Kavilca” Bread Prepared with an Ancient Anatolian Wheat from Türkiye ...	80
Production of Propionic Acid and Vitamin B12 by <i>Propionibacterium Freudenreichii</i> DSMZ	

20271 in the Environment of Fruit Pomace, Potato Wastewater, and Waste Glycerine	81
Using the Marker Based Metagenomic Data in Boron Mine Detection	82
Effects of Zinc Treatment on Expression Levels of Some Enzyme Genes in Selected Local Wheat Varieties	83
Breeding of Tomato (<i>Solanum Lycopersicum</i> L.) Lines Resistant to Tomato Yellow Leaf Curl (TYLCV) Virus and Tomato Spotted Wilt Virus (TSWV) By Molecular Marker Assisted Backcrossing Method	84
Optimization Of Haploid Plant Through Anther Culture In Safflower Plant (<i>Carthamus Tinctorius</i> L.)	85
Transcriptomics Of In Vitro Plant-Bacteria Interaction: a Case Study Of Fraser Photinia and Pgb_Invit Bacteria	86
Investigation of a New Plant-Based Enzymatic Protein Hydrolysate As a Seed-Soaking Agent for Wheat Seedlings Under Control and Water Deficit Conditions	87
Elevated Shikonin Production In Hairy Root Culture With a Biotechnological Approach	88
Identification of Bacteria Isolated from the Wheat Rhizosphere and Determination of Their Plant Growth-Promoting Properties	89
Effect of <i>Moringa Oleifera</i> on the Physiochemical and Organoleptic Properties of Surface Water	90
Potential Detoxification Properties Of Black Yeast Preparation In Relation To Aluminum – The Study In Yeast Cell Growth Culture	91
Effect of Predatory Protists on Active Bacterial Community in Paddy Field Soils	92
Colonization of Candidal in Diabetes Mellitus Patients Attending Ekiti State University Teaching Hospital, Ado- Ekiti	93
Comparative Evaluation of in Vitro Antioxidant Properties of <i>Abelmoschus Esculentus</i> Whole Fruit And Seed Extracts	94
Analysis of Boron Mineral Found in Agricultural Products and Endemic Plants in Tunceli and Elazig Regions	95
Bacteriological Profile and Resistance to Antibiotics of Strains of <i>Bacillus Cereus</i> Isolated from the Stools of Children (0 To 5 Years Old) at the General Hospital of Port-Bouet (Abidjan)	96
Evaluation in Silico and In Vitro of an Synthetic Peptide Bioinspired in Tsap-2 Scorpion Toxin	97

PREFACE

Dear colleagues and researchers,

The main objective of the “1st International Congress on Biotech Studies”, in which a multidisciplinary approach is aimed at Biotechnology Researches, is to organize an event to bring all highly reputable scientists in biotechnology to foster inspiration.

The Congress has the same name and perspective as the “Biotech Studies” Journal, which is an international, peer-reviewed, accessible, free, and scientific journal, published by Field Crops Central Research Institute in Ankara, TÜRKİYE. The Congress was organized as an online congress in the English language. More than 800 registrations from 17 different countries were made to the congress from universities, public institutions and organizations, the private sector, and non-governmental organizations. The Congress covered all the research areas that are subject of “Green Biotechnology (Agricultural Biotechnology), Yellow Biotechnology (Food Biotechnology), Gold Biotechnology (Bioinformatics, Nano biotechnology), Grey Biotechnology (Environmental Biotechnology), and Red Biotechnology (Health Biotechnology)”. Presented 75 abstracts are included in this Abstract E-Book. Also, 14 invited speakers, who are experts in their specific research areas from different countries, presented their research published in this E-Book. Moreover, full texts of some abstracts have been evaluated to be published in the “Biotech Studies”.

I am thankful to the Scientific Committee members for all their valuable contributions to this Congress. I also would like to thank the Organizing Committee members for their hard work and the Sponsor (Field Crops Central Research Institute in Ankara, TÜRKİYE) for their support to organize the Congress. Finally, I would like to thank all the participants of the “1st International Congress on Biotech Studies” for making the Congress an efficient and sustainable platform for Biotech Studies. I am looking forward to meeting with all the researchers at the 2nd International Congress on Biotech Studies.

Congress Chair
Dr. Hümeyra YAMAN

INVITED SPEAKERS

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

The Importance of Pharmaceutical Biotechnology in Health Sciences

Prof. Dr. Fusun Acaturk

Gazi University, Faculty of Pharmacy, Department of Pharmaceutical Technology, TÜRKİYE

acaturk@gazi.edu.tr

Biotechnology is key to the advancement of the pharmaceutical industry in the human health. In the development of new drugs against diseases, drugs produced by biotechnological methods are increasingly more effective than chemical drugs. When the two disciplines, pharmaceuticals and biotechnology come together, they result in many advantages for humankind in terms of healthcare. Pharmaceutical biotechnology is the biotechnological manufacturing of pharmaceutical products. Pharmaceutical biotechnology is a rapidly growing industry. Biologics are isolated from a variety of natural sources such as human, animal and microorganism. Biological products include a wide range of products such as vaccines, blood and blood components, allergenics, somatic cells, gene therapy, tissues, recombinant therapeutic proteins. Therapeutic proteins differ in many aspects from classical, small molecule drugs. They are large and complex molecules. They are a mixture various active molecules, i.e. heterogenous molecules. Production and impurity profiles are subject to minor changes. Structural stability, i.e. physical stability is very limited. Therapeutic proteins perform specific functions by interacting with other small and large molecules such as cell-surface receptors, binding proteins, nucleic acids, carbohydrates and lipids. Therapeutic proteins are in globular form. They have folded structure. The functional properties of proteins are derived from their folding into distinct three-dimensional structures. Tertiary structure is usually conformational, native, and active. The tertiary structure of the protein is essential for its function. In order for a biotechnology product to reach the pharmacy from the research stage, it must be proven that the drug is effective and reliable. It should be aimed to develop a stable formulation without any physical-chemical changes while developing peptide-protein formulations. Development of a peptide-protein formulation is much more difficult than conventional small molecular weight pharmaceuticals. It is very difficult to develop stable formulations due to the complex structures and stability problems of proteins. Maintaining the integrity of the purified peptide-protein during routine processing and transport/storage are important issues. Biotech products are produced by Recombinant DNA Technology (rDNA) and Monoclonal Antibody Technology (MoAb). Parenteral delivery is the most effective administration route of therapeutic proteins. Parenteral formulations of biotech drugs are solution, lyophilized powder and drug delivery system (micro/nanoparticles, microemulsion, liposome). Protein stabilizing agents and lyophilization technique are used for enhancing storage stability of proteins. There are number of marketed parenteral, oral, nasal and pulmonary used protein products. Progress in biotechnology research will be at the core of numerous innovations that will reach society. Pharmaceutical biotechnology remains associated with life-saving new developments. Pharmaceutical biotechnology will be a survival tool in the coming years with the increasing number of lethal diseases and pandemics.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Advancing Crop and Seed Dietary Nutrient Systems

Prof. Dr. Gokhan Hacisalihoglu

Florida A&M University, Tallahassee, Florida 32307 U.S.A..

<http://www.drhaci.com/en/8/Contact.html>

Seed size and composition quality traits are important in food crop plants and can be affected by nutrient availability in the soil. Phosphorus (P) is an essential macronutrient, and its deficiency significantly limits soybean yield and quality. Soybean recombinant inbred lines (RILs) from the cross of Fiskeby X Mandarin were grown under contrasting P availability environments to investigate the association of seed and plant traits in low and high P environments. Traits including seed weight, seed number, and pod plus seed weight were significantly affected by soil P levels and showed transgressive segregation among the RILs. The RIL phenotypes were used to identify and map quantitative trait loci (QTLs) controlling seed size and composition traits. Broad-sense heritability estimates were 0.78 (individual seed weight), 0.90 (protein), 0.34 (oil), 0.98 (seed number). Five QTLs were significant in low P environments, and one QTL was significant in optimal P environments. QTLs were detected for seed weight (SeedwtQTL4.1; SeedwQTL4.3; and SeedwQTL6.1), pod plus seed weight (PodplswtQTL4.2), volume (VolQTL6.2), and and protein (ProtQTL20.1). In summary, detection of specific QTLs under contrasting P levels together with transgression of seed and plant characteristics will help our understanding and improvement of soybean performance under limited P conditions. The QTLs identified can be used for molecular marker assisted breeding with their differential expression contributing to seed traits and low P tolerance in soybean. The current status of this project will be presented including the further research results.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Genetically-modified Mammalian Cells as Biological Therapeutics

Prof. Dr. Gunes Esendagli

Hacettepe University Cancer Institute, Ankara, TÜRKİYE

gunese@hacettepe.edu.tr

In this talk, the biotechnological applications for health sciences will be presented and discussed. Genetic modification technology in mammalian cells relies on transient genetic modification which is usually performed through random insertion or deletion of genetic material. Alternatively, Cre recombinase – Locus of x-over (Cre-Lox) system Zinc Finger Nucleases (ZFN), Transcription Activator-Like Effector Nucleases (TALEN), Clustered regularly interspaced short palindromic repeats – CRISPR-associated protein 9 (CRISPR-Cas9) take advantages of targeted and stable insertion or deletion of a target gene. Production of protein-structured drugs with “right” conformation, post-translational modifications without foreign contaminants is the main purpose of Genetically modified Mammalian Cells which aims to produce therapeutics such as monoclonal antibodies and hormones and growth factors. Moreover, the cells can be directly transformed into “living drugs” for GM/GE Stem Cell Therapy and GM/GE Cellular Immunotherapy. Replacement of the missing cellular component is also possible with stem cell transplantation for treatment of inborn errors. Induced pluripotent stem cells (iPSC) can be the most important example. Activation of suppressed immune responses for cancer therapy, regulation of excess responses for inflammatory diseases, GM dendritic cells, and chimeric antigen receptor (CAR) T-cell therapy form the basis for the immunotherapy approaches achieved by genetic modification. In conclusion, genetical modification of mammalian cells provides a plethora of possibilities and challenges for producing biological therapeutics.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Pathogenomics-Assisted Plant Breeding For Disease Resistance

Prof. Dr. Mahmut Tor¹, Emeka C. Okechukwu¹, Deniz Gol¹, Rachel Osborn¹, Sanu Arora², Claire Domoney², Jane Thomas³, Tom Wood³

1-Department of Biological Sciences, School of Science and the Environment, University of Worcester, Henwick Grove, Worcester, WR2 6AJ, UK.

2- The John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, UK.

3-NIAB, Cambridge, CB3 0LE, UK.

m.tor@worc.ac.uk

Plant breeding has long been a crucial aspect of agriculture, with the goal of producing crops that are resistant to pests, diseases, and environmental stresses. In recent years, the use of pathogenomics, which involves the study of the genomic basis of host-pathogen interactions, has emerged as a promising tool for plant breeding. By identifying the genes and pathways that are involved in the plant's defence against pathogens, plant breeders can select for plant lines that are more resistant to diseases. Additionally, pathogenomics can also help identify virulence factors of the pathogen, as well as design molecular markers for detection of the pathogen and population studies. Overall, the integration of pathogenomics into plant breeding has the potential to significantly improve crop yields and reduce the need for chemical pesticides, greatly advancing our ability to produce healthy and sustainable crops. We have been working on the pulse-downy mildew (DM) pathosystem, caused by the sexually reproducing obligate biotrophic oomycetes *Peronospora viciae* f.sp. *pisi* (*Pvp*) and *Peronospora viciae* f.sp. *fabae* (*Pvf*), which can cause yield losses of up to 45-75 % in pea and 40-50% in faba bean. We have a collaborative project for the identification of new *R*-genes for breeding purposes, the development of tools for accurate detection and diagnostics of *Pvp*/*Pvf* isolates using genomics, and the use of biologics to suppress downy mildew pathogens. Screening germplasm has identified new sources of resistance in pea and faba beans against DM and the use of genome-wide association studies (GWAS) allowed us to develop molecular markers linked to the loci involved. Draft reference genomes of *Pvp* and *Pvf* have been assembled and more than 40 isolates of *Pvp* have been collected and being sequenced to identify genetic variation between isolates. We want to generate isolate specific molecular markers and test them in the laboratory and on the populations. The latest data will be presented.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Food Biotechnology for the Future

Prof. Dr. Remziye Yilmaz

Hacettepe University, Department of Food Engineering, FoodOmics Laboratory, Beytepe Campus,
06800, Ankara, TÜRKİYE

remziye@hacettepe.edu.tr

Modern humanity could not exist without biotechnology. FAO (March, 2000) said that biotechnology provides powerful tools for the sustainable development of agriculture, fisheries, and forestry, as well as the food industry. When appropriately integrated with other technologies for the production of food, agricultural products, and services, biotechnology can be of significant assistance in meeting the needs of an expanding and increasingly urbanized population in the next millennium. The Convention on Biological Diversity (CBD) defines biotechnology as: "*any technological application that uses biological systems, living organisms, or derivatives thereof, to make or modify products or processes for specific use*".

Food is a complex ecosystem constituted of raw materials and microorganisms. Knowing food ecosystems helps improve food production and quality. Innovative molecular technologies permit a reliable study of food ecosystems. Food biotechnology is the use of technology to modify our food sources.

In the FoodOmics Laboratory, current studies are carried out in the fields of food microbiology, microbial biotechnology, and plant biotechnology by using classical methods and omics technologies such as genomics, transcriptomics, and metabolomics. The research area of the laboratory is the development of new foods and food analysis methods; food safety, biosecurity and risk assessment and ensuring food security. In traditional fermented foods, classical cultural methods and culture-independent (qPCR, sequencing, metagenomics, MALDI-TOF mass spectrometry) and their combination methods are used to discover microbiota diversity and beneficial microorganisms. Microencapsulation of probiotic bacteria and the use of the obtained microcapsules in the development of new food products are carried out in the laboratory, which has a culture collection containing original and local lactic acid bacteria and yeasts. The transcriptomic interaction that occurs as a result of fermentation in microorganisms such as *Saccharomyces cerevisiae* isolated and identified from Anatolia is examined and studies are carried out on the production of microbial protein, which is an alternative to plant and animal proteins. Studies on the development of vegetable protein-based products by fermentation using *Saccharomyces boulardii* are ongoing. In addition, a study has been initiated to determine the distribution and types of CRISPR-Cas loci of lactic acid bacteria. In the field of plant biotechnology, first of all, local wheat varieties and their bio-fortification as a result of the expression levels of some antioxidant enzyme genes were investigated. Furthermore, highly specific DNA-based methodology, such as RT-PCR and Nano-biosensor, has also been developed to detect and quantify genetically modified organisms (GMOs). The risk assessment methodology is being studied using bioinformatics tools from the perspective of multi-omics technologies of GMOs.

Lastly, biotechnology holds one of the most promising keys: it's already changing the foods we eat, replacing ingredients in foods we use, and improving novel foods.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

***In-situ* (Bio)remediation As an Advanced Technology of Sustainable Agriculture**

Prof. Dr. Selim L. Sanin,

Department of Environmental Engineering, Hacettepe University, Ankara, TÜRKİYE

sanin@hacettepe.edu.tr

Agricultural activities, cause diffuse pollution with their current methodologies. Fertilizers, pesticides and herbicides find their way to soil and groundwater. In addition, their chemical formulas are also changing in time. The change in agricultural methodologies also cause environmental stress. To reduce pollution caused by the agricultural activities, *in-situ* (bio)remediation methods became the most effective and economically feasible approach, in these difficult to define ecosystem. (e.i. soil and groundwater). *In-situ* remediation technologies need to advance to improve their efficacy. Advances in *in-situ* remediation technologies are investigated using model pollutants (e.g., s-triazines, endosulfan, phenol and neonicotinoids) for potential uses, in this talk.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Biochemicals, Feed and Food From Lignocellulose Hydrolysate by Oleaginous Yeasts

Prof. Dr. Volkmar Passoth, Jule Brandenburg, Mikołaj Chmielarz, Giselle Martín-Hernandez,
Yashaswini Nagaray, Bettina Müller, Johanna Blomqvist

Food Biotechnology, Department of Molecular Sciences, Swedish University of Agricultural Sciences,
Uppsala, SWEDEN

volkmar.passoth@slu.se

Vegetable oils belong to the most rapidly growing food commodities of the world. They are used for animal feed, as food additives, and to produce biofuels. The high demand for vegetable oils can result in monocultures, rainforest clearings and land use changes, which results in high greenhouse gas emissions during their production. Microbial oils represent a potential alternative to vegetable oil, especially from oleaginous yeasts. Those yeasts are the fastest known lipid accumulating organisms; many of them can convert low value side products such as lignocellulose hydrolysate or crude glycerol to lipids and other high value compounds.

We have established methods for controlled cultivation and intracellular lipid quantification. Following the kinetics of lipid accumulation in different strains, a high variability in lipid formation was observed, even between very closely related oleaginous yeast strains on both, wheat straw hydrolysate and crude glycerol. For example, on complete wheat straw hydrolysate we saw that one *Rhodotorula glutinis* strain, when starting assimilating xylose also assimilated the accumulated lipids, while a *Rhodotorula babjevae* strain could accumulate lipids on xylose.

Apart from microbial oil, *R. toruloides* also produces carotenoids. First attempts of extraction using the classical acetone- based method showed that β -carotene is the major carotenoid. However, there are indications that there are also substantial amounts of torulene and torularhodine, which have a very high potential as antioxidants.

To understand the genetic basis of the physiology of oleaginous *Rhodotorula*-yeasts, we established genomic analysis by a combination of long- and short read sequencing. DNA-molecules could be assembled that largely represent chromosomes. Different levels of ploidies were found in different strains. Transcriptional analysis showed splice variants and antisense transcription for some genes.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Blurring Disciplinary Boundaries to Offer Healthier, Safer Life to Individuals Through Nutritionally Enhanced, Safe Food or Better Diagnostics

Assoc. Prof. Sachin Rustgi

Department of Plant and Environmental Sciences, Pee Dee Research and Education Centre, Clemson Univ., Florence, SC, USA

srustgi@clemson.edu

In this day and age, disciplinary boundaries are blurring, and most research is interdisciplinary. In our group, we researched to find solutions for some fundamental problems, such as insensitivity to staple foods like wheat, allergy to peanuts and wheat, peanut aflatoxin contamination, and unavailability of sensitive and affordable detection tools for SARS-CoV2 diagnosis. Allergies to staple food like peanut and wheat carry a prevalence of 2.9% and 0.5% of the US population, respectively. Whereas wheat, specifically the gluten proteins, is responsible for autoimmune celiac disease. The current remedy to these foodborne disorders is an abstinent diet, which is difficult to follow and has associated penalties. For instance, removing wheat from the diet deprives consumers of essential dietary fibers and mineral nutrients. Similarly, removing peanuts deprives consumers, specifically vegetarians and vegans, of dietary proteins and fats. Given these challenges, we investigated the possibility of developing reduced immunogenicity wheat and peanut genotypes using gene stacking (via genetic crossing) and genome editing approaches. In the case of celiac disease, another strategy adopted was to express glutenases in wheat grains and use such grains as oral immunotherapy for celiac disease. Aflatoxin contamination of peanuts is another major issue facing the peanut industry, resulting in export restrictions and local consumption leading to significant wastage. We investigated two strategies, the use of nucleic acid as fungicides and the use of non-revertible atoxigenic strains (developed using a CRISPR-mediated gene drive) to displace the toxigenic *Aspergillus* strains. Both of these strategies are environment friendly as the nucleic acid pesticides being target specific, are safe for human consumption and the ecosystem. Since the covid19 pandemic is not yet over and is likely to stay, there remains a need to develop rapid and affordable early diagnosis tools that could facilitate the prevention of spread in the vulnerable population. In this direction, we investigate the possibility of using an in silico SELEX (Systematic Evolution of Ligands by EXponential Enrichment) process to identify candidate aptamers. We tested these candidates for the kinetics and affinity of molecular interactions via Bio-Layer Interferometry (BLI). The BLI analysis identified two aptamers that showed faster association rates and additionally identified an aptamer that showed affinity in the sub-micromolar range. The utility of these fundamental inventions in solving these massive problems will be discussed during the presentation.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Environmental Biotechnology Application Areas and Recent Developments

Assoc. Prof. Tugba Keskin Gundogdu*(<https://orcid.org/0000-0001-9354-7774>)

Izmir Democracy University, Engineering Faculty, Department of Industrial Engineering, Izmir,
35140, TÜRKİYE

tugba.keskingundogdu@idu.edu.tr

Sustainability has three dimensions; environmental, social, and economic. One of the important areas to develop environmental sustainability is biotechnology and biotechnology has a wide area of applications. Grey Biotechnology is focuses on the processes and products that are used for conservation of environment covering flora, fauna, inorganic elements that are necessary for life. Main areas for grey biotechnology are biofuels, biodegradation, bioremediation, bioaugmentation, conservation of flora and fauna etc. In line with the United Nations development goals, Governments have defined their paths and started to act. This study is a general summary of the actions taken to protect environment. Biofuel technologies are very advantageous because of the chance to use organic waste materials. Different biofuel production technologies, especially novel methods, and industrial scale applications such as biogas, bioethanol, biodiesel, biohydrogen and advantages and disadvantages of these different technologies were discussed. Possible waste sources for biofuel technologies were given for each different technology. Additionally, methods of bioremediation were explained and the novel developments for different technologies, such as bioinformatics and application of nanotechnology were also summarized. Protecting the nature and leaving a livable world to future generations is the common responsibility of all humanity and grey biotechnologies offers significant opportunities.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Grape Pomace as a Source of Bioactive Extracts

Assist. Prof. Claudio Ferrante

Department of Pharmacy, «G. d'Annunzio» University Chieti-Pescara.

claudio.ferrante@unich.it

Vitis vinifera (grape) is a multiuse crop rich in biomolecules with recognized health-promoting effects. In the wine-making industry, pomace is the main by-product, representing up to 20% of the whole biomass. However, the pomace deriving from the pressing may represent innovative raw materials

In the present study, we aimed to evaluate the effects of a water extract of grape pomace (WEGP) in colorectal cancer cell line SW480 and in an ex vivo experimental model of colon inflammation constituted by isolated mouse colon challenged with *E. coli* lipopolysaccharide (LPS). The grape pomace was the by-product of the vintage (year 2020) of a DOC red wine, the Montepulciano d'Abruzzo variety (Villamagna doc).

The results of the study indicated the efficacy of the water extract from grape pomace in reverting the burden of inflammation and oxidative stress occurring in isolated colon specimens exposed to LPS. Whereas, the reduction of human colon cancer SW-480 cell viability, and the modulation of the gene expression of proteins involved in carcinogenesis, further support protective effects in the colon. The mechanism underlying these effects could involve more than one phytochemicals. However, in SW480 cells the prominent phenolic compound, namely catechin, could be the putative responsible of the inhibitory effects on VEGFA, HIF1 α , and TRPM8 gene expression.

Considering also the large amount of grape pomace, about 20% of all processed plant material during wine-making, the present study supports the use of the pomace as a high quality by-product. This could also lead to an overall improvement of the chain production, and this would be of particular importance for local native-ecotypes, in most cases showing high quality wines, such as the Villamagna DOC, but with low productivity.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Harmonizing Nano-scale Technologies with Extracellular Vesicles for Disease Diagnostics

Assist. Prof. Fatih Inci ^{a,b,*}

^a UNAM—National Nanotechnology Research Center, Bilkent University, Ankara 06800, TÜRKİYE

^b Institute of Materials Science and Nanotechnology, Bilkent University, Ankara 06800, TÜRKİYE

finci@bilkent.edu.tr

Extracellular vesicles (EVs) are host-derived cargos that transfer information through cell–cell communication. EVs are secreted dynamically from many types of cells and organisms. Although EVs were initially defined as artifacts or cell dust, there is growing evidence for their essential roles as messengers in physiological functions and for their contribution in developing and propagating many diseases. Recent evidence represents EVs as promising biological agents for *both* diagnostic and therapeutic approaches in personalized medicine and precision health. However, isolating such nano-sized objects in size-dependent manner is one of the most challenging steps in EV research since conventional methods (ultracentrifugation, size exclusion chromatography or polymer-based isolation) are expensive; prone to loss of different sized EVs; or they potentially lead to accumulate contaminations on the isolated vesicles, hindering the quality of further investigations. Herein, we harmonize microfluidics and biosensing strategies to isolate and identify EVs from clinically-related specimens, thereby developing a diagnostic and screening scheme for point-of-care (POC) settings, where individuals can easily self-monitor their health status for “precision health” applications. Our research perspective aligns the design and development of platforms with biological and medical clues to diagnose and screen the diseases. Therefore, detecting such tiny EV markers, yet big players will be not only a “game-changer” in medicine, and also find new avenues for precision health and clinical management.

Acknowledgment: Fatih Inci gratefully acknowledges support from the Scientific and Technological Research Council of Turkey (TÜBİTAK) 2232 International Fellowship for Outstanding Researchers (Project No: 118C254) and the Turkish Academy of Sciences Outstanding Young Scientists Award Program (TÜBA-GEBİP). This work was also supported by the Young Scientist Awards Program (BAGEP) award from the Science Academy.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

The Era Of Multi-Omics Approaches in Crop Science

Dr. Ani Akpınar* (<https://orcid.org/0000-0001-6863-7436>)

Montana BioAgriculture, Inc., Missoula, MT 59802, USA

aniakpinar@gmail.com

Steady improvements in crop yields are becoming increasingly critical in the face of a fast-growing world population and worsening climatic changes. OMICs technologies, broadly referring to large-scale experiments targeting entire genomes, epigenomes, transcriptomes, proteomes, metabolomes, and phenomes, have been in use to support crop production. Recent advances in the throughput and accessibility of these experimental platforms, however, now allow the use of multi-omics approaches that can provide unprecedented insights into whole organisms, populations and species. While achieving a reference genome sequence for a given species had been a milestone for earlier studies, pangenomics approaches combine reference-quality genomes of several genotypes within a species, revealing significant intra-specific variation both for coding and non-coding features. Similarly, transcriptomics, proteomics and metabolomics studies, which have been around for a long time, now offer increased resolution, specificity and multiplicity. Importantly, phenomics approaches employing non-invasive imaging techniques, can provide large-scale phenotypic data to complement other omics approaches. Today, multi-omics technologies can be applied to hundreds of individuals in a single experiment, in search of not only candidate genes but also candidate pathways that can be exploited in breeding schemes. Consequently, we stand at a position where it is no longer challenging to access big data but to analyze it. These challenges also bring unique opportunities that can ensure the food security of upcoming generations.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Exploiting Genome Editing into Elite Wheat Cultivars by Deploying Morphological Gene

Dr. Sadiye Hayta

John Innes Centre, Department of Crop Genetics, Norwich Research Park, Norwich, Norfolk, NR4 7UH.

s.hayta@ues.ac.uk

New breeding technologies such as genome editing allow precise DNA manipulation, but its potential is limited by low regeneration efficiencies in tissue culture and lack of transformable genotypes. Wheat is one of the most recalcitrant crops to transform.

We developed, in the hexaploid spring wheat cultivar ‘Fielder’, an efficient and reproducible *Agrobacterium*-mediated transformation system. This high-throughput robust transformation system has been used effectively to introduce genes of interest, for over-expression, RNAi and for CRISPR-Cas based genome editing. Transformation efficiencies of up to 33% in ‘Fielder’ and 10% in the tetraploid durum wheat ‘Kronos’ were achieved.

The wheat Growth-Regulating Factor 4 (GRF4) and its cofactor GRF-Interacting Factor 1 (GIF1) is a recent development for wheat transformation by the Dubcovsky Lab at UC Davis, USA. When this protein fusion is overexpressed, it improves the regeneration of *in vitro* growing plant cells. We included and tested this technology with our wheat transformation protocol, the transformation efficiencies increased to 77.5% in ‘Fielder’, 70% in ‘Kronos’ and we expand the technology into different wheat varieties like Cadenza and elite wheat cultivars.

The GRF4-GIF1 technology results in fertile transgenic plants, giving a “normal” phenotype in low transgene copy plants without the need of specialized promoters or transgene excision, overcoming some of the limitations of transformation technologies with other morphogenic developmental regulating genes. It is an ideal technology to expand the utilization of genome editing technology to crops with low regeneration efficiencies.

It is envisaged that these developmental regulators alleviate some of the cultivar dependence of wheat transformation and, so doing, enable the more efficient and rapid transformation and genome editing of elite wheat cultivars. Presently, we are using this system in range wheat varieties looking at gene function and trait improvement.

ORAL PRESENTATIONS
FOOD AND INDUSTRIAL BIOTECHNOLOGY
YELLOW/WHITE SESSIONS

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

The Effect of Microwave Treatment on Gene Expression Level of Argonaute (AGO) and Phosphoglycerate Kinase (Pgk3) Genes in Maize (*Zea mays*) L. Flours

Begüm Zeynep Hancerliogullari¹, Umut Toprak², Remziye Yilmaz¹

¹Hacettepe University, Faculty of Engineering, Department of Food Engineering, FoodOmics Laboratory, Ankara, 06800, TÜRKİYE

²Division of Neuroblastoma Genomics, German Cancer Research Center (DKFZ), Im Neuenheimer Feld 280, Heidelberg, 69120, GERMANY.

Argonaute (AGO) proteins play a role in the basis of transcriptional gene silencing. The maize (*Zea mays*) genome encodes 17 AGO proteins among plants. Further, in plants, Phosphoglycerate Kinase (PGK, E.C. 2.7.2.3) is a key enzyme involved in both glycolysis and photosynthetic carbon metabolism. *Zea mays* var. B73 genome contains five genes putatively encoding PGK, and ZmPgk3 is important to produce ATP. As the members of the maize gene family, ZmAGO1a and ZmPgk3 gene expressions may respond to environmental conditions. In this study, the expression level of two different maize genes, ZmAGO1a and ZmPgk3, were investigated under microwave heat treatment using reverse transcription-quantitative polymerase chain reaction (RT-qPCR). Accordingly, absolute quantification analysis was performed separately by comparison of the gene expression levels between MIR604 and MON810 maize flours with different GM content (%) and their microwave-treated counterparts. Statistically significant differences in expression levels between these samples were identified using Post Hoc Tukey tests, $p < 0.05$. Consequently, for ZmAGO1a, it was found that no significant difference between MIR604 (0% GM) and its microwave-treated sample. However, the expression of ZmAGO1a in MIR604 (75% GM) slightly changed, about the one-log fold, compared to its heat-treated sample. Furthermore, it was observed that gene expression levels of ZmAGO1a were close to each other for MON810 maize flour samples with 0% and 5% GM content, in response to heat treatment. Subsequently, qPCR revealed that the expression of ZmPgk3 in MIR604 (0%) down-regulated about the one-log fold, which was similar to the pattern of gene regulation in MIR604 (75%) under microwave treatment. Besides, the microwave heat treatment had no significant effect in both MON810 0% and 5% for the studied ZmPgk3 gene. These results provide information for further study on the function of AGO and PGK genes under different heat treatments in maize flour.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Food Grade Biopigments Versus Synthetic Colorants

Didar Ucuncuoglu¹

¹Çankırı Karatekin University, Çankırı, TÜRKİYE

²Yoka Fonksiyonel Gıda San. Tic. Ltd. Şti., Çankırı, TÜRKİYE

Spirulina, Chlorella, Phaeodactylum, Nannochloropsis, Dunaliella, Cryptothecodinium, Schizochytrium, and Nitzschia which are the microbial photoautotrophic species listed on "Generally Recognized as Safe" (GRAS) as a safe source of food colorant by the Food and Drug Administration (FDA), USA. Microalgae-derived pigments are commonly used in the food industry as a functional food additive type. Moreover, carotenoid compounds are utilized as color enhancers and additives because of their excellent antioxidant properties that prevent oxidative reactions in lipid-rich food products. The pigments extracted from microalgae are scientifically proven with their several health-promoting effects and the unique properties of being harmless to the environment. As a result, the demand for commercial use is gradually increasing. However, producing algae on a huge scale is limited due to some cultural or environmental parameters. Accordingly, algal strains should be optimized genetically to improve the synthesized pigment amount. This review's scope is to summarize the biotechnological production of pigments and demonstrate current implementations in the food industry. Further, the expected studies are discussed for near-future applications.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

In Silico CRISPR-Cas Based Screening of *Lactococcus lactis* ASM2046375v1

Bilge Yilmaz¹, Remziye Yilmaz¹

¹Hacettepe University, Ankara, TÜRKİYE

It is of great importance to ensure the quality of food, which has become one of the most important factors in the food industry today, and to prevent both food and raw material losses. Considering lactic acid bacteria such as *Lactococcus lactis*, which is frequently used in the cheese industry, it is very important to eliminate the bacteriophage problem. The bacteriophages to which bacteria can be exposed are one of the biggest problems in the industry and directly affects the use of bacteria in the food production process. For this reason, CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats)-Cas (CRISPR-related endonuclease protein) technology, which was developed based on the autoimmune system developed by bacteria against bacteriophages, has gained great importance, especially in recent years. The detection of CRISPR-cas loci that affect the phage immunity of bacteria that are frequently used in the industry plays a critical role in the selection of cultures used in the production process, the control of the fermentation process, and the prevention of food losses. It aimed to perform an analysis of the formation of CRISPR-Cas systems in the genomes of *L.lactis* ASM2046375v1 (NZ_CP059048.1) bacteria in silico phase of this study. As a result of the study, it is important to determine the Endonuclease Cas9 gene regions which are unique for CRISPR Type II-A systems. For this purpose, various databases such as NCBI (US National Biotechnology Information Center) and CRISPRCasFinder were used in this study. Thanks to the databases; whole genome sequences, spacers, and Cas contents of bacteria can be obtained easily. For further study, it will be possible to investigate the CRISPR-Cas loci of lactic acid bacteria with instrumental studies to be carried out following DNA isolation and a comparative analysis of the obtained information on the database.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Towards The Determination Of Plant Species That Constitute Bingöl Honey Though Recent Meta Molecular Analysis

Veysel Süzerer¹ , İlkay Ünal² , Yelda Özden Çiftçi²

¹Bingöl University, Bingöl, TÜRKİYE

²Gebze Technical University, Kocaeli, TÜRKİYE

Bingöl honey is a flower honey that contains the nectar of many plants and has received degrees in many international organizations. There are many methods in order to determine the botanical origins of honey. Among them, melissopalynology, the traditional method used in this sense, is based on microscopic examination of the pollen content of honey. Although successful results are obtained with this method, the technique not only requires experts with experience to separate pollen grains of different morphology which is also laborious, but also takes a relatively long time. However, it is difficult to determine the whole plant diversity in honey with melissopalynological analysis. With the development of molecular techniques, this problem is tried to overcome by especially using metagenomics and metabarcoding of environmental DNA (e-DNA) isolated from honey. Hence, In this study, e-DNA is isolated from Bingöl honey were subjected to both metabarcoding and shotgun metagenomic studies. As a result of the bioinformatics analyzes obtained after the next generation sequencing, the plants that contribute to Bingöl honey were identified on the basis of family, genus and species. In the light of the information obtained, not only the flora content of Bingöl honey but also the prokaryotic content was defined. In conclusion, our results demonstrated that these molecular approaches could be used to reveal out botanical origins of Bingöl honey as well as other national and international honeys. This work was supported by ScientificResearch Projects Coordination Unit of Bingöl University. Project number PİKOM-AR1-2019.003

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Approaches for Metagenomic Examination of Fermented Food Products

Ozlem Isik Dogan¹ , Remziye Yilmaz¹

¹FoodOmics Research Laboratory, Department of Food Engineering, Hacettepe University, Beytepe Campus, 06800 Ankara, TÜRKİYE

²Central Research Institute of Food and Feed Control, 16160 Bursa, TÜRKİYE

Fermentation is an ancient food preserving technique that improves both functional and textural properties of food product. Various microbial interactions, e.g. competition, elimination and microbial adaptation, take place during fermentation process, and the end-product is a result of these activities. In this study, a food fermentation process involving both lactic acid bacteria and yeast fermentations was chosen as a model system to present a flow chart for high throughput sequencing analysis of the microbiota. Here, metagenomic DNA extraction and isolation of food samples were applied with QIAamp® Fast DNA Stool Mini Kit (Qiagen), and DNA concentration was measured via PicoGreen. Illumina MiSeq platform was used for high throughput sequencing after amplification of V3-V4 regions of bacterial 16S rRNA gene and ITS3-ITS4 regions of fungal 18S rRNA gene. As bioinformatics, quality analysis of reads via FastQC, trimming of adapters via CUTADAPT and merging via USEARCH were performed. After generation of operational taxonomic units, taxonomy assignments were determined regarding >60% confidence level. Also, alpha diversity calculations measured via Phyloseq and Vegan. The results of this study provided a method for metagenomic analysis of a fermented food at species level. Further studies could enable to examine the microbial interactions from raw materials to end-product during fermentation process in terms of controlled and enhanced food production.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Role of Nanotechnology in Food and Biotechnology Sector

Simple Sharma¹

¹I.K. Gujral Punjab Technical University, Kapurthala, Jalandhar

Nanotechnology involves the study and manipulation of materials at atomic, molecular, and macromolecular scale and macromolecular scales. The study of properties that vary significantly from those at a larger scale. It involves the characterization, fabrication, and/or manipulation of structures, devices, or materials that have at least a dimension of approximately 1-100 nm in size. Nanotechnology is advancing technology in the field of food and biotechnology. In food industries, the potential of nanotechnology utilized in functional food, design of nutritional supplements and nutraceuticals containing nano-sized ingredients and additives such as; vitamins, antimicrobials, antioxidants, and preservatives are currently available for enhanced taste, absorption, and bioavailability. During food processing, nanoparticles have been applied to improve nutritional quality, flow properties, flavor, color, and stability or to increase shelf life. Indeed, nanotechnology might help in the development of healthier food with lower fat, sugar, and salts to overcome many food-related diseases. The nanotechnology role in the biotechnology discipline provides approaches that are developed to improve the traditional biotechnological aspects. Nanobiotechnology remarkably improved the efficiency of different techniques including drug delivery, soil and water remediation, and enzymatic processes. It also involves the interaction of cellular and molecular components and engineered materials. It has immense opportunities to target and modify the behavior of cells and tissues at the nanoscale. Integration of bio- and nanotechnologies is transforming the way we detect, treat and monitor disease and thus resolve to exist and emerging medical problems. In its widest sense, nanotechnology is a natural part of food processing and conventional foods because the characteristic properties of many foods rely on nanometre-sized components. As developments in nanotechnology continue to emerge, its applicability to the food industry and biotechnology will increase potentially.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Analysis of Protein Secretion by Baker's Yeast (*Saccharomyces cerevisiae*)

Ipek Ceren Yesildag¹, Remziye Yilmaz¹, Hilal Akin², Hilal Ruzgar², Serafettin Yazici²

¹Hacettepe University Department of Food Engineering FoodOmics Research Laboratory, Ankara,
TÜRKİYE

²Tunay Food, Ankara, TÜRKİYE

Baker's yeast (*Saccharomyces cerevisiae*) is one of the most important and widely used cell factories for protein production. Nevertheless, Its productivity is still relatively low, and with increasing market demand, it is important to identify new strains which are valuable hosts for the production of protein with a wide array of applications. Here, we analyzed the protein secretion level of the original (*Saccharomyces cerevisiae*) strains to understand their capability of protein production. The original and local (*S.cerevisiae*) strains in the FoodOmics Laboratory Culture Collection were evaluated according to their ability to secrete microbial protein. Grape juice was chosen as the medium and in order to enhance the secretory pathway, 1% yeast extract powder was added to grape juice and fermentation was carried out for 72 hours at 28°C. During the fermentation, to compare the original (*S. Cerevisiae*) (HUF16M1C0004, HUF16M2K10004, HUF16M3G11088 and HUF16M3H11101) and control (HUF16M1C0002) strains, the growth of the strains and the amount of secretion protein were monitored. As a result, specific growth rate coefficients of the studied strains were found in the range of 0.23-2.52 h⁻¹. The 0.66–1,62 g/L of microbial protein was obtained after 48 hours of fermentation, and 1,64-1,96 g/L at the end of 72 hours. The protein content was found to be significantly higher than some previous studies on (*S. Cerevisiae*). And we have successfully detected extracellular levels of proteins to choose some strains for further studies.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Use Of Real-Time PCR And High-Resolution Melting Analysis For The Identification And Discrimination Of *Saccharomyces boulardii* Strains By *AAD15* And *MAL11* Genes

Beyza Sayman¹ , Remziye Yilmaz¹

¹Hacettepe University, Ankara, TÜRKİYE

With the awareness of healthy nutrition developing around the world, foods have ceased to be only for nutritional purposes, and the demand for functional foods has increased at a high rate. Functional foods are frequently preferred due to their features such as providing basic nutritional requirements as well as having a positive effect on chronic diseases and gastrointestinal health. Various microorganisms can be used for foods to have functional properties. *Saccharomyces cerevisiae* var. *boulardii* is a probiotic yeast that can provide functionality. The use of *S. boulardii*, a variety of *S. cerevisiae* which is one of the most used microorganism worldwide, is frequently preferred in the food industry. *S. boulardii*, which has been proven to be effective especially in the treatment of diarrhea by *in vivo* and *in vitro* studies, can provide advantage against other microorganisms, mainly due to its ability to grow optimally at body temperature and to remain viable even at gastric pH. The aim of this study was to design a new High-Resolution Melting Analysis (HRMA) assay to differentiate *Saccharomyces boulardii* with *Saccharomyces cerevisiae* by two new primers specifically designed for both *AAD15* and *MAL11* genes for this study. HRMA is a cost effective and fast method being used for gene scanning and genotyping. For the rtPCR-HRMA all of the *Saccharomyces cerevisiae* strains were provided by FoodOmics Culture Collection. Considering the optimum growth temperatures and viability at gastric pH, one of the strains were suitable for DNA extraction followed by HRMA. For control *S. cerevisiae* var. *boulardii* CNCM I-745® and *S. cerevisiae* ATCC®9763 were used. As a result, both primers for *AAD15* and *MAL11* genes were successfully able to differentiate *S. cerevisiae* var. *boulardii* strains by using rtPCR-HRMA.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Effect of Bitter Melon Peel Powder on Functional Properties of Edible Films

Nurcennet Erturk¹, Suzan Biran Ay²

¹Eskisehir Technical University, Eskişehir, TÜRKİYE

²Eskisehir Technical University, Eskişehir, TÜRKİYE

Bitter melon (*Momordica charantia*) has been known for ages and it has been used in many traditional and folk medicines for a wide range of medical applications such as obesity, bacterial and viral infections, bone, and skin diseases. The fruits of the plant are rich in phytochemicals offering nutritional and nutraceutical components. Addition of these nutraceuticals to edible film formulations can enhance the functional properties of packaging materials, increase the nutritional value and extend the shelf-life of the food. In this study, bitter melon peel powder was used to increase the antioxidant content of rye flour-based films plasticized with ethylene glycol. In the composite preparation, 5% (w/v) rye flour was mixed with different concentrations of ethylene glycol (40-100% (w/w flour)) in water and cooked for half an hour; then, it was cooled to 40°C and bitter melon peel powder (25-50% (w/w rye flour)) was added and the mixtures were poured into petri dishes to dry overnight at 35°. Characterization of the films was performed by thermogravimetric analysis (TGA) and Fourier transform infra-red (FTIR) spectroscopy. Films' thickness, opacity, percent elongation and tensile strength, water vapor permeability, water solubility, antioxidant activity and total phenolic content were also investigated. In general, increasing concentrations of ethylene glycol and *Momordica charantia* peel powder, resulted in increased thickness, solubility, total phenolic content (TPC) and antioxidant activity. The thickness of films varied between 0.078 and 0.153 mm, solubility between 55 and 74%, TPC between 0.9 and 3.6 mg gallic acid equivalents/g film, and antioxidant activity between 0-5% inhibition. While the tensile strength of films decreased from 7.47 to 1.62 MPa, the water vapor permeability remained as 1.02 ng/m.s.Pa, and percent elongation around 32%. *M. charantia* powder reduced the mechanical strength, but improved the TPC of composites, making them suitable as inner packaging materials for food.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

**Investigation of Antibacterial Effects of Some Safflower (*Carthamus L.*,
Asteraceae) Flowers Against *Salmonella enteritidis*, *Escherichia coli*,
Staphylococcus aureus and *Bacillus cereus***

Melike Erol Demirbilek¹, Gozde Celik Ozer², Canan Yagci Tuzun³, Oguzhan Aydin⁴, Burcu Tarikahya Hacıoglu⁵, Yusuf Arslan⁶, Ilhan Subasi⁶

¹Field Crops Central Research Institute, Biotechnology Research Center, Ankara, TÜRKİYE

²General Directorate Of Agricultural Research And Policies, Department of Field Crops Research, Ankara, TÜRKİYE

³Mediterranean Fisheries Research, Production And Training Institute, Department of Aquaculture, Ankara, TÜRKİYE

⁴Field Crops Central Research Institute, Department of Breeding and Genetics, Ankara, TÜRKİYE

⁵Hacettepe University, Faculty of Science, Ankara, TÜRKİYE

⁶Bolu Abant İzzet Baysal University, Faculty of Agriculture, Bolu, TÜRKİYE

Carthamus (*Carthamus* spp.- Asteraceae), is an annual fat plant and resistant to drought. Its flowers are used in food as coloring, flavoring and stabilizing. *Carthamus* (safflower) is known to have antibacterial activity. Antibacterial activity is an effect that kills bacteria or prevents bacterial development and reproduction. It also destroys any pathogenic/non-pathogenic undesirable bacteria in foods. Using random, unconscious and long-lasting antibacterials/synthetics cause a series of animal anomalies, animal food contamination, economic loss and the spread of multiple resistant bacterial strains. The use of plant extracts as antibacterial is increasing in order to minimize bacterial contamination and prolong food preservation period. Therefore, it is recommended that plant extracts which have antibacterial activity be used against pathogenic bacteria in the poultry, livestock, food, feed, agriculture and health sectors. The aim of our study was to reveal the antibacterial effect of safflower flowers against *Salmonella enteritidis*, *Escherichia coli*, *Staphylococcus aureus* and *Bacillus cereus* that are pathogenic for poultry, food and human. For this purpose, methanol extracts of flowers of *Carthamus tinctorius* L. cv Dinçer, *C.lanatus*, *C.tenius*, *C.persicus*, *C.glaucus* and *C.dentatus* were prepared. Antibacterial activity studies were performed according to the disk diffusion (Kirby Bauer) method. Each flower sample was investigated at seven different concentrations and studied in duplicate. EUCAST quality control discs were used as positive controls. According to our studies, all samples exhibited antibacterial activity against *S.aureus* in the range of 25-200 mg/ml extract concentrations. Only 100 mg/ml concentration of *C.tinctorius* flower showed antibacterial activity against *E.coli*, although flowers of four plants showed antibacterial activity at 75 mg/ml concentration against *B.cereus*. None of the extract showed any activity against *Salmonella enteritidis*. Consequently, because of antibacterial effect against *E.coli*, *S.aureus* and *B.cereus*, *Carthamus* extracts can be used in many areas especially food, health, pharmacy, feed and raising livestock.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Differences in Technological Properties Between *Saccharomyces Cerevisiae* and Non-*Saccharomyces* Yeast

Elif Bircan Muyanli¹ , Remziye Yilmaz¹

¹Hacettepe University, Department of Food Engineering, FoodOmics Research Laboratory, Beytepe Campus, 06800, Ankara, TÜRKİYE

In many studies conducted in recent years, the importance of using non-*Saccharomyces* yeasts in fermentation has been demonstrated in solving current problems in the production of quality wine and in the fermentation industry. In this study, differences in technological properties of *Saccharomyces cerevisiae*(Sc) and non-*Saccharomyces Metschnikowia pulcherrima*(Mp) yeasts used in alcohol fermentation were demonstrated. This study aims to detect the differences between the fermentation characteristics of Sc and Mp strains. For this purpose, the study focuses on monitoring the technological properties of strains during fermentation using Mp, Sc pure cultures. In the study, 16 Sc and 6 Mp strains isolated from different regions of Anatolia and identified in previous studies have been used in Hacettepe University FoodOmics Research Laboratory Culture Bank. Then, technological properties such as growth at high temperature, growth at low pH and fermentation rates of all selected Mp and Sc strains were investigated. The development of strains at 37 and 42 °C grape juice was monitored and their growth characteristics at high temperature were investigated. The growth characteristics of the strains at low pH were determined by examining their growth in grape juices adjusted to different pH values. In order to examine the fermentation rates of the strains, alcohol production, sugar consumption and foam formation were monitored during pure culture fermentation of Sc and Mp strains. In conclusion, in the study, obvious differences were found between the technological properties of Mp and Sc yeast isolated and identified from original/local sources. As a result of pure culture fermentation of strains, % Brix-Day graph slopes of Sc strains varied between (-2.11)-(-1.99). This value is (-0.68)-(-0.54) in Mp strains. In addition, alcohol production in Sc pure culture fermentation occurred on the 5th day of fermentation, while alcohol production was detected on the 11th day in Mp pure culture fermentation.

**ORAL PRESENTATIONS
BIONFORMATIC AND NANOBIO TECHNOLOGY
GOLD SESSION**

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Rnai Silencing by Prokaryotic Gene Sources

Omur Baysal¹ , Esra Demiral¹

¹Muğla Sıtkı Koçman University, Muğla, TÜRKİYE

The productivity and quality of plants are significantly affected by plant diseases and pests. Pesticides increase agricultural productivity by the protective effect on plants but cause non-target contamination which endangers human health and leads to environmental pollution. Uncontrolled pesticide application results in habitat destruction, the extinction of some insect species, climate change, and increasing residue on foods. Therefore, it is critical to develop environmentally friendly and user-friendly solutions for sustainable agriculture. RNA interference (RNAi) is a type of natural gene silencing. It is an effective tool for studying gene function and biological control of agricultural pests and pathogens. RNAi applications in agriculture are based on transgenic approaches in transgenic plants expressing double-stranded RNAs (dsRNA) in sequence-specific silencing of the target gene. RNA Interference (RNAi) is the silencing of a target gene based on its sequence. In eukaryotic organisms, RNAi silencing technology is widely used. We shifted our focus to prokaryotes in search of small fragments that could effectively interfere with RNA. We believe that small non-coding RNA like fragments in genome of prokaryotes could be used the RNAi mechanism to attack eukaryotes and their control in practice. Our bioinformatic analysis and data have shown its possibility on the selected sequences of whole genome sequences of reference genome data belonging to *Bacillus amyloliquefaciens* EU07.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Liposomal Encapsulation of Green Synthesis Silver Nanoparticles Using Green Algae (*Ulva lactuca*) and Investigate of Antibacterial Effect

Hilal Yavuz¹ , Inci Tuney Kizilkaya² , Mehmet Kahraman³ , Munevver Muge Cagal¹

¹Bursa Technical University, Bursa, TÜRKİYE

²Ege University, İzmir, TÜRKİYE

³Gaziantep University, Gaziantep, TÜRKİYE

The green synthesis method is environmentally, friendly and reliable for silver nanoparticles. Liposome structures are using as drug delivery systems or biological membranes. The aim of this study is to compare the antibacterial effects of silver nanoparticles (AgNPs) and liposome encapsulated silver nanoparticles (LE-AgNP), using reliable and nontoxic methods. AgNPs were biosynthesized from the aqueous extract of *Ulva lactuca*, a type of green algae. The aqueous extract was prepared from the algae, which was dried and cut into small pieces, at a concentration of 5% g/mL at 60 degrees for 30 minutes. Then, 45 mL of 1mM AgNO₃ and 5 mL of 5% extract were boiled for 2 hours and then stirred for 24 hours at room temperature on a magnetic stirrer. AgNP formation was checked in UV-spectrophotometer for certain periods. Characterization of AgNPs was done by SEM. The liposome solution was prepared by homogenization method with the help of a sonicator and the AgNPs were loaded into it. Liposome-AgNP ratio was prepared as 1:1, 1:0.50,1:0.25. Encapsulation activities were measured. Antibacterial effects of the samples were observed on *Escherichia coli* ATCC 25922 and *Staphylococcus aureus* ATCC 25923 by three repetitive disk diffusion method. The results showed that the antibacterial effect of LE-AgNP at a ratio of 1:1 with AgNPs was almost the same. No antibacterial effect was observed at other ratios. The study showed that; the same antibacterial effects can be achieved by using less AgNP with liposomal encapsulation. Also, the toxic effect of silver at high doses can be reduced by the help of liposomal formulation.

**ORAL PRESENTATIONS
AGRICULTURAL BIOTECHNOLOGY
GREEN SESSION**

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

The Mutant B-Type Response Regulator Hst1 Gene Regulates Transcriptomic Response to Provide Salinity Tolerance by Reprogramming Transcription Factors and Cytokinin Signaling Genes In Rice (*Oryza Sativa L.*)

Murat Aycan¹, Lutfun Nahar², Marouane Baslam¹, Toshiaki Mitsui¹

¹Laboratory of Biochemistry, Faculty of Agriculture, Niigata University, Niigata, JAPAN.

²Department of Life and Food Sciences, Graduate School of Science and Technology, Niigata University, Niigata, JAPAN.

Salinity is one of the serious environmental problems that limit plant yield in almost half of the agricultural fields. The hitomebore salt tolerant 1(hst1) is a mutant B-type response regulator gene that was reported to improve salinity tolerance in YNU plants. The sister line (SL) is salt-sensitive, and the nearest genomic relative of the YNU plant has the OsRR22 gene, which is the non-mutant form of the hst1 gene. Comprehensive transcriptome analysis of SL and YNU plants was performed to clarify the salinity tolerance mechanism-mediated by hst1 gene. Various transporter and gene-specific transcriptional regulator genes up-regulated in presence of hst1 gene under saline conditions, identifying that post-stress transcription factors (OsBHLH056, OsH43, OsGRAS29 and OsMADS1) contributed to improved salinity tolerance in YNU plants. Specifically, OsSalT, miR156, and OsLPT1.16 genes were up-regulated, while upstream (OsHKs and OsHPs) and downstream (plant hormone regulation, ion uptake, and cell elongation genes) regulators of the OsRR22 gene were down-regulated in YNU plants under saline conditions. Notably, the reprogramming of transcription factors, hormone regulations, and ion uptake genes indicate that these pathways are transcriptionally regulated by the hst1 gene. The findings of the regulatory role of the hst1 gene on plant transcriptome provide a greater understanding of hst1-mediated salt tolerance in rice plants. This knowledge will contribute to the understanding of the salinity tolerance mechanism in rice and the evolution of salt-tolerant crops with the ability to withstand higher salinity to ensure food security during climate change.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Isolation of LEAFY- and TERMINAL FLOWER 1-like Genes from Two *Tricyrtis* spp. Showing Different Inflorescence Architectures

Sota Takanashi¹, Masahiro Otani², Masaru Nakano²

¹Graduate School of Science and Technology, Niigata University, Niigata, JAPAN

²Faculty of Agriculture, Niigata University, Niigata, JAPAN

In *Arabidopsis thaliana*, LEAFY (LFY) and TERMINAL FLOWER 1 (TFL1), which encode plant-specific transcriptional factors, play a key role in the transition from vegetative to reproductive phases. LFY and TFL1 promotes and suppresses floral meristem induction, respectively. Interaction between LFY and TFL1 has been reported to regulate inflorescence architecture. The liliaceous ornamental plants *Tricyrtis* spp. show two types of inflorescence architecture: *T. hirta* produces both apical and axillary flowers, whereas *T. formosana* produces only apical flowers. In the present study, we isolated LFY- and TFL1-like genes from these species two as a first step toward elucidation of a molecular mechanism of inflorescence architecture determination in *Tricyrtis*. Both LFY-like genes (ThirLFY for *T. hirta* and TforLFY for *T. formosana*) encode 411 amino acid residues, and there are three amino acid substitutions between them. On the other hands, both TFL1-like genes (ThirTFL1 for *T. hirta* and TforTFL1 for *T. formosana*) encode 173 amino acids residues, and there is no amino acid substitution between them. LFY-like and TFL1-like genes have highly conserved LFY- and TFL1-specific regions, respectively. Phylogenetic analysis based on the deduced amino acid sequence showed that both LFY-like genes belong to the monocot clade and are closely related to LILFY1 (*Lilium longiflorum*) with 67.1-67.6 % identities. Both TFL1-like genes also belong to the monocot clade and are closely related to TgTFL1 (*Tulipa gesneriana*) with 84.4 % identity. We are now analyzing the function of both LFY- and TFL1-like genes by a genome-editing strategy.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

The Potential Biostimulant Effects of Macroalgae (*Cystoseira barbata*) Extracts on Broccoli Plant under Greenhouse Conditions

Yagmur Arıkan¹, Hande Mutlu Durak¹, Bahar Yıldız Kutman¹

¹Gebze Technical University, Institute of Biotechnology, Kocaeli, 41400, TÜRKİYE

Macroalgae represent the primary group of biostimulants due to their advantages because of abundant bioactive components in increasing plant growth without any negative effect on crop quality. *Cystoseira barbata*, a kind of brown seaweed that is common in Turkey, has an important potential for plant development and has never been used as a biostimulant. Broccoli is a high-value crop with rich content of mineral nutrients and phytochemicals that promote human health. The aim of the research is that the *C. barbata* extracts, prepared as 3 different extracts applied by irrigation at two different concentrations, have been tested to increase the growth parameters of broccoli (*Brassica oleracea* L. cv. Maraton) grown under greenhouse conditions. After 100 days, the plants were harvested, and plant growth characteristics were evaluated. At the intermediate period of the plants, chlorophyll, flavonoid, and anthocyanin were measured in the leaves. In addition, seaweed extracts were subjected to tests for biochemical characterizations of the extracts to better understand the potential effects of biostimulants. It was observed that increases of up to 55% of the dry weight of broccoli heads in the group treated with a low concentration of acid extraction. It was also reported that the total dry weight of the plants increased by almost 43% with a high concentration of hot water extraction application. Recent work reports the promising biostimulating effects of different extracts of *C. barbata* on broccoli grown in soil system. It can be said that various levels of potential bioactive components can have different effects on biostimulants. This research will contribute to more sustainable farming practices, increased food security worldwide, and lower production-related economic losses for broccoli. Resources from the national bioeconomy of our country can be turned into valuable goods and boost the economy. This study was supported by TUBITAK 2244 (Project number: 119C030).

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Marker-Assisted Selection (MAS) in Pepper Breeding

Cansu Simsek¹ , Duran Simsek¹ , Nedim Mutlu² , Feride Genc¹ , Dilsan Boylu¹

¹Areo Seed Co. Nebraska, USA

²Akdeniz University, Antalya, TÜRKİYE

Biotechnology is one of the trending topic in today's agriculture. Thanks to the effective integration of molecular markers into classical plant breeding, breeding for resistance has gained momentum. Marker-assisted selection (MAS) makes it possible to identify individuals within segregating populations that resistant to several diseases and selected for their superior agronomic traits. Pepper (*Capsicum annuum* L.), which is among the vegetables that is produced and consumed intensively both in the World and in our country, was used as the main material in this study. Pepper lines that will be used in the development of new hybrid varieties from the genetic sources of Areo Seed Co. have been determined on the basis of quality criteria, and it is aimed to improve resistance to these lines against Pepper Mild Mottle Virus (PMMoV), Tomato Spotted Wilt Virus (TSWV), *Phytophthora capsici* and Root-Knot Nematode using MAS method. In this context, fluorescent-labeled sequence-specific probe-based RT-PCR (real-time) method was used to determine the resistance against these diseases. In this way, the use of MAS in pepper breeding contributed to development of faster and more reliable multi-disease resistant parental lines for new hybrids.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Comparison of Biochemical and Antioxidant Activities in Different Solvent Extracts Obtained from Olive Leaves

Damla Onder¹ , Umit Erdogan² , Sercan Onder²

¹Süleyman Demirel University, Isparta, TÜRKİYE

²Isparta University of Applied Sciences, Isparta, TÜRKİYE

Olive (*Olea europaea*) leaves are considered to have great potential as natural sources of antioxidants and phenolic compounds. In this study, dried olive leaves were extracted with 4 different solvents (water, methanol, ethanol and 80:20 methanol-water) and biochemical (total phenolics and flavonoid, total protein, free amino acids, soluble and reducing sugars) and antioxidant activities (CUPric reducing antioxidant capacity (CUPRAC), 2,2-diphenyl-1-picrylhydrazyl (DPPH), ferric reducing antioxidant potential (FRAP) and ferrous ion-chelating ability) of these extracts were evaluated. Total phenolics content was significantly ($p \leq 0.05$) affected by the different solvents and the highest total phenolics content was obtained in methanol-water extraction. The highest total flavonoid and total protein contents were observed in methanol and ethanol extraction. The free amino acids content was lowest in ethanol (1.5 mg g⁻¹), while it was highest in water (2.3 mg g⁻¹) and methanol-water (2.2 mg g⁻¹) extraction. The highest total soluble sugars content was obtained from methanol-water (70.4 mg g⁻¹) and ethanol (65.4 mg g⁻¹) extraction, while the highest total reducing sugars content was found in methanol (112.2 mg g⁻¹) and methanol-water (111.6 mg g⁻¹) extraction. While methanol-water extraction showed the highest antioxidant capacity with 0.63 mmol TR g⁻¹ CUPRAC value, it also showed the strongest radical scavenging activity with 1.09 mmol TR g⁻¹ DPPH radicals value and 0.065 mmol TR g⁻¹ ferric reducing antioxidant potential value. The ferrous ion-chelating ability was higher than the water extraction. Correlation analysis between biochemical and antioxidant activities revealed 5 significant correlations and 4 of which were positive. Methanol and methanol-water (80:20) solvents are the most effective extractions for measuring phenolic and antioxidant activities.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Cold Tolerance in Some Camelina (*Camelina Sativa* (L.) Crantz) Genotypes Under Controlled Conditions

Banu Efeoglu¹ , Ozge Celik² , Melike Erol Demirbilek¹ , Nilufer Kocak Sahin³ , Oguzhan Aydin¹ , Ilhan Subası⁴ , Yusuf Aslan⁴

¹Central Research Institute for Field Crops, Ankara, TÜRKİYE

²İstanbul Kültür University, İstanbul, TÜRKİYE

³Ankara University, Ankara, TÜRKİYE

⁴Abant İzzet Baysal University, Bolu, TÜRKİYE

Camelina plant (*Camelina sativa* (L.) Crantz) is an alternative annual oilseed crop which has an increasing economical importance of late years and planned to be actively cultivated in Turkey. When it is used as winter cultivar, low temperature affects plant growth and causes significant crop yield especially in rosette stage. Therefore, cold tolerant camelina genotypes are necessary to develop suitable cultivars for winter planting and to improve camelina production in cold highlands. Degree of tolerance to cold stress of some camelina genotypes was evaluated by means of physiological and biochemical analyses in the proposed study. For this purpose, controlled freezing tests were applied to 34 genotypes provided from U.S.A. seed gene bank and one camelina line named Aslanbey developed by Central Research Institute for Field Crops proportional injury and malondialdehyde concentrations were determined. Degree of tolerance of the genotypes to cold stress were evaluated according to the results. Genotypes which have cold tolerance can be recommended as suitable gen source for breeding programs.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Callus and Suspension Culture Techniques Optimized for Use in Carrot Breeding Studies (*Daucus Carota Ssp. Sativus var. atrorubens Alef* and *D. carota*)

Damla Turan Buyukdinc¹ , K. Yaprak Kantoglu² , Arzu Karatas¹ , S. Sebnem Ellialtioglu³

¹*Recep Tayyip Erdogan University, Faculty of Agriculture, Department of Horticulture, Pazar-RİZE, TÜRKİYE

²Turkish Energy Nuclear and Mineral Research Agency, Nuclear Energy Research Institute - Ankara, TÜRKİYE

³Ankara University, Ankara Üniversitesi Teknokent, Doqutech Academy Ltd. Şti.,Gölbaşı-Ankara, TÜRKİYE

The callus and suspension culture methods for in vitro mutant breeding in carrots were optimized in this study (*Daucus carota ssp. sativus var. atrorubens Alef* and *D. carota*). Following this, the generated mutant lines were selected using in vitro salt stress. In the study, which started with the sowing of carrot seeds in Murashige and Skoog's (1962) basic nutritional medium at 6 g/L, 7 g/L, 8 g/L, and 15 g/L, the agar dose at which germination and plant growth were the best in the initial stage was discovered. First and 50% germination, root, cotyledon and genuine leaf formation in carrot seedlings whose plant development was tracked for two weeks were inspected and analyzed daily in the study, was continued with the determined 7g/L agardose. The cotyledon and hypocotyl explants collected from the carrot seedlings were cultivated for callus production in mixtures of MS-1, MS-2, and MS-3 nutritional medium. Second and fourth weeks following the second subculture, callus production percentages and weights were measured. The MS-3 (1 mg/L 2,4-D + 0.5 mg/L kinetin)(Herdem 1998)) nutritional medium and hypocotyl explant were found to be particularly effective at producing callus. The data from the second subculture, which was acquired from carrot calluses subcultured every three weeks, revealed that the MS nutritional medium with 0.2 mg/L TDZ was the optimal medium for plant regeneration. The scattered calli were cultured on a nutrient medium made up of MS + 0.1 mg/L kinetin that was intended for suspension culture. After three weeks, the scattered calli were subcultured in MS solid nutritional medium without plant growth regulator and found to be the most effective medium for plant regeneration. The results obtained with the optimization steps were used in ongoing study. Selection studies carried out on plants which were regenerated from carrot callus tissues exposed to mutation applications and subsequently salt stress.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Comparative Response of Coated and Commercial Urea on Lettuce Production and Nitrogen Contents

Saima Kalsoom Babar¹ , Mahnoor Baloch¹ , Shakeel Ahmed Babar²

¹Department of Soil Science, Sindh Agriculture University Tandojam, 70060, PAKISTAN

²Agriculture Research Centre Tandojam, PAKISTAN

Nitrogen (N) losses from agricultural fields are observed especially from urea. Coated urea might be one of its solutions, as it may improve crop yield by limiting the hazardous emission of ammonia (NH₃). The present study compared the response of coated and commercial urea on lettuce production and N contents based on these objects: 1) to compare performance of palm stearin coated urea with commercial urea for lettuce production and 2) to determine the N-concentration in lettuce plants. A controlled greenhouse conditions' experiment was conducted at Department of Soil Science, Sindh Agriculture University Tandojam. Treatments in CRD with four replications were applied, T1: control, T2 & T3: 120 & 140 kg N ha⁻¹ conventional urea, T4 & T5: 120 & 140 kg N ha⁻¹ coated urea. The results showed that the substantial effect of coated urea in efficient N use on biomass production and N accumulation in lettuce plants. The maximum fresh weight (93.50 g pot⁻¹), dry weight (5.72g pot⁻¹), No of leaves (22 pot⁻¹), N contents in plants (4.49 %), N contents in soil (1.05 %) after harvesting were recorded at the rate of 140 kg N ha⁻¹ from coated urea application. There was also a significant effect ($p < 0.05$) between variable rates and methods. It is concluded that the urea can be applied in coated form with natural polymers in order to reduce N losses and increase crop yield. However, coated urea maintained higher growth of lettuce as compared to conventional urea. It is suggested to compare the efficiency of coated urea on various seasonal crops and evaluated N-uptake in contrast to commercial urea.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Seaweed Liquid Extracts (*Cystoseira barbata*) as a Biostimulant Agents for Wheat Plant

Hande Mutlu Durak¹ , Yagmur Arikan¹ , Bahar Yildiz Kutman¹

¹Gebze Technical University, Institute of Biotechnology, Kocaeli, 41400, TÜRKİYE

It is crucial to do research to improve seed performance, which is crucial for the plant's healthy life cycle, and to use biostimulants prior to planting in the plant. One of the most significant types of biostimulants that can be used in a variety of application methods is seaweed extracts. It is well known that seaweed extracts, which have a biostimulant effect because of their abundant bioactive ingredients, significantly improve the primary and secondary metabolism of plants. The brown seaweed *Cystoseira barbata*, which is widely distributed in Turkey and has a significant potential to influence plant development through biostimulants, has never been the focus of biostimulant study. Different concentrations of different seaweed extracts (water, alkali, and acid) were utilized as a seed treatment agent, and the potential effects of various seaweed extracts derived from *C. barbata*, a brown algae species collected from the Tuzla coast, were studied on germination and short-term growth of summer durum wheat (*Triticum durum* cv. Sariçanak-98). To better understand the potential effects of *C. barbata* extracts, biochemical tests that are thought to play an active role in the mechanism of action on the plant were performed. According to the findings, seaweed-based biostimulants may help wheat seedlings perform better and have a positive impact on several short-term growth parameters including shoot and shoot length, as well as root morphology system-related parameters including root biomass, root length, root area and root volume. As a result, *C. barbata* extracts can be used as a biostimulant in agriculture may help to reduce crop production costs and promote sustainable farming practices and global food security. Macroalgae may be transformed into distinctive bioeconomy resources, resulting in high-value-added, renewable, promising, and sustainable commercial products that could lessen the need for chemical fertilizers. This study was supported by TUBITAK 3501 (Project number: 121Z215).

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Optimization of Indole-3-Acetic Acid Biosynthesis in a Native *Bacillus subtilis* Isolate

Nil Basak Top Kilic¹ , Omer Can Unuvar² , Ercan Selcuk Unlu¹

¹Bolu Abant İzzet Baysal University, Faculty of Arts and Science, Department of Chemistry, Bolu, 14030, TÜRKİYE

²Bolu Abant İzzet Baysal University, Faculty of Arts and Science, Department of Biology, Bolu, 14030, TÜRKİYE

Plant growth promoting bacteria (PGPB) are promising alternative to support plant growth in sustainable agriculture. *Bacillus subtilis* is a well-known PGPB with notable effects on promoting plant growth along with root elongation. Its ability to synthesize indole-3-acetic acid (IAA) is associated with enhancement of root quality. Thus, IAA is a highly demanded natural biocontrol agent in agricultural activities. There are limited number of studies related with increasing the yield of IAA biosynthesis in native *B. subtilis* species. The primary goal of the study is to optimize the culture conditions for increased IAA biosynthesis in *B. subtilis* strain ESU181 which was isolated from the roots of a local Einkorn wheat. IAA production was monitored for bacterial cells incubated at different temperatures (30°C and 37°C) and pH conditions (6.5, 7.5, and 8.5). The experiments were continued for 96 hours while taking measurements for every 24-hour intervals. Since there are two known mechanisms of IAA biosynthesis regarding to tryptophan dependency, we used two sets of growth media that include the same nutrient content with or without additional tryptophan. Our data showed that the highest IAA concentration was obtained at the 96th hour when bacteria were incubated in tryptophan supplemented media at pH 8.5 and 37°C. Our results also showed that biosynthesis of IAA is highly dependent on the differences of pH conditions while the impact of the additional tryptophan on IAA biosynthesis was not as high as expected in *B. subtilis* strain ESU181. The data presented in this study can be adapted for stimulating in situ IAA biosynthesis in soil and for the biotechnological production of IAA.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Drought Stress Induces Pattern-Triggered Immunity Highly Associated With Quantitative Disease Resistance In Brassica Oleracea

Hicret Asli Yalcın¹, Abraham G. Gutierrez², Christopher J. Ridout², Burkhard Steuernagel³, Peter G. Walley⁴

¹Life Sciences, Industrial Biotechnology Research Group, TÜBİTAK Marmara Research Center, Kocaeli TÜRKİYE

²Department of Crop Genetics, John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, UK

³Department of Computational and System Biology, John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, UK

⁴Department of Biochemistry and Systems Biology, Institute of Systems, Molecular & Integrative Biology, University of Liverpool, Liverpool, L69 7ZB, UK

Brassicas are major agricultural crops grown throughout the world and include a diverse range of crop types such as a great diversity of leaf and root vegetables. Their production is threatened by diseases and abiotic stresses such as drought which cause significant losses to farmers. This study aims to improve knowledge on the signalling crosstalk in the immune system of brassicas to improve their resilience to abiotic and biotic stresses. The first layer of active defence system in plants is based on the perception of Pathogen Associated Molecular Patterns (PAMPs) leading to PAMP-triggered immunity (PTI). PTI contributes to quantitative disease resistance (QDR), a desirable breeding trait that potentially provides durable control of diseases in plants. This work is focussed on understanding the effect of abiotic stress on PTI and disease resistance in *B. oleracea*. Induction of PTI by drought stress was determined by quantifying the PAMP-induced reactive oxygen species (ROS) production in mapping population of *BolAGDH*. The results revealed transgressive segregation for drought-induced ROS phenotype and for increased disease resistance to the necrotrophic fungal pathogen *Botrytis cinerea*. QTLs associated with QDR against *B. cinerea*, and drought-induced ROS production were identified. RNA-Seq data from extreme lines were used to identify differentially expressed genes (DEGs) induced by drought stress conditions. Our investigation provides the first insight into the effect of drought stress on PTI and QDR in *B. oleracea*, a globally important vegetable crop.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Development of IoT Based Hydroponic Smart Garden

Kubra Tutkun¹ , Bahar Yildiz Kutman¹

¹Gebze Technical University, Kocaeli, TÜRKİYE

According to the data of the United Nations, the world population, which was approximately 7.8 billion in 2020, is expected to reach 9.8 billion in 2050. Increasing population, global climate change, limited agricultural land put pressure on agricultural production. Soilless farming technologies can enable humanity to produce healthy, nutritious, and sufficient food to ensure global food security. Soilless farming systems can increase fertilizer and water use efficiency, reduce the need for pesticides, allow fresh production and reduce the storage and transportation costs and provide higher yield per unit area. With university-industry collaboration, a smart garden with deep water culture, LED technology and mobile application has been developed. In this system the plant production strategies are optimized for different leafy vegetables including lettuce, mint, basil, parsley, etc. Based on the germination and growth experiments, plants with similar growth properties were grouped in the same growing kits. The plants were subjected to both shoot and root pruning for ease of handling. The system was tested at room, extra light or dark conditions and the plant growth was compared in the different environments. The plant leaves were tested for their mineral content, vitamin C, chlorophyll levels to determine their nutritional quality. The device is on the market with the brand name Arzum x Vahaa Smart Garden. This work was a result of university-industry partnership between VAHAA DİKEY TARIM ÇÖZÜMLERİ VE TEKNOLOJİ A.Ş. and Gebze Technical University. This study was funded by The Scientific and Technological Research Council of Turkey (TUBITAK Project number: 130614).

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Genetic Variation and Population Structure of *Medicago sativa* L. Using SSR Markers

İsmail Bezirganoglu¹ , Busra Nur Akgul¹ , Busra Yazicilar¹ , Merve Simsek Geyik¹ , Ummu Gulsum Koc¹ , Fatma Ozge Aslan¹ , Dogan Ilhan²

¹Erzurum Technical University, Erzurum, TÜRKİYE

²Kafkas University, Erzurum, TÜRKİYE

Medicago sativa L (alfalfa) is a perennial forage plant with high nutritional value, belonging to the legumes (Fabaceae) family. It is the most preferred plant species among leguminous forage crops due to its longevity and resistance to different environmental conditions. In this study, the genetic diversity of alfalfa populations collected from different parts of Turkey, which has a large share in alfalfa cultivation, will be determined. It is aimed to contribute to breeding programs to develop clover varieties suitable for the region, which have economic importance for our country. In the light of this information, 72 alfalfa populations collected from different parts of Turkey were used in the study and the genetic distances between the populations were determined with the simple sequence repeat (SSR) molecular marker technique. The seeds collected from different regions were planted in MS medium, their DNA was isolated from the young leaf samples taken from the seedlings according to the CTAB method, and the polymorphism rate of the populations was determined from the bands formed as a result of PCR processes with selected SSR primers. The obtained data were analyzed with the NTSYS-pc program and a genetic relatedness diagram was created. As a result of the study, the genetic diversity of alfalfa gene sources belonging to different parts of Turkey has been revealed by molecular markers.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Exploring the Potential of Psychrophilic Organisms for Crop Production under Cold Conditions

Munevver Aksoy¹ , Ilker Uz² , Raziye Yildiz² , Faik Kantar¹

¹Akdeniz University, Faculty of Agriculture, Dept. of Agricultural Biotechnology, TÜRKİYE

²Akdeniz University, Faculty of Agriculture, Dept. of Soil Sciences and Plant Nutrition, TÜRKİYE

Biofertilizers include bacteria, cyanobacteria, fungi and microalgae. But the species found in the literature are mostly mesophilic species that can grow in room temperature. Utilization as biofertilizer of true psychrophilic organisms with intrinsic adaptation to sub-optimal temperatures may boost crop production under adverse cold conditions. But to our knowledge, there is no work on psychrophilic biofertilizers in Türkiye. Only a portion of chemical fertilizers applied to soil can be used by plants, because nutrients can become insoluble in soil. Application of biofertilizers can make the nutrients bio-available for plants. This practice would be beneficial for both plant productivity and the environment. Aim of this study was to isolate and compare growth rates of bacterial strains isolated from low altitude and high altitude regions of Antalya. Our results show that bacterial strains isolated from high altitudes have higher growth rates at room temperature and temperatures as low as 2 °C, comparing to strains isolated from low altitudes. This suggests that strains that can grow at 2 °C also would have higher enzymatic activities at low temperatures which makes them better candidates for development of biofertilizers for colder soils. Using cold adapted biofertilizer would have positive effect on plant productivity in agricultural areas located in cold regions of Türkiye. Therefore, isolation of these organisms and exploring their potential is important for our agricultural applications.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Wheat (*Triticum aestivum*) is Protected by Arbuscular Mycorrhizae from the Combined Effects of Boron Toxicity and Salinity Stress under Low- and High-Phosphorus Conditions.

Burak Tuncbas^{1,2}, Umit Baris Kutman¹

¹Institute of Biotechnology, Gebze Technical University, Kocaeli, TÜRKİYE

²Gübretaş R&D Center, Kocaeli, TÜRKİYE

The combined effects of salinity and B toxicity on crops differ from their main effects because of conditional interactions between them. Arbuscular mycorrhizae (AM) are fungal root-colonizing endophytes from the phylum Glomeromycota. The mutualistic symbiosis can enhance plant growth, contribute to mineral nutrition, and increase tolerance to abiotic stress factors. The availability of phosphorus (P) in the soil is closely related to mycorrhizal colonization. Bread wheat (*T. aestivum* cv. Nusrat) plants were grown at different levels of salinity, B toxicity and P availability in either autoclaved or autoclaved and AM-inoculated soil under greenhouse conditions. For inoculation, a commercial product containing three different *Glomus* species was used. The main effects of salinity and B toxicity and the effects of their interaction on vegetative growth, mineral homeostasis, oxidative damage, and yield parameters were determined. Mycorrhizal colonization was documented in root samples by light microscopy. While both salinity and B toxicity significantly reduced shoot dry weight at the vegetative stage, their interaction was not significant in terms of growth parameters. Inoculation with AM and high soil P application increased the shoot biomass by 35% and 32%, respectively. Shoot B accumulation was decreased by salinity and mycorrhizal inoculation. Mycorrhizal inoculation significantly increased different yield parameters and enhanced grain P concentration by 17%. Although the co-occurrence of salinity and B toxicity may increase the total stress burden on wheat, they can partially mask the adverse effects of each other. Arbuscular mycorrhizae may increase the growth and yield of wheat in the presence of combined salinity and B toxicity stress by minimizing ionic toxicities and improving the overall mineral homeostasis under both low-P and high-P conditions, indicating that P fertilization in conventional agriculture does not negate the benefits of AM. Inoculation with AM is promising as an effective tool to grow wheat sustainably in stress-prone areas.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

**Use of *Arthrobotrys* Spp. in Biocontrol of the Root-Knot Nematode
*Meloidogyne incognita***

Cafer Eken¹, Gulsum Uysal², Dudu Demir³, Selda Çaliskan², Emre Sevindik¹, Kardelen Caglayan³

¹Department of Agricultural Biotechnology, Faculty of Agriculture, Aydın Adnan Menderes University, Aydın, TÜRKİYE

²Batı Akdeniz Agricultural Research Institute, Antalya, TÜRKİYE

³Department of Agricultural Biotechnology, Faculty of Agriculture, Isparta University of Applied Sciences, Isparta, TÜRKİYE

Plant parasitic nematodes have been known as serious pathogens of many crops worldwide. Among the plant parasitic nematodes, root-knot nematodes (*Meloidogyne* spp.) are the economically important limiting factors in agricultural productivity and the quality of crops. One of the most destructive species of root-knot nematodes is *Meloidogyne incognita* among the most important plant pests which cause severe problems in economically important crops such as vegetables, fruits, and ornamental plants. *Meloidogyne* spp. can be managed by resistant cultivars, crop rotation, cultural practices, or chemical nematicides and biocontrol agents. The use of nematicides can cause significant problems including environmental pollution and long-term residue issues. Therefore, fungal biological control is agriculturally useful an exciting and rapidly developing research area and there is growing attention to the exploitation of fungi for the control of nematodes. Nematophagous fungi are an important group of soil microorganisms that can suppress the populations of plant-and animal-parasitic nematodes. These fungi can be divided into four categories: endoparasitic fungi, nematode-trapping fungi which parasitize eggs and females, and toxin-producing fungi. Among the nematophagous fungi, nematode-trapping fungi are the most studied. Nematode-trapping fungi are natural enemies of nematodes. The nematode-trapping fungi develop hyphal structures, such as adhesive networks, adhesive knobs, and constricting rings to capture nematodes. *Arthrobotrys* spp. are a well-known nematode-trapping fungus with biocontrol potential against root-knot nematodes, including *Meloidogyne incognita*. The objective of this paper is to summarize the data on the potential for use of *Arthrobotrys* spp. in biocontrol of the root-knot nematode *Meloidogyne incognita*. This study was supported by a grant from the Scientific and Technological Research Council of Turkey (TUBITAK-TOVAG 221O399).

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Phenotyping the Races of *Puccinia striiformis* fsp. *tritici* in Central Anatolia and Future Genotyping Studies

Merve Nur Ertas Oz¹ , Emine Burcu Turgay¹

¹Field Crops Central Research Institute, Ankara, TÜRKİYE

Stripe rust caused by *Puccinia striiformis* f. sp. *tritici*, biotrophic and heteroecious fungus, is a common fungal disease on cereal crops wheat, barley, some cultivated grass, and much wild grass. To be able to cope with the pathogen, it is necessary to understand the races in the populations of stripe rust in the related region. Therefore, breeding studies can be shaped around these informations and appropriate varieties could be suggested to farmers. In addition to phenotyping studies, it is significant to determine the races genotypically. In previous study, stripe rust isolates collected from various provinces of Central Anatolia were identified phenotypically. In future studies, DNA will be extracted using CTAB method (Justesen et al. 2002) and the quality and quantity will be checked in NanoDrop (Thermo Fisher Scientific, USA). For the PCR analysis, SSR markers will be used to identify the Pst groups (Bahri et al 2008, Ali et al. 2011, Ali et al. 2014, Thach 2016). Until now 16 different group has been reported and these genetic groups are differantiated from each other with 20 SSR markers. This study aims to investigate the future study for detection of genetic groups of the materials, phenotypically identified from previous study.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Screening of Stem Solidness Gene Content of Some Grain Varieties with SSR Markers

Mikail Caliskan¹ , Erhan Kocak² , Ayse Yildiz³

¹Central Research Institute for Field Crops, Ankara, TÜRKİYE

²Isparta Applied Science University, Isparta, TÜRKİYE

³Directorate of National Botanical Garden of TÜRKİYE

Stem Solidness is an important factor in increasing yield and quality in all grains, especially wheat (*Triticum aestivum* L.). The development of thick-walled cultivars between basal internodes is an effective way to increase lodging resistance in cereals. Grains with solid stems are known to be resistant to lodging in excessively rainy regions or seasons, to pests such as *Cephus pygmaeus* and *Trachelus tabidus*, and to pathogens such as *Fusarium*. A number of genes located on chromosome 3D in wheat have been shown to be associated with QTLs that control stem solidness. In the study, analyses were made on 28 genotypes, including 10 triticale, 1 rye, 3 oats, 14 barley, with Xgwm114, Xgwm181, Xgwm247, Xgwm340 and Xgwm547 SSR primers developed for the determination of stem solidness genes in wheat. No gene regions expressed by the screened markers were found in oat and barley cultivars. While Xgwm114 and Xgwm181 gene regions were not found in triticale cultivars, only Xgwm247 gene region was determined in "Aslım" rye cultivar, which is the only rye included in the study. The presence of the Xgwm247 and Xgwm547 gene regions was determined in all triticale cultivars, while the Xgwm340 gene region was found to exist in 5 triticale cultivars. The usability of the markers determining the stem resistance genes in wheat plant in some selected cereals was investigated and a preliminary information was formed for breeding programs.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

The Story of Constructing the First Barley Mapping Population in Turkey for Developing Molecular Markers Related to Some Foliar Diseases

Gulden Cetin Ozkan¹, Ulku Selcen Haydaroglu¹, Arzu Celik Oguz⁴, Aziz Karakaya⁴, Namuk Ergun¹, Fatih Olmez³, Sinan Aydogan¹, Emine Burcu Turgay¹, Erdem Sefa Sahin², Muhammed Bahattin Tanyolac⁵, Cuma Karaoglu¹

¹Field Crops Central Research Institute, Ankara, TÜRKİYE

²Aegean Agricultural Research Institute, İzmir, TÜRKİYE

³Sivas University of Science and Technology Faculty Of Agricultural Sciences And Technology, Sivas, TÜRKİYE

⁴Ankara University, Faculty of Agriculture, Department of Plant Protection, Ankara, TÜRKİYE

⁵EGE UNIVERSITY Faculty of Engineering, İzmir, TÜRKİYE

Barley is produced in a significant part of our country's agricultural lands and its a very important place in animal nutrition and malt industry. Disease factors are at the forefront of the biotic factors that affect the yield of this strategic product. Rhynchosporium commune, which is the most important leaf spot disease in barley, and Pyrenophora teres, can cause significant yield losses. In order to breed a new variety in cereals, a long time such as 10-12 years and an intensive labor force are required by using classical breeding methods. Using double haploid lines in plants; It facilitates the breeding work and saves time by shortening the breeding period. The homozygosity process, which takes 5-6 years in classical breeding studies, can be completed in 1 year, and breeding studies that take 10-12 years can be completed in 5-7 years. In this study, double haploid mapping populations were created by using hybrid populations of varieties known to be resistant and susceptible to diseases in order to develop new markers that can be used against important fungal leaf diseases that are a problem in barley. During the formation of double haploid lines, 3 different pretreatment, 2 different callus formation media (induction) and 4 different regeneration media were tried. A total of 286 lines were obtained, which were determined to be double haploid as a result of ploidy tests. The resulting DH populations were phenotypically tested for both diseases. The DH population will be characterized by the GBS (genotyping by sequencing) technique; New markers will be developed that can distinguish resistant individuals with high accuracy through bioinformatic analysis. It is aimed to integrate the reliable and applicable markers that will be developed at the end of the project into the barley breeding programs in our country and to contribute to the breeding process.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

The Effects of High Temperature-time Stress Pretreatments on Callus Induction and Regeneration in Anther Culture of Some Bread Wheat Varieties (*Triticum Aestivum* L.)

Cuma Karaoglu¹, Nesrin Karaca Sanyurek², Seyda Ozdemir¹, Asli Avci¹, Ayten Salantur¹

¹ Field Crops Central Research Institute, Biotechnology Research Center, Ankara, TÜRKİYE

² Munzur University, Faculty of Engineering, Department of Food Engineering, Tunceli, TÜRKİYE

Callus formation is one of the necessary ways to obtain haploid plants through anther culture. In bread wheat, researchers have reported many stress factors applied to stimulate androgenesis, such as cold, heat, nutrient deficiencies, colchicine, osmotic shock. The most commonly applied stress factors are cold, heat and nutrient deficiencies pretreatment alone or in combination. Heat treatment of isolated anthers in anther culture is an important stress factor that increases the efficiency of androgenesis induction. Three different wheat varieties were used in our study. Anthers of these cultivars were isolated in vitro. The effect of high temperature (32°C) and different time (1, 2 and 3 hours) on callus formation was investigated. After removing the top and bottom spikelets of the surface sterilized ears in a sterile cabinet, approximately 30 anthers were carefully removed without injury and placed in 60 mm x 15 mm petri dishes containing 10 ml of liquid callus formation medium (CHB3). Afterwards, the petri dish was wrapped with parafilm and kept at 32°C for 1-2 and 3 hours, respectively, and then incubated for 1 month in the dark in a conventional incubator with 29±1°C and 80% relative humidity. At the end of the incubation, it was determined that the callus formation was higher in the varieties taken into the incubation cabinet after the petri dishes were kept for 1 hour at 32 degrees. As a result of this study; application of high temperature stress can be one of the preliminary applications that can be used to induce callus formation in anther culture.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

**The Effect of MS And Sucrose Doses on Direct Shoot Organogenesis of
Saintpaulia ionantha Wendl**

Nur Koyuncu¹, Yusuf Coskun¹, Ali Aykut Tekin¹, Kubra Ayaz¹, Elif Seda Atasoy¹

¹Field Crops Central Research Institute, Ankara, TÜRKİYE

African violet is a popular commercial and ornamental plant and contains many cultivars with varied colors and shapes. These plants are most commonly propagated by vegetative leaf cuttings, but micropropagation techniques are used to produce large numbers of true-to-type plants in a relatively short period of time. Studies to date have shown that plant regeneration can be achieved from any part of the plant through somatic embryogenesis or shoot organogenesis. Here, we studied the effect of different levels of MS and sucrose on in vitro growth, morphogenesis, and survival percentage of *Saintpaulia ionantha* Wendl plantlets. In vitro-grown African violet shoots of 0.5-1 cm height were planted in Murashige and Skoog (MS) salt medium at ½, ¼ concentration supplemented with 7.5, 15, and 30 g/l sucrose. All media did not contain any plant growth regulators. While higher shoot number and clump diameter were obtained at 30 g/l sucrose concentration at both MS doses, the highest shoot length and leaf diameter were obtained at ½ MS-15 g/l sucrose concentration. All plantlets were easily rooted on ½ MS-15 g/l sucrose medium containing 1 mg/l IBA or in peat irrigated with 1 mg/l IBA. A high survival percentage (100 %) was obtained when the plants were transferred to greenhouse conditions.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Response of Some Turkish Rice (*Oryza Sativa L.*) Varieties to Anther Culture on Different Culture Medium

Nur Koyuncu¹ , Ali Aykut Tekin¹ , Yusuf Coskun¹

¹Field Crops Central Research Institute, Ankara, TÜRKİYE

Anther culture is one of the most used techniques in the production of doubled haploid plants in cereals. With DH plant production, the breeding process is shortened by ensuring that homozygous plants are obtained in one generation compared to conventional methods which require at least 6-7 generations. Embryogenic callus induction from microspores and regeneration of green plants from these calli are two important stages of another culture. There are different factors affecting another culture's efficiency such as genotype, physiology of donor plant, low-temperature pre-treatment, and culture medium. This study was conducted to examine callus induction and plant regeneration capacity of three Turkish rice cultivars (Kızılırmak, Karadeniz, and Bafra Yıldızı) for another culture. Anthers from cold-pretreated (10 °C for 8 days) panicles of the rice cultivars were cultured in N6 and RZM basal media. Best callus induction frequencies were obtained in all cultivars in RZM medium containing 4% (w/v) maltose, 2,4-D, NAA, and kinetin. For callus regeneration MS medium supplemented with BAP, NAA and kinetin were used and plants were transferred to hormone-free half-strength MS medium for rooting. The highest number of regenerated plants was obtained in Kızılırmak, Bafra Yıldızı, and Karadeniz varieties, respectively. This information can be used in the development of doubled haploids for better yield and grain quality by parental use of these cultivars.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

The First Studies of Adaptation, Spring Growth Behavior, Water Requirement and Temperature Response of Promising Multiple Developed Primary (Tcpt) and Secondary (Tcst), Tritipyrum, Under Three Different Irrigation Methods in Türkiye

Hossein Shahsavand Hassani^{1,2,3}, Khalid Mahmood Khawar³, Ayten Salantur¹, Erdal Eren Yeler¹, Murat Balaban¹, Hamza Sahin¹, Mine Ertem¹, Cuma Karaoglu¹, Firdevs Ozbek¹, Leyla Cure¹, Merve Nur Ertas Oz¹, Selim Uygun¹, Nesim Yildiz¹

¹Field Crops Central Research Institute, Ministry of Agriculture and Forestry, 06170, Ankara, TÜRKİYE

²Department of Crop Production and Genetics, School of Agriculture Shiraz University, Shiraz İRAN

³Department of Field Crops. Faculty of Agriculture Ankara University, 06110, Diskapı, Ankara, TÜRKİYE

After a 3 decade of chromosome manipulation and improvement, new cereal, Tritipyrum, stand out as a crop of adequate biomass and grain yield potential, which generally is close to normal wheat and triticale in normal agricultural areas. The first new developed promising set of 14 promising primary Tritipyrum (TCPT: $2n=6x=42$, AABBEbEb) and a new developed promising set with 15 main crosses of TCPT lines (200 TCST inbred lines :AABBEb(1-7)"D(1-7)") have been chosen from Iranian Tritipyrum collection in Shiraz University and evaluated for their field adaptation and agronomical traits in Iran for few years. The set of 33 Iranian genotypes including TCPT and TCST lines with two bread wheat and 2 triticale genotypes were transferred to Türkiye for 121CO36 Tubitak project in March, 2022. The objective of this studies were to investigate the adaptation, photoperiod response, spring growth behavior, water requirement and temperature reaction on 14 TCPT and 15 substituted tritipyrum combinations with 200 potential TCST in April, 2022 in comparison with 5 Turkish wheat and 2 triticale cultivars in 3 different fields of Haymana (Field Crop Central Research Institute of Turkish ministry of agriculture and forestry) with 440 plots under 0, 1 and 5 frequency of irrigation, respectively, but the EC of last irrigation was 32 ds/m² of NaCl and CaCl₂. Twenty morphological and agronomical traits per one and 6 square meter were measured. The preliminary results showed that new cereal, Tritipyrum, is growing like wheat in Türkiye very well and more information will be provided by analyzing all data of these 3 trials. With first trait-oriented selection can reinforce breeding Tritipyrum for both broad and specific adaptation in Türkiye for the first time. All TCPT and TCST lines can grow either irrigation or non-irrigation in Turkey and their behavior to spring sowing were much better than Turkish wheat.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

The Evaluation of Promising Trans Chromosomal Lines of Primary (TCPT) and Secondary (TCST) Under Salinity of Na/CaCl₂ For Seed Germination and Seedling Emergence Stages

Hossein Shahsavand Hassani^{1,2,3}, Cuma Karaoglu², Ayten Salantur², Khalid Mahmood Khawar³, Cansu Tekin², Mine Ertem², Merve Nur Ertas Oz², Erdal Eren Yeler², Fatma Betül Sade², Murat Balaban², Nesim Yildiz³

¹Department of Crop Production and Genetics, School of Agriculture Shiraz University, Shiraz İRAN

²Field Crops Central Research Institute, Ministry of Agriculture and Forestry, 06170, Ankara, TÜRKİYE

³Department of Field Crops. Faculty of Agriculture Ankara University, 06110, Diskapı, Ankara, TÜRKİYE.

Salinity stress is a serious problem world over and could result in a loss of 50% of arable lands by the middle of the 21st century that will damage yield, growth and development of many crops. Improving tolerant salt crops like Tritipyrum wheat is one way to help production areas which the soil and water salinity are problems. After two decades of chromosomal manipulation and improvement, Tritipyrum stand out as a new crop with a reasonable biomass and grain yield potential. Tritipyrum is a derivative of Thinopyrum bessarabicum ($2n=2x=14$, EbEb) with 350 mM NaCl tolerant. Few researches have already shown that Tritipyrum lines can present large genetic diversity for salt resistance that has not yet been fully explored as a valuable stress tolerant cereal on its own for breeding cereals. Because of its high salt tolerant it might become as important as wheat or better on a global scale but in saline soils and brackish water. In this study 30 Tritipyrum primary and secondary lines were compared for their salt resistance at seed germination and seedling emergence ratio under 0, 8, 16, 24 and 32 ds/m² of NaCl + CaCl₂ salts from planting to the 14th day and continued to 28th day in comparison with Iranian and Turkish commercial wheat and triticale cultivars. The results showed all TCPT lines could germinate in EC=24 and in EC=32 des/m², with germination rate of 80% and 40%, respectively, but the TCST lines were variable so that most of them were not germinated at EC=24 ds/m². The variation of seedling length and emergence in all TCPT and TCST lines will be useful in breeding programs for salt tolerance in future. This is the first report of TCPT and TCST promising Tritipyrum lines for germination behavior to NaCl/CaCl₂ salts in Türkiye under the 121CO36 TUBITAK project.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

The First Study of Photoperiod Sensitivity and Vernalization Genes in the Promising Primary and Secondary Lines of New Salt Tolerant Cereal, Tritipyrum

Hossein Shahsavand Hassani^{1,2,3}, Cuma Karaoglu¹, Ayten Salantur¹, Khalid Mahmood Khawar³, Mine Ertem¹, Merve Nur Ertas Oz¹, Erdal Eren Yeler¹, Murat Balaban¹, Fatma Betül Sade¹, Leyla Cure¹, Firdevs Ozbek¹, Emine Burcu Turgay¹

¹Field Crops Central Research Institute, Ministry of Agriculture and Forestry, 06170, Ankara, TÜRKİYE

²Department of Crop Production and Genetics, School of Agriculture Shiraz University, Shiraz İRAN

³Department of Field Crops. Faculty of Agriculture Ankara University, 06110, Diskapı, Ankara, TÜRKİYE.

Bread wheat, as winter or spring type plant, is one of the major worldwide crops and provides the main source of calories for the world's population. Winter wheat needs to experience low temperatures for several weeks to promote its flowering situation as vernalization requirement that was controlled by Vrn genes designated as Vrn-A1, Vrn-B1 and Vrn-D1, located on the long arms of chromosome 5A, 5B and 5D, respectively. Salinity is a serious problem world over which will ultimately decreased the yields and growth of many crops. The first new primary (2n=6x=42, AABBEBEb) and secondary (AABBEB(1-7)"D(1-7)") Chromosomally inbred lines (CRIL) of so called, Tritipyrum, have been produced and evaluated for their field adaptation traits under 150 to 250 mM NaCl; respectively. In order to find out their vernalization +(4-6)°C and photoperiod sensitivity behavior, 37 CRIL genotypes were evaluated 4, 5, 6, 7 and 8 week vernalization along with no vernalization +(20-26)°C and natural vernalization (-8 to +20)°C treatments in comparison with commercial Iranian and Türkiye's wheat cultivars. The facultative behavior of Tritipyrum CRILs to winter environment have been tried for few years but its molecular basis is not clear for winter and spring growth habit. Information on the distribution of vernalization genes and their association with growth habit is crucial to understanding the adaptability of new promising primary and secondary CRILs to different environments. The DNA evaluation of all lines for finding the involvement of Vrn A5, Vrn B5 and VrnE5 gens will be carried out, too. The results showed the vernalization behavior of primary CRILs almost are same but for the secondary CRILs were more variable. This is the first comprehensive report of promising primary and secondary CRILs of Tritipyrum to vernalization treatments, as a new salt tolerant cereal, in the world under the 121CO36 TUBITAK Project.

**ORAL PRESENTATIONS
ENVIRONMENTAL BIOTECHNOLOGY
GREY SESSION**

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Predatory Protists Enhance Rice Plant Growth Through Regulating Rhizobacterial Community Composition

Rasit Asiloglu¹ , Oloruntoba Solomon Samuel¹ , Kazuki Suzuki¹ , Naoki Harada¹

¹Niigata University, JAPAN

To overcome the global problem of food shortage through supporting sustainable life on Earth, we must appreciate the critical importance of soil microorganisms. Among the microbial groups, bacteria are the key drivers of the essential ecosystem services for humans, including nutrient cycling and plant productivity. However, bacterial communities and functions are mainly determined by predators, especially protists. Here we focused on the effect of protists on rhizobacterial community composition and its outcome for rice plant growth. Sterile rice seedlings were grown in sterilized soil that was inoculated with protist isolates, and an indigenous protist-free bacterial community. The impact of protists on bacterial community structure was investigated by high throughput sequencing. The results showed that protists altered the community composition of bacteria. In particular, Sphingobacteriia, Azospirillum, Rodospirillales, Massilia, Caloramator, and Agrobacterium benefited from the presence of protists, while Sphingomonadales, Ralstonia, Burkholderia, and Rhodoferrax decreased in the protist inoculated microcosms. In addition to the rhizobacteria, protists altered the plant root microbiome, namely endophytes. The protists enhanced the rice plant growth, total nitrogen content, and bacterial gene abundances involved in nitrogen fixation. This study provides a novel insight into underground plant-microbe interactions.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Impact of Water Pollution on Vital Organs of Fish Species

(Oreochromis Mossambicus)

Amedeo J.J¹

¹malankara Catholic College, Mariagiri

Tamil Nadu 629153, INDIA

Freshwater is a chief natural resource used for various types of activities in our daily life for drinking as well as different developmental purposes. An increase in pollution level leads to instability in our natural environment and harm both the physical systems and living organisms dwelling in the ecosystem. Various harmful substances present in polluted water bodies in the form of insecticide, pesticides, heavy metals, mills waste, and crude oil are frequently released into the aquatic ecosystem. Tilapia like other fish such as Nile tilapia and trout, are opportunistic omnivores and will feed on algae, plant matter, organic particles, small invertebrates and other fish. OBJECTIVES ➤To estimate the amount of protein in vital organs (brain, liver and gills) of Oreochromis mossambicus. ➤To estimate the amount of carbohydrate in vital organs (brain, liver, and gill) of Oreochromis mossambicus. ➤To analyse the enzyme activity (AST and ALT) in vital organs (brain, liver and gills) of Oreochromis mossambicus. ➤To analyze the LDH activity in vital organs (brain, liver and gills) of Oreochromis mossambicus. Different types of impurities and toxins enter into the aquatic ecosystem and impact the water quality and disturb life cycle of aquatic organisms. Some pollutants are very active to damage the aquatic organisms both morphologically and metabolically. Nevertheless, there is only inadequate evidence that water impurities and pollutants are truly accountable for the expansion of disease in aquatic animals.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Evidences Showing Significant Alterations in Metabolic Processes in Selected Bacterium *Cellulosimicrobium Cellulans*

Paushali Ghosh¹

¹Banaras Hindu University

Pradesh 221005, Hindistan

Bacteria are among the first components of the biota in the ecosystem affected by diverse environmental stimuli. However, their integral genetic and metabolic capabilities make them essential targets to combat adverse environmental conditions. Although bacteria, as a group, are important agents in determining the form and distribution of metals in the environment, they themselves are subjected to metal toxicity. The present study deals with the effects of two heavy metals, mercury (Hg) and cadmium (Cd) on the physiological status, morphology and expression of cellular proteins in the bacterium *Cellulosimicrobium cellulans*. Employing standard microbiological techniques, *C. cellulans* was isolated and identified by 16S rRNA sequencing. Exposure of bacterial cultures to Hg (0 to 0.07 mM) and Cd (0 to 1.2 mM) for 12 h duration showed LD50 at 0.03 mM for Hg and 0.4 mM for Cd. Cultures exposed to heavy metals Hg and Cd at LD50 concentrations for a duration of 0 to 8 h caused acceleration in the production of ROS, increase in the level of oxidatively damaged proteins and decrease in free thiol groups with increasing duration of exposure. Cell response against heavy metals exposure, Hg and Cd at sub lethal concentrations for 12 h duration, includes distinct morphological changes leading to the enlargement of cell volume under stress conditions as evident by SEM. TEM reveals different stages of bacterial cell lysis after exposure to both the metals. FTIR of both control and metal exposed biomass was performed to understand the functional groups involved in the surface binding mechanism of heavy metals. Analysis of protein profile by SDS-PAGE was also performed which depicted significant alterations in the expression of proteins of the bacteria under heavy metals stress. In conclusion, findings of this study clearly demonstrate that heavy metals stress induce significant metabolic changes in the selected bacterial isolate.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Diatoms and New Biotechnological Approaches

Bulent Akar¹, Utku Avci²

¹Gümüşhane University, Faculty of Engineering and Natural Sciences, Department of Food Engineering, Gümüşhane, 29000, TÜRKİYE.

²Eskişehir Osmangazi University, Faculty of Agriculture, Department of Agricultural Biotechnology, Eskişehir, 26160, TÜRKİYE.

In recent years, especially due to the increase in human population, excessive consumption of natural resources and cost increases have become inevitable. For these reasons, new pursuits are being considered. In these pursuits, microalgae have become one of the preferred organisms for biotechnological studies in recent years, as they can multiply rapidly and increase their biomass, adapt to extremely salty, extremely acidic or extremely alkaline environments, and produce industrially useful compounds using carbon dioxide. Diatoms, which have approximately 100,000 defined species and subspecies taxa within the Bacillariophyta division, are single-celled algal organisms that can survive in all moisture-containing environments, especially in fresh and salt waters. They account for 40% of the primary production in the oceans and 25% of the net primary production in the world. Additionally, they contribute to the carbon and silicon cycle in the world with their siliceous cell wall and ability to absorb silicon in their environment. In addition to their ecological importance, they also have biotechnological importance. In particular, the fact that diatoms have siliceous cell walls at micro and nanoscale make them stand out for developing new biomimetic approaches at nanoscale and creating silicon-based micro devices with specific properties. For example, there are studies in this direction such as molecular filtrations, biophotonics, biosensors, drug/gene delivery, bioimaging/biosensing, solar cells, microfluidics, and photodynamic therapy. In addition, nanoporous biosilica fabrication is important for anticancer drug targeting. In this study, biotechnological applications of diatoms will be discussed along with their high resolution images.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Prediction of the Bioremediation Potential Of Microbial Diversity in Hypersaline Tuz Lake

Suzan Sahin Dogan¹ , Aytac Kocabas¹

¹Karamanoglu Mehmetbey University, Karaman, TÜRKİYE

Non-extremophilic microorganisms are predominantly preferred in bioremediation studies. However, the removal of organic pollutants at high salt concentrations by non-extremophilic microorganisms would be needed pretreatment processes to overcome negative salt effects. Halophilic microorganisms have unique enzymatic structures that provide them to adopt extreme saline environment. Halophiles effectively use hydrocarbons as their sole carbon and energy sources; therefore they appear favorable bioremediation agents for the treatment of hypersaline waters contaminated with toxic compounds. Therefore, extremophilic microorganisms stand out as an efficient source of removal of organic pollutants at high salt concentrations. In this study PICRUSt2 tool was applied to predict bioremediation enzymes of prokaryotic diversity in Tuz Lake using 16S amplicon sequencing data. As a result of functional analysis, various enzymes related to bioremediation process were detected in Tuz Lake metagenome data. Arsenite transporter ATPase (EC:3.6.3.16), arsenate reductase (EC:1.20.4.1), molybdopterin molybdotransferase (EC:2.10.1.1), molybdopterin synthase (EC:2.8.1.12), (S)-2-haloacid dehalogenase (EC:3.8.1.2), nitrate reductase (EC:1.7.99.4), catechol 2,3-dioxygenase (EC:1.13.11.2) enzymes were found in high abundance.

ORAL PRESENTATIONS
HEALTH BIOTECHNOLOGY
RED SESSION

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Neuroprotective Role of Chrysin Against Bupivacaine Induced Apoptosis and Oxidative Stress in SH-SY5Y Cell Line

İlknur Cinar Ayan¹ , Ebru Guclu¹

¹Necmettin Erbakan University, Meram Faculty of Medicine, Department of Medical Biology, Konya, TÜRKİYE

Local anesthetics such as bupivacaine are known to induce apoptosis, oxidative stress and mitochondrial dysfunction in neurons. Chrysin, a natural flavonoid, has a strong neuroprotective effect in many neurodegenerative diseases. Therefore, we aimed to investigate the neuroprotective effect of chrysin against bupivacaine-induced neurotoxicity in SH-SY5Y cells. The cytotoxic effect of bupivacaine and chrysin on SH-SY5Y cells was evaluated by XTT test. Cells were treated with bupivacaine for 24 hours and with chrysin for 24 hours dose-dependent manner. It was also applied in combination with bupivacaine for 18 hours after pre-treatment with chrysin for 6 hours. According to the results of XTT analysis, the non-toxic concentration of chrysin was determined and the cells were treated with bupivacaine alone and together with this determined chrysin dose. Changes in the expression level of target genes associated with apoptosis (CASP3, -7, -8, -9) and antioxidant enzyme mechanism (NOS2, SOD1,-2,-3, CAT) were evaluated by RT-qPCR analysis. The differences of CAT and SOD expression were determined by ELISA. According to the results of RT-qPCR analysis, the level of caspases increased in the group treated with only bupivacaine compared to the control group, while the expression of antioxidant enzymes decreased. When compared with the group treated with bupivacaine alone, it was determined that while the expression of caspases decreased in the group in which bupivacaine and chrysin were treated together, the expression of antioxidant enzymes increased. According to the ELISA results, SOD and CAT activity were decreased in the group treated with bupivacaine alone compared to the control group. SOD and CAT activities increased in the presence of chrysin treated with bupivacaine compared to the group treated with bupivacaine alone. The obtained data showed that chrysin may play a neuroprotective role by inducing the expression of antioxidant enzymes while inhibiting apoptosis against bupivacaine-induced neurotoxicity in SH-SY5Y cells.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Investigations of Antimicrobial Activities and DNA Interactions of Phosphazenes

Desi Nurjanah¹, Leyla Acik¹, Güler İnci Tanrikulu², Aytug Okumus³, Zeynel Kilic³

¹Department of Biology, Gazi University, Ankara, TÜRKİYE

²Department of Chemistry, Amasya University, Amasya, TÜRKİYE

³Department of Chemistry, Ankara University, Ankara, TÜRKİYE

Background/Aim: The main property of phosphazenes is that they can provide substitution reactions to different groups. these features have led to an expansion in the field of phosphazenes use. In addition, phosphazenes has antimicrobial activity properties. It has also been found that phosphazenes can cause DNA cross-linking to break, thereby damaging DNA. This study focused on the investigations of the antimicrobial activity and DNA interaction, phosphazenes with plasmid DNA. **Materials and Methods:** Microdilution method were used to examine the antimicrobial activity and minimal inhibitor concentration (MIC) values of the phosphazenes. In the DNA interaction, studies the electrophoretic image was observed by treating with the plasmid DNA compounds in the supercoiled structure. Restriction enzyme digestion of the compound-DNA mixture was used to determine compound binds to which nucleotides. The data obtained from control and treatment groups were evaluated and compared. **Results and Discussion:** According the result of this research with compound 30 exhibited potential activity on the bacterial strain *S. aureus*. Also compound 30 show strong activity on yeast strains *C. albicans* and *C. tropicalis*. MIC value of the compounds from <19.54 to >2500 µM. Moreover, MBC/MFC values of the compounds from <19.54 to >2500 µM. The compounds inhibited DNA restriction indicating the compounds binds to A/A and G/G nucleotides. **Conclusions:** Some of the compounds used as result of research that have been carried out have antimicrobial activity. Also has effect on DNA.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Pyrogallol Prevents the Progress of Glioblastoma Multiforme Cells by Regulating Apoptotic Cell Death

Aynur Aliyeva¹, Sona Eminova¹, Hasibe Vural¹, Hatice Gul Dursun¹

¹Necmettin Erbakan University, Meram Faculty of Medicine, Department of Medical Biology, Konya, TÜRKİYE

Glioblastoma multiforme (GBM) is the most aggressive, common and difficult to treat malignant brain tumor in adults. In the treatment of the disease, methods such as chemotherapy, surgical resection and immunotherapy are used. However, conventional chemotherapeutic agents are not specific to tumor cells and show severe cytotoxic effects on healthy cells. Therefore, it is very important to investigate the anticancer effects of natural products with less side effects. Pyrogallol is a phenolic compound found in various natural products such as green tea, coffee, avocado, apricot, and mango. It has also been shown that pyrogallol has important pharmacological properties such as antibacterial, antiviral, anti-hepatotoxic, anti-ulcer, anti-inflammatory, antioxidant, anti-mutagenic and anti-cancer. The aim of this study was to investigate the possible anticancer activity of pyrogallol in U87 human glioblastoma cells. The cytotoxic effect of pyrogallol in U87 cells was evaluated by XTT analysis. Cells were treated with pyrogallol at a dose range of 5-100 μ M for 24, 48 hours. After determining the % viability values for each concentration of pyrogallol, the IC₅₀ dose was calculated using the Graphpad prism 8.02 program. Then, RNA isolation was performed from control group and dose group cells treated with IC₅₀ dose of pyrogallol and cDNA was synthesized. Obtained cDNAs were used in qRT-PCR analysis and differences in mRNA expression levels of genes associated with apoptosis and metastasis (CASP3, CASP8, CASP9, BAX, BCL-2, MMP2, TIMP1) were evaluated in dose group cells treated with pyrogallol. Colony formation was significantly reduced in U87 cells treated with pyrogallol compared to control cells. According to the results of qRT-PCR analysis, pyrogallol treatment significantly increased the expression levels of CASP3, CASP9 BAX and TIMP1 genes, while significantly decreased the expression levels of BCL-2 genes.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

An Investigation on the Protein Profile and Enzyme Activities of *Walterinnesia Morgani* (Desert Black Cobra) Venom

Nasit Igci¹

¹Nevşehir Hacı Bektaş Veli University, Faculty of Science and Arts, Department of Molecular Biology, Nevşehir, 50300, TÜRKİYE

Snake venom is a complex cocktail consisting of various bioactive proteins and peptides as major constituent, and other organic molecules and inorganics as minor components. Enzymes make up a significant portion of snake venom proteins. Snake venom proteins and peptides have diagnostic and therapeutic potential. Desert Black Cobra (*Walterinnesia morgani*) is a venomous snake distributed mainly in the Middle East including southeastern Türkiye (Şanlıurfa and Kilis provinces). The aim of the present study is to investigate the key enzyme activities and protein profile of *W. morgani* venom originating from southeastern Türkiye (Şanlıurfa). After determination of the protein content, venom sample was subjected enzymatic activity assays to assess phospholipase A2, protease, L-amino acid oxidase, hyaluronidase, 5'-nucleotidase and phosphodiesterase activities by a spectrophotometry-based method. Protease activity was also assessed by gel zymography. Additionally, fibrinogenolytic activity of the venom was evaluated using fibrinogen zymography and SDS-PAGE. Protein profile of *W. morgani* venom was obtained by SDS-PAGE and reversed phase HPLC methods. According to the results, 11 protein bands between approximately 12-240 kDa were observed on non-reduced SDS-PAGE gel while there were 8 bands between 12-140 on reduced gel. Venom proteins of *W. morgani* distributed predominantly between 25-12 kDa. Venom proteins separated into at least 13 protein groups (peaks) by HPLC analysis. Venom of *W. morgani* showed phospholipase A2, L-amino acid oxidase, hyaluronidase, 5'-nucleotidase and phosphodiesterase activities but no protease activity in our experimental conditions. This study revealed the key enzymatic activities of *W. morgani* venom and will guide the future purification and characterization studies. Acknowledgements: This study was supported by the Research Fund of Nevşehir Hacı Bektaş Veli University (Project No: BAP18F26).

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

***In Vitro* Effects of *Montivipera Xanthina* (Ottoman Viper) Crude Venom and Its Fractions on Endothelial Tube Formation**

Secil Karahisar Turan¹ , Elif Karacaoglu¹ , Nasit Igci²

¹Hacettepe University, Faculty of Science, Department of Biology, Ankara, 06800, TÜRKİYE

²Nevşehir Hacı Bektaş Veli University, Faculty of Science and Arts, Department of Molecular Biology, Nevşehir, 50300, TÜRKİYE

Snake venom is a molecular cocktail that contains different bioactive molecules. It is mainly composed of proteins and peptides, which are responsible for its key activities. Viper venoms contain proteins and peptides interfering with the cardiovascular system and blood coagulation. Some of these molecules were used for the development of drugs and diagnostic products and some of them are under investigation. Ottoman Viper, *Montivipera xanthina*, is one of the medicinally important venomous snake species distributed mainly in the western and southwestern parts of Türkiye. Its understudied venom is promising for the discovery of new bioactive proteins and peptides. Angiogenesis is a key process that is crucial for a healthy physiology. However, it is also associated with diseases such as cancer which makes this mechanism a target for therapies. This study aimed to investigate the in vitro effects of *M. xanthina* crude venom and its fractions on endothelial tube formation, as a model to assess angiogenesis. Crude venom was fractionated by gel filtration chromatography and the protein contents of each fraction were determined. In vitro tubulogenesis assay was carried out using human umbilical cord endothelial cells (HUVEC). The half maximal Inhibitory concentrations (IC₅₀) of each fraction and crude venom for their cytotoxic effects were determined by an initial study using MTT assay. One-tenth of the IC₅₀ values were used as an exposure concentration for the tubulogenesis assay. As a result, crude venom showed antiangiogenic effects in general while some of the fractions promoted tube formation compared to the negative control, and some of them inhibited tubulogenesis. These results showed that *M. xanthina* venom contains active proteins with both proangiogenic and antiangiogenic activities, which might be valuable for the development of new molecules affecting angiogenesis. Acknowledgements: This research is supported by Hacettepe University Scientific Research Projects Coordination (Grant No: FBA-2020-18841).

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Rhein Inhibits Cell Proliferation Through Induced Mrna Level of Apoptosis Related Genes and Supressed Mrna Level of Tgfb Pathway and Metastasis Related Genes in *Glioblastoma Multiforme* Cells

Sumeyra Gultekin¹

¹Biotechnology Research Center of Ministry of Agriculture and Forestry, Ankara, TÜRKİYE

Rhein (4,5-dihydroxyanthraquinone-2-carboxylic acid) is one of the natural compounds found in rhubarb roots. Rhein has long been widely used in traditional Chinese medicine. Studies so far have shown that rhein inhibits cell proliferation, migration, invasion and stimulates apoptosis in many types of cancer. In our study, it was aimed to investigate the antiproliferative, apoptotic and antimetastatic effects of rhein in U87 GBM cells. For this purpose, U87 cells were treated with different concentrations (5-10-15-20-30-40-50-75-100 μ M) of rhein as time (24 and 48 hours) dependents manner, and the % viability values were calculated for each concentration. Colony formation assay was performed by treating cells with IC50 dose of rhein. Afterwards, RT-qPCR test were carried out to evaluate the the mRNA expression level of genes associated with apoptosis, TGF β pathway. According to the results of the XTT assay, the IC50 dose of rhein was determined as 10 μ M at 24 hours. Compared to the control group, it was determined that the colony formations in the dose group cells were significantly reduced. According to the results of RT-qPCR analysis, mRNA levels of CASP3, -8, -9, BAX and SMAD7 genes increased significantly in dose groups treated with rhein's IC50 dose; A significant decrease was observed in SMAD2, SMAD4, TGF β R2 genes. As a result, it has been shown that rhein induces apoptosis in U87 GBM cells, suppresses metastasis and TGF β pathway, and exerts antiproliferative and antimetastatic effects.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

The Response of Plant Secondary Metabolites on Climate Change

Reyhan Bahtiyarca Bagdat¹ , Sevinc Demir¹ , Pinar Cinar²

¹Central Research Institute of Field Crops, Ankara, TÜRKİYE

²Ankara University Agricultural Faculty, Ankara, TÜRKİYE

The detrimental effect of global warming can be witnessed in any kind of crop production and diversification of crop patterns in the farming systems, recently. Medicinal and Aromatic Plants (MAPs) are valuable sources of promising crop rotation systems, thanks to their secondary metabolites, which are a kind of defense mechanism against different stress factors. While different biotic and abiotic stress factors have a reducing effect on yield and biomass production, they promote the formation of secondary metabolites in different ways. Positive changes in phenolic components, antioxidant activities, flavonoids, alkaloids, tannins, pigments, saponins, PALM enzymes, carotenoids, and in glucosinolates of plants have been recorded in those plants exposed to UV-B radiation, to extreme temperatures, to different irrigation regimes and irrigation stresses, to phytocompetition, to salinity, and to heavy metals. Plant secondary metabolites with noteworthy biological activity are considered an alternative to most synthetic drugs represent highly economically valuable products and can be used as high-value chemicals such as drugs, fragrances, flavors, insecticides, dyes, etc. There is a crucial demand for new pharmaceutical agents to overcome serious illnesses and new sources of bioactive secondary metabolites with novel activities. Considering those effects, they are also an important input that provides added value to semi-finished or final products.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

An Investigation on the Antifungal Effect of Some Benzimidazole Compounds

Seda Kulen¹ , Durmus Erdurmus²

¹Field Crops Central Research Institute, Ankara, TÜRKİYE

²Plant Protection Central Research Institute, Ankara, TÜRKİYE

Benzimidazole compounds are among the important heterocyclic compounds. They have been the subject of research in many fields, especially in the agricultural chemistry and medicine. In general, a benzimidazole ring consists of a phenyl structure and an imidazole ring and has a fundamental role in biological systems. As an example, benzimidazole ring found in the structure of vitamin B12 complex is a typical one. The structure of purine bases, which is an important part of the biological system, is similar to the numerous synthesized benzimidazole derivatives having antibacterial, antiulcer, antihypertensive, anticancer, antifungal, antiviral effects. An important class among them is Schiff bases. These compounds having carbon nitrogen double bond, -CH=N-, in their structure are widely used in various pharmaceutical and biological systems. Two benzimidazole derivatives, namely 2-methyl-5-nitro-1H-benzimidazole-6-amine and Schiff base 2-[(2-methyl-5-nitro-1H-benzimidazol-6-yl)imino]methyl}phenol were used to investigate their effect in vitro on the antifungal activity against binucleate *Rhizoctonia* AG-A pathogen at different concentrations (0.1; 1; 10; 50 ppm). The effect of 2-methyl-5-nitro-1H-benzimidazole-6-amine against this pathogen was similar to the control solution, and no inhibitory or activating effect was observed. According to the measurements on the 5th day, Schiff base compound had an inhibition effect at 10 ppm and 50 ppm compared to the control sample on binucleate *Rhizoctonia* AG-A pathogen.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

The Monetary Losses Due to Fasciolosis in Cattle in Muğla

Mehmet Acioz¹ , Faruk Bozkaya² , Ali Ihsan Yilmaz³

¹Province Directorate of Agriculture and Forestry, Datça, Muğla, TÜRKİYE

²Faculty of Veterinary Medicine, Department of Genetics, Harran University, 63200 Eyyubiye, Şanlıurfa, TÜRKİYE

³Province Directorate of Agriculture and Forestry, Menteşe, Muğla, TÜRKİYE

This study aimed to investigate prevalence and seasonal distribution of fasciolosis in slaughtered cattles of Muğla province and monetary losses caused by fasciolosis. Slaughter records kept in 2019 in Muğla were analyzed retrospectively. For direct losses liver condemnations were considered while for indirect losses reduction in carcass yield, milk yield, liver weight and fecundity were taken into account. The prevalence of cattle fasciolosis was found to be 0.18% in Muğla. The direct economic loss was determined as 6300 TL (\$1045). Total indirect yield losses arising from reduction in milk yield, carcass yield liver weight and fecundity were calculated as 144.498TL (\$23964), 7.7760 TL (\$12896), loss of 31.646 TL (\$5248), of 14.572 TL (\$2417), 20.520 TL (\$3403) respectively. The total economic losses due to cattle fasciolosis were 150.798,451 TL (\$25009). In conclusion, based on the data on slaughtered cattle in Muğla province in 2019 it was suggested that fasciolosis caused remarkable economical losses is in Muğla city.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Cytotoxicity Screening of the Skin and Parotoid Gland Secretions of (*Salamandra infraimmaculata* ssp. *Semenovi*) from Anatolia

Mert Karis¹

¹Nevşehir Hacı Bektaş Veli University, Nevşehir, TÜRKİYE

The diversity of chemical compounds in the parotoid and skin glands of salamanders makes them important sources for the development of new potential therapeutic agents. The main aim of this study is to reveal the cytotoxic potential the skin-parotoid gland secretions of *Salamandra infraimmaculata* ssp. *semenovi* from Anatolia on cancerous cell lines (HeLa, MPanc-96, PC-3, MDA-MB-231), a healthy cell line (HEK-293) and rabbit red blood cells at concentrations of 0.5, 5, 50 µg/ml. Secretions are obtained via non-invasive mild electrical stimulation on body surface and by manual compressing of the parotoid glands from four salamander specimens. Each sample is rinsed with ultra-pure water into the tubes and pooled, then centrifuged and supernatant is snap-frozen by liquid nitrogen then lyophilized. 4 mg lyophilized sample is dissolved with 1 ml ultra-pure water (4 mg/ml), homogenized, filtered then protein content is determined by BCA assay kit. Protein amount is found ca. 1400 µg/ml. IC50 values and cell viabilities are determined by MTT assay. The results are showed that the crude *S. i. semenovi* skin-parotoid gland secretions have moderate cytotoxic effects on both cancerous and healthy cell lines. The highest cytotoxic effects revealed on cancerous cell lines, HeLa (cervical) and MPanc-96 (pancreas) with IC50 values 44.99 µg/ml and 46.60 µg/ml, respectively. No hemolytic activity is observed on rabbit red blood cells even at the highest concentration of 50 µg/ml. Further studies are needed to focus on the purification of the biologically active components from *S. i. semenovi* skin-parotoid gland secretions.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Guar Gum-Based Biofilms Containing Momordica Charantia Fruit Extract and Biogenic Silver Nanoparticles (AgNP) for Medical Applications

Suzan Biran Ay¹, Rabia Sevval Engin¹, Fikri Yigit Vuranok¹

¹Eskisehir Technical University, Eskişehir, TÜRKİYE

The aim of this study was to produce biocompatible and biodegradable films, functionalized by an addition of medical plant extract and biogenic AgNP, with healing and antibacterial properties, suitable for use in the medical field. Guar gum (GG) was used as the main material and propylene glycol (PG) was added as a plasticizer. Momordica charantia fruit extract (Ext) and AgNO₃ solution were used to produce silver nanoparticles (AgNP) by green synthesis. Biocomposites of different GG (0.5%, 0.75, 1.0% w/w) and PG (40%, 60%, 80% (w/w GG)) concentrations were prepared to evaluate the physical properties of the films. Selected composites were further developed by addition of Ext-AgNP solutions (1mL, 2mL, 3mL) to the formulation. The composites were characterized by Scanning electron microscopy (SEM), Fourier Transform Infrared Spectrum (FTIR) analysis, water vapor permeability, swelling and mechanical tests, as well as antimicrobial evaluation. The films had a thickness ranging between 0.01 and 0.04 mm. They demonstrated a good endurance and elasticity with tensile strength values between 30.1 to 60.5 MPa, and elongation at break between 16 and 26%. The water holding capacity of the films was determined according to the swelling tests, where a maximum of more than 7500% increase in mass was measured. The water vapor permeability of the films was calculated between 2.8 and 4.0 g/dm²/day. Lastly, the antimicrobial properties of the composites against Gram negative Escherichia coli, Gram positive Staphylococcus aureus were determined by disc diffusion method. The results demonstrated the promising use of the composites as wound dressings in biomedical applications.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Anti-Wood-Decay Fungal Activity of the Simultaneous Hydrodistillation of *Salvia Rosmarinus* Spenn and *Cedrus Atlantica* Manetti

Annemer Saoussan¹, Ez zoubi Yassine², Satrani Badr³, Stambouli Hamide⁴, Assouguem Amine¹, Bouayoun Taoufik⁴, Farah Abdellah¹

¹Laboratory of Applied Organic Chemistry, Faculty of Sciences and Techniques, University Sidi Mohammed Ben Abdellah, Fez B.P. 2202, Morocco

²Biotechnology, Environmental Technology and Valorization of Bio-Resources Team, Department of Biology, Faculty of Sciences and Techniques Al-Hoceima, Abdelmalek Essaadi University, Tetouan, Morocco

³Forestry Research Center - Rabat, Avenue Omar Ibn Al Khattab, BP 763, - Rabat-Agdal. 10050, Morocco

⁴Institute of Forensic Sciences of Gendarmerie Royal, Rabat-Institute, B.P. 6597, Morocco

This study aimed to determine the antifungal activity of the combined *Salvia rosmarinus* Spenn and *Cedrus atlantica* Manetti essential oils obtained by simultaneous hydrodistillation. The extraction of *S. rosmarinus* and *C. atlantica* essential oils was obtained by hydrodistillation, and their combinations (75%:25%, 50%:50%, 25%:75%) were obtained by a combined simultaneous hydrodistillation using a mixture design methodology. The antifungal activity was assessed using the macrodilution method, and the effective concentration for 50 percent of maximal effect (EC50) was determined against four fungi responsible for wood decay: *Coniophora puteana* (*C. puteana*), *Coriolus versicolor* (*C. versicolor*), *Gloeophyllum trabeum* (*G. trabeum*), and *Poria placenta* (*P. placenta*). The results of the yield of the extracted essential oils by the previous methods revealed that with the increased proportion of *Cedrus atlantica* Manetti in the mixture, the yields of the essential oil mixtures increased considerably. Gas chromatography /mass spectrometry (GC/MS) essential oil analysis identified myrtenal as a new component appearing in binary combinations. The results showed that simultaneous hydrodistillation improved the antifungal activity of these essential oils. The highest or optimum antifungal activity was found in a combination of 60% *S. rosmarinus* and 40% *C. atlantica* essential oils, providing an EC50 value of 9.91 ± 1.91 and 9.28 ± 1.55 $\mu\text{g/mL}$ for *C. puteana* and *C. versicolor*, respectively. The optimum antifungal activity for *G. trabeum* and *P. placenta* was observed in the combination of 55% of *S. rosmarinus* and 45% of *C. atlantica* essential oils, with an EC50 value of 11.48 ± 3.73 and 22.619 ± 3.79 $\mu\text{g/mL}$, respectively. This activity indicated that *C. versicolor* was the most susceptible fungi to a binary combination of essential oils, while the least susceptible fungi were *G. trabeum* and *P. placenta*. Combined simultaneous hydrodistillation could be used to improve antifungal activity and protect wood against wood-decay fungi.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Effects of Corneal Alkaline Burns on Intraocular Pressure in Rabbits

Yasemin Kiraz¹ , Prof. Dr. Gultekin Atalan²

¹Kayseri Gıda Kontrol Laboratuvar Müdürlüğü, Kayseri, TÜRKİYE

²Erciyes Üniversitesi Veteriner Fakültesi, Kayseri, TÜRKİYE

Cornea; It is the avascular, transparent structure that together with the sclera forms the fibrous structure, the outermost layer of the eyeball. Corneal ulcers; it is one of the most common eye diseases that can be seen in many pets. They are inflammatory phenomena characterized by tissue losses related to corneal epithelium and stroma that do not heal spontaneously. In this study, it was aimed to investigate the effects on intraocular pressure (IOP) values by creating experimental alkaline corneal burns that cause ulceration in rabbits. In our study, 4 groups of 8 rabbits were formed to use different agents. IOP values of healthy rabbits on day 0 and intraocular pressure values of rabbits with corneal alkaline burns on day 1 were measured using rebound tonometry. On a total of 32 rabbits; An experimental corneal alkaline burn was created by absorbing 1 N NaOH onto a 3 mm diameter filter paper, keeping it on the cornea for an equal time in each rabbit, and then washing it with physiological saline solution for an equal amount of time. One-Way ANOVA was used to test whether there was a statistically significant difference between the groups, and from which group this difference originated. Wilcoxon Paired Two Samples test was used to evaluate the difference between two measurements. Day Zero 1st measurements 12.25±0.1637 mm/Hg, 12.25±0.1637 mm/Hg, 12.13±0.1250 mm/Hg, 12.13±0.1250 mm/Hg; day 1 2nd 24.50±0.6547 mm/Hg, 24.63±0.5957 mm/Hg, 24.63±0.7055 mm/Hg, 24.50±0.6547 mm/Hg measurements respectively in the same groups of data were obtained. According to the results of one-way analysis of variance for IOP values, there was no significant difference between the groups on days 0 and 1. As p<0.05 in Wilcoxon Paired Two-Sample Test Result performed to evaluate the difference between Day 0 and Day 1, it was determined that corneal alkaline burns affect intraocular pressure.

POSTER PRESENTATIONS

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Utilization of Food Wastes in Production of Bacterial Cellulose

Pelin Ozkaya¹

¹Manisa Celal Bayar University, Faculty Of Engineering, Department Of Food Engineering, Manisa, 45030, TÜRKİYE

Cellulose is defined as a polymer which exists in cell wall of plant tissues and being widely used in many fields of industry. However, forests have recently been exposed to the danger of disappearing and this threat has pushed the researchers to find alternative sources instead of wood for cellulose production. Hence, researchers have focused on particular bacteria, such as Acetobacter, Glucanobacter, Alcaligenes, Pseudomonas, etc., since they are known as capable of producing cellulose. Researchers claim that these two types of cellulose (plant originated and bacterial cellulose) are similar; so, bacterial cellulose possesses a big economical and commercial potential depending on the purpose and the method of production, since these factors are directly effective on physical and mechanical properties. Substrates to be used for production also vary, including several fruit juices or syrups, konjac flour, etc. Main utilization of obtained bacterial cellulose in food applications can be alined as fat replacer, rheology modifier, immobilizer of probiotics and enzymes, stabilizer of pickering emulsions, food coatings and ingredient of green packaging films. Recently, it has become more prominent to use food wastes as production inputs such as beet and sugar cane molasses, fruit wastes (peels of pineapple, melon, etc.), wastewater rice wine distillery, coffee cherry husk, dry olive mill residue, wheat straw. So, utilization of these agro-forestry residues and industrial by-products as carbon sources has been providing significant advantages such as increasing yield and reducing the cost. In this way, bacterial cellulose production seem to be quite open to progress through waste management perspective. This study aims to present a general look related to bacterial cellulose production in combination with the usage of different food wastes and future trends.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

An Attempt to Obtain Intracellular Melanins from the Biomass of *Aureobasidium Pullulans* A.P.–3

Katarzyna Pobiega¹, Małgorzata Gniewosz¹

¹Department of Food Biotechnology and Microbiology, Institute of Food Sciences, Warsaw University of Life Sciences – SGGW

Aureobasidium pullulans is a fungus, it is often called black fungus because of its melanin production. *A. pullulans* is one of the most widespread saprophytic fungi in the environment, therefore it is widely used in biotechnology, agriculture, pharmaceutical and food industries. It has been found in both terrestrial and aquatic habitats, and lives in both tropical and temperate environments. It can be isolated from air, sewage, fruit, vegetables, water, wood or the needles of gymnosperms. Melanin is present in the cell wall of spores produced by asexual reproduction, e.g. conidia and fungal chlamydo spores. The fungal conidia cell wall may be saturated with melanins to prevent water loss and contribute to increased resistance to biological, chemical and physical factors. The presence of melanin promotes the growth of fungi in the environment, allowing them to grow under difficult conditions and reducing the possibility of degradation. The aim of the study was the biotechnological synthesis of intracellular melanins by *A. pullulans* A.p.–3 and extraction the melanin preparation from biomass. The batch cultivation of the fungus was grown at 28°C for 96 hours. Melanins were extracted from biomass with NaOH and KOH for 0 h, 24 h and 48 h, then the biomass was autoclaved at 115°C/10' and 20' and 121°C/10' and 20'. Methods of loosening the fungal cell wall were investigated: microwave and ultrasound. It was found that the higher content of intracellular melanins was extracted from the biomass using KOH. The studies showed 0.312 g melanin/g d.m. The extraction time had an effect on the melanin content depending on the autoclaving conditions and the extractor used. Additional methods of loosening the cell wall did not influence the increased extraction of melanins from the cell wall of the fungus.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Phenolic Profile of “Kavilca” Bread Prepared with an Ancient Anatolian Wheat from Türkiye

Elif Feyza Aydar¹ , Evren Demircan¹ , Zehra Mertdinc¹ , Tülay Kahraman² , Beraat Ozcelik³

¹Istanbul Technical University, İstanbul, TÜRKİYE

²Unmaş Unlu Mamüller Indust. Trade Ltd., İstanbul, TÜRKİYE

³Bioactive Research & Innovation Food Manufac. Indust. Trade Ltd., İstanbul, TÜRKİYE

In many cultures, bread is a crucial component of the diet and makes up a sizeable share of the daily carbohydrate energy consumption. Hexaploid (2n=42 chromosomes) *Triticum aestivum* L., sometimes referred to as "common wheat," "bread wheat," or "modern wheat," is a high-yielding wheat that accounts for around 95% of global wheat production. However, due to their unique flavor characteristics, dietary and nutritional value, ancient grains are growing in popularity. The "kavilca" variety of *Triticum turgidum* ssp. *dicoccum*, which is grown in Kars, Türkiye, is rich in minerals, fibers, and phytochemicals. The major phenolic acid in wheat is ferulic acid, which accounts for up to 55-77% of total phenolic. Previous studies have reported the importance of the food matrix and on phenolic profile. The different phenolic compounds found in the bread samples may be sourced from the different food matrixes. Fermentation and heating processes may also induce diversification of the phenolic profile. Moreover, flour type and environmental factors influence phenolic yield. The aim of this study was to determine the phenolic profiles of “Kavilca” bread and modern bread. The phenolic profiles of samples consisted of 3,4-hydroxybenzoic acid, trans-cinnamic acid, epigallocatechin gallate (EGCG), and syringic acid. The kavilca bread was rich in terms of EGCG and syringic acid while modern bread was rich in terms of gallic acid and trans-cinnamic acid.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Production of Propionic Acid and Vitamin B12 by *Propionibacterium Freudenreichii* DSMZ 20271 in the Environment of Fruit Pomace, Potato Wastewater and Waste Glycerine

Paulina Chraniuk¹ , Kamil Piwowarek¹

¹Warsaw University of Life Sciences, Institute of Food Sciences, Department of Food Biotechnology and Microbiology, Warsaw, 02-776, POLAND

Ever-increasing food production results in more and more side-streams, which burden the environment. Moreover, industrial residues are a major financial problem – due to the high cost of disposal. Continued degradation of the natural environment is promoting scientists to seek alternative methods of managing the by-products of technological processes. The needs are being met by biotechnology, which offers the possibility of microbiological utilization of waste biomass (in the form of the culture media) with simultaneous production of microbial metabolites (metabolites of propionic acid bacteria, for instance). Nowadays, propionic acid and vitamin B12 are produced on an industrial scale using chemical processes (harmful to the environment), mainly due to low costs. Therefore, it is necessary to look for alternative methods of obtaining these compounds, at the same time reducing production costs, and thus – their market price. The aim of this study was to examine the possibility of propionic acid and vitamin B12 production by *Propionibacterium freudenreichii* DSMZ 20271 bacteria in media containing only post-production residues (apple pomace, blue honeysuckle berry pomace, potato wastewater, waste glycerine). The obtained results allowed concluding that fruit pomace and waste glycerine can serve as carbon sources (sugars + glycerol) in the culture of propionic acid bacteria, while potato wastewater – as a source of nitrogen. It was found that the examined strain is capable of growth and production of both propionic acid and vitamin B12 in media containing waste materials only, without additional supplementation. The highest production of propionic acid was observed in the medium containing all tested residues (0,994 g/100 mL). The data obtained showed that glycerol stimulates the synthesis of propionic acid by the tested strain at the expense of acetic acid synthesis. The bacteria produced vitamin in the tested media in the range of 1439,36-1500,95 µg/100 g wet biomass.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Using the Marker Based Metagenomic Data in Boron Mine Detection

Ilayda Nur Belen¹ , Prof. Dr. Omur Baysal¹ , Prof. Dr. Ilkay Kuscu¹

¹Muğla Sıtkı Koçman Üniversitesi, Muğla, TÜRKİYE

Mining exploration programs are risky investments that involve serious costs, so mining companies need to identify potential areas where the most efficient decarbonizations are found in a short time by conducting successful mining exploration programs. However, once a biological method targeting biological mass in the soil instead of comparing the metal concentration and the metal concentration in certain parts of the mining exploration has been developed, it will be the main method as a powerful method that could be transferred into practice as cost-effective programs. In this project proposal, target mineralization has been selected and aimed to develop a biological method that will provide economic and cost-effective measurements in the detection of boron mines due to its great sectoral importance. There are various boron minerals in nature, and most reserves are present in Turkey in Eskişehir, Balıkesir, Bursa, and Kütahya. We have done a metagenomics analysis to determine uncultured or uncultured microorganisms from the samples collected from these regions. As a result, a significant affinity was detected between boron-related protein in bacteria found in the soil and colemanite as boron a component. Further studies will be carried out on this subject more in detail.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Effects of Zinc Treatment on Expression Levels of Some Enzyme Genes in Selected Local Wheat Varieties

Aysegul Bilge Uguz¹ , Remziye Yilmaz¹ , Ayten Salantur²

¹Hacettepe University, Faculty of Engineering, Department of Food Engineering, FoodOmics Research Laboratory, Beytepe Campus, 06800, Ankara, TÜRKİYE

²Ministry of Agriculture and Forestry, Field Crops Central Research Institute, TAGEM, Ankara, TÜRKİYE

Wheat is a high adaptability cereal that can be grown in several locations due to its ability to grow in different climates and soil conditions. Recent trends in nutrition have led to the popularity of "healthy foods." One reason for this trend is the development of new wheat varieties with high levels of flavonoids and antioxidants. Scientists need to understand the biosynthesis process of these compounds in order to develop new strategies for their production. This is why they use omics technologies such as transcriptomics. In this study, we aimed to investigate the changes in the expression levels of one of the antioxidant enzyme gene Catalase (CAT) and one of the flavonoid biosynthesis enzyme gene Phenylalanine Ammonium Lyase (PAL) in the wheat genotypes selected (*Triticum dicoccum* (3), *Triticum durum* (3), *Triticum spelta* (1)). For this purpose, wheat genotypes were germinated two different pot trials were performed, and foliar zinc biofortification was applied in one pot test. Wheat leaves were harvested 20 days after planting, and RNA isolation and cDNA synthesis were performed immediately. Obtained cDNA samples were used in further gene expression analysis. At this stage, the effect of foliar zinc biofortification on the expression levels of CAT and PAL genes was evaluated, it has been revealed *Triticum dicoccum* and *Triticum durum* genotype can use foliar-applied Zn-fertilizer better than *Triticum spelta* and that foliar applied Zn fertilizer affects the expression level of different genes at different rates. In here, activity changes in antioxidant enzyme and flavonoid biosynthesis enzyme genes depending on genotype differences were revealed in local wheat genotypes with a transcriptomic analysis approach. In addition, it was revealed that the change in the expression profile of these genes with the application of Zn from the leaves was in the direction of a more even distribution.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Breeding of Tomato (*Solanum Lycopersicum L.*) Lines Resistant to Tomato Yellow Leaf Curl (TyLCV) Virus and Tomato Spotted Wilt Virus (TSWV) by Molecular Marker Assisted Backcrossing Method

Sevde Nur Yemsen¹ , Ece Akkul¹ , Nedim Mutlu¹

¹Akdeniz University, Antalya, TÜRKİYE

Numerous viruses seriously reduce tomato yield and quality. An indeterminate fresh market tomato variety with highly commercial potential was susceptible to both TYLCV and TSWV viruses. The aim of this study was to transfer Ty-3 and SW5 genes into parental line via marker assisted backcross breeding approach. By using highly reliable markers both genes were transferred into one of the parents. To achieve this, the "202 F1" heterozygous resistant against both virus was crossed with the susceptible parental line #51. At the seedling stage, the segregating population F1 plants (pseudo-BC1F1) were tested using the molecular markers, and double resistant (Ty-3 and Sw-5) plants were grown. Marker assisted selection followed by single plant selection for plant and fruit characteristics were continued. The resistant BC3F1 plants were selfed to obtain homozygous resistant plants against both virus. The homozygous double virus resistant BC3F2 plants were crossed. The 12 different BC3F2 plants carrying both Ty-3 and Sw-5 at homozygotes were used to create potential double virus resistant hybrids. The resistant parents were selfed further and stable lines have been used to develop four precommercial hybrids. The resistant hybrids are expected to reduce yield and quality losses caused by these viral diseases.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Optimization of Haploid Plant Through Anther Culture in Safflower Plant (*Carthamus tinctorius* L.)

Gulden Cetin Ozkan¹ , Humeyra Yaman¹ , Meryem Sagkol¹ , Ersin Aksor¹ , Oguzhan Aydin¹

¹Central Research Institute for Field Crops, Ankara, TÜRKİYE

Since our country has diverse geography with different ecological conditions, it is very important to select plants resistant to cold, drought and have high adaptability. Safflower is an important oilseed plants with a high level of unsaturated fatty acids, and oil quality is suitable for industrial use with different areas of use in almost every field. Since, the plants have high oil contents and low plant soil requirements, it is necessary to accelerate research on safflower breeding. Since 1980s, breeders are inclined towards rapid breeding techniques tended towards shortening the breeding process by integrating biotechnological tools with traditional breeding methods. Anther culture is frequently used in plant breeding; to obtain homozygous lines for rapid breeding. The aim of this study; was the optimization of the anther culture methods in the safflower to breed new varieties and reduce the time to breed for cold tolerance. It is possible to obtain one generation in a year through classical breeding studies. By optimizing the anther culture study in safflower, it will be possible to reach full homozygosity in a short period of time. In this context, donor plants were grown in the hybrid garden of the Field Crops Central Research Institute. F2 stage trays of the hybrid populations were obtained by different crosses of 5 different safflower genotypes and brought to the laboratory. They were subjected to cold pretreatment at +4 °C for 3-4 days. Thereafter, sterilization process was performed with 20% bleach for 20 minutes and they were cultured on starting media prepared with different concentrations of BAP, NAA, and 2,4-D. Callus and shoot induction was noted within 28-30 days, but rooted shoots are yet to be recovered. The work is currently ongoing for developing effective rooting protocols.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Transcriptomics of *In Vitro* Plant-Bacteria Interaction: a Case Study of Fraser Photinia and PGB_Invit Bacteria

Nil Turkolmez¹, M. Hamit Ekinci¹, Stuart J. Lucas², Ozlem Akkaya¹, Mine Gul Seker¹, Ceyhan Kayihan³, Yelda Ozden Ciftci⁴

¹Gebze Technical University, Faculty of Basic Sciences, Department of Molecular Biology and Genetics, 41400, Kocaeli, TÜRKİYE

²Sabancı University Nanotechnology Research and Application Centre (SUNUM), Orhanlı, 34956 Istanbul, TÜRKİYE

³Department of Molecular Biology and Genetics, Başkent University, 06790 Etimesgut, Ankara, TÜRKİYE

⁴Gebze Technical University, Smart Agriculture Research and Application Center, 41400, Gebze, Kocaeli, TÜRKİYE

Biotization of in vitro plant cultures with plant growth promoting Rhizobacteria (PGPR) gained importance recently as these microorganisms could fix nitrogen and produce different plant growth regulators and siderophores which promote the in vitro proliferation of plant cultures. Hence, physiological, biochemical and molecular aspects of plant-PGPR interaction became one of the hot topics in tissue culture studies. Among them, different omics approaches especially transcriptomics could shed more light to understand molecular interactions among those organisms. Thus, this method was utilized as a case study in this report to assess interactions of an endophytic beneficial bacterium (PGB_invit) with its host plant, Fraser's Photinia (*Photinia × fraseri* Dress.) since this interesting bacterium promotes in vitro proliferation of Fraser's Photinia microshoots without requiring periodic subculture up to 16 months. After 60 days of continuous in vitro culture, RNA was isolated from control plants (non-inoculated), active group (106 cfu ml⁻¹ PGB_invit inoculated) plants and inactive group (106 cfu ml⁻¹ heat-inactivated PGB_invit inoculated) plants and sequenced. As a result of RNA-Seq, altered levels of expression of different genes were found and qRT-PCR was performed for the validation of gene expression differences. Among these genes, E2 ubiquitin-conjugating enzyme and predicted E3 ubiquitin-protein ligase RHA1B-like genes were found to play important roles in plant immunity and stress. The down-regulation of these genes in PGB_invit inoculated plants demonstrated that PGB_invit does not evoke plant immune system and has a positive effect on reducing stress on Fraser's Photinia. In conclusion, transcriptomics approach could provide more clues to reveal out not only beneficial but also detrimental aspects of plant-bacteria interaction. This study was supported with TÜBİTAK project No. (117R002).

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Investigation of a New Plant-Based Enzymatic Protein Hydrolysate as a Seed-Soaking Agent for Wheat Seedlings under Control and Water Deficit Conditions

Burak Tuncbas¹ , Burak Tuncbas² , Umit Baris Kutman¹

¹Institute of Biotechnology, Gebze Technical University, Kocaeli, TÜRKİYE

²Gübretaş R&D Center, Kocaeli, TÜRKİYE

Plant biostimulants offer an ecofriendly, innovative, and sustainable contribution to crop yields and global food security. Protein hydrolysates are categorized as biostimulants because of the growth-promoting effects of free amino acids and peptides in their composition. This study was conducted to evaluate the biostimulant effects of a novel protein hydrolysate (PH) on wheat seedlings in the absence or presence of drought stress when applied to wheat seeds as a seed soaking agent. The PH used in this study is obtained from corn gluten through a proprietary enzymatic process. In the first experiment, bread wheat (*Triticum aestivum* cv. Nusrat) seeds were soaked in dH₂O (control), 2%, and 5% PH for 12h. In this experiment, vegetative growth parameters were examined. In the second experiment, which was carried out to study the effects of different concentrations of PH on the root traits, shoot mineral accumulation, and drought tolerance of wheat seedlings, seeds were soaked in dH₂O, 0.1%, 1.0%, and 2.0% PH solutions for 12h. After uniform emergence, half of the pots were kept well-watered whereas the other half were not watered. In the first experiment, PH treatment had no effect on shoot fresh weight two weeks after sowing whereas it significantly enhanced shoot fresh weight of three-week-old plants. Low (2%) and high (5%) PH treatments increased plant height by 14% and 23%, respectively. In the second experiment, seed soaking with 2% PH enhanced various root traits. Mineral analysis revealed increases in the shoot contents of some essential mineral nutrients including Ca, K, Mg, and Zn. The experimental corn gluten-based PH is effective as a low-cost biostimulant. Stimulation of root growth may contribute to seedling establishment under drought. Further studies are needed to document the effects of seed soaking with this PH on crops and establish the benefits in the absence and presence of abiotic stress factors.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Elevated Shikonin Production in Hairy Root Culture with a Biotechnological Approach

Mine Gul Seker¹ , Melike Tepe¹ , Veysel Suzerer² , Yelda Ozden Ciftci³

¹Gebze Technical University, Molecular Biology and Genetics Department, Gebze/ Kocaeli, 41400, TÜRKİYE

²Bingöl University, Vocational School of Health Services, Department Medical Services & Techniques, Program Medical Laboratory Tech, Bingol, 12000, TÜRKİYE

³Gebze Technical University, Smart Agriculture Research and Application Center, Gebze/Kocaeli, 41400, TÜRKİYE

Hairy root cultures are produced with the transfer of rol genes that induces rooting in plants. Therefore, these cultures were utilized widely to biotechnologically produce various economically important secondary metabolites especially for the pharmaceutical industry. Among them, shikonin which is a naphthoquinone compound that has several biological activity including antibacterial and anticancer. Due to these importance, hairy root cultures were initiated from roots excised from in vitro germinated-*Echium italicum* L. seeds. Then, the production of shikonin derivatives were tried to elevated by inclusion of several elicitors together with application of temporary immersion bioreactor. At the end of 4 weeks of in vitro culture of hairy roots, shikonin was extracted from roots and culture medium and the production of shikonin derivatives was assessed via TLC and HPLC. Our results showed that the highest production was achieved by inclusion of methyl jasmonate to the culture medium and immersion of roots to medium for 12 minutes every 6 hours. This project supported by TÜBİTAK with 119Z092 project number.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Identification of Bacteria Isolated from the Wheat Rhizosphere and Determination of Their Plant Growth-Promoting Properties

Senanur Acet¹ , Mine Gul Seker¹ , Ozlem Akkaya¹ , Stuart J. Lucas³ , Yelda Ozden Ciftci²

¹Gebze Technical University, Basic Sciences Faculty, Department of Molecular Biology and Genetics, Gebze/ Kocaeli, 41400, TÜRKİYE

²Gebze Technical University, Smart Agriculture Research and Application Center, Gebze/Kocaeli, 41400, TÜRKİYE

³Sabancı University, Nanotechnology Research and Application Centre (SUNUM), 34956 Orhanlı, Istanbul, TÜRKİYE

Wheat with its high nutritional and economic value is one of the most widely grown cereals in Türkiye and the world. The use of chemical fertilizers and uncontrolled water consumption to enhance yield in wheat cultivation not only increase cost, but also have a negative impact on the environment. The use of plant growth promoting bacteria (PGPB) with abilities such as nitrogen fixation, inorganic phosphate solubilization, siderophore and phytohormone production as biofertilizer has gained importance in recent years for sustainable agriculture. One of the innovative approaches in developing biofertilizer is to identify plant specific microbiomes and to formulate new plant-specific microbial consortia from these microbiomes. Hence, the aim of this study is to determine the bacteria that could be used to produce a wheat-specific microbial consortium-based biofertilizer. For this purpose, soil samples were collected from wheat cultivated fields in Tekirdağ, Ankara, Diyarbakır, Konya and Sivas provinces and wheat was grown in those soils under greenhouse conditions. 500 bacterial isolate were isolated from the rhizosphere of wheat from which 100 of them were selected in accordance with the different isolation fields. Afterwards, descriptive biochemical tests were performed to determine plant growth promoting properties such as nitrogen fixation ability, solubilization of inorganic phosphate compound, indole-3-acetic acid, siderophores and biofilm production. Overall results demonstrated that 19 isolates with different biochemical characteristics have potential to promote plant growth and those were selected as candidates for the members of microbial consortium to be formulated. Studies are currently underway to determine the potential beneficial influence on wheat growth. This study is supported by TÜBİTAK with 121O649 project number.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Effect of Moringa Oleifera on the Physicochemical and Organoleptic Properties of Surface Water

Olaniyi Omoyajowo¹, Jacob Oluyeye¹

¹Ekiti State University, Ado Ekiti, Nigeria, JAPAN

The implementation of the sustainable development goal (SDG 6) which involves ensuring availability and sustainable management of water and sanitation for all had triggered the search for biological based coagulants substitutes such as Moringa oleifera. The study aimed at effect of defatted Moringa oleifera on physicochemical and organoleptic properties of water. Freshly plucked matured and healthy Moringa oleifera seeds were obtained, air-dried, crushed into small pieces, and were defatted using soxhlet extractor. Different dosages of defatted Moringa oleifera used ranging from 0g, 0.1g, 0.2, 0.3g, 0.4g were added to 1 Litre of water in sterilised bottles, and thereafter shaken before allowing to settle for two (2) hours. The supernatant (water) was decanted for analysis. Twenty man panels were set up to evaluate the taste, clarity, appearance, odour and overall acceptability with scores ranging from 0 to 5 with 0 being the least and 5 being best. The data obtained were subjected to descriptive statistical analyses using one-way ANOVA at $P = 0.05$ and Duncan multiple range test. The result showed that an increase in the concentration of defatted Moringa oleifera (MO) changed the pH of the water from 7.1 to 7.2, with corresponding increase in the conductivity from 0.41 to 0.44ms/cm. Addition of Moringa oleifera (MOC) does increase the TDS, but increase in coagulant dosage does not affect TDS. 87% of turbidity of the water was removed (15NTU to 2NTU). The statistical analysis revealed the significant difference between raw water, water treated with Moringa oleifera and commercially produced water, but no significant difference between water treated with Moringa oleifera and commercially produced water samples in terms of odour, colour, taste and overall acceptability. This study suggests that defatted Moringa oleifera removes turbidity, colour and organic matter from the water and wastewater, therefore making it a viable alternative for chemical coagulants.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Potential Detoxification Properties of Black Yeast Preparation in Relation to Aluminum – The Study in Yeast Cell Growth Culture

Dominika Popielarz¹, Alicja Synowiec¹, Katarzyna Pobiega¹, Anna Bzducha-Wróbel¹

¹Warsaw University of Life Sciences, Institute of Food Sciences, POLAND

Toxic forms of aluminum, i.e. the ion in the +3 oxidation state (Al³⁺) may disrupt different biological functions. They show strong prooxidative properties resulting in oxidative stress which is considered to be the main mechanism of aluminum toxicity to living organisms. Solutions to limit the toxic effects of aluminum are being sought which may consist in the use of effective detoxifying agents, e.g. adsorbents that reduce the availability of aluminum in environment. The study evaluated whether the autolyzed biomass of black yeast - *Aureobasidium pullulans* may have protective effect on the *Saccharomyces cerevisiae* yeasts cells growing in the presence of inhibitory aluminum concentrations. We used yeast cells as a model organism to test toxic aluminium activity and potential protective effect of *A. pullulans* preparation. The first stage of the experiment estimated the minimum inhibitory concentrations of aluminum in relation to seven different *Saccharomyces cerevisiae* strains using microplates technique. The preparation of *A. pullulans* was applied in concentrations of 5 and 10 mg L⁻¹ to evaluate its influence on the growth of *S. cerevisiae* cultivated in the presence of designated toxic doses of aluminum. The inhibitory dose of aluminium concentration was noted to be 36 mg mL⁻¹ for all tested *S. cerevisiae* strains, while the dose of 18 mg of aluminium per mL⁻¹ significantly reduces their growth. Obtained results showed the protective effect of *A. pullulans* preparation on yeast growth in the presence of aluminum with dose dependent manner. We assume that the observed antitoxic activity of the preparation may be related to aluminum adsorption. The exact mechanism of action of the *A. pullulans* autolyzed biomass will be the aim of our further studies. We assume that potential detoxifying activity of the tested *A. pullulans* preparation would allow it to be used as an ecological method of aluminum detoxification.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Effect of Predatory Protists on Active Bacterial Community in Paddy Field Soils

Mayu Fujino¹, Naoki Harada², Kazuki Suzuki³, Rasit Asiloglu²

¹Graduate School of Science and Technology, Niigata University, JAPAN

²Institute of Science and Technology, Niigata University, JAPAN

³Institute for Research Promotion, Niigata University, JAPAN

Predatory protists are one of the core components of the soil microbiome. They feed on bacteria. Their predatory effects alter microbiome composition and functionality. Studies showed that predatory protists are major eukaryotic organisms in the paddy field, and they control bacterial community. However, our knowledge of prey-predator interaction between protists and bacteria almost exclusively comes from DNA-based. Still, less is known about the effects of predatory protists on the active bacterial communities. Here we aimed to analyze the effects of three predatory protists on total and active bacterial communities in two different paddy field soils. Three predatory protists represent the common soil protists, an amoeba, a ciliate, and a flagellate. Soil samples were andosol and gley soil. We had five treatments for each soil type: 1) only protist-free bacterial inoculum, 2-4) protist-free bacterial inoculum and each protist isolate, 5) protist-free bacterial inoculum and a combination of three protist isolates. The microcosms were destructively sampled on days 0, 7, 21, and 35, and soil DNA and RNA were extracted. Amplicon sequencing analyzed the effect of protists on bacterial communities. The results showed that the active bacterial communities of the two soils differed significantly, with Oxalobacteraceae and Prolixibacteraceae families dominating in the Andosol, while Burkholderiaceae and Azospirillaceae families dominating in the gley soil. The effect of protists on bacterial community composition was analyzed with LEfSe, which showed that the relative abundance of bacterial groups in both soils was altered by predatory protists. Compared to the Andosol community, more bacterial groups were affected by the protists in gley soil. Each protist isolate had a different effect on bacterial communities. The effect of protist species was changed depending on the soil type, which indicates that soil habitat is an essential determinant of the microbial trophic interactions.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Colonization of Candidal in Diabetes Mellitus Patients Attending Ekiti State University Teaching Hospital, Ado- Ekiti

Temidayo Odianosen Faloye¹ , Oluwole Moses David¹

¹Ekiti State University of Ado Ekiti, Ekiti State Nigeria, JAPAN

Candida species are opportunistic yeast that pose serious threat to immunocompromised patients. Diabetes has been reported to be a predisposing factor to fungi infection. This study aimed at determining the rate of Candida species among diabetic patients and to also determine antifungal susceptibility among the isolates recovered from diabetic patients attending Ekiti State University Teaching Hospital, Ado-Ekiti. A total of 245 non-repeat samples comprising of 115 urine, 123 saliva and 7 wound swabs were screened for the presence of Candida species. The frequency of Candida species was higher in diabetic subjects compared to non-diabetic (control group). Out of 245 samples screened, 149 were positive for Candida species which included Candida albicans [n=91(61.0%)] followed by Candida glabrata [26 (17.44%)], Candida tropicalis [10(6.71%)], Candida krusei [5 (3.22%)] and other Candida species [17(1.4%)]. Likewise, Candida albicans was the most frequent species 21 (42.8%) in the non-diabetic individual. The demographic data showed high association of Candida with diabetic patients within 31-59 years old [118 (48.16%)], followed by those that are more than 60 years in age [93 (37.95%)]. The susceptibility profile of the isolates to antifungals showed that 64.8% of Candida albicans were susceptible to fluconazole and 56.0% to griseofulvin. The research shows that there is high incidence of Candida albicans among diabetic patients. Proper attention must be given to patients with diabetes mellitus because of the high incidence in fungal infection.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Comparative Evaluation of *In Vitro* Antioxidant Properties of *Abelmoschus Esculentus* Whole Fruit and Seed Extracts

Oluwatunmise Falana¹, Adeniyi Philip Adebule², O. R. Moleyin¹

¹Ekiti State University, Ado Ekiti, Ekiti State, NIGERIA

²University of KwaZulu-Natal, SOUTH AFRICA

The present study was designed to evaluate and compare the antioxidant potential and inhibitory effect of aqueous extract of *Abelmoschus esculentus* whole fruit and *Abelmoschus esculentus* seed; a popular vegetable used widely as medicinal plant in traditional medicine. The inhibitory effect and antioxidant potential of both extract of whole fruit and seed were assessed using Lipid peroxidation assay, Ferric reducing antioxidant power (FRAP) assay, 2,2-azinobis (3- ethylbenzo-thiazoline- 6-sulfonate) (ABTS) radical scavenging ability, Iron chelation ability and the phenolic content (total Phenol and total flavonoids) were as well assessed. The result of the phenolic content of *Abelmoschus esculentus* whole fruit and seed were 5.00 ± 0.59 and 2.95 ± 0.22 (mgGAE/g) and the ferric reducing antioxidant property were 3.84 ± 0.29 and 2.185 ± 0.261 (mg/ Ascorbic acid equivalent /g) of sample, and a high inhibitory effect on malondialdehyde (MDA) by sample, respectively. The result revealed that *Abelmoschus esculentus* whole fruit had significantly ($p < 0.05$) higher phenolic content than the *Abelmoschus esculentus* seed. *Abelmoschus esculentus* also exhibit significantly ($p < 0.05$) high ABTS scavenging ability, Iron chelation ability and Ferric reducing antioxidant property in both whole fruit and seed of *Abelmoschus esculentus*, however the whole fruit shows a high antioxidative potential than the seeds. The antioxidant and inhibitory properties of the vegetable revealed could be attributed to their high phenolic contents; therefore, it is a good vegetable for dietary consumption, nutritional health supplements and as herbal medicine.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Analysis of Boron Mineral Found in Agricultural Products and Endemic Plants in Tunceli and Elazig Regions

Ulku Ozbey¹ , Sibel Aydin²

¹Munzur University Faculty of Health Sciences, Department of Nutrition and Dietetics, Tunceli
,TÜRKİYE

²Munzur University, Pertek Sakine Genç Vocational School, Department of
Biotechnology, Tunceli, TÜRKİYE

Boron (B) is needed by plants in trace amounts and the limits for required and toxic levels are quite close to each other. Sufficient B levels are essential for optimum growth and yield in plant production practices. Boron plays various significant roles in carbohydrate and protein metabolisms of plants, tissue differentiation, auxin and phenol metabolisms, membrane permeability, pollen germination and pollen tube growth. The aim of this study is to determine whether there is boron mineral in the agricultural products and endemic plants grown in Tunceli and Elazig regions. This study analyzed boron content in commonly consumed foods in Elazig and Tunceli Turkey. Boron content was analyzed on 34 different foods using Inductively coupled plasma mass spectrometry (ICP-MS). Nine species of fruit (apricot, green apple, yellow apple, ışkın, peach, cherry, strawberry, plum), twelve species of vegetable (eggplant, tomato, pepper, cucumber, zucchini, garlic, green beans, onion, spring onion, basil, mint, cutlet), were included to this study. Vegetables and fruits were analyzed by Inductively coupled plasma mass spectrometry (ICP-MS) technique. It was determined that the B concentration in foods varied between 0.0676-46.0120 mg/kg. ICP-MS is one of the most common, reliable, and powerful method for B determination. The results of our study show that the B content in foodstuffs can be determined by spectrophotometric method. In addition, more detailed studies on the boron content of all other foods in Turkey and a boron database should be created.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Bacteriological Profile and Resistance to Antibiotics of Strains of *Bacillus Cereus* Isolated from the Stools of Children (0 To 5 Years Old) at the General Hospital of Port-Bouet (Abidjan)

Kalpy julien Coulibaly¹, Adompo Jaures Cedric Yapi¹, Alice Britoh-mlan¹, Syndou Meité¹, Mireille Dosso¹

¹Pasteur Institute of Côte d'Ivoire

²Felix Houphouët Boigny University of Côte d'Ivoire

Diarrheal diseases are one of the main causes of morbidity and mortality in children under 5 in Africa. Diarrhoea due to *Bacillus cereus* is rare, relatively mild and difficult to confirm. The general objective of this work was to describe the main phenotypic characteristics of strains of *Bacillus cereus* isolated from the stools of children aged 0 to 5 years with diarrhoea at the general hospital of Port Bouet. Stool culture performed on stools taken from children aged 0 to 5 years revealed 16 strains of *Bacillus cereus*. The description of the cultural and morphological bacteriological characters was carried out. The clinical bacteriology unit of the Pasteur Institute of Cocody (Abidjan) was our study framework with the collaboration of the medical paediatrics department of the General Hospital of Port Bouet. In our study, 50% of patients were under 12 months old with a sex ratio of 1.28. The identification of presumptive colonies of bacteria of the *Bacillus cereus* group was carried out by morphological characterization and by performing biochemical tests. Confirmation was made using a haemolysis test on fresh sheep blood agar. An antibiogram of the *B. cereus* group was carried out using the classic agar diffusion method according to the Kirby Baueur method. All our strains of *Bacillus cereus* were resistant to benzylpenicillin, ampicillin, amoxicillin and trimethoprim. *Bacillus cereus* deserves to be considered in standard or investigation stool cultures. The study of its ecosystem and the genotypic characterization will make it possible to better describe its involvement in the occurrence of gastroenteritis.

November 9-11, 2022

Abstract E-Book of the 1st International Congress on Biotech Studies

Evaluation in Silico and in Vitro of an Synthetic Peptide Bioinspired in Tsap-2 Scorpion Toxin

Adriel Lacerda¹

¹Universidade Católica Dom Bosco

Campo Grande, BRASIL

The remarkable need for new efficient drugs in the treatment of bacterial infections, mainly those resulting from resistant pathogens, stimulates the applicability of biotechnological devices such as the search for bioactive compounds in animals, including the scorpion, which has high scientific relevance. The present work aims to evaluate the antibacterial activity of a peptide bio-inspired by the TsAP-2 toxin from *Tityus serrulatus*. The methodology consisted of three steps: two in silico and one in vitro. In the first in silico step, was the selection and the construction of the one analog peptide. For the second in silico step were used APD, HeliQuest and I-TASSER software to evaluated and to predict the three-dimensional structure based on physicochemical characteristics. In the third step, were evaluated the in vitro effect. The activities minimum inhibitory concentration, minimum bactericidal concentration, antibiofilm and hemolytic effect of the parental peptides TsAP-2 and Ts-MAP1 analog were carried out. However, only Ts-MAP1 showed activity against *S. aureus* MRSA, *A. baumannii*, *E. coli* ATCC, *E. coli* KPC, *K. pneumoniae* ATCC and *K. pneumoniae* KPC at the respective concentrations 4.1, 8.1, 16.2, 4.1, 32.2 and 4.1 μM . In addition, it was able to completely inhibit the biofilm formation of *A. baumannii* at 8 μM , however, it showed 80% hemolysis at 8 μM against mouse erythrocytes. TsAP-2 and Ts-MAP1 reduced cell viability by 20%, although only the analog demonstrated the ability to reduce the BV-2 inflammatory process. Despite the high hemolytic effect, the proposed peptide has high antimicrobial activity and with new rational design adjustments it could represent an anti-inflammatory and antibacterial pharmacological tool against resistant and biofilm-forming bacteria.