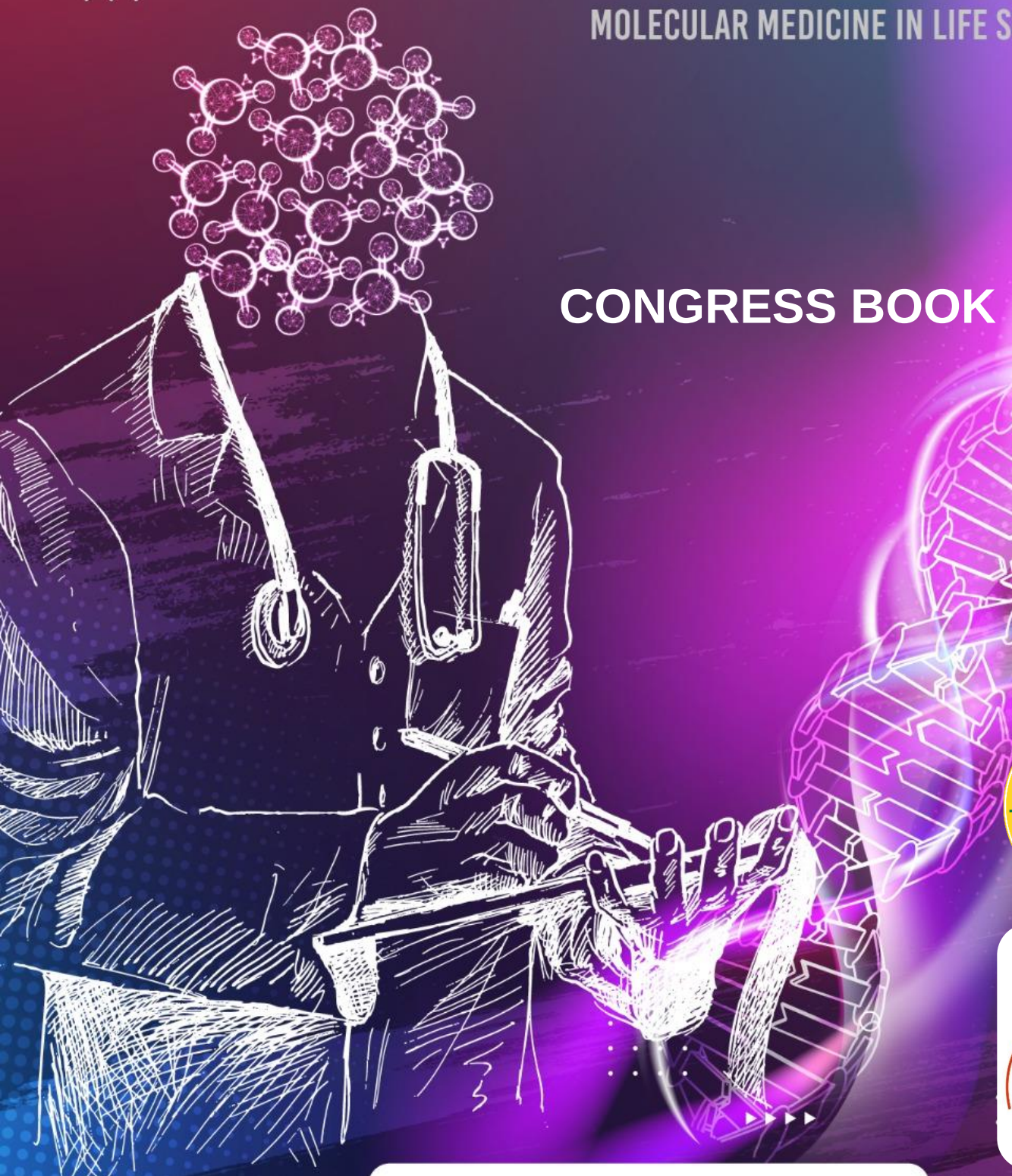
IX. INTERNATIONAL CONGRESS OF MOLECULAR MEDICINE

ONLINE CONFERENCE

18-20 DECEMBER 2023

MOLECULAR MEDICINE IN LIFE SCIENCES



CONGRESS BOOK

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1999 Turkish Society of Molecular Medicine

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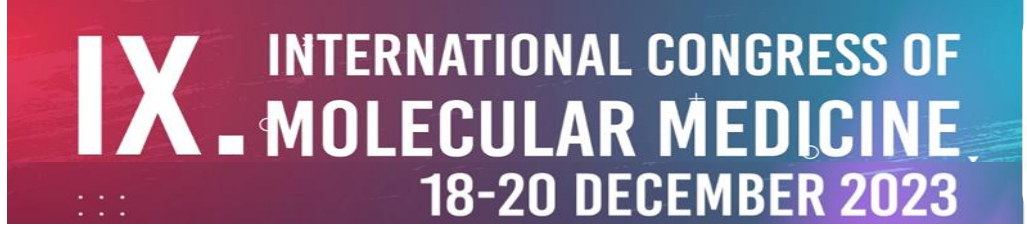

Dear Colleagues,

On behalf of the Organizing Committee I am delighted to invite you to the 9th International Congress of Molecular Medicine that will be held in Istanbul, Türkiye on 18th – 20th of December under the auspices of Istanbul University in cooperation with the Turkish Society of Molecular Medicine.

The congress biennial of molecular medicine is an important forum for researchers and clinicians from Türkiye and all around the world to focus on the latest developments in molecular medicine.

Trends, technologies and clinical applications in areas including, "Cancer Genetics, Epigenetics" "Tumor Micro-Environment", "Anti-Cancer Agents", "Genetic and Metabolic Aspects in Sportive Performance", "Nutritional and Epigenetic Aspects to Diseases", "Metabolic Syndrome", "Prospective Methods in Molecular Medicine", "Molecular Aspects in Diabetes", "Forensic Science", "Cancer Bioinformatics", "Novel Aspects in Personalized Medicine", "Autoimmunity and Molecular Medicine" shall be discussed during the congress.

We will be looking forward to meet you in December 2023 for this outstanding congress we are organizing for the 9th time online this year, with leading scientists in their field and researchers who will make their valuable contributions.

Prof. Dr. Ümit Zeybek
Chair of the Turkish Society of Molecular Medicine,
Istanbul University, Department of Molecular Medicine,
Aziz Sancar Institute of Experimental
Medicine, Istanbul, Türkiye

Main Theme

- Molecular Medicine in Life Sciences

Main Scientific Topics

- Cancer Genetics, Epigenetics
- Tumor Micro-Environment
- Anti-Cancer Agents
- Genetic and Metabolic Aspects in Sportive Performance
- Nutritional and Epigenetic Aspects to Diseases
- Metabolic Syndrome
- Prospective Methods in Molecular Medicine
- Molecular Aspects in Diabetes
- Forensic Science
- Cancer Bioinformatics
- Novel Aspects in Personalized Medicine
- Autoimmunity and Molecular Medicine

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CONGRESS PROGRAM
HALL - A

	18 December 2023 - Monday
09:30 – 10:30	**PROTOCOL - OPENING SECTION** - Zeybek Ümit - Congress President, Head of Turkish Molecular Medicine Association - Deniz Günnur - Istanbul, University Director of Aziz Sancar Institute of Experimental Medicine - Zülfikar Bülent - Istanbul University Rector, Congress Honorary President
10:45 - 11:30	**OPENING LECTURE** **Moderators:** Yücel Doğan, Girgin Sağın Ferhan - Özben Tomris Integrated Diagnostics: Evidence Based Therapy Guidance in Oncology from Tumor Markers to Liquid Biopsy and Imaging
11:45 – 13:15	**Panel 1 GENÇ ARAŞTIRMACILARIN AKADEMİK YOLUNDA REHBER İPUÇLARI** (Guiding Tips for Young Researchers in Their Academic Journey) **Moderators:** İsbir Turgay, Girgin Sağın Ferhan - Gürdöl Figen Ayın Karanlık Yüzü: Sıradışı Yayınlar (Dark Side of the Moon: Extraordinary Publications) - Güner Akdoğan Gül Orpheus ve Doktora Öğrenciliği (Orpheus and PhD Studentship) - Tanrıöver Gamze Tubitak Projesi Hazırlarken Dikkat Edilmesi Gereken Noktalar Nelerdir? (What are the points to be considered when preparing a Tubitak Project?)
13:30 – 14:15	**KEYNOTE LECTURE** **Moderators:** Akdoğan Güner Gül, Yaylım İlhan - Saso Luciano Pharmacological Modulation of Oxidative Stress
14:30 – 16:00	**Panel 2 CURRENT APPROACHES TO AUTOIMMUNE DISEASES FROM AN IMMUNOLOGICAL PERSPECTIVES** **Moderators**: Özdemir Alper, Zeybek Ümit - Özdemir Alper Tunga CAR-T Cell Approaches in The Treatment of Autoimmune Diseases - Özdemir Bilge Alterations of Costimulatory Molecule Expressions of Mesenchymal Stem Cells That Preconditioned With IFN-gama, IL-4 and IL-10 - Öztatlıcı Mustafa Immunomodulatory Effects of Exosomes

16:15 – 18:45	**Panel 3 MOLECULAR APPROACHES TO DIFFERENT CELL DEATH MECHANISMS IN DISEASES** **Moderators**: Turna Akif, Koçdor Hilal - Gözüaçık Devrim Autophagy and Cancer - Özel İshak Dark Side of Immune Aging and Inflammaging - Armagan Güliz Targeting Ferroptosis as a Therapeutic Approach - Alturfan Ebru Işık Endocrine Disrupting Chemical Exposure During Embryogenesis, Our Experiences in Zebrafish Embryos - Soysal Yasemin Epigenetics and Nutrition
19:00 – 19:45	**KEYNOTE LECTURE** **Moderators:** Ulukaya Engin, Ülker Çakır Dilek - Özpolat Bülent Development of Innovative microRNA Therapeutics for Solid Cancers

	19 December 2023 - Tuesday
08:30 – 10:30	**Panel 4 CELLULAR AND BIOCHEMICAL CURRENT APPROACHES TO AUTOIMMUN AND DEGENERATIVE DISEASES** **Moderators:** Tunalı Akbay Tuba, Cengiz Müjgan - Akkoç Tunç Otoimmunity and Cellular Therapies - Ulusu Nuray Biochemical Approaches to Amyotrophic Lateral Sclerosis - Attar Rukset Current Approaches to Etiopathogenesis of Endometriosis - Aslan Mutay Neurological Biomarkers Following Liver and Kidney Transplantation
10.45 – 12:15	**Panel 5 NEW CANDIDATE PANELS FOR PRECISION MEDICINE AND DRUG RESISTANCE IN CANCER** **Moderators:** Demokan Semra, Tanrıöver Gamze - Aktaş Safiye Use of Pancancer Panel in NGS for Precision Medicine - Altun Zekiye Exosomes and Drug Resistance in Cancer - Demokan Semra Current Developments That May Change The Clinic in Epigenetic-based Biomarker Panel Studies in Cancer

	SATALLITE PANEL - Next Generation Near Patient Molecular Testing, Dr. Gaye Tanrıöver (BioeXsen GmbH)
13:15 – 15:15	**Panel 6 NOVEL DEEP LEARNING APPLICATIONS AND NOVEL NANOTECHNOLOGICAL APPROACHES TO DISEASES** **Moderators:** Baysan Mehmet, Öztürk Melek - Durdağı Serdar MOL2DRUG: Development and Pretesting of a Deep LearningQSAR-Based Mobile Application on Prediction of Biological Activity and Toxicity of a Molecule from Provided Image - Kaya Mehmet The Role of Blood-brain Barrier For Treatment of Neurodegenerative Diseases:Novel Nanotechnological Approaches - Baysan Mehmet Facilitating Sequencing Analyzes and Evaluating Accuracy Rates -Çakmak Ali Mutation Wars: Vaccines vs. Viruses
15:30 – 17:00	**Panel 7 FORENSIC SCIENCES** **Moderators:** Yükseloğlu Hülya, Küçükhüseyin Özlem - Tarı Cömert Itır Mental Health and Psychology Practices from The Perspective of Forensic Social Sciences - Kalfoğlu Sotiri Forensics in Action: Crime Scene - Ebedi Meryem From Genes to Justice: Molecular Pathology's Role in Forensic Sciences
17:15 – 19:15	**Panel 8 RECENT DEVELOPMENTS IN DIABETES, SLE AND MICROBIOTA MODULATION** **Moderators:** Gürol Ali Osman, İşbilen Başok Banu - Bezirtzoglou Eugenia Functional Dairy Foods and Microbiota Modulation - Danilova İrina Hepatic Insulin Synthesis Increases in Rat Models of Diabetes Mellitus Type 1 and 2 Differently -Tsigalou Christina The Contribution of The Immunology Laboratory in The Diagnosis of SLE - Aydın Özgür Burçin What Are The Effects of Th Cell Subgroups in Type 1 Diabetes?

	20 December 2023 - Wednesday
08:45 – 10:45	**Panel 9 NEW THERAPEUTIC APPROACHES TO DISEASES** **Moderators:** Sepici Dinçel Aylin**,** Hepokur Ceylan - Açılan Ayhan Ceyda Targeting the Enemy: Precision Approaches - Bassiouny Ahmad Molecular Study on Nanocurcumin Effect on Formalin-induced Pain in Rat Model - Tutar Yusuf Characterization of Anticancer Properties of Quinoxalinone-thiazole Hybrid Structures - Farooqi Ammad Ahmad Diametrically Opposed Role of PI3K/AKT Signaling and Apoptosis in Carcinogenesis and Metastasis
11:00 – 12:30	**Panel 10 GENETICAL VIEW TO SPORTIVE PERFORMANCE** **Moderators:** Kayhan Fatih - Bıyıklı Türker The Importance of Genetic Data in Sports Performance - Tutkun Erkut Is My Child Talented? New Approaches to Talent Discovery - Ersöz Gözde Molecular Mechanisms Affecting Exercise and Brain Functions
	SATALLITE PANEL - Alternative Approaches for Protein, Cell Analysis, and Cell Separation. Türker Toktay (MEDSANTEK)
13:15 – 15:15	**Panel 11 NUTRITIONAL EFFECTS ON EPIGENETIC REGULATION** **Moderators:** Meral Gülsen, Timirci Kahraman Özlem - Al-Zoubi Mazhar Genetic Bases If Men Infertility in the Jordanian Population - Aslan Elif Sibel Harmony in Hashimoto's: Exploring the Epigenetic İnfluence of Nutrition - Meral Gülsen The Relationship between Vitamin D Deficiency and Its Epigenetic Regulation - Yılmaz İlker A Different Approach To Malnutrition-Related Appetite And Weight Loss In Cancer Patients: Is Saturation Enough At The Cell Level?

15:30 – 17:30	**Panel 12 A VIEW OF CURRENT CLINICAL, GENETICAL AND IMMUNOLOGICAL APPROACHES TO CANCER** **Moderators:** Kumar Shant, Koçtürk Semra - Jhanwar Suresh Cancer Genomics in Translational Research and Precision Medicine: A Brief Overview of Current Status and Future Prospects - Turna Akif Enhancing Anti-tumor Immunity Against Lung Cancer by Surgery - Ulukaya Engin Dying of Cancer Cells Feeds The Others to Create More Supressive Tumor - Alhudiri Inas Establishing a Biobank- a Libyan Perspective
17:45 – 19:45	**Panel 13 RECENT DIFFERENT PERSPECTIVES IN CLINICAL AND LABORATORY INVESTIGATIONS** **Moderators:** Yerer Mükerrem Betül, Karakuş Selcan - Üresin Yağız New Generation Clinical Research - Attar Erkut Quantum Biology - Soomro Razium Ali MXene and their composites for Electrochemical Devices - Görmüş DeGrigo Uzay Laboratories in The Technology Universe
20:00	- **Closing and Award Ceremony**

HALL – B

	18 December 2023 - Monday
14:30 – 15:30	**Panel 1** **Moderators:** Sacide Pehlivan, Kürşat Özdilli, Özlem Küçükhüseyin - Can Mitochondrial DNA Copy Number and Leukocyte Telomere Length Be Effective In The Prognosis of Multiple Myeloma? Yasemin Oyacı, Istemi Serin, Fatıma Ceren Tunçel, Mustafa Pehlivan, Sacide Pehlivan - Identification of Novel Androgen Receptor Conformations For Targeting Prostate Cancer Sefer Baday - Pioglitazone Increase Healthspan Possibly by Reducing Oxidative Stress in Fission Yeast Sümeyra Zeynep Çalıcı, Buse Özden, Çağatay Tarhan
15:45 – 16:45	**Panel 2** **Moderators:** Elif Özkök, Uğur Gezer, Cem Horozoğlu, - Effects of Gentisic Acid Rotenone-Induced Neurotoxicity in Zebrafish Derya Cansız, Ismail Ünal, Merih Beler, Ebru Emekli Alturfan - Investigation of the Effect of MAO-A and SLC6A4 Genes in Obsessive-Compulsive Disorder Jansed Berfin Yıldız, Efruz Irem Akkuş Yaylamış, Neşe Kocabaşoğlu, Müjgan Cengiz - Moringa oleifera Ethanolic Extract Prevents Oxidative Damage on Spleen Caused by Sodium Valproate Used in Epilepsy Treatment Sabina Ahmadova, Ismet Burcu Turkyilmaz, Umar Faruk Magaji, Ozlem Sacan, Refiye Yanardag - Exploration of the Effects of N-Cadherin Mimetic Sequence on the Regenerative Potential and Stem Cell Potency of Mesenchymal Stem Cells Demet Kaçaroğlu, Yelda Yüregir, Seher Yaylacı
17:00 – 18:15	**Panel 3** **Moderators:** Fahri Akbaş, Canan Cacına, Allison Pınar Eronat - Prognostic Importance of BRAF and PTEN Proteins in Patients with Malignant Melanoma Elif Bilgin, Ceren Tilgen Yasasever, Murat Serilmez, Faruk Taş, Derya Duranyıldız, Hilal Oğuz – Soydinç - Investigation of the Effects of Toothpastes with Different Contents on the Oxidant-Antioxidant System in Zebrafish Embryos Atakan Karagöz, Merih Beler, İsmail Ünal, Derya Cansız, Ebru Emekli Alturfan - Investigation of Leukocyte Telomere Length and hTERT Gene MNS16A VNTR Variant in Microtia Patients Sevde Sayın, Berker Büyükgüral, Fatıma Ceren Tunçel, Yasemin Oyacı, Mehmet Bekerecioğlu, Sacide Pehlivan

	- Assessing HSP70 and TCP1 Status of Circulating Tumor Cells in Metastatic Colorectal Cancer Dilek Pirim, Berkcan Doğan, Fatih Atilla Bağcı, Özgen Işık, Türkan Evrensel - Investigation of the Role of Rev-Erb α/β in Traumatic Brain Injury Mahmud Esad Pence

	19 December 2023 - Tuesday
09:00 – 10:00	**Panel 4** **Moderators:** Serap Kuruca, Ferda Arı, Ceylan Hepokur - Cytokine Detection with Bionanosensors in An in Vitro Sepsis Model Işık Neslişah Korkut, Ilhan Yaylım, Serap Kuruca, Selcan Karakuş - Attachment of Oxadiazole Ring to Tetrazole-Containing Proteasome Inhibitor Increases Cell Death İn ER+ Breast Cancer Cells Vildan Betul Yenigun, Hatice Ozkan, Ebru Kanımdan, Hamdi Ozkan, Abdurrahim Kocyigit - Knockdown of XPO5 delays cell wound healing and increase in apoptosis in larengeal cancer cells by regulating miR-138 Seren Gülşen Gürge, Ipek Canatar, Sibel Özdaş, Turan Gündüz - Valproic acid-Induced Autism Model in Zebrafish Embryos Gizem Eğilmezer, Merih Beler, İsmail Ünal, Derya Cansız, Ebru Emekli Alturfan
10:15 – 11.15	**Panel 5** **Moderators:** Sinem Bireller, Seda Güleç, Özlem Kurnaz Gömleksiz - Investigation of Chemokine LIGAND12 (CXCL12) Gene Polymorphism in Ovarian Cancer Among the Turkish Population Eman Ahmed Bouni, Rukset Attar, Seda Güleç Yılmaz, Turgay İsbir - Identification of The Epigenetic-Transcriptomic Changes Related to Clinical Outcome in Pancreatic Cancer Seçil Demirkol Canlı - Hormonotherapy in Pretreated Patients with Metastatic or Refractory Uterine Sarcoma Nijat Khanmammadov - Association between the Interleukin-1 beta (IL 1β) gene Polymorphism and Ovarian Cancer Sereen Shoubash, Rukset Attar, Seda Güleç Yılmaz, Abdulrazzaq B. M. Alhashimi, Turgay İsbir

13:00 – 14:15	**Panel 6** **Moderators:** Canan Küçükgergin, Nihal Şehkar Oktay, Huri Dedeakayoğlları - Investigation of the Cytotoxic Effects of ARUM DIOSCORIDIS Plant Extract on HT-29 Cancer Cells Faruk Kaan Çelik, Hayrani Eren Bostancı - Effects of Bisphenol A Exposure on Brain Oxidant-Antioxidant Status in Zebrafish Merih Beler, Derya Cansız, Ismail Ünal, Ebru Emekli Alturfan - PathwayMapper Reveals A Link Between β1-integrin and Wnt/β-catenin Pathway Secil Eroglu, Safiah Olabi - Evaluation of the Usability of Morphometric Measurements from Computed Tomography Images in Gender Determination of Adult Individuals (Preliminary Study of Thesis) Hilal Işık Rozan, Murat Dıramalı, Seval Bayrak - Exploring Functional Promoter SNPs in the Human TNF-A Gene: In Silico Analysis Abeer Babiker Idris, Semih YILMAZ, Aysun Cetin, Einass Babikir Idris, Mohammed A Hassan
14:30 – 15:30	**Panel 7** **Moderators:** Elif Öztetik, Emine Öksüzoğlu, Kevser Kuşat - The Cytotoxic Effects of the Lactarius Deliciosus and Paxillus Involutus Mushrooms on Breast Cancer Cells Ceylan Hepokur, Sema MISIR, İlhan YAYLIM - Investigation of the Relationship Between PLIN4 and IGFBP3 Genes and Obesity Risk Kerem Ozyavuz, Arezoo Gheybi, Zeliha Dogan, Umit Zeybek - Identification of Differentially Expressed Genes and Potential Inhibitors in Resistant Subtypes of Acute Lymphoblastic Leukemia Başak Özay, Ezgi Yağmur Tükel, Yağmur Kiraz, Gizem Ayna Duran
15:45 – 16:45	**Panel 8** **Moderators:** Mehmet Yaman, Ayşegül Cebi, Selcuk Daşdemir - The Effect of Polygonum Cognatum (Meissn.) on Cell Behaviours of Human Dermal Fibroblasts Seeded on 3D Thermoplastic Polyurethane Scaffolds Mehtap Yukselegrilmez, Ufkay Karabay, Sıla Aze Bakan, Resit Bugra Husemoglu, Keyvan Hemmatvand, Zehra Tavsan, Dilay Turu, Kerem Canlı - Phyllanthus Emblica Loaded Wound Dressing Materials Ipek Canatar, Sibel Özdaş, Gözde Baydemir Peşint - Investigation of Ghrelin ad NPY Polymorphisms in Diabetic Obese and Non-Obese Diabetic Groups in Turkey Saadet Büşra Aksoyer Sezgin, Şermin Durak, Arezoo Gheybi, Faruk Çelik, Ramazan

	Çakmak, Ali Osman Gürol, Ümit Zeybek - Gene Isoform Switches and Repeat-Arisen Transcripts in the Adipose Tissues of Individuals with Metabolic Syndrome and Obesity Cihangir Yandım

	20 December 2023 - Wednesday
09:00 – 10:15	**Panel 9** **Moderators:** Nazlı Arda, Tuba Tunalı Akbay, Pınar Aksoy Sağırlı - Lactobacillus rhamnosus GG alleviates BPA-induced oxidative damage Pınar Dede, Seren Ede Pazarbaşı, Doğancan Dörücü, Göksel Şener, Tuğba Tunalı Akbay - The Effects of Panax ginseng on the Blood Samples of the Rats Exposed to Bisphenol A Naji Ullah Fazalyar, Doğancan Dörücü, Seren Ede Pazarbaşı, Göksel Şener, Tuğba Tunalı Akbay - Investigation of Morphological and Behavioral Effects of Memantine Treatment in Zebrafish Embryos Efruz Irem Akkuş Yaylamış, Müjgan Cengiz, Ebru Emekli Alturfan - Investigation of The Relationship of Indoleamin 2,3 Dioxygenase-1 Gene with Foxm1 Pathway in Lung Cancer Cell Lines Venhar Çinar, Dilara Sönmez Zor, Mehmet Tolgahan Hakan, Islim Kaleler, Gultekin Iseyeva, Şeyda Demirkol, Ceylan Hepokur, Özlem Küçükhüseyin, Cem Horozoğlu, Akif Turna, Ş. Umit Zeybek, Dürdane Serap Kuruca, Zuhal Hamurcu, Bülent Özpolat, İlhan Yaylım - Investigation of Antiinflammatory and Antiapoptotic Effects of Sodium Phthalhydrazide in 1.1B4 Cell Line Burcin Ozgur, Günnur Demircan, Ali Osman Gürol, Irina Danilova, Musa Abidov, M. Temel Yilmaz
10:30 – 11:45	**Panel 10** **Moderators:** Kubilay Korkut, Gülbu Işıtmangil, Beyza Özçınar, - Assesment of Pathological Variations Associated with Autoimmunity and Inflammation through Whole Exome Sequencing in Granulomatous Mastitis Disease Beyza Ozcinar, Ozlem Timirci Kahraman, Zeynep Ocak, Baris Ertugrul, Bedia Cakmakoglu - Comparison of HLA B27 Gene Positivity and Negativity with MCV, WBC, MPV, PLT and PCT Values From Complete Blood Count Parameters in Patients with a Preliminary Diagnosis of Ankylosing Spondylitis Ali Osman Arslan - Characterization of ANA+ B Cell Subtypes in a Systemic Lupus Erythematosus Mouse Model Using Flow Cytometry Esin Bayrali Ulker, Munir Akkaya

	- The combined effects of ANGPTL8 (rs2278426), APOC1 (rs11568822), and APOA5 (rs662799) polymorphisms on CAD risk factors Aslıhan Gizem Bilgin, Aybike Sena Özuynuk Ertuğrul, Berkay Ekici, Aycan Fahri Erkan, Neslihan Çoban - Evaluation of The Potential Relationship Between ICAM1 and Lncrna NORAD in Laryngeal Squamous Cell Cancers (LSCC) in Terms of İnteractomic and RNA Expression. Cem Horozoglu, Dilara Sönmez Zor, Mehmet Tolgahan Hakan, Görkem Bal, Batuhan Kabadayı, islim Kaleler, Aysegul Verim, İlhan Yaylım
12:00 – 13:15	**Panel 11** **Moderators:** Melek Öztürk, Sacide Pehlivan, Mehtap Yüksel Eğrilmez - Casticin Regulates Autophagy in Lipopolysaccharide-activated Microglial Cells Mehtap Yuksel Egrilmez, Keyvan Hemmatvand - Effect of Cytokine Gene Variants on the Risk of Autism Spectrum Disorder Kübra Çiğdem Pekkoç Uyanık, Aysel Kalaycı Yiğin, Burak Doğangün, Mehmet Seven - The New Ubiquitously Chromatin Opening Models as a Strong Potential Tool for Recombinant Production and Gene Therapy Applications Omer Faruk Anakok - AMPK alpha-1 and TNFA Gene Expression Levels are Associated with Myocardial Infarction Markers Aybike Sena Ozuynuk Ertugrul, Nazli Dogan, Cenk Eray Yildiz, Ozan Onur Balkanay, Neslihan Coban
13:30 – 14:45	**Panel 12** **Moderators:** Gül Özhan, Güldal İnal Gültekin, Semra Koçtürk - Organoids and Spheroids: Emerging 3D Models to Advance Pancreatic Cancer Research Nazanin Jamshidi, Negar Jamshidi, Elahe Shams, Seyedeh Nasim Mirbahari, Vahid Chaleshi - The Effect of the POMC and UCP2 Genes on the Risk of Obesity Umit Yilmaz, Sermin Durak, Umit Zeybek - Evaluation of the Effects of Emotional and Violence Related Genes in Athletes Buse Sabiha Bozaslan, Emel Hülya Yükseloğlu, Şakir Ümit Zeybek - 9b, a novel HDAC6 inhibitor for treatment for Castration Resistant Prostate Cancer Arda Işıklar, Ipek Bulut, Buse Cevatemre, Büşra Yıldırım, Batuhan Mert Kalkan, Dusan Ruzic, Katarina Nikolic, Ceyda Açılan Ayhan - Expression Analysis of lncRNA-ATB in the PAC-treated Estrogen Receptor-positive Breast Cancer Cell Line Fatma Hande Karpuzoğlu

15:00 – 16:30	**Panel 13** **Moderators:** Bora Tüzüner, Hülya Yılmaz Aydoğan, Murat Kartal - The effect of Moringa oleifera extract on sodium valproate-induced oxidative changes of rat extraorbital lacrimal gland Burçin Alev Tüzüner, Sehkar Oktay, Eda Cergel, Gülsüm Elik, Umar Faruk Magaji, Ozlem Sacan, Refiye Yanardag, Aysen Yarat - Deciphering the Influence of Specific miRNAs on NRF2, TRAIL, and C-MYC Expression in Breast Cancer: A Bioinformatics Analysis Vida Pourteimoor, Mehmet Tolgahan Hakan, Özlem Küçükhüseyin, Vahid Chaleshi, Ilhan Yaylim - Evaluation Of The Anti-Cancer Properties of A Half-Sandwich (HS) Mono-Functional Ru(II) P-Cymene Complex Containing Biguanide Ligand Sabahattin Comertpay, Abdulmecit Gul, Ozge Gungor, Muhammet Kose - Research of the Relationship Between CETP and FABP2 Genes with Obesity Faruk Celik, Saadet Büşra Aksoyer Sezgin, Umit Zeybek - Gene Isoform Switches and Repeat-Arisen Transcripts in the Adipose Tissues of Individuals with Metabolic Syndrome and Obesity Cihangir Yandım
16:45 – 18:00	**Panel 14** **Moderators:** Didem Karakaş, Nazlıhan Aztopal, Yelda Birinci Kudu - Enhancing The Therapeutic Potential: Epigenetic Modulation of Lysosomal Sequestration and Exocytosis Increases Cisplatin Efficacy Baris Sergi, Neslihan Yuksel, Selahattin Can Ozcan, Hamzah Syed, Kirill Kiselyov, Ceyda Acilan Ayhan - Determination of the Transcriptional Regulation of ABCB1 Gene in Taxane Resistant Prostate Cancer by Genomic Locus Proteomics Busra Yildirim, Baris Sergi, S. Can Ozcan, Buse Cevatemre, Ipek Bulut, Ceyda Acilan Ayhan - Flavopiridol and Temozolomid Combination Suppresses Cell Proliferation and Colony Formation in U87-MG GBM Cells Ahsen Güler, Zühal Hamurcu - Optimization of Protocols for Neuronal Differentiation and Cancer-Neuron Interaction Experiments Didem Karakas - Synthesis and Selective Anticancer Activity of 3,5-Diiodosalicylaldehyde S-Methyl Thiosemicarbazone Zn(II) Complex Güneş Özen Eroğlu, Elif Avcu Altıparmak, Tülay Bal Demirci, İlhan Yaylım, D. Serap Kuruca

ORAL PRESENTATIONS ABSTRACTS

OP1

Hormonotherapy in Pretreated Patients with Metastatic or Refractory Uterine Sarcoma

Nijat Khanmammadov

Istanbul University, Institute of Oncology

Background: Uterine sarcoma arises from the myometrium, or connective tissue of the endometrium. The primary treatment of uterine sarcoma is surgery. In the metastatic spread, we can use hormonotherapy. This study aimed to assess the efficacy of hormonotherapy in patients with metastatic or refractory uterine sarcoma.

Method: We evaluated data of the patients with uterine sarcoma that was estrogen receptor-positive retrospectively. Data of the patients were assessed with SPSS 25 version. Also, we used the Kaplan-Meier method for survival analysis.

Results: Nine patients were included in the study. The median age was 50 (range, 44-65) years at diagnosis. Five patients (55.6%) had low-grade endometrial stromal sarcoma, three patients (33.3%) leiomyosarcoma, one patient (11.1%) undifferentiated uterine sarcoma. Six patients (66.7%) were de-novo metastatic. Eight patients (88.9%) had intraabdominal metastasis and two patients (22.2%) lung metastasis. Before hormonotherapy, all patients had undergone surgery. Four patients (44.9%) had received chemotherapy, and one patient (11.1%) radiotherapy. Six patients (66.7%) received megestrol acetate, and three patients (33.3%) aromatase inhibitors as hormonotherapy. One patient (11.1%) had a complete response, one patient (11.1%) partial response, four patients (44.5%) stable disease, and three patients (33.3%) progressive disease. Median progression-free survival was 12.4 (95% CI, 4.9-20.0) months. Toxicity (myalgia) was observed in one patient (11.1%).

Conclusions: In this study, we detected hormonotherapy's efficacy in pretreated metastatic or refractory uterine sarcoma. Despite a small and heterogeneous group of patients, we found that megestrol acetate and aromatase inhibitors were effective in estrogen receptor-positive uterine sarcoma.

Keywords: uterine sarcoma, hormonotherapy, megestrol acetate, aromatase inhibitors

OP2

Identification of novel androgen receptor conformations for targeting prostate cancer

Sefer Baday

Artificial Intelligence and Data Engineering Department Faculty of Computer Informatics and Engineering, Istanbul Technical University, Istanbul, Türkiye

Androgen receptor is an important drug target for the treatment of prostate cancer. However, mutations on drug binding site of the protein can transform antagonist molecules into agonists ones. Thus, drug resistance is an important issue in the treatment of the prostate cancer patients in the clinic. Therefore, novel drug molecules are needed in the clinic. Current drug discovery studies are limited to the testosterone bound Androgen receptor structure. Obtaining alternative protein conformations that can be utilized in structure-based drug discovery studies would be very important. Here a comprehensive structural analysis was made on the conformations obtained from accelerated and classical molecular dynamics simulations of Androgen receptor in apo form, bound to antagonist and agonists. First clustering of the trajectories is applied based on the ligand binding site. Then, docking of known antagonists and binders as well as non-binders and decoys was performed on the identified

protein conformations. Here it is aimed to discover conformations that can be used to discriminate binders/non-binders and antagonist/agonists. While ROC AUC score for when binders and non-binders using the X-ray structure is 0.7, several structures obtained from clustering yielded much higher ROC AUC scores. Therefore, Androgen receptor conformations obtained in this study could help us to develop novel drug molecules.

Keywords: MD simulations, Docking, Androgen Receptor, Prostate cancer

OP3

The new ubiquitously chromatin opening models as a strong potential tool for recombinant production and gene therapy applications

Omer Faruk Anakok

Bolu Abant İzzet Baysal University, Faculty of Medicine, Medicinal Biology and Genetics

Our new chromatin opening models we recently developed which free from potential mutation sites that reduce the size of the current UCOE models used in gene therapy and recombinant protein biotechnology studies, were tested on various cell groups, including mouse embryonic stem cells and human İPS cells.

It has been demonstrated in terms of replacing existing UCOE models that these new UCOE candidates we have developed are more efficient than the previous ones and that they are also a safer profile model for clinical gene therapy studies since they are free from additional enhancing vector cassette areas. These new UCOE models ubiquitously shows a powerfull resistance to DNA methylation-mediated silencing and also provides a higher and stable transfection profile.

To understand the potentiality of our new generation UCOE designs in gene therapy studies, it was tested whether the universal chromatin opening abilities will be retained stable of activation on human induced pluripotent stem cells by differentiating them into different tissue cell types as done before on mouse embryonic stem cells.

In the light of the obtained results, the new UCOE designs that we developed, have maintained their expression levels stably on human iPS cells before and after differentiation into three different tissue type cells. And additionally, they also showed their potential on monoclonal antibody production with CHO cells as producing mg and gr level of recombinant antibodies into two months of period in another parallel study we conducted.

Keywords: ubiquitous chromatin opening element (UCOE), embryonic stem cells, induced pluripotent stem cells, gene therapy, recombinant human mAb production

OP4

Comparison of HLA B27 Gene Positivity and Negativity with MCV, WBC, MPV, PLT and PCT values from complete blood count parameters in patients with a preliminary diagnosis of Ankylosing Spondylitis

Ali Osman Arslan

Department of Medical Biology, Department of Basic Medical Sciences, Faculty of Medicine, Bolu Abant İzzet Baysal University, Bolu, Turkiye

Aim: Ankylosing Spondylitis (AS), a type of spondyloarthropathy, is a chronic inflammatory condition primarily affects sacroiliac joint and spine. One of the most important genetic factors involved in its pathogenesis is the human leukocyte antigen HLA B27. Individuals carrying certain HLA alleles have been found to be more susceptible

to autoimmune diseases compared to those who do not. AS and HLA B27 relationship might be present as an example for this. In our study, we aimed to compare the results of MCV, WBC, PLT, MPV, and PCT in AS patients with positive and negative HLA B27 gene tests. Method: The AS patient samples were obtained from our university's hospital. 100 individuals with HLA B27-positive and negative types were obtained by Real-Time PCR genetic analysis results. In our retrospective study, data were obtained by scanning the patient results from Medical Genetics outpatient clinic.

Results: In our results, PCT was found to be significant in HLA B27-positive or negative individuals (p=0.052). Furthermore, PCT was statistically significant in females depending on HLA B27 result (p=0.044). Regarding other biochemical parameters concerning the HLA B27 result, we did not find significant results. Conclusion: In AS patients with a preliminary diagnosis, there were no significant differences in WBC, MCV, PLT, and MPV values between those with positive or negative HLA B27 results, contrary to the literature. We believe that this could be due to different patient populations, clinical variability, and environmental factors. We anticipate that studies with a larger sample size needs to be done.

Keywords: *HLA B27*, Ankylosing spondylitis, Hemogram parameters, PCT

OP5

Investigation of the cytotoxic effects of ARUM DIOSCORIDIS plant extract on HT-29 cancer cells

Faruk Kaan Çelik[1], Hayrani Eren Bostancı[2]

[1]Yıldız Technical University, Faculty of Arts and Sciences, Department of Molecular Biology and Genetics, İstanbul, Turkey
[2]Sivas Cumhuriyet University, Faculty of Pharmacy, Department of Biochemistry, Sivas, Turkey

The study investigates the potential anticancer properties of Arum dioscoridis, an endemic Middle Eastern plant. Using the MTT method, the research assesses the impact of Arum dioscoridis extracts on the HT29 cancer cell line and healthy L929 cell lines, by calculating IC50 values. Arum dioscoridis was collected, washed and dried for two weeks. Arum dioscoridis extracted using ethanol maseration. The extracts were purified and studied on cancer and healthy cells using the MTT method. Cell vitality was determined using the 575 nm reference range. The extracts were added to 96-well plates in different doses (2-400 µg/mL) for both cell lines, and the IC50 values were calculated using the Graphpad 8.0 program. The study measured the absorbance values of root and leaf extracts with the drug Cisplatin used in various cancers. IC50 values of HT-29 and L929 were determined as 31.29 ± 1.45 µg/ml, 347.1 ± 3.27 µg/ml, 89.29 ± 1.45 µg/ml and 166.2 ± 1.14 µg/ml in root and leaf for all cell lines, respectively. The IC50 value of cisplatin is 32.95 ± 2.98 µg/ml and 63.3 ± 4.29 µg/ml, respectively. The study showed that root extracts prepared with ethanol have a statistically more apoptotic effect than cisplatine, a drug used for HT29 colon cancer. Ethanol leaf extracts were less effective, but neither of them have been shown to have toxic effects on healthy cells. The results showed that Arum dioscoridis ethanol root extract could be a potential substitute for cisplatin in the treatment of colon cancer.

Keywords: Arum dioscoridis, Anticancer, Cell culture, Colon cancer

OP6

Optimization of Protocols for Neuronal Differentiation and Cancer-Neuron Interaction Experiments

Didem Karakas

Department of Medical Biotechnology, Graduate School of Health Sciences, Acibadem University, Istanbul, Turkiye

Primary mature neurons are cells that have lost the ability to divide, therefore, they cannot be propagated in cell culture environment. Furthermore, isolating neurons, especially for human-based studies, has ethical concerns. Therefore, primary neurons are often differentiated from other cell types by applying different compounds (stem cell, neuroblastoma cell) and used for numerous purposes. One of these purposes is cell-cell interaction studies to model the tumor microenvironment.

In this study, SH-SY5Y neuroblastoma cells were differentiated into neurons via all-trans retinoic acid (ATRA) treatment in different medium conditions. ATRA concentration was kept constant at 10 µM during the experiments, while different medium formulations and treatment periods were applied to the cells to evaluate the changes in the differentiation efficiency of the cells into neurons. Then, exosome isolation protocol from non-divided neurons was optimized. Furthermore, indirect co-culture experiments were performed to investigate the interaction between cancer cells and neurons. As a result of the study, although the seeding number, ATRA exposure time, and medium composition are important in cell differentiation, the most critical factor is defined as the passage number of the cells. Besides, in cancer-neuron interaction experiments, it was determined that the presence of ATRA and other additional components in the medium and the confluency of cancer cells can manipulate the experimental results.

In conclusion, the passage number of the cells and the presence of external factors should be taken into consideration for exosome isolation and cell-cell interaction experiments, respectively.

Keywords: neuron, cell differentiation, exosome, cancer

OP7

Identification of the epigenetic-transcriptomic changes related to clinical outcome in pancreatic cancer

Seçil Demirkol Canlı

Division of Tumor Pathology, Department of Clinical Oncology, Cancer Institute, Hacettepe University

Pancreatic cancer is recognized for its elevated fatality rates among various cancer types. Existing treatment modalities encompass surgical procedures and chemotherapy; nonetheless, a considerable number of patients exhibit unresectable tumors due to the aggressive nature of the disease. Recent advancements in high-throughput technologies have yielded extensive datasets harboring gene expression and methylation information. Methylation patterns are considered promising biomarkers due to their early and frequent occurrence in cancer, ease of detection, stability in DNA methylation over time in clinical samples, presence in body fluids, and cell-type specificity. Consequently, methylation patterns have been extensively studied as potential markers for cancer prognosis and diagnosis.

In this study, we employed a cross-validation methodology to pinpoint robust methylation-based markers associated with clinical outcomes in the TCGA pancreatic

adenocarcinoma cohort. Simultaneously, we explored changes in expression patterns potentially influenced by methylation alterations, which are associated with prognosis, aiming to identify the most robust expression-methylation patterns. Patients were randomly divided into two groups, each consisting of 92 patients, for 10 iterations, resulting in 20 distinct patient groups. Cox regression analyses were conducted, and p-values and hazard ratios (HR) were documented for each iteration. We identified CpGs significantly linked to prognosis in both discovery and test groups, consistently in the same direction across at least 9 iterations, with a mean beta value exceeding 0.1. Three genes (MET, NISCH, MYOF) met these criteria. These findings suggest that methylation-expression relationships undergoing fluctuations during tumor progression may serve as potential biomarkers for risk stratification.

Keywords: pancreatic cancer, prognosis, biomarkers, bioinformatics

OP8

Exploration of the Effects of N-Cadherin Mimetic Sequence on the Regenerative Potential and Stem Cell Potency of Mesenchymal Stem Cells

Demet Kaçaroğlu[1], Yelda Yüregir[2], Seher Yaylacı[1]

[1]Lokman Hekim University, Faculty of Medicine, Medical Biology Department, Ankara
[2]Dresden University of Technology, Regenerative Biology and Medicine Department, Dresden

Mesenchymal stem cells(MSCs) are morphologically similar to fibroblasts with high regenerative capacity, can differentiate into cells of mesodermal origin. Due to different therapeutic properties, MSCs are clinically used in haematological malignancies, cardiovascular diseases, neurological diseases, organ transplants, endocrine diseases and regenerative medicine. However, the regenerative properties and stem cell potency of ADMSCs cannot be adequately preserved by conventional cell culture techniques. To solve this problem, HAVDI pentapeptide sequence, which is located in the first extracellular part of N-cadherin and is involved in cell-cell interactions, was used. Although the environment increases MSC proliferation and chondrogenic differentiation, its effects on regeneration and stem cell potency have not been sufficiently investigated. In this study, experimental groups were formed using plastic surface, HAVDI and scrambled HAVDI sequences and cultured in 2D and 3D environment. ADMSCs were cultured for 48h and collected for PCR and Flow cytometry analysis. A fold increase in MMP2;13.2, VEGFR2;24.5 and PLAU;32.2 genes was observed in 3D HAVDI experimental group compared to 2D plastic surface. In the 2D HAVDI experimental group, an increase in the expression of CD90+8.7%, CD73+7.4%, CD105+8.1% surface markers was observed compared to 2D plastic surface. In the 3D HAVDI experimental group, increased expression of CD90+5.5%, CD73+8%, CD105+3.3% surface markers was observed compared to 2D. The results showed a significant increase in the expression of regenerative genes and stem cell markers in cell cultures with HAVDI peptide amphiphile. In conclusion, HAVDI peptide sequence can be considered as a strategy to increase the effectiveness of MSCs commonly used in clinics.

Keywords: HAVDI, ADMSCs, Regenerative medicine, N-cadherin

OP9

The effect of *Moringa oleifera* extract on sodium valproate-induced oxidative changes of rat extraorbital lacrimal gland

Burçin Alev Tüzüner[1], Sehkar Oktay[2], Eda Cergel[3], Gülsüm Elik[4], Umar Faruk Magaji[5], Ozlem Sacan[6], Refiye Yanardag[6], Aysen Yarat[2]

[1]Istanbul Gelisim University, Faculty of Dentistry, Biochemistry Department, Avcilar, Istanbul, Turkiye; Istanbul Gelisim University, Life Sciences and Biomedical Engineering Application and Research Centre, Istanbul, Turkiye
[2]Marmara University, Faculty of Dentistry, Basic Medical Sciences, Biochemistry, Maltepe, Istanbul, Turkiye
[3]Marmara University, Health Sciences Institute, Biochemistry Master of Science Student, Maltepe, Istanbul, Turkiye; Haliç University, Faculty of Health Sciences, Department of Nutrition and Dietetics, Eyupsultan, Istanbul, Turkiye
[4]Marmara University, Health Sciences Institute, Biochemistry Master of Science Student, Maltepe, Istanbul, Turkiye; Egil District State Hospital, Department of Nutrition and Dietetics, Egil, Diyarbakir, Turkiye
[5]Istanbul University-Cerrahpaşa, Faculty of Engineering, Department of Chemistry, Avcilar, Istanbul, Turkiye; Federal University Birnin Kebbi, Department of Biochemistry and Molecular Biology, Birnin Kebbi, Kebbi, Nigeria
[6]Istanbul University-Cerrahpaşa, Faculty of Engineering, Department of Chemistry, Avcilar, Istanbul, Turkiye

Dry eye disease, which occurs due to dysfunction of the lacrimal gland, is one of the most common eye diseases that causes corneal epithelial damage and results in significant vision loss and reduced quality of life. Maintaining a homeostatic microenvironment is crucial for a healthy ocular surface. Valproic acid/valproate is a broad-spectrum anti-epileptic drug. Although this drug has many side effects, its effects on the extraorbital lacrimal gland are unknown. *Moringa oleifera* (*M. oleifera*) is a plant widely used as food and folk medicine in Africa and Asia. It is stated that *M. oleifera* protects eye health with the high concentration of vitamin A. The lack of sufficient curative treatments for dry eye disease directs researchers to find more permanent and sustainable treatment options. In this study, the effects of sodium valproate and *M. oleifera* on the extraorbital lacrimal gland of rats were examined. The lipid peroxidation and total oxidant levels in groups, defined as control, control + moringa extract, sodium valproate and sodium valproate + moringa extract, were determined. Valproate induced oxidative stress by significantly increasing the total oxidant and lipid peroxidation levels in the rat extraorbital lacrimal gland. *M. oleifera* extract exhibited protective properties, reversing these valproate-induced changes due to its antioxidant and therapeutic attributes. This research suggests that moringa extract might serve as an alternative treatment approach for individuals using sodium valproate and experiencing extraorbital lacrimal gland issues.

Keywords: *Moringa oleifera*, sodium valproate, extraorbital lacrimal gland, lipid peroxidation, total oxidant status

OP10

Lactobacillus rhamnosus GG alleviates BPA-induced oxidative damage

Pınar Dede[1], Seren Ede Pazarbaşı[1], Doğancan Dörücü[2], Göksel Şener[3], Tuğba Tunalı Akbay[4]

[1]Marmara University, Institute of Health Sciences, Department of Biochemistry, Istanbul, Türkiye

[2]Marmara University, School of Medicine, Urology Department, Istanbul, Türkiye
[3]Fenerbahce University, Faculty of Pharmacy,

Department of Pharmacology, Istanbul, Türkiye
[4]Marmara University, Faculty of Dentistry, Department of Basic Medical Sciences, Istanbul, Türkiye

BPA is a chemical that disrupts the endocrine system by mimicking numerous hormones like estrogen in the human body or by having a xenobiotic effect on the organism. It is used in the production of many materials and materials that are used in daily life including cans, pet materials, food and beverage packaging, processed and heated papers, and various equipment used in dental treatment. The present study aimed to investigate if bisphenol A induces oxidative stress in the liver and kidney of rats and if co-administration of, Lactobacillus rhamnosus GG (LGG) a probiotic, can prevent oxidative stress in rat serum. LGG-type probiotics have been found to reduce oxidative damage and inflammation and increase antioxidant activity. For this purpose, twenty-four Wistar albino male rats were divided into three groups: control (1st group), Bisphenol A (2nd group), and Bisphenol A+ LGG (3rd group). 50 mg/kg Bisphenol A (2nd and 3rd group) was administered five days a week for six weeks and 1x109 colony forming unit/day will be applied to LGG (3rd group only). At the end of the sixth week, heart blood samples were collected. Total oxidant status, oxidative stress index, lipid peroxidation, and glutathione levels were measured in serum samples. In this study, it was determined that LGG increased serum antioxidant capacity in BPA-induced oxidative stress. The results of this study will guide future research into the potential benefit of probiotics in mitigating the toxic effects of various hazardous chemicals.

Keywords: bisphenol A, lactobacillus rhamnosus GG, endocrine disruptors, probiotic

OP11

Alpha Lipoic Acid Prevents the Damage to the Kidneys Caused by Valproic Acid Used in the Treatment of Epilepsy

Nigar Garayeva[1], Ismet Burcu Turkyilmaz[2], Refiye Yanardag[2]

[1]Istanbul University-Cerrahpaşa, Institute of Graduate Studies, 34320, Avcilar, Istanbul, Turkey
[2]Istanbul University-Cerrahpaşa, Faculty of Engineering, Department of Chemistry, 34320, Avcilar, Istanbul, Turkey

VPA, 2-propyl valeric acid (VPA), is a fatty acid derivative and an anticonvulsant but this drug causes the production of reactive oxygen species which is related to many organ toxicities and injuries. Alpha lipoic acid (ALA) is a powerful antioxidant and can remove a variety of reactive oxygen species, and regenerate antioxidant molecules to maintain normal antioxidant capacity. The human kidney plays a vital role in the filtration of blood, secretion of hormones, and regulation of blood pressure. In this study, we aimed to investigate the possible protective effects of ALA on VPA-induced kidney injury in rats. Female rats were divided into four groups as follows: Group I, control animals (corn oil per day for 15 days); Group II, ALA given group (50 mg/kg per day for 15 days); Group III, VPA administered group (500 mg/kg per day for 15 days) and Group IV, VPA and ALA given group at the same dose and time per day. On the 16th day, kidney tissues were taken. Kidney tissues were homogenized in cold saline and centrifuged. The reduced glutathione and lipid peroxidation levels, sodium potassium ATPase, and arginase activities were determined in all groups. The reduced glutathione levels and sodium-potassium ATPase activities were decreased while lipid peroxidation levels and arginase activities were increased in VPA group as compared to control group. Administration of ALA reversed these levels and activities in

VPA group. We may conclude that alpha lipoic acid can protect against kidney injury induced by VPA.

Keywords: Valproic acid, alpha lipoic acid, kidney

OP12

Evaluation of The Anti-Cancer Properties of o Half-Sandwoch (Hs) Mono-Functoonal Ru(II) P-Cymene Complex Containing Biguanide Ligand

Sabahattin Comertpay[1], Abdulmecit Gul[2], Ozge Gungor[3], Muhammet Kose[3]

[1]Kahramanmaras Sutcu Imam University, Department of BioEngineering and BioSciences, Kahramanmaras, TURKIYE
[2]Kahramanmaras Sutcu Imam University, Faculty of Agriculture, Department of Agricultural Biotechnology, Kahramanmaras, TURKIYE
[3]Kahramanmaras Sutcu Imam University, Faculty of Science, Chemistry Department, Kahramanmaras, TURKIYE

The development of chemotherapy drugs for treating brain tumors is constrained by the limited ability of these drugs to penetrate the blood-brain barrier. Furthermore, platinum-based agents, commonly employed in cancer treatment, face challenges such as resistance development in tumors and severe side effects. Ruthenium (Ru) complexes, on the other hand, emerge as potential alternatives to platinum-based agents with their versatile biological activity. In this TUBITAK-supported study (Project Nr. 122 Z 455), a novel half-sandwich (HS) mono-functional Ru(II)-p-cymene complex [Ru(p-cymene)(T2B)Cl]Cl of a biguanide ligand (T2B) containing L-borneol terminal unit was synthesized and characterized, and the complex's ability to traverse the blood-brain barrier and its anti-cancer properties were evaluated in vitro. Although both the T2B ligand and its ruthenium complex appeared incapable of crossing the blood-brain barrier in the ADME test, the ruthenium complex exhibited noteworthy potential surpassing the ligand alone.

Additionally, in MTS assay-based cytotoxicity assessments on YKG-1 glioblastoma cells and HUVEC healthy human cells, both agents demonstrated higher cytotoxicity against cancer cells compared to healthy cells ($p<0.0001$). However, the Ru complex was observed to require a larger concentration to reduce the viability of both cell types ($p<0.0001$). These preliminary findings suggest that i) the T2B ligand kills YKG-1 cells more efficiently than HUVEC cells, and ii) the addition of ruthenium to the ligand reduces its cytotoxicity. Although T2B here presents a potential to be used as an anti-cancer agent, further experiments with diverse cell types as well as animal models are crucial for a comprehensive assessment of this potential.

Keywords: Brain Tumor, Cytotoxicity, HUVEC, YKG-1, ruthenium

OP13

Investigation of the relation between suppressor of cytokine signalling (SOCS-1) gene polymorphism (-1478CA>del) and COVID-19 disease

Maya Ahmadova[1], Ergun Pınarbaşı[3], Mahir Budak[2], Ertan Mahir Korkmaz[2]
[1]Department of Molecular Biology and Genetics, Graduate School Of Natural and Applied Sciences, Sivas Cumhuriyet University, Sivas,Turkey
[2]Department of Molecular Biology and Genetics, Faculty of Science, Sivas Cumhuriyet University, Sivas, Turkey
[3]Department of Medical Biology,Faculty of Medicine,Sivas Cumhuriyet University, Sivas, Turkey

COVID-19 is an infectious disease caused by SARS-CoV-2. Despite being very active and infectious, its symptoms vary among individuals. The researches on the genetic background are essential for elucidating the reason why COVID-19 causes mild symptoms in some people but severe symptoms in others. A number of studies have revealed that inflammation contributes to a range of complex infections. Cytokines play a role in modulating humoral and transcellular immune pathways during immune response to inflammation. The cytokine storm in COVID-19 patients is strictly regulated by the SOCS family proteins, which suppress cytokine signalling. SOCS-1, one of the eight intracellular proteins in mammalian SOCS family, is involved in the regulation of the JAK/STAT and NF-κB pathways through ubiquitin-mediated proteasomal degradation. The dysfunction of this protein affects antiviral defence in the respiratory tract. When compared to the low-risk groups for COVID-19, the high-risk groups exhibit less interferon response. This results in an excessive inflammatory response, allowing the virus to reproduce and spread even faster. A polymorphism scan of the SOCS-1 gene in asthma patients has revealed the presence of 13 different polymorphisms. The -1478CA>del polymorphism located in the promoter region was discovered to have a significant relationship with adult susceptibility, resulting higher transcription levels in the human lung epithelial cell line. Here, we therefore investigated the distribution pattern of the -1478CA>del polymorphism in COVID-19 patients with different clinical characteristics. The effect of genetic variations on clinical outcomes was assessed by associating genotypes and allele frequencies with the severity of the disease.

Keywords: Pandemic, SARS-CoV-2, SOCS1, Polymorphism, RFLP

OP14

Assessing *HSP70* and *TCP1* Status of Circulating Tumor Cells in Metastatic Colorectal Cancer

Dilek Pirim[1], Berkcan Doğan[2], Fatih Atilla Bağcı[3], Özgen Işık[4], Türkan Evrensel[5]

[1]Bursa Uludag University, Faculty of Arts & Science, Department of Molecular Biology and Genetics, 16059, Bursa, Türkiye; Bursa Uludag University, Institute of Health Sciences, Department of Translational Medicine, 16059, Bursa, Türkiye

[2]Bursa Uludag University, Institute of Health Sciences, Department of Translational Medicine, 16059, Bursa, Türkiye; Bursa Uludag University, Faculty of Medicine, Department of Medical Genetics, 16059, Bursa, Türkiye

[3]Bursa Uludag University, Institute of Natural and Applied Sciences, Department of Molecular Biology and Genetics, 16059, Bursa, Türkiye

[4]Bursa Uludag University, Faculty of Medicine, Department of General Surgery, 16059, Bursa, Türkiye

[5]Bursa Uludag University, Faculty of Medicine, Department of Medical Oncology, 16059, Bursa, Türkiye

Colorectal cancer (CRC) remains a global public health problem. Accumulating evidence indicates that utilizing circulating tumor cells (CTCs) can be a promising approach for alleviating the global burden of CRC. The major limitation in CTC research is to define heterogenous CTC phenotypes precisely which require further investigation. HSP70 and TCP1 are key molecular chaperones and were previously reported to have crucial roles in cancer pathogenesis yet their clinical value for CTC characterization and CRC management remains unclear. Here, we aimed to assess the expression status of HSP70 and TCP1 on CRC-derived CTCs to evaluate their biomarker potential for CTC identification. Thus, peripheral blood samples collected from 47 metastatic CRC patients were immuno-

magnetically enriched for CTC detection, and the expression status of the *HSP70* and *TCP1* was analyzed by PCR-based AdnaTest (QIAGEN GmbH, Germany) protocol. The correlations of the analyzed genes with CRC-specific markers (*CEA*, *EpCAM*, and *EGFR*) and clinicopathological characteristics were also determined. *HSP70* positivity was observed in 26 of 47 cells (55.32%) of metastatic CRC patients. However, *TCP1* positivity was detected in only 6 samples. Nine samples (9/17) that were negative for CRC-specific markers (*CEA*, *EpCAM*, and *EGFR*) showed expressions of *HSP70* and *TCP1* expressions. Our preliminary data also implies that *HSP70* positivity is predominantly seen in rectum cancer patients. Our results suggest the clinical value of the *HSP70* for CTC characterization in CRC and provide information for its utility in liquid biopsy approaches for CRC monitoring and disease management.

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Keywords: Circulating tumor cells, colorectal cancer, HSP70, TCP1, liquid biopsy

OP15

Flavopiridol and temozolomid combination suppresses cell proliferation and colony formation in U87-MG GBM cells

Ahsen Güler, Zühal Hamurcu
Department of Medical Biology, Faculty of Medicine, Erciyes University, Kayseri, Turkey; Betül-Ziya Eren Genome and Stem Cell Center, Erciyes University, Kayseri, Turkey.

Glioblastoma multiforme (GBM) remains one of the most challenging solid cancers to treat due to its highly aggressive and drug-resistant nature. Surgical resection, followed by chemo- and radiotherapy, is currently the standard treatment for GBM in the clinic. The increase in temozolomid (TMZ) resistance is one of the main reasons for GBM treatment failure. Flavopiridol (FP) is a semi-synthetic flavonoid isolated from an Indian plant. FP has been shown to inhibit CDKs in G1/S or G2/M of cell cycle in solid tumors. Therefore, we investigated the effects of the combination of FP and TMZ on GBM cell proliferation. In our study, U87-MG cells were treated with various concentrations of FP (50-100 nM), TMZ (20-80 µM), the combination of FP and TMZ for 72 hours. MTS assay and clonogenic assay were performed to detect cell proliferation and colony formation. The expressions of Cyclin-D1 and p53 proteins, which play a role in the cell cycle, were determined by western blot analysis.

We found that the combination of FP and TMZ led to a significant reduced the cell proliferation and clonogenicity of GBM cells compared to only FP and TMZ in GBM cells ($p<0.001$). Furthermore, we demonstrated that treatment with FP significantly reduced expression of Cyclin-D1 and p53 protein, which is involved in cell cycle, in GBM cells ($p<0.001$). Our results showed, that FP may increases sensitivity of TMZ, and FP and TMZ combination could be a useful therapeutic strategy for GBM treatment. However, more studies are needed.

Keywords: Glioblastoma multiforme, Flavopiridol, Temozolomid

OP16

The Effects of Panax ginseng on the Blood Samples of the Rats Exposed to Bisphenol A

Naji Ullah Fazalyar[1], Doğancan Dörücü[2], Seren Ede Pazarbaşı[5], Göksel Şener[3], Tuğba Tunalı Akbay[4]
[1]Marmara University, Institute of Health

Sciences, Department of Biochemistry, Istanbul, Turkey
[2]Marmara University, School of Medicine, Urology Department, Istanbul, Turkey
[3]Fenerbahce University, Faculty of Pharmacy, Department of Pharmacology, Istanbul, Turkey
[4]Marmara University, Faculty of Dentistry, Department of Basic Medical Sciences, Istanbul, Turkey
[5]Fenerbahçe University, Vocational School of Health Services

Bisphenol A is one of the xenoestrogens that enters the human body through food, water, and inhalation, accumulating in tissues due to its fat-soluble nature. It exhibits toxic, mutagenic, and carcinogenic effects in living organisms. This study aimed to investigate if bisphenol A induces oxidative stress in the blood and whether Panax ginseng (PxG) may counteract it. PxG is a medicinal herb with a powerful anti-oxidant properties. It is not still approved by FDA for human use but it is claimed that its local effect takes part in regulating different body subsystems. It contains ginsenosides, saponins, nonsaponins, oils, phytosterols, polysaccharides, vitamins, minerals, enzymes, and organic acids. PxG and its components have also shown anti-diabetic, anti-tumor, anti-apoptotic, anti-hypertensive, anti-inflammatory, and anti-aging properties. In this study bisphenol A (50 mg/kg bisphenol A per day) and bisphenol A+PxG (100 mg/kg PxG per day) were orally administered to rats for six weeks. At the end of the six weeks, blood samples were collected. Total oxidant status, total antioxidant status, oxidative stress index, lipid peroxidation, and glutathione levels were measured in serum samples. PxG ameliorated the oxidative effects of bisphenol A in serum after six weeks of treatment. In conclusion, Panax ginseng has therapeutic potential to prevent bisphenol A-induced oxidative damage by strengthening antioxidant defense systems.

Keywords: Bisphenol A (BPA), Oxidative stress, Panax ginseng (PxG)

OP17

The combined effects of *ANGPTL8* (rs2278426), *APOC1* (rs11568822), and *APOA5* (rs662799) polymorphisms on CAD risk factors

Aslıhan Gizem Bilgin[1], Aybike Sena Özuynuk Ertuğrul[1], Berkay Ekici[2], Aycan Fahri Erkan[3], Neslihan Çoban[1]

[1]Istanbul University Aziz Sancar Institute of Experimental Medicine, Department of Genetics, Istanbul, Türkiye
[2]Ufuk University Faculty of Medicine, Department of Cardiology, Ankara, Türkiye
[3]Biruni University Faculty of Medicine, Department of Cardiology, Istanbul, Türkiye

Atherosclerosis, characterized by the accumulation of lipids in the arterial walls, is a leading cause of coronary artery disease (CAD). Angiopoietin like protein 8 (ANGPTL8), apolipoprotein C-I (ApoC-I), and apolipoprotein A-V (ApoA-V) play essential roles in atherosclerosis due to their associations with triglyceride (TG) metabolism and lipoprotein lipase (LPL). The most recent evidence suggests that ApoA-V induces LPL activity by suppressing the ANGPTL8/ANGPTL3 complex that inactivates LPL. This study aims to examine the associations between CAD and combined effects of *ANGPTL8* (rs2278426, C/T) with *APOC1* (rs11568822, TT/TTCGTT) and *APOA5* (rs662799 T/C) polymorphisms. A total of 443 individuals who underwent coronary angiography were included in this study. The study population was divided into non-CAD (<=30% stenosis) and CAD (>=50% stenosis). Genomic DNA was isolated from blood samples, and subjects were genotyped for selected polymorphisms. Minor allele carriage statuses of polymorphisms were demonstrated with (+) and (-) symbols. In the CAD group, *ANGPTL8(+)/APOA5(-)* patients had lower stenosis degree than *ANGPTL8(-)/APOA5(+)* patients (p=0.037). In addition, *ANGPTL8* minor (T) allele carrier CAD patients had lower TG levels than patients with

CC genotype (*p*=0.049) and CAD patients with *ANGPTL8(+)/APOC1(-)* had lower TG level (*p*=0.029), TG glucose (TyG) index (*p*=0.016) and TG/HDL ratio (*p*=0.040) than patients with *ANGPTL8(-)/APOC1(+)*. The findings show that the polymorphisms in these genes affect fasting TG levels and possible CAD risk factors such as TyG index and TG/HDL ratio. The findings indicate that ANGPTL8, a recently discovered member of the family, could be a promising target for managing CAD risk.

Keywords: *ANGPTL8*, *APOA5*, *APOC1*, atherosclerosis, polymorphism

OP18

Evaluation of the Effects of Emotional and Violence Related Genes in Athletes

Buse Sabiha Bozaslan[1], Emel Hülya Yükseloğlu[2], Şakir Ümit Zeybek[3]

[1]Turkey/ Istanbul/ Uskudar University/ Health Services Vocational School/ Assist Prof.
[2]Turkey/ Istanbul/ Istanbul Cerrahpasa University/ Institute Of Forensic Sciences, Department Of Natural And Applied Sciences/ Professor.
[3]Turkey/ Istanbul/ Istanbul University/Aziz Sancar Institute Of Experimental Medicine, Department Of Molecular Medicine/ Professor

The exploration of the human genome involves the examination of various factors such as gene function, structural features of the genome, chromatin organization, recombination rate, and mutations to accurately understand its complex relationship with physiology and diseases. With the sequencing of the human genome, there is a growing trend in studies investigating the influence of genes on the development of behavior and personality traits. Research indicates that complex behaviors and traits are regulated by multiple genes. In this regard, genes influencing the dopamine pathway are being studied in connection with the field of neuroscience. Sports genetics studies encompass a wide range of research, including the identification of genes affecting athletic performance, elucidation of the mechanisms of these genes, and determining individual predispositions for athletic performance. Considering the factors determining success in sports, the creation of training and nutrition programs tailored to genetic makeup is crucial, not only in individual sports but also in team sports. This study will present a review of the literature on the relationships associated with candidate genes, particularly catechol-O-methyltransferase, serotonin transporter, and monoamine oxidase, known to influence the personality and behavior traits of athletes, especially those related to aggression. Many studies in sports genetics cover a spectrum of research, including the identification of genes influencing athletic performance, the explanation of the mechanisms of these genes, and the determination of individual predispositions for athletic performance.

Keywords: Athletes, genetics, violence

OP19

Identification of Differentially Expressed Genes and Potential Inhibitors in Resistant Subtypes of Acute Lymphoblastic Leukemia

Başak Özay[1], Ezgi Yağmur Tükel[1], Yağmur Kiraz[1], Gizem Ayna Duran

[1]Faculty of Engineering, Department of Genetics and Bioengineering, Izmir University of Economics, 35330, Izmir, Turkey
[2]Faculty of Engineering, Department of Biomedical Engineering, Izmir University of Economics, 35330, Izmir, Turkey

Introduction and Aim: Acute lymphoblastic leukemia is a hematological malignancy often seen in children. While the 5-year survival rate for the disease is high, resistance to commonly

used chemotherapy drugs is still a problem. The aim of this study is to find differentially expressed genes (DEGs) related to the resistance of four drugs and identify potential inhibitors through *in silico* screening and docking.

Materials-Methods: Gene expression data of four types of resistant (asparaginase, daunorubicin, vincristine and prednisolone) and sensitive ALL patients were provided from GSE635 GEO dataset, and GSE22529 was used to obtain data of 11 healthy individuals. GSE19143 was used for validation. RMA normalization and LIMMA were used to analyze the CEL files. Molecular docking was done using PyRX and molecular dynamics (MD) simulations were performed on Gromacs.

Results: Based on Adj.p.value < 0.05, 25 hub genes were discovered and 1294 DEGs were identified in total. 12 of which including HSPA8 were found to be commonly overexpressed across four types of resistant groups. Kegg pathway analysis showed enrichment in the PI3K-Akt pathway. Two proteins were screened against 3556 molecules and three were identified as potential inhibitors. MD analysis of one of the proteins showed all drugs had potential to overcome drug resistance, with one showing superior results.

Conclusion: This study reveals the potential common target genes for resistant ALL subtypes and suggests inhibitor candidates to reduce current relapse rates via drug repurposing. Further cytotoxicity analyses on ALL cell lines will be conducted to validate these results.

Keywords: Acute lymphoblastic leukemia, drug resistance, differentially expressed genes, in silico screening

OP20

Cytokine Detection with Bionanosensors in An In Vitro Sepsis Model

Işık Neslişah Korkut[1], Ilhan Yaylım[2], Serap Kuruca[2], Selcan Karakuş[3]

[1]Department of Molecular Medicine, Aziz Sancar Institute of Experimental Medicine, Istanbul University, Istanbul, Türkiye
[2]Department of Molecular Medicine, Aziz Sancar Institute of Experimental Medicine, Istanbul University, Istanbul, Türkiye; Department of Physiology, Faculty of Medicine, Istanbul Atlas University, Istanbul, Türkiye
[3]Department Of Physical Chemistry, Department Of Chemistry, Faculty Of Engineering, Istanbul- Cerrahpaşa University, Istanbul, Turkey

Within the scope of the study, secreted cytokines in human blood were determined by bionanosensors with in vitro sepsis model. For the in vitro model of sepsis, blood from health and volunteers is treated with LPS. LPS increased cytokine secretion in the whole blood model. The aim of our study is to develop a biosensor that enables the clinical detection of cytokines secreted by organisms as a cause or consequence of many diseases, with much more sensitive measurements, and maintains its sensitivity in the in vitro sepsis model. Maca-based silver nanostructures were prepared. Electrodes are coated with prepared Ag nanostructures and cytokine levels of the blood-serum samples were measured. It has been determined that the bionanosensor measurement is a much faster and more sensitive measurement method used against ELISA measurements. It is aimed to enable future biosensors to rapidly and sensitively detect sepsis, a leading infectious disease, in the clinic.

Keywords: Sepsis, IL-6, Cytokine, Bionanosensor, silver nanoparticles

OP21

Expression analysis of lncRNA-ATB in the PAC-treated estrogen receptor-positive breast cancer cell line

Fatma Hande Karpuzoğlu

İstanbul University Istanbul Faculty of Medicine Department of Biochemistry

Breast cancer is still the leading cause of cancer death in women worldwide and conventional treatments remain insufficient despite years of research. Tumor size, lymph node involvement, and the expression levels of estrogen receptor (ER), progesterone receptor (PgR), and human epidermal growth factor receptor 2 (HER2) in tumors are among other factors that influence prognosis. The relationship between diseases and lncRNAs, with the elucidation of their biological and physiological roles, has become the subject of research. The role of lncRNA-ATB in cellular invasion, its influence on migration, and its potential impact on metastasis underscore its significance in shaping the aggressive behavior of breast cancer cells. In our study, we aimed to determine the expression changes in lncRNA-ATB level when treated with paclitaxel used in the treatment of estrogen receptor-positive breast cancer in vitro.

The IC50 value of the clinical drug paclitaxel (PAC) in an estrogen receptor-positive breast cancer cell line (MCF-7) was determined by the MTT viability test. After total RNA isolation, the difference in lncRNA expression levels of PAC treatment in the MCF-7 cell line was determined by qPCR. By the 2-ΔΔCT method, the lncRNA-ATB expression level was 0.52-fold decreased in the PAC-treated cell line compared to the untreated cell line, but statistical significance was not obtained. Since abnormal expression of lncRNAs is known to contribute significantly to the initiation and progression of cancer in breast cancer types, it is thought that low-expression lncRNAs may provide insight in terms of correct treatment and good prognosis.

Keywords: breast cancer, cell line, long noncoding RNAs ATB, lncRNAs ATB, paclitaxel

OP22

Moringa oleifera Ethanolic Extract Prevents Oxidative Damage on Spleen Caused by Sodium Valproate Used in Epilepsy Treatment

Sabina Ahmadova[1], Ismet Burcu Turkyilmaz[2], Umar Faruk Magaji[3], Ozlem Sacan[2], Refiye Yanardag[2]

[1]Istanbul University-Cerrahpaşa, Institute of Graduate Studies, Avcilar, Istanbul, Turkey
[2]Istanbul University-Cerrahpaşa, Faculty of Engineering, Department of Chemistry, Avcilar, Istanbul, Turkey
[3]Federal University Birnin Kebbi, Department of Biochemistry and Molecular Biology, Birnin Kebbi, Kebbi, Nigeria

Valproic acid/Valproate, a branched chain carboxylic acid, is widely used for its antiepileptic property. This drug has side effects on many tissues and organs. Moringa oleifera (MO) is a well-known herb in Africa region and is used for folk medicine. Its rich ingredients like natural antioxidants and vitamins make this plant valuable for treating many diseases. Spleen is the largest immune organ of the body and has many functions like immune response, blood filtration. In this study, we aimed to investigate the possible protective effects of MO ethanolic extract on sodium valproate-induced spleen injury in rats. Female rats were divided into four groups as follows: Group I, control animals (0.9% NaCl given orally for 15 days); Group II, MO ethanolic extract given group (0.3 g/kg for 15 days); Group III, sodium valproate given group (0.5 g/kg per day for 15 days) and Group IV, sodium valproate and MO ethanolic extract given group at the same dose and time. On the 16th day, animals were sacrificed, and spleen

tissues were taken. They were homogenized in 0.9% NaCl and centrifuged. In supernatants, reduced glutathione and lipid peroxidation levels were determined. The glutathione levels were decreased while lipid peroxidation levels were increased in sodium valproate group compared to control group. MO ethanolic extract increased glutathione levels while it decreased lipid peroxidation levels in spleen tissues of sodium valproate group. It can be concluded that Moringa oleifera ethanolic extract can protect spleen against sodium valproate toxicity.

Keywords: Moringa oleifera, sodium valproate, spleen

OP23

Effect of Cytokine Gene Variants on the Risk of Autism Spectrum Disorder

Kübra Çiğdem Pekkoç Uyanık[1], Aysel Kalaycı Yiğin[2], Burak Doğangün[3], Mehmet Seven[2]

[1]Department of Medical Biology, Faculty of Medicine, Haliç University, İstanbul, Turkey; Department of Medical Genetics, Cerrahpasa Faculty of Medicine, İstanbul University-Cerrahpasa, İstanbul, Turkey
[2]Department of Medical Genetics, Cerrahpasa Faculty of Medicine, İstanbul University-Cerrahpasa, İstanbul, Turkey
[3]Department of Child and Adolescent Psychiatry, Cerrahpasa Faculty of Medicine, İstanbul University-Cerrahpasa, İstanbul, Turkey

Background: Autism Spectrum Disorder (ASD) is a neurodevelopmental disorder caused by genetic, environmental and immunological factors. It is known that neural development processes are affected by immune functions. In autism, chronic active neuroinflammation and an increase in proinflammatory cytokines in serum and cerebrospinal fluid are observed. Interleukin 6 (*IL6*) and interleukin 1B (*IL1B*) genes are important cytokine genes that may be immunologically linked to autism. The aim of this study is to evaluate the relationship between cytokine gene polymorphisms in ASD. Methods: DNA isolations were performed in 95 children diagnosed with ASD and 84 unrelated healthy children, single-nucleotide changes in *IL6* (rs1800796) and *IL1B* (rs1143634) genes were determined by using Real-Time Polymerase Chain Reaction method. Results: *IL6* rs1800796 polymorphism presented an elevated risk for the development of ASD with CG genotype and dominant model (CG+GG vs. CC), CG+GG carriers (OR = 1.867, p = 0.057; OR = 1.847, p = 0.055, respectively). CT genotype in *IL1B* rs1143634 polymorphism associated with 2.33 times elevated risk of autism and showed a significant association compared to wild-type CC genotype (p = 0.02). *IL1B* rs1143634 polymorphism presented a significantly elevated risk for the development of ASD with recessive model (CC+CT vs.TT), TT genotype (OR = 8.145, p = 0.02).
Conclusion: This study concludes that rs1143634 is associated with the risk of ASD in Turkish children. Determining these polymorphisms in a larger sample group may contribute to understanding the etiology of ASD and developing new treatment protocols.

Keywords: Autism spectrum disorder, *IL6* gene, *IL1B* gene, polymorphism, real-time PCR

OP24

Pioglitazone Increase Healthspan Possibly by Reducing Oxidative Stress in Fission Yeast

Sümeyra Zeynep Çalıcı[1], Buse Özden[1], Çağatay Tarhan[2]

[1]Istanbul University, Institute of Science, Molecular Biotechnology and Genetics

[2]Istanbul University, Faculty of Science, Department of Molecular Biology and Genetics

Aging is characterized by a gradual reduction in physiological health, affecting functions at the molecular, cellular, tissue, and systemic levels, thereby increasing the probability of mortality. Pioglitazone is a commonly prescribed medication for diabetes, primarily known for its ability to enhance insulin sensitivity. Beyond its role in diabetes, Pioglitazone serves as an effective glycation inhibitor, indirectly modulating the expression of numerous metabolic genes by activating the gamma isoform of peroxisome proliferator-activated receptor-c (PPAR-c). This activation mimics the effects of calorie restriction and imparts antioxidative as well as anti-inflammatory properties. Additionally, Pioglitazone has been observed to affect the skin atrophy, contributing to its potential in mitigating signs of aging. In this research, our emphasis was on exploring the anti-aging properties of Pioglitazone using the model organism S. pombe. To achieve this objective, we identified the effective concentration of Pioglitazone and assessed its impact on chronological lifespan. Additionally, we conducted analyses for lipid peroxidation, total carbohydrate consumption, and the activity of SOD enzymes in cells treated with Pioglitazone at this determined concentration, comparing them to untreated cells. According to our results, it appears that Pioglitazone treatment increases healthy lifespan instead of chronological lifespan, encourages consuming existing glucose much faster, clearly reduces lipid peroxidation levels, and does not cause a significant change in SOD activity. Our results unveil the beneficial impact of pioglitazone on the aging process by enhancing specific parameters in S. pombe and showcasing a notable effect on glucose metabolism.

Keywords: Pioglitazone, S.pombe, Healthspan

OP25

Evaluation of the Usability of Morphometric Measurements from Computed Tomography Images in Gender Determination of Adult Individuals (Preliminary Study of Thesis)

Hilal Işık Rozan[1], Murat Dıramalı[1], Seval Bayrak[2]
[1]Bolu İzzet Baysal University, Faculty of Medicine, Department of Anatomy
[2]Bolu İzzet Baysal University, Faculty of Dentistry

Objective: Identifying the sex of skeletal remains through gender analysis is a crucial and fundamental step in forensic anthropology. Maxillary sinuses and adjacent anatomical structures, including the skull and other bones, can retain their integrity even in cases of severe damage, making them suitable for sex determination. In this study, we aimed to predict gender based on measurements obtained from cone-beam computed tomography images of patients. Materials-Methods: A total of 630 individuals who presented to the Bolu Abant İzzet Baysal University Faculty of Dentistry with no facial anomalies, trauma history, surgical history, missing or absent upper jaw teeth, and no history of orthognathic or orthodontic treatment were included in the study. Measurements were taken from the sections where the boundaries of the zygomatic arches were most distinct. Gender differences were analyzed using the Student's t-test, and machine learning models based on linear discriminant analysis were developed for parameters that showed statistical significance. Python 3.8.8 compiler and Jupyter Notebook 6.1.8 editor were used for data analysis and algorithm training. Results: The linear discriminant analysis yielded a gender prediction accuracy of 80.4% based on the right maxillary sinus width and right zygomatic arch height. Machine learning methods, including Random Forest, K-Nearest Neighbors, and Gaussian Naive Bayes

algorithms, achieved a higher accuracy rate of 81.7% in gender prediction. Conclusion: It was observed that gender prediction can be achieved using machine learning models based on right zygomatic arch height and right maxillary sinus height parameters.

Keywords: Anatomy, Gender Estimation, Linear Discriminant Analysis, Machine Learning Algorithms

OP26

AMPK alpha-1 and TNFA gene expression levels are associated with myocardial infarction markers

Aybike Sena Ozuynuk Ertugrul[1], Nazli Dogan[1], Cenk Eray Yildiz[2], Ozan Onur Balkanay[3], Neslihan Coban[1]

[1]Department of Genetics, Aziz Sancar Institute of Experimental Medicine, Istanbul University, Istanbul, Türkiye
[2]Cardiovascular Surgery, Institute of Cardiology-Istanbul University-Cerrahpasa, Istanbul, Türkiye
[3]Cardiovascular Surgery, Cerrahpasa Medical Faculty-Istanbul University-Cerrahpasa, Istanbul, Türkiye

Background and Aims: Epicardial adipose tissue (EAT) surrounds the heart and coronary arteries and is important for comprehending the pathogenesis of coronary artery disease (CAD). We aimed to evaluate the expressions of TNFA, and PRKAA1 (encodes for α1 subunit of AMPK), in EAT by comparing to visceral adipose tissue (VAT).

Methods: EAT samples from 93 individuals (63 CAD; 30 non-CAD) and VAT samples from 65 individuals (46 CAD; 19 non-CAD) were collected. PRKAA1 and TNFA expression levels were examined using quantitative real-time PCR. Biochemical measurements were done from the blood samples collected during the pre-operative period.

Results: The most striking result to emerge from the data is that PRKAA1 expression level is significantly lower, while TNFA is higher in EAT compared to VAT in CAD patients ($p<0.05$). PRKAA1 expression was found in negative correlation with Troponin T (hsTnT) and with creatine kinase (CK-MB), while EAT TNFA expression was found in positive correlation with systolic blood pressure and fasting glucose levels ($p<0.05$). Moreover, TNFA expression in VAT was positively correlated with CK-MB ($p<0.05$).
Conclusions: The lower expression of PRKAA1 in EAT than in VAT in CAD patients could be explained by the dysregulated energy metabolism occurring during CAD pathogenesis. The higher expression level of TNFA in EAT compared to VAT is due to increased inflammation in EAT during CAD. In addition, PRKAA1 and TNFA expressions in EAT are associated with myocardial infarction markers.

Keywords: epicardial adipose tissue, coronary artery disease, AMPK, TNFA

OP27

Investigation of the effect of MAO-A and SLC6A4 genes in obsessive-compulsive disorder

Jansed Berfin Yıldız[1], Efruz Irem Akkuş Yaylamış[1], Neşe Kocabaşoğlu[2], Müjgan Cengiz[1]

[1]İstanbul University-Cerrahpaşa, Cerrahpaşa Faculty of Medicine, Department of Medical Biology, Istanbul, Türkiye
[2]İstanbul University-Cerrahpaşa, Cerrahpaşa Faculty of Medicine, Department of Psychiatry, Istanbul, Türkiye

Obsessive-compulsive disorder (OCD) is a

psychiatric condition characterized by uncontrollable, reoccurring thoughts and repetitive behaviors. Serotonin is a chemical neurotransmitter commonly found in the human brain. Serotonin levels are controlled by intraneuronal monoamine oxidases. Monoamine oxidase A (MAO-A) regulates monoamine levels in the brain by metabolizing serotonin. MAO-A enzyme is associated with various psychiatric disorders. SLC6A4 gene encodes the serotonin transporter protein and is a candidate gene for the development of OCD. The aim of this study was to investigate the association of MAO-A and SLC6A6 genes with OCD. The study groups consisted of 95 patients diagnosed with OCD and 70 healthy volunteers. OCD severity of the patients was determined with the Yale-Brown Obsessive Compulsive Scale administered by an expert psychiatrist. Single nucleotide polymorphism analyses of rs909525 in MAO-A and rs16965628 in SLC6A4 were performed using real-time PCR. A significant difference was found between the genotype distributions of rs909525 (C/T) in MAO-A in OCD patients and healthy controls ($p<0.001$). Likewise, a significant difference was obtained between the genotype distributions of rs16965628 (G/C) in SLC6A4 in the study groups ($p<0.001$). Comparison of the polymorphic genotype distributions of MAO-A and SLC6A4 in the patient and control groups yielded significant data and showed that they may be associated with OCD. It is thought that this study will contribute to the literature in understanding the effects of imbalance in serotonergic system genetics on OCD.

This study was supported by Istanbul University-Cerrahpaşa Scientific Research Projects Coordination Unit. Project number: 35679.

Keywords: Obsessive-Compulsive Disorder, SLC6A4, MAO-A, Serotonin, Polymorphism

OP28

Investigation of Leukocyte Telomere Length and hTERT Gene MNS16A VNTR Variant in Microtia Patients

Sevde Sayın[1], Berker Büyükgüral[2], Fatıma Ceren Tunçel[1], Yasemin Oyacı[1], Mehmet Bekerecioğlu[3], Sacide Pehlivan[4]

[1]Institute of Graduate Studies in Health Sciences, Istanbul University
[2]Specialist of Plastic and Reconstructive Surgery, İstanbul, Turkey
[3]Gaziantep University, Department of Plastic, Reconstructive and Aesthetic Surgery, Gaziantep, Turkey
[4]Istanbul University, Istanbul Faculty of Medicine, Department of Medical Biology

Telomeres are the basis of replicative senescence in somatic cells and control cell division. It has been shown in some studies that telomere shortening is associated with growth retardation and congenital malformations. Microtia is a congenital ear deformity in which the external ear is malformed and underdeveloped.

This study aimed to determine whether leukocyte telomere length (LTL) and the MNS16A variable number tandem repeat (VNTR) polymorphism of the hTERT gene are associated with the risk of microtia in the Turkish population. A total of 38 volunteers, 18 patients diagnosed with microtia and 20 healthy controls, were included in the study. LTL analysis was performed with the Quantitative PCR (Q-PCR) method, and relative T/S ratios of patients and controls were calculated. hTERT-MNS16A-VNTR analysis was performed by PCR method. When patients and healthy controls were compared in terms of genotype/allele frequencies; No statistically significant difference was detected in the genotype and allele frequency of the hTERT-MNS16A-VNTR variant. However, when the T/S ratios of the patients were compared with the healthy group, borderline significance was

detected in terms of the shortening rate (p=0.055).
Our study is the first study in the literature to examine the relationship between microtia and LTL and hTERT-MNS16A-VNTR. Our results suggest that the hTERT-MNS16A-VNTR variant may not be associated with microtia, but telomere shortening may have a causal relationship with microtia. Since microtia is a rare congenital anomaly with different prevalence among populations, studies in different ethnicities will provide further elucidation of the relationship between microtia and LTL/hTERT-MNS16A-VNTR.

Keywords: Microtia, telomere, VNTR, PCR

OP29

Investigation of the Role of Rev-Erb α/β in Traumatic Brain Injury

Mahmud Esad Pence

Istanbul Medipol University Faculty of Medicine, Department of Medical Biochemistry

Traumatic brain injury (TBI) presents significant health challenges due to its association with high mortality and morbidity. This study explores the impact of RevErbα/β, a protein whose expression is modifiable via lentiviral vectors, on TBI pathophysiology. Employing 8–12-week-old male Balb/C mice, we manipulated Rev-Erbα/β protein levels using lentivirus and then induced TBI. Our primary objective was to understand how variations in Rev-Erbα/β levels influence TBI outcomes, specifically focusing on brain edema, infarct volume, blood-brain barrier (BBB) permeability, neuronal survival, and DNA fragmentation.

Our results revealed that increased RevErbα levels notably reduced DNA fragmentation and enhanced neuronal survival post-TBI. Similarly, elevated RevErbβ or combined RevErbα/β expression reduced infarct volume and DNA fragmentation, improved BBB integrity, and boosted neuronal survival. Conversely, decreasing RevErbα levels was associated with increased neuronal death and DNA fragmentation. Inhibition of RevErbβ led to increased injury volume, BBB permeability, and neuronal death. Suppressing both RevErbα and RevErbβ exacerbated these adverse outcomes.

Furthermore, proteomic analysis using liquid chromatography-mass spectrometry revealed that Rev-Erbα/β overexpression altered 46 different proteins, while its inhibition affected 402 proteins. These findings underscore the critical roles of Rev-Erbα/β in the pathophysiological processes following TBI. This study contributes to a deeper understanding of TBI's molecular dynamics, potentially guiding future therapeutic strategies targeting RevErbα/β for improved TBI management

Keywords: Circadian rhythm, Lentivirus, Proteomics, RevErb, TBI

OP30

Investigation of Ghrelin ad NPY Polymorphisms in Diabetic Obese and Non-Obese Diabetic Groups in Turkey

Saadet Büşra Aksoyer Sezgin[1], Şermin Durak[2], Arezoo Gheybi[3], Faruk Çelik[3], Ramazan Çakmak[4], Ali Osman Gürol[5], Ümit Zeybek[3]

[1]Department of Medical Biology and Genetics, Istanbul Yeni Yuzyil University, Istanbul, Turkey
[2]Department of Medical Microbiology, Istanbul University Cerrahpaşa, Istanbul, Turkey
[3]Department of Molecular Medicine, Istanbul University, Aziz Sancar Institute of Experimental Medicine, Istanbul, Turkey
[4]Department of Internal Medicine, Istanbul University Medical Faculty, Istanbul, Turkey

[5]Department of Immunology, Istanbul University, Aziz Sancar Institute of Experimental Medicine, Istanbul, Turkey

Obesity is a healthcare concern interacting with chronic diseases, promoting the production of pro-inflammatory factors that are involved in the pathogenesis of insulin resistance. As one of the most studied genes in obesity, Ghrelin controls glucose homeostasis by playing important roles in insulin resistance, glucose metabolism, and metabolic syndrome. One of the Single-Nucleotide Polymorphisms(SNPs) of Ghrelin is Gln90Leu(rs4684677). Ghrelin increases Neuropeptide-Y(NPY) expression in the hypothalamus by binding to the Ghrelin-Receptor. As a result, increased NPY-signaling contributes to the development of diabetes and obesity. It has also been reported the rs16147 is associated with obesity, glucose, and lipid metabolism from adolescence to adulthood.
A total of 99 diabetic obese and 99 non-obese diabetic individuals were examined in the present study. RT-PCR was used to detect Ghrelin(rs4684677) and NPY(rs16147)SNPs. No significant differences were detected between the genotype&allele distributions of the Ghrelin-polymorphism between the groups. However, NPY-polymorphism genotype distribution was significant between the groups(p<=0.0001). NPY-polymorphism T-allele was found to be significantly higher in the diabetic obese group(p<=0.0001), C-allele was significantly higher in the non-obese diabetic group(p=0.006). It was found that the risk of obesity increased ~13-fold in diabetic-patients who carried the NPY-polymorphism T-allele. The BMI increased at a significant level in the diabetic-obese patients who carried the NPY-polymorphism C-allele(p<=0.001). Although the mechanism of increased BMI that is associated with the NPY-variant is considered to occur because of increased food consumption, there is little evidence in epidemiological studies supporting this hypothesis. Further studies are needed to elucidate the molecular mechanisms underlying the observed relationships.

Keywords: Ghrelin, NPY, Polymorphisms, obesity, diabetes

OP31

Casticin regulates autophagy in lipopolysaccharide-activated microglial cells

Mehtap Yuksel Egrilmez, Keyvan Hemmatvand
Department of Molecular Medicine, Institute of Health Sciences, Dokuz Eylül University, Izmir, Türkiye

Microglia are the myeloid lineage cells which play important roles in homeostasis, inflammatory responses, and tissue repair in the brain. Microglial activation is involved in neuroinflammation which is associated with neurodegenerative diseases. Autophagy is a lysosome-dependent pathway for degradation and turnover of proteins and organelles in the cells. Autophagic dysfunction in microglial cells is suggested to contribute to neuroinflammation. Casticin is a polymethylflavone which has anti-cancer, anti-inflammatory, and anti-oxidant activities. This study aims to investigate the effect of casticin on autophagy in lipopolysaccharide (LPS)-activated microglial cells in vitro.N9 murine microglial cells were used in the study.N9 microglial cells were incubated with 1 µg/mL LPS for 2, 4, 8 and 24 h.The cells were pretreated with 0.1, 0.5 and 1 µM of casticin for 24 h.Cell viability was measured using WST-1 assay. The protein expression levels of LC3-II and p62 were determined by Western blotting.0.1 and 0.5 µM of casticin did not affect cell viability, whereas 1 µM casticin decreased.LC3-II and p62 protein expression levels were increased after LPS incubation.0.1 µM casticin increased LPS-induced LC3II protein expression, however 0.5 µM casticin

decreased compared to 0.1 µM casticin.0.1 µM casticin also increased LPS-induced p62 protein expression while 0.5 µM casticin decreased compared to 0.1 µM casticin. Our results indicated that LPS induced autophagosome formation, however, prevented autophagosome degradation leading to inhibition of autophagy.Lower dose of casticin increased LPS-induced inhibition of autophagy while higher dose of casticin induced autophagy suggesting a neuroprotective potential for neuroinflammation. These findings reveal that different doses of casticin have different effects on LPS-activated microglial autophagy.

Keywords: Microglia, lipopolysaccharide, neuroinflammation, autophagy, casticin

OP32

Attachment of oxadiazole ring to tetrazole-containing proteasome inhibitor increases cell death in ER+ breast cancer cells

Vildan Betul Yenigun[1], Hatice Ozkan[2], Ebru Kanımdan[1], Hamdi Ozkan[3], Abdurrahim Kocyigit[1]

[1]Bezmialem Vakıf University, Faculty of Medicine, Department of Medical Biochemistry, İstanbul, Turkey
[2]Bezmialem Vakif University, Faculty of Medicine, İstanbul, Turkey
[3]Gazi University, Faculty of Science, Department of Chemistry, Ankara, Turkey

Introduction: Breast cancer is one of the most common malignancies in the world that leads to women's death. Proteasomes remove damaged proteins from the body through an enzyme called proteolysis, and the proteasome inhibitors block the activity of proteasomes, which are responsible for breaking down proteins and regulating gene expression through various signaling pathways. Many proteasome inhibitors have been developed by targeting the 26S proteasome complex for antitumor effects. These proteasome inhibitors have shown anticancer action by activating apoptosis in different tumor types. The purpose of this study was to investigate the anticancer activity of a unique molecule with proteasome inhibitory properties that contains tetrazole and oxadiazole ring on breast cancer cells.
Methods: In this study, ER+ breast cancer cells (MCF-7) were used. Cell viability was analyzed by MTT assay, and the half-maximal inhibitory concentration (IC50) value with the most effective time was determined. The apoptosis was detected by Flow cytometry using Annexin V/PI in addition to Acridine Orange/Ethidium Bromide (AO/EB) staining.
Results: Cell viability results revealed that new designed proteasome inhibitor induced cytotoxicity and decreased viability of ER+ breast cancers best at 72hrs, and the inhibitor containing tetrazole and oxadiazole rings has lower IC50 value (200µM) comparing to inhibitor with only tetrazole. Flow cytometry analysis and AO/EB staining results also supported viability data.

Conclusion: The results of this study showed that the addition of an oxadiazole ring to the proteasome inhibitor containing a tetrazole ring leads to an increase in cell death caused by the inhibitor.

Keywords: Breast Cancer, Proteasome Inhibitor, Apoptosis, Cell Death

OP33

Valproic acid-Induced Autism Model in Zebrafish Embryos

Gizem Eğilmezer[1], Merih Beler[1], İsmail Ünal[1], Derya Cansız[2], Ebru Emekli Alturfan[3]

[1]Marmara University, Institute of Health Sciences, Faculty of Pharmacy, Department of

Biochemistry, Istanbul, Turkey
[2]Department Medipol University, Faculty of Medicine, Medical Biochemistry, Istanbul, Turkey
[3]Marmara University, Faculty of Dentistry, Department of Basic Medical Sciences, Istanbul, Turkey

The complex neurodevelopmental deficits and etiology of autism spectrum disorder (ASD) are associated with both hereditary and environmental variables. Therefore, in order to comprehend the fundamental mechanisms of ASD, it is imperative to create animal models with traits similar to ASD. In humans, rodents, and most recently, zebrafish, prenatal exposure to valproic acid (VPA) resulted in symptoms resembling ASD. In this study, the utilization of VPA exposure to create an ASD model in zebrafish was examined through studies in the literature and our preliminary experiments. Zebrafish embryos were exposed to VPA for 72 hpf and locomotor activites were examined. Results of studies in literature and our preliminary experiments showed that VPA caused alterations in locomotor activities related with the progression of ASD.

Keywords: Autism spectrum disorder, valproic acid, zebrafish embryos

OP34

Investigation of morphological and behavioral effects of memantine treatment in zebrafish embryos

Efruz Irem Akkuş Yaylamış[1], Müjgan Cengiz[1], Ebru Emekli Alturfan[2]

[1]Istanbul University-Cerrahpaşa, Cerrahpaşa Faculty of Medicine, Department of Medical Biology, Istanbul, Türkiye
[2]Marmara University, Faculty of Dentistry, Department of Basic Medical Sciences, Istanbul, Türkiye

Memantine is a moderate-affinity and non-competitive antagonist for N-methyl-D-aspartate receptors (NMDAR). Memantine is currently indicated for the treatment of neurodegenerative diseases such as Alzheimer's disease and Parkinson's disease, and neuropsychiatric disorders such as depression and obsessive-compulsive disorder. The aim of this study was to investigate the effects of memantine treatment on morphological and locomotor activity during development in zebrafish embryos. Memantine was obtained from Ebixa® containing 10 mg memantine hydrochloride by dissolving in dimethyl sulfoxide (DMSO) and diluted in E3 medium to give the requisite test concentration. Zebrafish embryos were treated with various doses of memantine up to 72 hours post fertilization (hpf). The control group consisted of zebrafish exposed to DMSO. Developmental alterations, mortality and hatching rates were monitored and documented daily throughout embryonic development. Embryos were evaluated in terms of locomotor behavior by touch-evoked response method at 72 hpf. Memantine caused dose dependent alterations in the parameters investigated in zebrafish embryos. We continue our research to determine the molecular mechanisms of the alterations caused by memantine.

Keywords: Memantine, neurodegenerative diseases, development, locomotor activity, zebrafish embryos

OP35

Effects of Bisphenol A Exposure on Brain Oxidant-Antioxidant Status in Zebrafish

Merih Beler[1], Derya Cansız[2], Ismail Ünal[1], Ebru Emekli Alturfan[3]

[1]Marmara University, Institute of Health Sciences, Faculty of Pharmacy, Department of Biochemistry, Istanbul, Turkey

[2]Department Medipol University, Faculty of Medicine, Medical Biochemistry, Istanbul, Turkey
[3]Marmara University, Faculty of Dentistry, Department of Basic Medical Sciences, Istanbul, Turkey

Endocrine disruptors are natural or synthetic chemicals disrupting the normal functioning of the body by mimicking or blocking hormones. They act by changing the activity of endogenous peptide or steroid hormones, activating or antagonizing nuclear receptors in the hypothalamus, adipose tissue, liver and other organs. Bisphenol A (BPA) is included to the plastic material to harden the plastics. BPA is an estrogenic endocrine disrupting chemical used as food containers, baby bottles, adhesives, dye powders and dental fillers. We aimed to determine effects of BPA in zebrafish focusing on the oxidant-antioxidant status in brain. Adult zebrafish were exposed to BPA for 30 days. At the end of 30 days oxidant-antioxidant parameters were determined in the brain tissues. Results of our study showed that BPA disrupted the oxidant-antioxidant status in brain in zebrafish.

Keywords: Bisphenol A, zebrafish, brain, oxidant-antioxidant status

OP36

Investigation of the Effects of Toothpastes with Different Contents on the Oxidant-Antioxidant System in Zebrafish Embryos

Atakan Karagöz[1], Merih Beler[1], İsmail Ünal[1], Derya Cansız[2], Ebru Emekli Alturfan[3]

[1]Marmara University, Institute of Health Sciences, Faculty of Pharmacy, Department of Biochemistry, Istanbul, Turkey
[2]Medipol University, Faculty of Medicine, Medical Biochemistry, Istanbul, Turkey
[3]Marmara University, Faculty of Dentistry, Department of Basic Medical Sciences, Istanbul, Turkey

Embryogenesis is an important process that also has an impact on the future life. Aim of this study was to evaluate the effects of toothpastes with different active ingredients on the development of zebrafish embryos. For this purpose, zebrafish embryos were studied in 3 repetitions with at least 20 embryos in each of the control group and exposure groups consisting of different toothpastes according to their contents. Exposure studies continued up to 72 hours post fertilization. At the end of the experiment, oxidant-antioxidant parameters including lipid peroxidation, nitric oxide, and glutathione S-transferase (GST) were evaluated in homogenates. Significant differences were observed in the oxidant-antioxidant status of the embryos exposed to different toothpastes according to their detergent contents. These results showed the need to examine the effect of toothpastes on embryogenesis in more detail.

Keywords: Toothpaste, oxidant-antioxidant status, zebrafish embryos

OP37

9b, a novel HDAC6 inhibitor for treatment for Castration Resistant Prostate Cancer

Arda Işıklar[1], Ipek Bulut[1], Buse Cevatemre[2], Büşra Yıldırım[1], Batuhan Mert Kalkan[1], Dusan Ruzic[3], Katarina Nikolic[3], Ceyda Açılan Ayhan[4]

[1]Graduate School of Health Sciences, Koç University, Istanbul, Turkey
[2]Research Center for Translational Medicine, Koç University, Istanbul, Turkey
[3]Department of Pharmaceutical Chemistry, Faculty of Pharmacy, University of Belgrade, 11000 Belgrade, Serbia
[4]School of Medicine, Koç University, Istanbul, Turkey; Research Center for Translational Medicine, Koç University, Istanbul, Turkey

Primary prostate cancers can be treated with radiotherapy, but treatment options are limited for metastatic "castration resistant" (CR) phases. While some patients initially benefit from taxane treatment, unfortunately chemoresistance can develop. Tumor epigenetic alterations, particularly involving histone deacetylase (HDAC), is one of the mechanism that is responsible for this resistance. Specifically, HDAC6, which is non-lethal and reduces tumor size, emerges as a promising therapeutic target. This project aims to identify new HDAC6 inhibitors that synergizes with taxanes or reverse resistance in CRPCa cells.

In this study, we synthesized a total of 4 HDAC6i and tested their efficacy on parental and taxane resistant CRPCa cells. Initially, we performed viability screen in the presence of HDAC6i's either without or with taxanes via SRB and CTG assays; resulting 2 inhibitors for further testing. Target engagement of HDAC6i in cells was determined by CETSA on HDAC6 among with other HDAC's. Their effects on invasion and migration were tested with wound healing and Matrigel invasion assays among with western blotting and qPCR to investigate HDAC6i effects on HDAC6's nuclear and cytosolic targets.

In summary, among 4 HDAC6i, 9b was the most potent, based on IC50, specificity and selectivity. Interestingly, targeting CRPCa cells with 9b shown synergetic effects in combination with taxanes without affecting sensitive parental lines. Currently, we are investigating the mechanism of action of 9b and efficacy in reduction of tumor size in mice. We hope that our studies will provide a basis for the development of new treatment modalities for taxane resistant patients.

Keywords: Chemoresistance, Epigenetic, Prostate Cancer, Histone Deacetylase

OP38

Gene Isoform Switches and Repeat-Arisen Transcripts in the Adipose Tissues of Individuals with Metabolic Syndrome and Obesity

Cihangir Yandım

Dept. of Genetics and Bioengineering, Izmir University of Economics, Izmir, Turkey

Metabolic syndrome and obesity, arising from complex dysregulatory events in hormonal homeostasis and gene regulation, present a multifaceted molecular pathology. While genes implicated in metabolic syndrome are well-documented, further exploration is needed to fully reveal its uncovered dimensions where cellular machineries deviate. This study employs RNA sequencing data from subcutaneous adipose tissues of 14 metabolically healthy lean (MHL), 25 metabolically healthy obese (MHO), and 27 metabolically unhealthy obese (MUO) individuals to identify pathological gene isoform switches and dysregulations in the expressions of repeat-arisen transcripts. Utilizing a comprehensive bioinformatics pipeline with state-of-the-art tools such as IsoformswitchR and RepEnrich, obesity-induced isoform switching was observed in genes associated with cardiovascular (e.g., PKP2, SPP1), immune (e.g., C5AR1, LILRB4), and retinal diseases (e.g., CPAMD8), irrespective of the presence of metabolic syndrome. Notably, additional isoform switches in genes related to cardiovascular (e.g. Angiogenin) and immune disorders (e.g. BTK, LSP1), and several cancer-related genes (e.g., MAPKAPK3, RASL10B), were identified exclusively in MUO individuals. A significant finding was the isoform switch in the FBP1 gene, crucial for gluconeogenesis, occurring only in MUO individuals with potential implications in the onset of metabolic syndrome. Additionally, an increase in signal recognition particle expression and dysregulations in various transposable

elements were also noted. This study is the first to describe gene isoform switches and dysregulatory events in repeat-arisen transcripts in the adipose tissues of metabolically unhealthy individuals, underscoring the need for further research in this avenue into the complex molecular pathology of metabolic syndrome and obesity.

Keywords: metabolic syndrome, obesity, transposon, bioinformatics, gene regulation

OP39

PathwayMapper Reveals A Link Between β1-integrin And Wnt/β-catenin Pathway

Secil Eroglu[1], Safiah Olabi[2]

[1]Department of Medical Biology, Faculty of Medicine, Gaziantep Islam Science and Technology University, Gaziantep, Turkiye
[2]Institute for Tissue Engineering and Regenerative Medicine (iTERM), Helmholtz Center, Neuherberg, Munich, Germany

Understanding adhesion receptor signalling dysregulation in cancer settings is vital for the effective and safe incorporation of adhesion-targeted therapeutics in the clinic. β1-integrin is a major extracellular matrix adhesion receptor that has been shown to control important processes such as proliferation, cell cycle progression, apoptosis and cell migration. β1-integrin signalling pathway is complex and can cross-talk with many tumorigenic pathways. It is therefore not surprising that enhanced β1-integrin signalling has been reported to correlate with progression and therapy resistance in many types of cancers. Therefore, a complete understanding of the pathways and genes altered in all cancer types is essential to identify novel therapeutic options specific for certain cancer types. In this study, a pan-cancer analysis was performed to identify alterations of β1-integrin and most dysregulated cancer-related genes (106 genes, Kegg map05200) using 2565 patients whole genomes data (ICGC/TCGA, 2020). OncoPrint, mutations, copy number alterations (CNA), mutual exclusivity and pathway enrichment were conducted using cBioPortal. PathwayMapper, an interactive graphical editing tool allowing collaborative curation was used to view altered genes and pathways with alteration frequencies. Pathway enrichment analyses related to genetic alterations identified the Wnt signaling was the most frequently altered pathway. Mutual exclusivity analyses showed that β1-integrin-Wnt; β1-integrin-LRP5 and β1-integrin-FZD pairs exhibited co-occurrence, two sided fisher exact test indicates $p < 0.001$. This has shown a link between β1-integrin and Wnt/β-catenin pathways. Genetic alterations of β1-integrin receptor, whether these mutations will cause an activation of the Wnt/β-catenin pathway and their effects on overall survival and metastasis will be further examined.

Keywords: β1-integrin, Wnt signaling, Pan-cancer, Pathway enrichment

OP40

The effect of Polygonum cognatum (Meissn.) on cell behaviours of human dermal fibroblasts seeded on 3D thermoplastic polyurethane scaffolds

Mehtap Yukselegrilmez[1], Ufkay Karabay[2], Sıla Aze Bakan[2], Resit Bugra Husemoglu[3], Keyvan Hemmatvand[1], Zehra Tavsan[4], Dilay Turu[5], Kerem Canlı[6]

[1]Department of Molecular Medicine, Institute of Health Sciences Dokuz Eylul University, Izmir, Türkiye
[2]Pathology Laboratory Techniques Program, Vocational School of Health Services, Izmir Tinaztepe University, Izmir, Türkiye

[3]Department of Biomechanics, Institute of Health Sciences, Dokuz Eylul University, Izmir, Türkiye
[4]Faculty of Education, Department of Science Education, Dokuz Eylul University, Izmir, Türkiye
[5]Department of Biology, Graduate School of Natural and Applied Science, Dokuz Eylül University, Izmir, Türkiye
[6]Department of Biology, Faculty of Science, Dokuz Eylül University, Izmir, Türkiye

Tissue scaffolds provide a structural environment for cells to adhere and proliferate. Thermoplastic polyurethanes (TPUs) are linear polymers that have high biocompatibility, biodegradability and superior viscoelastic behaviour. They are used in medical applications such as wound dressings. 3D printing is an innovative tool for tissue engineering. Dermal fibroblasts play an essential role in skin wound healing. Polygonum cognatum Meissn. (PC) is a wild plant rich in vitamin C and carotenoids. It has antioxidant, antimicrobial, and antidiabetic activities. The aim of this study is to investigate the effect of PC on the viability, distribution and collagen expression of human dermal fibroblasts (HDFs) seeded on 3D TPU scaffolds. 3D TPU scaffolds were prepared using a fused deposition modeling printer. HDFs were seeded on 3D TPU scaffolds and treated with 250 µg/mL of PC for 24 and 48 h. Cell viability was measured by WST-1 assay. Cell distribution was analyzed by hematoxylin and eosin (H&E) staining. Collagen expression in HDFs was stained with Masson's trichrome (MT). The viability of HDFs on 3D TPU scaffolds treated with PC was significantly higher than HDFs on 3D TPU scaffolds at 48 h. H&E staining demonstrated that HDFs on 3D scaffolds treated with PC maintained their tissue-specific morphology and have larger cell and nucleus sizes. Collagen expression by MT staining was more intense in HDFs on 3D scaffolds treated with PC. Our results show that PC increases viability and collagen expression of HDFs on 3D TPU scaffolds and may promote wound healing through modulation of cell behaviours.

Keywords: Regenerative medicine, 3D cell culture, Human dermal fibroblast

OP41

Enhancing The Therapeutic Potential: Epigenetic Modulation of Lysosomal Sequestration and Exocytosis Increases Cisplatin Efficacy

Baris Sergi[1], Neslihan Yuksel[1], Selahattin Can Ozcan[3], Hamzah Syed[3], Kirill Kiselyov[2], Ceyda Acilan Ayhan[4]

[1]Koc University, Graduate School of Health Sciences, Istanbul, Turkey
[2]University of Pittsburgh, Department of Biological Sciences, Pittsburgh, USA
[3]Koc University, Research Center for Translational Medicine (KUTTAM), Istanbul, Turkey
[4]Koc University, School of Medicine, Istanbul, Turkey

Epigenetic modifications profoundly influence gene expression, steering oncogenic transformations and instigating drug resistance. Lysosomes, integral to signaling and managing cellular components, have recently emerged as key players in cancer cell survival through strategies like lysosomal sequestration and exocytosis, evading programmed cell death. This study probes the epigenetic orchestration of these processes, proposing that epigenetic modifier drugs (epidrugs) capable of suppressing lysosomal activities could serve as effective therapeutics, amplifying the efficacy of cisplatin. Our investigation involved thorough screenings of epidrugs, evaluating their impact on lysosomal exocytosis (β-hex assay), lysosomal content (LysoTracker staining), and combined cytotoxicity with cisplatin (cell viability assay). Notably, MS023, type I PRMT inhibitor,

emerged as a promising candidate, demonstrating efficacy in diminishing exocytosis and enhancing cisplatin cytotoxicity. Significantly, silencing individual PRMT targets (PRMT1, 6, and 8) proved less effective in reducing exocytosis compared to MS023, suggesting the necessity for concurrent inhibition of multiple PRMTs or the involvement of an unidentified target. Molecular insights into MS023-induced alterations were explored through RNA-seq and gene ontology studies, unveiling potential biological processes and functions responsible for changes in exocytosis and drug response. Differentially expressed genes (DEGs) identified three notable candidates—ABCA1, ABCA3, and SerpinE1—previously linked to drug resistance. Focusing on ABCA3, displaying the highest fold change and lysosomal localization, we found that knocking down all MS023 target PRMTs led to a reduction in ABCA3 expression.

In summary, MS023 emerges as a promising epidrug impacting secretory pathways and drug efflux processes, aiming to establish future targets for cancer intervention and ultimately enhancing drug efficacy.

Keywords: Epigenetic Regulation, Lysosomal Exocytosis, Cancer Chemotherapeutics, Cisplatin

OP42

Can Mitochondrial DNA Copy Number and Leukocyte Telomere Length Be Effective In The Prognosis of Multiple Myeloma?

Yasemin Oyacı[1], Istemi Serin[2], Fatıma Ceren Tunçel[1], Mustafa Pehlivan[3], Sacide Pehlivan[4]

[1]Institute of Graduate Studies in Health Sciences, Istanbul University, Istanbul, Turkey
[2]Department of Hematology, Agri Training and Research Hospital, Ibrahim Cecen University, Agri, Turkey.
[3]Department of Hematology, Basaksehir Cam and Sakura City Hospital, Istanbul, Turkey
[4]Istanbul University, Istanbul Faculty of Medicine, Department of Medical Biology, Istanbul, Turkey

In this study, it was investigated whether leukocyte telomere length (LTL) and mtDNA copy number showed a difference between Mutiple Myeloma (MM) disease before treatment (BT) and after treatment (AT), and whether there was a relationship with clinical parameters. Peripheral blood samples of 30 MM patients were taken BT and AT, and a total of 60 genomic DNAs were obtained. Leukocyte telomere length analysis and mtDNA copy number analysis were performed using the qPCR method, and the patients' BT and AT results were compared by calculating with the 2-ΔΔCt formulation.

When LTL was compared in the BT/AT groups of 30 MM patients; It was determined that the rate decreased in 14 patients and increased in 16 patients compared to before treatment. LTL Artışıyla Objektif yanıt oranı arasında (ORR) istatistiksel olarak anlamlı bir ilişkisinin olduğu belirlenmiştir (p:0.039). When mtDNA copy number results are compared; According to BT, mtDNA copy number was observed to decrease in 18 patients and to increase in 12 patients. When response to treatment status was examined, it was observed that there was no significant relationship with mtDNA copy number (p:0.232). However, a borderline significance was determined between 2-year overall survival and mtDNA increase (p:0.059). Our results show that LTL and mtDNA copy number may be related to treatment response and prognosis in MM.

Keywords: Multiple Myeloma, mtDNA, telomere length, qpcr

OP43

Prognostic Importance of BRAF and PTEN Proteins in Patients with Malignant Melanoma

Elif Bilgin, Ceren Tilgen Yasasever, Murat

Serilmez, Faruk Taş, Derya Duranyıldız, Hilal Oğuz Soydinç

Istanbul University, Oncology Institute

Malignant melanoma is a tumor that originates from pigment cells and metastasizes frequently. In this tumor, the incidence of which is increasing day by day worldwide and resulting in high rates of death in advanced stages, the follow-up of the disease is very important in terms of survival. The very short life expectancy in metastatic disease has necessitated the identification of new marker molecules for early diagnosis. BRAF genes encode the BRAF molecule, which is an effective transcription factor in the Raf-ERK pathway. The Ras/BRAF/MEK/ERK pathway is defined in various cancers with oncogenic mutations.

PTEN, a tumor suppressor gene, participates in cell signaling in the PI-3K pathway. With the loss of function of PTEN with mutation, excessive activation of oncogenic proteins in the pathway and uncontrolled stimulation ensure the proliferation of tumor cells. In our study, the expressions of BRAF and PTEN genes and protein products in serum samples of 60 patients and 20 healthy controls were evaluated by RT-PCR and ELISA methods. mRNA and protein expression levels of BRAF and PTEN molecules in patients were found to be highly significant compared to the control group ($p<0.05$).

As a result of the Spearman correlation test, a correlation was found between the protein levels of BRAF and PTEN molecules in the patient group ($p<0.05$).

Keywords: Malignant melanoma, BRAF, PTEN

OP44

Determination of the Transcriptional Regulation of ABCB1 Gene in Taxane Resistant Prostate Cancer by Genomic Locus Proteomics

Busra Yildirim[1], Baris Sergi[1], S. Can Ozcan[2], Buse Cevatemre[2], Ipek Bulut[2], Ceyda Acilan Ayhan[3]

[1]Koc University, Graduate School of Health Sciences, Istanbul, Turkey
[2]Koc University, Research Center for Translational Medicine, Istanbul, Turkey
[3]Koc University, School of Medicine, Istanbul, Turkey

Prostate cancer (PCa) progresses to a challenging "castration-resistant" (CR) phase where treatment options like Docetaxel and Cabazitaxel become less effective due to taxane resistance. Understanding the mechanisms behind this resistance and identifying new targets to reverse it is crucial. Resistance in cancer can result from various factors, in taxane-resistant cases, overexpression of the multidrug resistance gene ABCB1 (MDR1) is a primary cause of therapeutic failure. While inhibiting ABCB1 can reverse resistance, chemical inhibition has undesirable side effects on the immune system. We hypothesized that targeting master regulators governing ABCB1 expression could restore taxanes as a treatment option.
Numerous epigenetic modulators and transcription factors have been associated with ABCB1 regulation. However, our in-silico analysis revealed potential transcription factors not previously linked to ABCB1. Moreover, the expression of these factors does not always correlate with ABCB1 expression in cancer. This project aims to identify proteins directly binding to or interacting with the ABCB1 promoter in resistant cell lines. An unbiased approach using Genomic Locus Proteomics (GLoPro) is employed, the CASPEX (dCas9-APEX2) fusion protein is guided to the ABCB1 promoter with gRNAs which are then confirmed by ChIP assays, biotinylating nearby

proteins. This method captures not only direct promoters but also enhancer-bound proteins, offering a comprehensive view. The biotinylated proteins will be identified via mass spectrometry and selected based on specific criteria. Further validation will be conducted using qPCR and ChIP. Finally, candidate regulatory proteins will undergo shRNA/CRISPR/Cas9 knockout to assess their impact on taxane resistance.

Keywords: prostate cancer, multidrug resistance, genomic locus proteomics, transcriptional regulation

OP45

Investigation of antiinflammatory and antiapoptotic effects of sodium phthalhydrazide in 1.1B4 cell line

Burcin Ozgur[1], Günnur Demircan[1], Ali Osman Gürol[2], Irina Danilova[3], Musa Abidov[4], M. Temel Yilmaz[5]

[1]Demiroglu Bilim University, Faculty of Medicine, Department of Medical Biology and Genetics, Istanbul, Turkey
[2]Istanbul University, Aziz Sancar Institute of Experimental Medicine, Department of Immunology, Istanbul, Turkey
[3]Immunology and Physiology of the Ural Branch of the RAS, Immunology and Physiology of the Ural Branch of the RAS, Yekaterinburg, Russia
[4]Immunopathology and Preventive Medicine, Immunopathology and Preventive Medicine, Ljubljana, Slovenia
[5]Demiroglu Bilim University, Faculty of Medicine, Department of Internal Medicine, Istanbul, Turkey

β-cell lines represent valuable tools in understanding autoimmune β-cell destruction. Sodium phthalhydrazide is available for over two decades in Russian Federation under Tamerit1/Galavit1 name, has been applied in parallel with different standard therapies for patients with viral and bacterial infections. Different doses of Tamerit treatment was planned for 1.1B4 cells in cell culture in order to elucidate pathological insulitis process and resulting β-cell destruction mechanism in Type 1 Diabetes (T1D), and to modulate responsible pathways and inflammation steps in this process. After Tamerit and cytokine addition, MTT analysis was performed and cell metabolic activity was measured. In 1.1B4 cell line; IL-1β, TNF-α and IFN-γ proinflammatory cytokines were used to simulate T1D environment. IL-1β cytokine levels were measured for anti-inflammatory effect, BcL2 for antiapoptotic effect, and Catalase for antioxidant effect of Tamerit. All measurements were evaluated on an ELISA reader. Bcl-2 levels were significantly increased in both Tamerit dosed groups compared to control (C) ($p<0.0001$); Tamerit 2nd (T2) dose cytokine group (CG) ($p=0.003$) and Tamerit 1st (T1) dose applied CG showed significant increase ($p=0.038$) compared to CG. IL1-β levels were increased in CG compared to C ($p<0.0001$), and it was found to be significantly lower in Tamerit-treated CG compared to CG ($p<0.0001$). Catalase levels, T2 applied to CG showed significant increase compared to T1 ($p=0.012$). Cytokines significantly decreased cell viability compared to C. ($p<0.0001$), and cell viability increased ($p<0.0001$) with addition of Tamerit to CG.

Keywords: Bcl-2, Sodium phthalhydrazide, IL-1β, Catalase

OP46

Assesment of Pathological Variations Associated with Autoimmunity and Inflammation through Whole Exome Sequencing in Granulomatous Mastitis Disease

Beyza Ozcinar[1], Ozlem Timirci Kahraman[2], Zeynep Ocak[3], Baris Ertugrul[2], Bedia Cakmakoglu[2]

[1]Department of General Surgery, Istanbul Medical Faculty, Istanbul University, Istanbul, Turkey
[2]Department of Molecular Medicine, Aziz Sancar Institute of Experimental Medicine, Istanbul University, Istanbul, Turkey
[3]Department of Medical Genetics, Medical Faculty, Istinye University, Istanbul, Turkey

Introduction: Granulomatous mastitis (GM) is a chronic inflammatory disease of the breast. Despite numerous studies conducted to date, conclusive evidence regarding the etiology of the disease has not been reached. This study aimed to identify the pathological variations using whole exome sequencing. This study represents the first investigation focused on the genetic etiology of GM.
Method: We collected genomic DNA from 22 patients and 22 control group individuals for the SNP and CNV analysis. Genomic DNA samples were sequenced with Paired End Sequencing using Illumina. The raw sequencing data (FASTQ files) were obtained and assessed for quality using tools such as FastQC. For genome mapping and alignment, we utilized BWA (Burrows-Wheeler Aligner) Version 0.7.17-r1188. The sequencing reads were aligned to the reference human genome GRCh37/UCSC hg19 using the BWA. To identify genetic variants including SNPs and CNVs, we employed the Genome Analysis Toolkit (GATK) Version 4.4.0.0. Variants were called using GATK's HaplotypeCaller. For the annotation of identified variants, we developed an in-house script that integrated information from various databases and annotation sources.

Results: The whole exome sequencing study revealed a total of 1066 variants of 776 genes. A total of 462 variants were assessed as tolerated, while 53 were classified as deleterious. The most common variants associated with GM were identified in genes related to autoimmunity (C3, HLA-DRB1) and inflammation (HLA-DQA1, HLA-DQB1, HLA-DRB1, SLC39A4).

Conclusion: The findings of this study may potential value in GM diagnosis and treatment.

Keywords: Granulomatous mastitis, variations, whole exome sequencing, NGS

OP47

Characterization of ANA+ B Cell Subtypes in a Systemic Lupus Erythematosus Mouse Model Using Flow Cytometry

Esin Bayrali Ulker, Munir Akkaya
Division of Rheumatology and Immunology, Department of Internal Medicine; College of Medicine, The Ohio State University, Columbus, Ohio.

Systemic Lupus Erythematosus (SLE) is a complex autoimmune disease characterized by the production of antinuclear antibodies (ANA) and dysregulation of B cells. In this study, we aimed to elucidate the specific subtypes of ANA+ B cells in SLE using flow cytometry techniques. A well-established SLE mouse model was developed to mimic the disease's pathophysiology in vivo. Peripheral blood and splenic B cells were isolated from both control and SLE mice. Subsequently, flow cytometry was employed to analyze surface markers and intracellular factors associated with B cell activation and differentiation. The results revealed distinct subpopulations of ANA+ B cells with varied phenotypic characteristics, suggesting a heterogeneous B cell response in SLE. Furthermore, the in vivo SLE mouse model provided valuable insights into the dynamic changes in B cell populations during the progression of the disease. Our findings shed light on the complexity of B cell dysregulation in SLE and emphasize the importance of understanding specific B cell subtypes in the context of autoimmune pathogenesis. This comprehensive characterization of ANA+ B cell subtypes contributes to a deeper understanding of the immunological

mechanisms underlying SLE. Such insights may pave the way for targeted therapeutic interventions aimed at modulating specific B cell populations to alleviate the symptoms and progression of systemic lupus erythematosus.

Keywords: Systemic Lupus Erythematosus (SLE), Autoimmune Disease, B cells

OP48

Organoids and Spheroids: Emerging 3D Models to Advance Pancreatic Cancer Research

Nazanin Jamshidi[1], Negar Jamshidi[1], Elahe Shams1[1], Seyedeh Nasim Mirbahari[2], Vahid Chaleshi[1]

[1]Gastroenterology and Liver Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
[2]Department of Genetics, Reproductive Biomedicine Research Center, Royan Institute for Reproductive Biomedicine, ACECR, Tehran, Iran.

Pancreatic ductal adenocarcinoma (PDAC) is the fourth leading cause of cancer-related deaths due to its resistance to chemotherapy, making it almost universally fatal. Many drugs show promise in preclinical studies but fail in clinical trials, highlighting the limitations of conventional two-dimensional cell culture models used in early drug screening. Three-dimensional (3D) culture systems better mimic the native tumor microenvironment and have shown advantages over 2D models in morphology, proliferation, drug response, and protein expression. Tumor organoids and spheroids are two 3D culture platforms that recapitulate aspects of pancreatic tumor biology, each generated by different methods. These next-generation models demonstrate enhanced similarity to original tumor tissues and provide greater clinical relevance for in vitro and in vivo cancer research compared to standard cell lines. In this review, we examine the techniques, tissue sources, and applications of pancreatic cancer spheroids and organoids. Comparing these 3D culture systems can guide researchers in selecting the optimal model design suited to their specific experimental aims for studying pancreatic cancer and developing improved therapeutics.

Keywords: 3D cell culture, Spheroid, Organoid, Pancreatic cancer, in-vitro cancer model

OP49

Investigation of The Relationship of Indoleamin 2,3 Dioxygenase-1 Gene with Foxm1 Pathway in Lung Cancer Cell Lines

Venhar Çinar[1], Dilara Sönmez Zor[2], Islim Kaleler[2], Gultekin Iseyeva[2], Ceylan Özsoy[3], Özlem Küçükhüseyin[2], Cem Horozoğlu[4], Akif Turna[5], Ş. Umit Zeybek[2], Zuhal Hamurcu[1], Bülent Özpolat[6], Ilhan Yaylım[2]

[1]Erciyes University, Faculty of Medicine, Department of Medical Biology, Kayseri/Türkiye
[2]Istanbul University, Experimental Medicine Research Institute, Department of Molecular Medicine, Istanbul/Türkiye
[3]Cumhuriyet University, Faculty of Pharmacy, Department of Biochemistry, Sivas/Türkiye
[4]Haliç University Faculty of Medicine, Department of Pathology, Istanbul/Türkiye
[5]Istanbul University-Cerrahpaşa, Cerrahpaşa Faculty of Medicine, Department of Thoracic Surgery, Istanbul/Türkiye
[6]Houston Methodist Research Institute and Neil Cancer Center, Department of Nanomedicine, Texas/USA

It was aimed to investigate the effect of the indoleamine2,3,dioxygenase-1 enzyme (IDO-1)

pathway, which is the enzyme involved in tryptophan metabolism, on cell proliferation in the progression of small cell lung cancers (SCLC).HCC-827 cells were used in our study, and the expression of the IDO-1 gene in the cells was silenced by transfecting these cells with two different IDO-1 siRNAs specific to the IDO-1 gene. MTS analysis was performed to measure viability levels in siRNA-transfected cells. IDO-1 expression level and expression levels of proteins that may be associated with proliferation were measured by western blot analysis.A significant decrease in IDO-1 protein expression level was found after western blot analysis in HCC-827 cells transfected with IDO-1 siRNA.In cells transfected with two different IDO-1 siRNAs, viability/proliferation was found to be significantly suppressed as a result of MTS analysis compared to cells transfected with control siRNA ($p<0.001$).In addition, a significant decrease in the expression levels of FOXM1 and eEF2K proteins, an important proliferation pathway element in cancer, was found in cells transfected with two different IDO-1 siRNAs by western blot analysis ($p<0.001$).Our findings showed that the IDO-1 gene when silenced by IDO-1 siRNA led to a significant reduction in proliferation in SCLCs.In addition, western blot analysis results showed that there was suppression of the oncogenic transcription factor FOXM1 and eEF2K pathway in cells with the IDO-1 gene silenced.In conclusion, our study suggests that FOXM1-related IDO-1 is a new molecule that can be used as a therapeutic agent in the treatment strategy of lung cancer patients.

Keywords: Lung Cancer, IDO-1, siRNA, FOXM1

OP50

The effect of the POMC and UCP2 genes on the risk of obesity

Umit Yilmaz[1], Sermin Durak[2], Umit Zeybek[3]

[1]Department of Physiology, Faculty of Medicine, Karabuk University, Karabuk, Turkey
[2]Department of Medical Microbiology, Istanbul University Cerrahpasa, Istanbul, Turkey
[3]Department of Molecular Medicine, Aziz Sancar Institute of Experimental Medicine, Istanbul University, Istanbul, Turkey

Proopiomelanocortin (POMC), secreted by POMC neurons located in the arcuate nucleus of the hypothalamus, is a neuropeptide that reduces food intake and plays an important role in the regulation of energy balance. Uncoupling protein 2 (UCP2), located in the inner membrane of mitochondria, plays a role in regulating energy metabolism by ensuring that energy stored in adipose tissue is released as heat. The aim of this study is to investigate the relationship between POMC and UCP2 genes and the risk of obesity. Two-hundred individuals were included in this study and divided into four groups (n=50). Individuals according to BMI; they were grouped as non-obese (BMI<25), overweight (25<=BMI<30), obese (30<=BMI<35) and morbidly obese (35<=BMI). The DNA sequence analysis, RPA, and qPCR analysis were applied to the extracted DNAs. According to the results of three genetic analyses, individuals with the TT genotype for the rs1042571 polymorphism of the POMC gene are at risk of developing obesity. Individuals with the TT genotype were found to have increased BMI and to be prone to the development of non-syndromic and morbid obesity. Individuals with the AA genotype for the rs659366 polymorphism of the UCP2 gene were found to be at risk of developing obesity. Individuals with the AA genotype was found to be prone to an increase in BMI, and in the density of abdominal and visceral adipose tissue. The TT genotype for the POMC gene and the AA genotype for the UCP2 gene were found to be at risk for the development of obesity.

Keywords: Obesity, POMC, UCP2

OP51

Knockdown of *XPO5* delays cell wound healing and increase in apoptosis in larengeal cancer cells by regulating miR-138

Seren Gülşen Gürge[1], Ipek Canatar[2], Sibel Özdaş[2], Turan Gündüz[1]

[1]Celal Bayar University, School of Vocational Health Service, Department of Histology and Embryology, Manisa, Türkiye
[2]Adana Alparslan Türkeş Science and Technology University, Faculty of Engineering Sciences, Department of Bioengineering, Adana, Türkiye

Disregulated expression of microRNAs (miRNAs) and dysregulation of the mechanisms that regulate them are associated with carcinogenesis. XPO5, a member of the Karyopherin family, is a protein responsible for the transfer of pre-miRNAs from the nucleus to the cytoplasm. The aim of our study is to determine the role of XPO5 in laryngeal cancer and to investigate the effect of XPO5 expression on miR-138 level. XPO5 gene expression was strongly suppressed (knockdown) by XPO5-siRNA transfection, verifying that it was suppressed at the mRNA, protein and intracellular level by qRT-PCR, Western-blot analysis and immunofluorescence staining, respectively. Silencing XPO5 with siRNA caused delay in cell wound healing and increase in apoptosis in larengeal cancer lines compared to control, and these increases-decreases were more observed in metastatic cells compared to primary cells by migration and TUNEL assay, respectively. Also, XPO5-siRNA transfection caused the expression of miR-138 to be upregulated in laryngeal cancer lines compared to control. As a result, it was concluded that XPO5 can be used as a promising biomarker in the diagnosis, treatment and follow-up of laryngeal cancer and as a potential therapeutic target molecule against the disease. **Acknowledgment:** This study was financially supported by Manisa Celal Bayar University Scientific Research Projects Coordination Unit (Project No: 2020/043).

Keywords: Knockdown, XPO5, larengeal cancer

OP52

***Phyllanthus emblica* Loaded Wound Dressing Materials**

Ipek Canatar, Sibel Özdaş, Gözde Baydemir Peşint

Adana Alparslan Türkeş Science and Technology University, Faculty of Engineering Sciences, Department of Bioengineering, Adana, Türkiye

Since ancient times, plants have played a vital role in therapeutic approaches for a variety of diseases and ailments. *Phyllanthus emblica (P. emblica)* has been described in many studies to have multiple therapeutic activities and is considered an important part of Ayurvedic and Unani medicinal systems. The study sought to examine the effect of synthesized *P. emblica* loaded cryogels on wound healing and their potential in wound dressing applications. For this purpose, polyvinylalcohol/gelatin (PVA/Gel) based cryogels were synthesized containing 0.5% (PVA/Gel/*P.emblica*-0.5), 1% (PVA/Gel/*P.emblica*-1), 1.5% (PVA/Gel/P.emblica-1.5), 2% (PVA/Gel/P.emblica-2) *P. emblica* extract. The results of characterization studies revealed that *P. emblica* loaded PVA/Gel cryogels was increased with increasing the amounts of *P. emblica* by swelling tests and Brunauer-Emmett-Teller (BET). Morphological results displayed that the cryogels had a dense, interconnected pore morphology and a macroporous structure. 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT), trypan blue exclusion and live/dead assay results revealed that adding of P. emblica into cryogels led to enhanced cell

proliferation, increased cell number, and improved cell viability. Based on the phase contrast microscope, scanning electron microscope (SEM), immunofluorescence and giemsa images of the HaCaT cells on *P. emblica* loaded PVA/Gel cryogels, it was observed that *P. emblica* promoted cell attachment, proliferation and penetration. In conclusion, it has been shown that PVA/Gel/*P.emblica* cryogels are suitable for use as wound dressing materials and can be developed with further studies.
Acknowledgment: This study was financially supported by Adana Alparslan Türkeş Science and Technology University, Scientific Research Projects Coordination Unit with project number 22303016.

Keywords: *Phyllanthus emblic*a, Wound Dressing Material, Cryogels

OP53

Research of the relationship between CETP and FABP2 genes with Obesity

Faruk Celik[1], Saadet Büşra Aksoyer Sezgin[2], Umit Zeybek[1]

[1]Department of Molecular Medicine, Aziz Sancar Institute of Experimental Medicine, Istanbul University, Istanbul, Turkey
[2]Medical Biology and Genetics Department, Yeni Yuzyil University, Istanbul, Turkey

Association of a cholesteryl ester transfer protein (CETP) rs5882 polymorphism with CETP activity, HDL-C transportation and risk of coronary artery disease (CAD). CETP is a glycoprotein that transfers cholesteryl ester from HDL to apolipoprotein (Apo) B-containing lipoproteins. It collects triglycerides from very-low-density or low-density lipoproteins and exchanges them for cholesteryl esters from HDL. CETP regulates HDL-C level and polymorphisms in this gene have been associated with changes in plasma HDL-C. CETP polymorphisms are also associated with metabolic syndrome (MetS) and increased level of TG and lower HDL-C levels. One of the most important gene families associated with obesity is the Fatty acid-binding protein (FABP), coding the superfamily of small intracellular lipid-binding proteins. The FABP2 gene is located on the long arm of chromosome4 and encodes the intestinal form of Fatty binding protein (IFABP) involved in the uptake, intracellular metabolism, and transport of long-chain fatty acids. Besides, the FABP2 gene is thought to play a role in maintaining energy homeostasis by functioning as a lipid sensor. In our research was for groups with 50 patients each (A-BMI<25,B-25<= BMI<30,C-30<= BMI <35,D-35<= BMI). The results of our research shows us that as the obesity rises the risk is getting higher in patients in both genes specifically in FABP2 (CETP %1AA-Risk, %75AG-Low Risk and %24GG-Normal) wich is responsible for predisposition to weight gain associated with abdominal obesity and HDL-cholesterol levels and (FABP2 %23AA-Risk, %70AG-Low Risk and %7GG-Normal) is related to obesity due to factors such as increased body fat mass, carbohydrate sensitivity, insulin resistance.

Keywords: Obesity, CETP, FABP2, Polymorphism

OP54

Effects of Gentisic Acid Rotenone-Induced Neurotoxicity in Zebrafish

Derya Cansız[1], Ismail Ünal[2], Merih Beler[2], Ebru Emekli Alturfan[3]

[1]Department of Medical Biochemistry, Istanbul Medipol University, Istanbul, Turkey
[2]Department of Biochemistry, Institute of Health Sciences, Faculty of Pharmacy, Marmara University, Istanbul, Turkey

[3]Department of Basic Medical Sciences, Faculty of Dentistry, Marmara University, Istanbul, Turkey

Parkinson's disease (PD) is the second most prevalent neurological condition that affects the motor system.In recent years, the pharmacological activities of natural products have been evaluated leading to the synthesis of new treatments for the management and treatment of PD. Phenolic acids are well-known phytochemical elements that have positive therapeutic benefits. They are produced as secondary plant products from tyrosine or phenylalanine and are typically found in plants like fruits and vegetables. Gentisic acid (2,5-dihydroxybenzoic acid) is a diphenolic chemical derived from benzoic acid. Gentisic acid has a strong ability to scavenge free radicals and has been reported to have antiatherogenic, anticancer, antioxidant, and skeletal muscle relaxant properties. We aimed to determine effects of gentisic acid in rotenone induced PD model in zebrafish focusing on the oxidant-antioxidant status in brain. Adult zebrafish were exposed to rotenone and gentisic acid for 30 days.At the end of 30 days locomotor activities were determined. Lipid peroxidation, nitric oxide, superoxide dismutase, glutathione S-transferase (GST), and acetylcholinesterase activities were determined in the brain tissues. Results of our study showed that gentisic acid ameliorated the locomotor activity and the oxidant-antioxidant status in rotenone induced PD model in zebrafish.

Keywords: Parkinson's disease, gentisic acid, brain, oxidant-antioxidant status

POSTER PRESENTATIONS ABSTRACTS

PP1

Alpha Lipoic Acid Prevents the Damage to the Kidneys Caused by Valproic Acid Used in the Treatment of Epilepsy

Nigar Garayeva[1], Ismet Burcu Turkyilmaz[2], Refiye Yanardag[2]

[1]Istanbul University-Cerrahpaşa, Institute of Graduate Studies, 34320, Avcilar, Istanbul, Turkey
[2]Istanbul University-Cerrahpaşa, Faculty of Engineering, Department of Chemistry, 34320, Avcilar, Istanbul, Turkey

VPA, 2-propyl valeric acid (VPA), is a fatty acid derivative and an anticonvulsant but this drug causes the production of reactive oxygen species which is related to many organ toxicities and injuries. Alpha lipoic acid (ALA) is a powerful antioxidant and can remove a variety of reactive oxygen species, and regenerate antioxidant molecules to maintain normal antioxidant capacity. The human kidney plays a vital role in the filtration of blood, secretion of hormones, and regulation of blood pressure. In this study, we aimed to investigate the possible protective effects of ALA on VPA-induced kidney injury in rats. Female rats were divided into four groups as follows: Group I, control animals (corn oil per day for 15 days); Group II, ALA given group (50 mg/kg per day for 15 days); Group III, VPA administered group (500 mg/kg per day for 15 days) and Group IV, VPA and ALA given group at the same dose and time per day. On the 16th day, kidney tissues were taken. Kidney tissues were homogenized in cold saline and centrifuged. The reduced glutathione and lipid peroxidation levels, sodium potassium ATPase, and arginase activities were determined in all groups. The reduced glutathione levels and sodium-potassium ATPase activities were decreased while lipid peroxidation levels and arginase activities were increased in VPA group as compared to control group. Administration of ALA reversed these levels and activities in VPA group. We may conclude that alpha lipoic acid can protect against kidney injury induced by VPA.

Keywords: Valproic acid, alpha lipoic acid, kidney

PP2

A Different Approach To Malnutrition-Related Appetite And Weight Loss In Cancer Patients: Is Saturation Enough At The Cell Level?

Mahmut Ilker Yılmaz[1], Mustafa Ozturk[2], Zeynep Demir[3], Muhammet Fatih Demir[1], Beste Alimert[4], Vahit Arslan[5], Engin Onalan[6], Murat Aydin[7], Fatih Muhammed Kaya[8], Yaprak Demir[9], Koray Kocak[4], Mahmut Can Yagmurdur[10]

[1]Epigenetic Health Solutions, Unit of Nephrology, Ankara, Turkey
[2]Private Tekden Hospital, Department of Oncology, Denizli
[3]Wake Forest Institute for Regenerative Medicine, Winston-Salem, NY, USA
[4]Epigenetic Health Solutions, Unit of Nutrition, Ankara, Turkey
[5]Private Losante Hospital, Department of Emergency Medicine, Cankaya, Ankara, Turkey
[6]Private Mim Hospital, Department of Emergency Medicine, Cankaya, Ankara, Turkey
[7]Private Anadolu Hospital, Department of Biochemistry, Eskisehir, Turkey
[8]Igdir Hospital, Department of Physical Therapy and Rehabilitation, Igdir, Turkey
[9]Arztekammer Berlin, Germany
[10]Edumed Academy, Ankara, Turkey

Cancer is one of the most important, most common and dangerous diseases of our age. The following three important mechanisms remain dominant in the pathogenesis of chronic diseases: inflammation, oxidative stress and endothelial dysfunction. It is of great importance that these three mechanisms operate correctly on the path to health.

The aim of this study is to investigate the effects of 3 functional food supplements on 98 people with Stage 4 metastasis cancer patients. The 52-week study was completed with 51 men and 47 adult women. The initial weight of the patients included in the study was between 31-44 kg. In this study, Morinda citrifolia (anti-atherosclerotic liquid- AAL) (3 mL once per day orally) Omega-3 (anti-inflammatory capsules-AIC) (3 capsules once per day orally) extract with Alaskan blueberry and 21 different red purple fruit vegetables (anti-oxidant liquid-AOL) (30 mL once per day orally) have been used.

With 52 weeks of follow-up, 74 of the patients included in the study were still alive at the end of the first year. The body weights of 74 surviving patients were between 48-76 kg. Positive results were obtained in all biochemical and radiological parameters of the three mechanisms, indicating the correct functioning of the mechanisms.

With the intake of these three foods, both weight gain and life expectancy and quality of life were increased.

Malnutrition is corrected with micronutrition at the cellular level, and a significant improvement in appetite and weight gain prolongs the person's survival and also increases the quality of life.

Keywords: Inflammation, Oxidative Stress, Endothelial Dysfunction, Nutrition, Quality life

PP3

Investigation of Anti-Cancer Potential of Omeprazole in Prostate Cancer Cells

Nejdet Memiş[1], Ümmühan Demir[2], Büşra Gündoğdu[1], Muhammed Hamza Müslümanoğlu[3]

[1]Department of Molecular Biology and Genetics, Faculty of Arts and Sciences, Yıldız Technical University, 34220, İstanbul, Turkey; Istanbul Medeniyet University Science and Advanced Technologies Research Center (BILTAM), İstanbul, Turkey

[2]Department of Molecular Biology and Genetics, Faculty of Engineering and Natural Sciences, İstanbul Medeniyet University, 34700, İstanbul, Turkey; Istanbul Medeniyet University Science and Advanced Technologies Research Center (BILTAM), İstanbul, Turkey

[3]Department of Molecular Biology and Genetics, Faculty of Arts and Sciences, Yıldız Technical University, 34220, İstanbul, Turkey

Prostate cancer is the second most common type of cancer in men worldwide. Proton pump inhibitors used widely in gastritis disease are used as anti-cancer agents by drug repurposing. Omeprazole is a proton pump inhibitor and an FDA-approved anti-acidic drug used in acid-related diseases. The anti-cancer potential of omeprazole has been demonstrated in many cancer types. This study aims to demonstrate the anti-cancer potential of omeprazole in prostate cancer. To reach the aim of our study 2D and 3D cell culture studies were performed. Scratch assays were used to determine the effect of omeprazole on the migration capabilities of cancer cells. Glucose consumption and pH change were determined in response to omeprazole. Finally, a new drug combination was tested. The IC50 scores of PC-3, and LnCap were lower than control CCD1072-sk cells. Omeprazole inhibited significantly the numbers and size of PC-3 colonies. Surprisingly, a higher amount of glucose in the medium of the control group and the acidity of the medium in the drug-treated group suggested higher glycolysis in omeprazole treatment. The combination of omeprazole with GLUT inhibitor WZB117 resulted in a synergistic effect. Omeprazole doesn't only inhibit V-ATPase but also suppresses the FASN enzyme, which plays an important role in lipid metabolism in cells. In light of these findings, cancer cells may use the glycolytic pathway more actively in response to this, since omeprazole suppresses lipid metabolism. Therefore, it is important to target

lipid and glucose metabolism at the same time in prostate cancer.

Keywords: Prostate cancer, drug repositioning, proton pump inhibitor, omeprazole

PP4

Bioactivity-guided Isolation of Anti-cancer Compounds from Endemic Gypsophila eriocalyx Extracts

Büşra Gündoğdu[1], Ümmühan Demir[2], Hüseyin Servi[3], Muhammed Hamza Müslümanoğlu[1]
[1]Yıldız Technical University, Graduate School of Science and Engineering, Molecular Biology and Genetic Department, İstanbul, Türkiye
[2]İstanbul Medeniyet University, Molecular Biology and Genetic Department, İstanbul, Türkiye
[3]İstanbul Yeni Yüzyıl University, Pharmacy Faculty, Pharmacognosy Department, İstanbul, Türkiye

Gypsophila eriocalyx is a taxon of Gypsophila L. genus, a member of Caryophyllaceae family, and spreads to Iran-Turan region. While it is well-known to have a high saponin content of Gypsophila species; antiviral, antidiabetic, antifungal, and antiproliferative activity of G. eriocalyx has also been reported. In this study, the dried powdered aerial parts of G. eriocalyx were macerated with ethyl acetate, methanol, and methanol:water (7:3) respectively. The extracts were evaporated under vacuum to dryness to give crude extracts. PC3 cell line was used to test the extracts' antiproliferative properties. The ethyl acetate extract was shown to have maximum activity following the activity test. By using column chromatography to separate the ethyl acetate extract into fractions, seven major fractions were produced. After examining the antiproliferative activity of the seven fractions, it was found that fraction 3 had highest activity. Fraction 3 was separated into two sub-fractions by molecular sieve chromatography (Sephadex LH-20). The 3.2 coded fraction was shown to have the most activity against the PC3 cell line with 29.5 µg/ml IC50 value. Colony formation tests performed on LNCAP with this extract also supported antiproliferative effect. Thin layer chromatography studies were carried out with different mobile phase systems to separate the substances in this fraction and six subfractions were obtained. 3.2.2 coded fraction had lowest IC50 value and selected for further analysis. This study is the first study in the literature to isolate bioactive compounds for cancer treatment from Gypsophila eriocalyx. The bioactive molecule separation and activity studies are ongoing.

Keywords: Gypsophila eriocalyx, anti-cancer activity, bioactive molecule

PP5

Effects of VOL Complex on Diabetic Stomach Tissue

Fatma Gulnaz Karakus[1], Sevim Tunali[2], Tulay Bal Demirci[3], Bahri Ülküseven[3], Refiye Yanardag[2]

[1]Istanbul University-Cerrahpaşa, Institute of Graduate Studies, 34320 Avcilar, Istanbul, Turkey
[2]Istanbul University-Cerrahpaşa, Faculty of Engineering, Department of Chemistry, Biochemistry Division, 34320 Avcilar, Istanbul, Turkey
[3]Istanbul University-Cerrahpaşa, Faculty of Engineering, Department of Chemistry, Inorganic Chemistry Division,34320 Avcilar, Istanbul, Turkey

In the treatment of diabetes, vanadium has been shown to mimic insulin. When compared to inorganic vanadium salts, complexes of vanadium with appropriate organic ligands can improve permeation, tissue uptake, and effectiveness, and reduce toxicity. The aim of

the present study was to determine whether thiosemicarbazone-based oxidovanadium (IV) complex (VOL) treatment has a positive effect on biochemical parameters in the stomach tissue of streptozotocin (STZ)-rats. Animals were randomly selected into four experimental groups as follows: two control groups divided as (Group 1) control group-intact (n=5) and (Group 2) treated control-which received VOL (n=5) (0.2 mM/kg/day); two diabetic groups separated as (Group 3) diabetic control (n=6) (65 mg/kg of STZ) and (Group 4) VOL treated diabetic group (n=5) (receiving the same doses of STZ and VOL). The rats were sacrificed after 12 days of the experimental period. The levels of glutathione, lipid peroxidation, non-enzymatic glycosylation, and the activities of lactate dehydrogenase and xanthine oxidase were measured in stomach tissue of all the experimental animals. Although VOL treatment to diabetic rats increased the stomach glutathione levels; lipid peroxidation, non-enzymatic glycosylation were decreased. On the other hand lactate dehydrogenase and xanthine oxidase activities were decreased. The results obtained indicate that VOL treatment has a curative effect on the stomach tissue of diabetic rats. This effect is possibly accomplished through the insulin-mimic and antioxidant activity of VOL observed in diabetic animals. Consequently, VOL may be a candidate for therapeutic treatment of diabetes.

Keywords: Diabetes mellitus, VOL complex, stomach tissue, rat

PP6

Novel Hybrid Gene Therapy for Wilson's Disease Treatment

Neslihan Yüksel[1], Barış Sergi[1], Batuhan Altay[1], Ayça Açar[1], Mehri Ahmadian[2], Cavit Ağca[2], Ceyda Açılan Ayhan[1]

[1]Health Sciences Institute, Koç University, Istanbul, Turkey
[2]Faculty of Engineering and Natural Sciences, Sabancı University, Istanbul, Turkey

Wilson's disease (WD) is a rare genetic disorder that causes disruption of copper homeostasis due to pathogenic variants of ATP7B gene. ATP7B gene has a crucial role in excretion of excessive copper. Symptoms of Wilson's disease show around age 5, due to copper accumulation in the body. The disease manifests itself as decrease in liver function, jaundice, central nervous system problems, and Kayser-Fleischer rings. Current treatment plans are low copper diet, copper chelators and zinc salts. However, such treatments are not effective for all patients. Drug treatment unresponsive patients are treated by liver transplantation. Due to side effects of drug treatments and drug response rate, new therapy methods are needed. WD is a monogenic disease which makes it a good candidate for gene therapy as a lifelong treatment. In this project, we aim to generate split ATP7B carrying Adeno Associated Virus (AAV) due to ATP7B being a large gene. We will express the ATP7B gene under its endogenous promoter. We have designed the ATP7B promoter using firefly luciferase assay. Also, dTomato expressing AAV is intravenously injected into the mice to observe virus distribution. Virus distribution were checked with IVIS and flow cytometry. To sum up, AAV based Wilson's disease therapy is a promising approach for monogenic diseases.

Keywords: rare diseases, genetic therapy, hepatitis

PP7

The role of MLL Interacting Proteins Menin and LEDGF for the Taxane Resistance in Castration Resistant Prostate Cancer

Ipek Bulut[1], Buse Cevatemre[2], Hamzah Syed[2], Idil Ateş[3], Ceyda Açılan Ayhan[3]

[1]Koc University, Graduate School of Health Sciences, Istanbul, Turkey
[2]Koc University, Research Center for Translational Medicine, Istanbul, Turkey
[3]Koc University, School of Medicine Istanbul, Turkey

Prostate cancer (PC) is usually hormone dependent, and androgen deprivation therapy (ADT) is the standard of care for advanced tumors [1]. Conventional chemotherapeutics such as Docetaxel (DTX) and Cabazitaxel (CBZ) are used frequently either in combination or as a follow up of hormone therapies, yet some tumors still relapse [2].
We generated resistant CRPC cell lines, library drug screen revealed epigenetic targets and they were knocked out via CRISPR cas9 system, furthermore, RNA-sequencing and ChIP experiments were performed to uncover the essential effects of these factors in the resistant cell genome.
Proteomics and RNA sequencing approaches revealed that, the previously described ABCB1, was the top hit, between DTX and CBZ resistant cells. Our epigenetic screen showed, two MLL complex inhibitors MI-2 (iMLL-Menin) and WDR5-0103 (iMLL-WDR5) synergized with both taxanes and significantly induced apoptosis when combined with the taxols. The absence of the N-terminus MLL partners Menin and LEDGF had no effect on the parental cells, they significantly halted the growth of the resistant cells. Parental cells require Menin expression for the acquisition of the drug resistance. Menin and LEDGF knockout cells were examined through RNA-sequencing and ChIP experiments. Menin targets were identified and verified through qPCR. Our chromatin pulldown showed that Menin is highly enriched in Myc promoter in the resistant cells.
MLL-Menin and MLL-WDR5 inhibition, reverts taxane resistance in CRPC. Menin knockout showed vulnerability in resistant cell and Menin expression is crucial for the acquisition of DTX resistance.

Keywords: prostate cancer, epigenetics, menin inhibitors, docetaxel reversion

PP8

Investigating the effects of metformin on heterogeneous population of prostate cancer due to metabolic shift by nutrient manipulation

Merve Erkisa Genel[1], Kubra Onbasli[2], Didem Karakas[3], Ilhan Yaylim[4], Havva Funda Yagci Acar[5], Engin Ulukaya[6]

[1]Department of Medical Biology, Istanbul Health and Technology University, Istanbul, Turkiye
[2]Department of Metallurgical and Materials Engineering, Istanbul Technical University, Istanbul, Turkiye
[3]Pancreatic Cancer Research Center, Acibadem University, Istanbul, Turkiye
[4]Department of Molecular Medicine, Aziz Sancar DETAE, Istanbul University, Istanbul, Turkiye
[5]Department of Chemistry, Koc University, Istanbul, Turkiye
[6]Department of Clinical Biochemistry, Faculty of Medicine, Istinye University, Istanbul, Turkiye

Cancer cells exhibit metabolic flexibility to accumulate biomass, supply increased demand for energy production, and maintain redox homeostasis. The dependence on different nutrients determines the metabolic phenotype that cancer cells adapt to overcome all these processes. Within the scope of this study, the

possible anti-cancer effect mechanisms of nanoformulation (NPcetuximab&metformin) prepared with metformin, a widely used metabolic drug in the treatment of type 2 diabetes, on parental PC-3 (PT) and prostate cancer stem cells (PCSCs) enriched from these cells were investigated. Successful enrichment of PCSCs from PT cells has been demonstrated by flow cytometry and immunofluorescence staining methods. The effects of different glucose and glutamine concentrations on the viability of PC-3 and PCSCs were determined by the MTT assay. The amount of intracellular ATP was measured using the luminescence-based ATP kit. Cell death assays were evaluated by measuring phosphatidylserine translocation and caspase 3/7 activity in flow cytometry. The effects on the metastasis process were analyzed with wound healing, matrigel invasion test, 3D matrigel invasion test and colony formation experiments. In conclusion, glucose and glutamine represent important metabolites for different cell populations within prostate tumor and that deprivation of metabolites reduces proliferation of prostate cancer cells. Furthermore, we suggest that the combination of targeted metformin therapy with nutrient deprivation may provide an effective therapeutic benefit for prostate cancer.

Keywords: Metabolism, Metformin, Nanoparticles, Prostate cancer

PP9

Investigation of Candidate Genes and miRNAs Associated with the Complement System in Conversion from Clinically Isolated Syndrome to Multiple Sclerosis

Aysegul Turk[1], Cem Ismail Kucukali[2], Tugba Kose[3], Zerrin Karaaslan[2], Murat Kurtuncu[4], Ozlem Timirci Kahraman[1]

[1]Department of Molecular Medicine, Aziz Sancar Institute of Experimental Medicine, Istanbul University, Istanbul, Turkey
[2]Department of Neuroscience, Aziz Sancar Institute of Experimental Medicine, Istanbul University, Istanbul, Turkey
[3]Department of Genetic and Bioengineering, Bilgi University, Istanbul, Turkey
[4]Department of Neurology, Istanbul Faculty of Medicine, Istanbul University, Istanbul, Turkey

The aim of this study is to evaluate the potential of C1qA gene expression and its targeting miR-335-5p expression as biomarkers for disease progression by examining their relationship among clinically isolated syndrome (CIS), relapsing-remitting multiple sclerosis (RRMS) and healthy control groups. For the determination of C1qA gene and target miR-335-5p expression levels, PBMC (peripheral blood mononuclear cells) were obtained from 18 CIS, 32 RRMS, and 16 control blood samples. RNA isolation and quantitative Real-Time PCR (qRT-PCR) were performed. The sensitivity and specificity of C1qA and miR-335-5p between the study groups were verified through ROC curve analysis. In addition, sandwich ELISA method was applied to determine the C1qA protein levels in serum samples from the study groups. According to the obtained data, significant increases were observed in both C1qA gene expression ($p=0.0291$) and miR-335-5p expression ($p=0.0196$) in CIS patients compared to controls. In RRMS patients as well, an increase in expression levels was observed for these two parameters compared to controls, but statistical significance was not detected. Both CIS and RRMS patients showed a decrease in both C1qA and miR-335-5p expression levels. Additionally, statistical significance was achieved for miRNA ($p=0.0442$). There was no significant difference in C1qA protein levels among the study groups ($p>0.05$).
In conclusion, our project, being the first study conducted on C1qA and miR-335-5p in MS,

holds the potential to contribute to the development of new therapeutic approaches and can pave the way for advancements in the literature.

Keywords: CIS, RRMS, C1qA, miR-335-5p, Expression

PP10

Investigation of GAL-9, CD40-CD40L plasma levels in bladder cancer

Levent Verim[1], Onur Dülger[2], Vida Pourteimoor[3], Dilara Sönmez[3], Şeyda Demirkol[4], Mehmet Tolgahan Hakan[3], Kemal Kayar[5], Mehmet Fatih Gülçer[5], Özlem Küçükhüseyin[3], Ilhan Yaylım[3]

[1]Yalova Medical Faculty, Urology Department - Yalova, Turkey
[2]Department of Pathology, Cerrahpaşa Medical Faculty, İstanbul University-Cerrahpaşa, İstanbul, Turkey
[3]Department of Molecular Medicine, Aziz Sancar Institute of Experimental Medicine, İstanbul University, İstanbul, Turkey
[4]Department of Molecular Biology and Genetics, Biruni University, Istanbul, Turkey
[5]Haydarpasa Numune Training Hospital, Urology Department, Istanbul, Turkey

Background: Bladder cancer ranks as the ninth most prevalent cancer globally, with an estimated more than 573,000 new cases reported in 2020. Recent advances in bladder cancer therapy include developing targeted and immune therapies. Cancer cells exploit this interaction by expressing high levels of CD40 and CD40L, making them more resistant to immune surveillance and promoting tumor growth while evading immune responses. Changes in the concentration of CD40 and CD40L in bladder cancer cells significantly impact the immune system, even with low expression. Galectin-9 (GAL-9) is expressed on the surface of cancer cells, immune cells, and stromal cells, making it a crucial player in cancer biology.
Objective: We aimed to investigate whether the plasma level of GAL-9 may contribute more systemic impacts on personalized therapies for bladder cancer taking into consideration the GAL-9/CD40-CD40L pathway.
Methods: Plasma levels of GAL-9, sCD40, and sCD40L were assessed using ELISA in 22 bladder cancer patients and 61 controls. Ethical approval was obtained from Haydarpasa Numune Training Hospital, and volunteers gave both verbal and written consent. Standard protocols for blood collection, plasma isolation, storage at -20 ◦C, and biomolecule measurement were rigorously adhered to.
Results: We observed lower levels of GAL-9 and CD40/CD40L in the plasma of bladder cancer patients compared to healthy individuals. CD40 levels were higher in patients with high-grade bladder cancer than in low-grade patients. These results may serve as an important parameter for the future diagnosis and selection of treatment for patients with bladder tumors.

Keywords: bladder cancer, GAL-9, CD40, CD40L