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

[Abstract:0112]

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

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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

[Abstract:0113]

Cytokine Detection with Bionanosensors in An In Vitro Sepsis Model

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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

[Abstract:0115]

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

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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-