

ORAL PRESENTATION ABSTRACTS

S001

THE EFFECT OF AEROBIC EXERCISE ON SERUM IRISIN AND PREPTIN LEVELS IN OVERWEIGHT SEDENTARY WOMEN

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Objectives: This study investigated the effect of aerobic exercise on serum irisin, preptin levels in overweight women and their relationship with routine biochemical tests.

Methods: The study included 25 healthy controls and 25 overweight sedentary women (BMI>25). The exercise training was performed 3 days a week for 12 weeks. Anthropometric measurements were performed and fasting blood samples were collected before and after exercise period. All samples were centrifuged at 1500xg for 10 minutes and the serum was separated. Serum irisin and preptin levels were analyzed by ELISA method. Routine biochemical parameters were assayed by spectrophotometric, hsCRP levels by nephelometric and insulin levels by immunoassay method using auto analyzers.

Results: There was a significant decrease in BMI and fat mass in the post-exercise group compared with pre-exercise (p<0.001). Serum irisin levels were significantly lower in pre- and post-exercise group compared to controls (p<0.001), but no significant change was observed after exercise period. Preptin levels were significantly higher in the pre-exercise group (median/IQR, 558.2 /351,2-756,8 pg/ml) compared to the controls (median / IQR, 137.1/85.2-427.9 pg/ml), and significantly reduced in post-exercise group (medium/IQR, 243.1/179.2-330 pg/ml) compared to pre-exercise group. In the pre-exercise group, a significant negative correlation was observed between

irisin and body mass index (r=-0.443, p=0,027), while a positive correlation was found between preptin and body weight (r=0.438, p=0.029).

Conclusions: Twelve weeks of aerobic exercise in overweight sedentary women has lowering effect on serum preptin levels but no effect on serum irisin levels.

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Keywords: irisin, preptin, aerobic exercise, overweight

S002

THE STUDY OF THE PLASMA AMINO ACIDS PROFILE IN PATIENTS WITH HASHIMOTO THYROID DISEASE

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Objectives: HT is a chronic autoimmune thyroid disorder characterized by the production of thyroid autoantibodies against thyroid peroxidase and thyroglobulin. In addition to genetic factors, environmental factors also play an important role in the development of Hashimoto's thyroiditis (HT). Infiltration of lymphocytes in thyroid gland and subsequent development of metabolic and inflammatory disorders. Our aim is to determine possible role of plasma amino acids in HT and after treatment.

Methods: 60 HT patients and 30 healthy individuals were included in this study. The demographic data of the patients were recorded. Plasma amino acid profile was measured by 8045 LC-MS/MS device. Multivariate statistical analysis of studied parameters was performed.

Results: When HT patients treated with levothyroxine and untreated Euthyroid HT patient groups were compared with the control group, plasma levels of only 1-methyl histidine, alanine, asparagine, histidine, isoleucine, lysine, methionine, norvaline, ornithine, phenylalanine, proline, sarcosine, threonine, tyrosine, valine aspartic acid, cystine, glutamic acid, homocitrulline and taurine were found to be lower significantly ($p<0.005$).

Conclusions: Some studied amino acids may be potential biomarkers in the diagnosis, prognosis, treatment and follow up of HT

Keywords: Hashimoto thyroiditis Amino acids LS-MSMS

S003

TRIMETHYLAMINE N-OXIDE AND LIPO-POLYSACCHARIDE BINDING PROTEIN AS POTENTIAL BIOMARKERS IN VITAMIN D, VITAMIN B12, AND IRON DEFICIENCY

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Objectives: We aimed to evaluate the levels of trimethylamine N-oxide (TMAO), a gut microbial metabolite, and lipopolysaccharide binding protein (LBP), recommended as a biomarker for intestinal permeability, in patients with vitamin D, vitamin B12, and iron deficiency.

Methods: This study was performed in 33 patients with iron deficiency, 30 with vitamin B12 deficiency, 33 with vitamin D deficiency, 32 with combined deficiency, 24 patients who received vitamin D supplementation and 32 healthy controls. Serum TMAO and LBP levels were determined by enzyme-linked immunosorbent assay.

Results: TMAO values were found lower

in patients with iron deficiency and combined deficiency compared with the controls ($p<0.01$). LBP values were lower in the vitamin D supplemented group compared to the controls ($p<0.05$). There was a correlation between TMAO and creatinine ($r=0.188$, $p<0.05$), ferritin ($r=0.153$, $p<0.05$) and iron ($r=0.296$, $p<0.001$) levels. TMAO levels were negatively correlated with glucose levels ($r=-0.174$, $p<0.05$). A negative correlation was found between LBP and ferritin levels ($r=-0.178$, $p<0.05$).

Conclusions: Observation of changes in TMAO and LBP levels and their relationship with biochemical parameters in this study shows that these biomarkers play a role in the pathogenesis of micronutrient deficiencies.

Keywords: Iron deficiency, Vitamin B12 deficiency, Vitamin D deficiency, Trimethylamine N-oxide, Lipopolysaccharide binding protein

S004

THE EFFECT OF FUNCTIONAL TRAINING ON INSULIN, HDL, AND LDL LEVELS IN SEDENTARY WOMEN

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Objectives: The insulin is the uptake of glucose in the bloodstream by cells for the purpose of energy production. HDL assists in transporting cholesterol from tissues and arteries to the liver, LDL is responsible for transporting cholesterol from tissues to the areas. The purpose of this study is to examine the acute effects of functional training on insulin, sedentary women and to investigate the acute effects of functional training on HDL and LDL levels.

Methods: 10 sedentary female individuals with an average age of 21.2 ± 1.54 voluntarily participated in the study. After measurements of age height and weight of the participants,

a pre-defined 30-minute functional training session was applied acutely. Insulin, LDL, and HDL levels were measured using the Roche 6000 analyzer series.

Results: The insulin value before exercise was 13.19 ± 2.26 , and the insulin value after exercise was 10.72 ± 2.43 . Statistically significant in insulin levels was observed after exercise ($p < 0.05$). HDL levels before exercise was 56.60 ± 8.14 , and the HDL levels after exercise was 57.90 ± 8.26 . The average LDL before exercise was 98.90 ± 24.87 , and the average LDL value after exercise was 68.10 ± 19.41 . Statistically significant in HDL and LDL levels was observed after exercise ($p < 0.05$).

Conclusions: The results obtained in this study have demonstrated that functional training, as expected, acutely decreases insulin levels. Moreover, acute exercise significantly decreases LDL levels, which are normally expected to decrease in a chronic process after a prolonged exercise, and it also increases HDL levels after acute exercise.

Keywords: Functional Training, Insulin, HDL, LDL
S005

EVALUATION OF THE RELATIONSHIP BETWEEN HbA1C AND VITAMIN D LEVELS IN TYPE 2 DIABETES AND PREDIABETIC CASES

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Objectives: Besides its skeletal effects, the extraskeletal effects of vitamin D, mainly its association with the development of Diabetes Mellitus, attracted considerable attention in several studies. In this study, we aimed to investigate the relationship between vitamin D levels and diabetes mellitus development in prediabetic, and diabetic individuals.

Methods: Patients over 18 years old who applied to the Endocrinology Department of Tokat Gaziosmanpasa University Hospital between June and August 2023 were included in the study. The study population consisted of three groups. The control group consisted of nondiabetic participants with $HbA1c < 5.7$ ($n=46$). The prediabetic group included individuals with $HbA1c$ between 5.7 and 6.4 ($n=24$). Finally, the diabetic group consisted of diabetes mellitus patients with $HbA1c > 6.4$ ($n=28$). Vitamin D (25(OH)D3) and glycosylated hemoglobin (HbA1c) were measured in the study individuals, and statistical analysis was performed.

Results: Vitamin D showed lower levels among diabetes mellitus patients 12.7 (5.11-44.81), compared to prediabetic 16.1 (4.86-42.82) and normal individuals 20.2 (5.74-40.5); $p < 0.05$. A statistically significant difference was observed in vitamin D levels between the control group 20.2 (5.74-40.5) and the diabetes mellitus group 12.7 (5.11-44.81); $p < 0.05$. However, no significant difference was observed in vitamin D levels when comparing the prediabetic group 16.1 (4.86-42.82) with the controls 20.2 (5.74-40.5). Additionally, vitamin D levels were observed to be inversely correlated with HbA1c ($P = 0.03$, $r = -0.219$).

Conclusions: The negative relationship between vitamin D levels and HbA1c suggests that improving vitamin D levels may reduce the risk of developing diabetes mellitus.

Keywords: Diabetes Mellitus, HbA1C, Vitamin D

S006

INVESTIGATION OF THE EFFECT OF KRILL OIL ON IRISIN AND UCP1 LEVELS IN A HIGH-FAT DIET-INDUCED OBESE RAT MODEL

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Objectives: Obesity is characterized by an abnormal increase in the number and volume of adipocytes. Adipose tissue is an endocrine organ, stores energy and synthesizes bioactive molecules called adipokines. Irisin is a novel myokine and adipokine that has gained much attention recently due to its mechanisms of action. Irisin is secreted following proteolytic cleavage of its precursor fibronectin typeIII domain containing 5 (FNDC5). Following its release, irisin exerts its major action by increasing the expression of mitochondrial uncoupling protein 1 (UCP 1), which facilitates the conversion of white adipose tissue(WAT) into beige adipose tissue. Krill oil is a dietary supplement derived from Antarctic krill that have been shown to have beneficial effects on lipid metabolism. This study aims to investigate the effect of krill oil on irisin and UCP1 levels.

Methods: In this study, 21 *Sprague Dawley* 6-8 weeks old male rats were divided into three groups as control, high-fat diet, high-fat diet+krill oil. Rats were fed ad libitum with krill oil 600 mg/kg by oral gavage every day for 13 weeks. At the end of the experiment, serum irisin and UCP1 levels were analyzed by ELISA method.

Results: As a result of the analysis, both irisin and UCP1 levels increase in the high-fat diet and krill oil group compared to the control group. However, this increase was not found to be statically significant.

Conclusions: Irisin is the hormone that provides a different approach to globalizing health problems despite conflicting results. The results obtained by conducting more long-term and complex studies should be supported.

Keywords: irisin, UCP1, obesity, krill oil

S007

THE TEST THAT TOUCHED HUMAN LIFE "TETRAHYDROBIOPTERIN LOADING TEST IN HYPERPHENYLALANINEMIA"

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Objectives: The enzymes responsible for the synthesis of tetrahydrobiopterin (BH4) are abnormal in about 3% of phenylketonuria (PKU). In cases where hereditary hyperphenylalanin is suspected, the BH4 loading test should be applied for the differential diagnosis of biopterin metabolism disorder. According to the results of this loading test, the treatment plan and management of the patients are determined.

Methods: BH4 loading tests of 2 sisters who applied to Başakşehir Cam and Sakura City Hospital Pediatric Metabolism Clinic were studied in our laboratory. The patients were administered sapropterin 20 mg/kg. Phenylalanine (FA) measurements were taken at 0, 4, 8, 16 and 24 hours after sapropterin administration. FA levels in the test were studied in Sciex Triple Quadripol 3500 and HPLC Shimadzu devices as new born screening test.

Results: A simultaneous Bh4 loading test was performed in cases aged 4 and 7 years. A decrease of more than 30% in FA level is considered as a BH4 response. Accordingly, it was determined that there was a 96.4% decrease in the 1st case and a 95.5% decrease in the 2nd case.

Conclusions: This loading test is the gold standard for changing the course of diagnosis and treatment. Much more effective and successful results are obtained by both the removal of the lifelong FA-restricted diet and the drug treatment response of the patients with response. Especially with the removal of the dietary requirement, the patient's lack of food restriction, the cost and social difficulties it brings to the family are overcome.

Keywords: Phenylalanine, Tetrahydrobiopterin

S008

ANTIGLYCATION EFFECT OF PYRIDOXAMINE, COMBINATION WITH CHILI PEPPER EXTRACT AND CAPSAICIN IN STZ-INDUCED DIABETIC RATS

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Objectives: The objective of this study was to evaluate the antiglycation effects of red chili pepper extract (RC) and capsaicin (CAPS), the main bitter ingredient in red peppers and pyridoxamine (PM), a vitamin B6, one by one or in combination, in STZ-induced diabetic rats.

Methods: 96 Male Sprague Dawley rats (8 wk old), each weighing 200-300 grams, were divided into 12 groups of 8 rats each. A single dose of STZ (50 mg/kg body weight) was administered to induce experimental diabetes in rats. Group 1 was normal control, group 2 was diabetic control. Groups 3 and 4, 200 and 400 mg/kg RC, groups 5 and 6, 6 and 8 mg/kg CAPS and group 7, 4 mg/mL PM and group 8 were receiving 300 mg/kg metformin. Groups 9 and 10, 200 and 400 mg/kg RC+ 4 mg/mL PM and groups 11 and 12 were diabetic rats treated with 6 and 8 mg/kg CAPS + 4 mg/mL PM.

Results: Our findings indicate that when high doses of KC+PM (400 mg/kg/day + 4 mg/mL/day) and CAPS+PM (8 mg/kg/day + 4 mg/mL/day) are used in combination, Hemoglobin A1C and fructosamine (FA) levels are significantly reduced.

Conclusions: Our findings strongly imply that extract combinations may have powerful antiglycaemic effects on the healing of diabetes-related damage. This is the first study to look at the antiglycation impact of these substances, and as far as we are aware, there have been no prior reports

Keywords: Diabetes, Glycation, Red chili pepper extract, Pyridoxamine, Capsaicin

S009

COMPARISON OF GENE EXPRESSIONS IN INDIVIDUALS WITH G6PD MEDITERRANEAN MUTATION AND HEMOLYTIC ANEMIA

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Objectives: G6PD enzyme is the most common enzyme deficiency and affects more than 500 million people. Even the patients with Gd-Med mutation are exposed to oxidative agents, some of the patients experience health issues such as hemolytic anemia. In our study, we aimed to clarify the relationship between G6PD enzyme kinetics and mRNA expression levels of the G6PD gene in Gd-Med patients with and without hemolytic anemia.

Methods: The study group consisted of 30 cases with Gd-Med mutation and 30 cases with enzyme activity levels in the reference range. G6PD enzyme was partially purified and its kinetic parameters were studied. Gd-Med mutation was genotyped and the expression levels were calculated.

Results: In our study, a significant difference was found between the Km_{NADP^+} and Km_{G6P} values of the cases with Gd-Med mutation and the control group. There was no significant difference between Km_{NADP^+} and Km_{G6P} values in Gd-Med mutated patients with and without hemolytic anemia. Gene expression of 18 patients without hemolytic anemia were significantly higher than 12 patients with hemolytic anemia. In addition, there was a significant difference between these variables and the control group.

Conclusions: In the light of our data, the substrate binding site of the enzyme in cases with Gd-Med mutation may have undergone post-transcriptional or post-translational modifications, and therefore gene expression might be changed. As a further study, the decrease in gene expressions of patients with hemolytic anemia with Gd-Med mutation can be clarified by evaluating the promoter side of the gene.

Keywords: Enzyme Kinetics, Gene Expression, Glucose-6-phosphate Dehydrogenase, Hemolytic Anemia

S013

DEVELOPMENT OF LC-MS/MS BASED METHODS FOR 2ND TIER ANALYSIS OF SUAC, MMA AND BIOMARKERS OF MSUDMurat Emrah Mavis, Gokce Goksu Gursu, Sule Yalcin

Altium International Lab. Cih. A.ş., Ar-ge Merkezi

Objectives: The main objective of this study was to develop LC-MS/MS based 2nd tier tests or i) Tyrosinemia type I (*primary targeted analyte: SUAC*)

ii) Methylmalonic Acidurias (*primary targeted analyte: MMA*)

iii) Maple Syrup Urine Disease (*primary targeted analyte: allo-isoleucine*) using DBS specimen.

Methods: According to Jassem methodology, 3 mm punches of DBS were extracted using 100 µL extraction reagent specific for both SUAC and MSUD biomarkers at room temperature for 15 min. Following the extraction step, extract was subjected to Agilent 6465B (Ultivo) system. The total run times for SUAC and MSUD biomarkers were 5.5 min and 10.5 min respectively. For the measurement of MMA, 3 mm DBS punch was extracted by 100 µL extraction reagent at room temperature for 15 min. After that, the extract was injected Ultivo system. The analysis time was 10.0 min.

Results: The linearity and accuracy of the methods were evaluated using four DBS-based calibrators and two DBS-based internal quality controls for all works in this paper. For three methods linearity, RSD % (inter-intraday) and accuracy were within the analytical acceptable ranges.

Conclusions: The measurement of biomarkers in the context of 2nd tier using original DBS sample provides reducing number of false positives (increasing positive predictive value) thereby avoiding unnecessary parental anxiety, follow-up efforts and costs. *The proposed* LC-MS/MS methods are centred on quick sample preparation (without derivatization, extraction, and injection) contributing reliable results.

Besides, the methodologies developed are in conjunction with the NBS screening kit and confirmation kits for amino acidurias and organic acidemias.

Keywords: Mass spectrometry, liquid chromatography, metabolic disorder, dried blood spot, second tier test

S014

THE EFFECT OF EDTA ON FLOW CYTOMETRY CROSSMATCH OUTCOMESRasime Derya Güleç¹, Fatma Demet Arslan²¹ Health Sciences University, Tepecik Training and Research Hospital, Tissue Typing Lab. İzmir, Türkiye² Bakırçay University, School of Medicine, Department of Medical Biochemistry, İzmir, Türkiye

Objectives: Flow cytometry crossmatch (FCXM) assesses immunological risk before solid organ transplantation. When ethylenediaminetetraacetic acid (EDTA) is applied to serum, it eliminates high antibody titers, prozone effects, or interacting substances that induce a blocking effect. Our aim is to reveal the possible interference preventive effect of EDTA on outcomes within patient sera during routine FCXM studies.

Methods: Lymphocytes of 21 different kidney transplant candidate-donor pairs were separated and standard tricolor FCXM protocol was applied. For each patient, FCXM tests with EDTA-treated and untreated serums were conducted using donor cells against negative-positive controls and patients' serum, and patient cells (autologous) against patient serum. CD3, CD19, and anti-IgG staining data in cells were acquired using the DxFlex flow cytometer. The ratio of the median fluorescent values of positive control, patient sample, or autologous sample to negative control was calculated. The ratio of EDTA-treated and untreated studies of 21 patients was compared with each other.

Results: While T-cell reactivity in autologous samples after the EDTA-treated significantly decrease (p=0.009), the increase in the positive control (p=0.807), and the decrease in the patient samples (p=0.578) was not significant. On the other hand,

B cell reactivity after the EDTA-treated significantly decreased in positive controls ($p=0.049$), in patient samples ($p=0.024$), and in autologous ($p=0.008$) samples.

Conclusions: A significant reduction in the reactivity of both T and B cells was seen in EDTA-treated autologous samples in the FCXM assay. Our study showed that EDTA treatment can reduce non-specific binding, especially in B-cells.

Keywords: Flow cytometry, crossmatch, ethylenediaminetetraacetic acid, interference

S015

REVIEW OF THE DIAGNOSIS OF DIABETES ACCORDING TO GLUCOSE MEASUREMENT UNCERTAINTY

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Objectives: Measurement uncertainty is the expression of the statistical dispersion of the values attributed to a measured quantity that is reported together with the patient result. When the measurement uncertainty is calculated and given with the test result; it indicates the limits within which the measurement can be found. In our study, our aim was to investigate the effect of glucose measurement uncertainty in the diagnosis of diabetes mellitus.

Methods: The glucose and HbA1c measurement uncertainty was calculated according to the Eurachem/CITAC Guide CG4 using a five-stage measurement uncertainty calculation model. According to the obtained glucose measurement uncertainty, patient results were examined between March-April-May 2023, retrospectively. The patients who were affected from the glucose measurement uncertainty in the diagnosis of diabetes mellitus were also evaluated by HbA1c results and HbA1c uncertainty.

Results: The measurement uncertainty value of glucose was calculated as ± 5.6 mg/dL at a 95% confidence interval. According to this result which effects the diagnosis of Diabetes Mellitus, 681 of 77131 (0.88%) glucose results were close to the threshold value (126 ± 5.6 mg/dL). According to the obtained glucose measurement uncertainty, the number of people with glucose results below 126 mg/dL and HbA1c values above 6.4% was 34 (0.04%).

Conclusions: Since measurement uncertainty is highly important in the diagnosis and clinical decisions of diabetes, it should be to further reduce measurement uncertainty with stricter analytical performance requirements.

Keywords: Glucose, Uncertainty, Quality Control, Standardization

S016

COMPARISON OF CREATININE LEVELS MEASURED BY JAFFE AND LC/MS/MS METHOD

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Objectives: As one of the most requested analyzes in clinical laboratories, creatinine is an important analyte for the prediction of kidney and muscle damage. Many methods are used to determine creatine levels. In the study, we aimed to compare creatine levels which measured by Jaffe and LC/MS/MS method.

Methods: The serum samples were taken from 102 healthy subjects who came to the 29 Mayıs state hospital for control purposes between January and April 2021. The creatinine levels were measured and compared in Mindray BS-800 device

using the Jaffe method using the archem kit and API 3200 tandem mass device measuring with the Liquid Chromatography Tandem Mass/Mass Spectrometer method. The samples were stored at -80 °C until analysis and were dissolved during analysis following the establishment of the measurement method and measured in API 3200 Mass Spectrometer and Mindray BS-800 device in our routine biochemistry laboratory.

Results: Correlation coefficient of all data (n=102) was measured as 0.9958. Mindray BS-800M-Archem Crea-J/LC/MS/MS for creatinine' s reference levels under 0.5 (n=32) was determined as 0.4938. Creatinine' s reference levels between 0.5-1.3 mg/dL (n=39) was determined as 0.9689 for jaffe an LC/MS/MS method. Creatinine' s reference levels above 1.4 mg/dL (n=31) was determined as 0.9924.

Conclusions: The correlation coefficients of the all data, between 0.5-1.3 mg/dL levels and above 1.4 mg/dL levels show a good correlation. However, the level of under reference levels 0.5 mg/dL did not show a well correlation.

Keywords: Jaffe method, LCMSMS, creatinine

S017

INTERCHANGEABILITY OF K3-EDTA AND SODIUM CITRATE TUBES FOR HBA1C MEASUREMENT BY CAPILLARY ELECTROPHORESIS

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Objectives: Glycated hemoglobin (HbA1c) is a vital parameter for Diabetes Mellitus diagnosis and monitoring. Traditionally, HbA1c measurements are performed using K3-EDTA tubes. This study aims to compare HbA1c results obtained from K3-EDTA and Sodium Citrate tubes using capillary electrophoresis.

Methods: Blood samples from 67 patients were collected in Greiner VACUETTE 2 ml K3-EDTA and Greiner VACUETTE 2 ml Sodium Citrate tubes (Greiner Bio-One, Kremsmünster, Austria).

Measurements were conducted with a Sebia Capillary 3 Tera analyzer (Sebia, Lisses, France). For data presentation, conformity to normal distribution was evaluated by Kolmogorov-Smirnov test. Since the data did not fit the normal distribution, the results were presented as median (interquartile range). Passing-Bablok regression analysis and Bland-Altman plots were used for comparison. Statistical significance was set at $p < 0.05$ with a 95% confidence interval.

Results: Median HbA1c levels were 4.7% (5.6% - 9.4%) for K3-EDTA and 4.6% (5.5% - 9.5%) for Sodium Citrate. Passing-Bablok regression yielded the equation $y \text{ (Sodium Citrate)} = 0.000 \text{ (95\% CI: -0.147-0.000)} + 1.000 \text{ (95\% CI: 1.000-1.019)} x \text{ (K3-EDTA)}$. The Bland-Altman plot showed a mean difference of 0.115%.

Conclusions: Results indicate that K3-EDTA and Sodium Citrate tubes are interchangeable for HbA1c measurement by capillary electrophoresis, ensuring flexibility in blood collection tube selection.

Keywords: Diabetes mellitus, Hemoglobin A1c, capillary electrophoresis, blood collection tube, method comparison.

S018

THE PERFORMANCE ASSESSMENT OF HEMOGRAM PARAMETERS: SIGMA VALUES WITH DIFFERENT TOTAL ALLOWABLE ERROR GOALS

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Objectives: Six sigma process analysis is widely used to evaluate the performance of tests in clinical laboratories. This study aimed to compare the sigma values determined by using the total allowable error (TEa) goals of The Clinical Laboratory Improvement Amendments (CLIA) and The European Federation of Clinical Chemistry and Laboratory Medicine (EFLM) to evaluate the performance of some hemogram parameters.

Methods: The study was conducted in Kastamonu Teaching and Research Hospi

January-June 2022. Leukocyte, erythrocyte, hemoglobin, hematocrit, and platelet parameters studied on the Sysmex XN-1000 (Kobe, Japan) hematology autoanalyzer were included in the study. The 6-month mean bias and coefficient of variation (CV) were obtained retrospectively from proficiency test and internal quality control results, respectively. Sigma values were determined with the formula '(TEa-bias)/CV'. The acceptable sigma level was considered as 3.

Results: All tests had sigma values above 3 when CLIA TEa goals were used (i.e., process performance was acceptable). Six-month mean sigma values according to CLIA and EFLM TEa goals were 9.3 and 2.5 for leukocyte, 4.7 and 2.4 for erythrocyte, 6.2 and 2.8 for hemoglobin, 3.9 and 2.2 for hematocrit, and 6.1 and 2.2 for platelet, respectively.

Conclusions: The TEa goals set by CLIA and EFLM are different, and this causes significant differences in the sigma values of hemogram parameters. Tests that perform well according to CLIA goals have unacceptable performance according to EFLM. Consequently, a consensus should be achieved in the guidelines for standardizing hematology performance specifications.

Keywords: six sigma, performance specifications, hemogram, total allowable error

S019

EVALUATION OF PERFORMANCE CHARACTERISTICS OF ROCHE COBAS T511 COAGULATION DEVICE

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Objectives: The aim of this study was to evaluate the analytical performance characteristics of prothrombin time(PT), activated partial thromboplastin time(aPTT) and fibrinogen tests performed on the Cobas t511(Roche Diagnostics, Germany) coagulation device and to verify the reference intervals determined by the manufacturer.

Methods: In the study, precision and bias validation was performed using CLSI EP15 A3 and method comparison was performed using CLSI EP9 A3 standards. Method comparison study was performed with STA-R Max-2(Diagnostica Stago SAS). In the method comparison, 160 plasma samples for PT and aPTT and 44 plasma samples for fibrinogen were used. Indirect reference interval determination was performed for reference interval assessment. For this purpose, data of 435 patients aged <18 years and 4700 patients aged >18 years for PT and aPTT tests and 1033 patients for fibrinogen, which were studied on Cobas t511 device, were used. Statistical analyses were performed with SPSS ver.21 and Excel Analyze-it package programs.

Results: Intra-study, total %CV values for normal and high control samples used in the study were PT: 0.57-0.69, 1.58-0.79 aPTT: 0.32-0.4, 1.7-2.88 and fibrinogen: 2.06-1.84, 2.65-2.35. Mean %bias values were PT: 2.45%, aPTT: 3.45%, fibrinogen: 5.54%. Regression equations for PT, aPTT and fibrinogen in device comparison were cobas t511=-0.56+0.68 STA-R max, cobas t511=-9.67+1.21 STA-R max, -cobas t511=-4.18+STA-R max and r was 0.872, 0.870, 0.995, respectively. In the reference interval study performed using the indirect method for Cobas t511; PT <18 years: 8.2-10.5s, >18 years: 7.9-10.6s, aPTT: <18 years: 23.4-34.6s, >18 years: 22.4-32.8s, and fibrinogen: 193-580 mg/dL.

Conclusions: The results of our validation studies for PT, aPTT, fibrinogen on the Cobas t511 analyzer show that the device performs adequately for routine use in our laboratory.

Keywords: Coagulation, Method comparison, Verification, Prothrombin time, Activated partial thromboplastin time

S020

ANALYTICAL VERIFICATION OF THE HEMATOLOGY ANALYZER DYMIND DH615

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Objectives: The Dymind DH615 is a new automated hematology analyzer that provides a complete blood count (CBC) including a 5-part WBC differential count. The purpose of this study was to test the Dymind DH615 automated analyzer and compare it to the Sysmex XN1000.

Methods: Analytical verification included estimation of repeatability, within-run precision, within-laboratory precision, and bias for low, normal, and high control samples. Acceptance criteria for analytical verification were defined using the European Federation of Laboratory Medicine (EFLM) 2019 Biological Variation Database. Method comparison between the Dymind DH615 and the Sysmex XN1000 with respect to hematologic parameters was performed on 31 patient samples.

Results: The Dymind DH615 demonstrated excellent repeatability and within-run precision for all CBC and WBC differential parameters for all level controls. Within-laboratory precision was within acceptable ranges, with the exception of eosinophils (11.9%, 12.10%), red blood cells (2.11%, 3.30%), hemoglobin (3.6%), mean cell volume (0.7%, 0.9%, 1.0%), and platelets (6.8%). The Dymind DH615 and Sysmex XN1000 analyzers showed very good correlation coefficients (R²) except for monocytes, basophils, and MPV (0.7758, 0.8222, and 0.6639, respectively).

Conclusions: We conclude that the Dymind DH615 is a competent analyzer to provide reliable and accurate diagnostic results. In our opinion, the clinical performance of the Dymind DH615 Hematology Analyzer compares favorably with the analyzer Sysmex XN1000 and meets the requirements for clinical use in medium to large-sized hematology laboratories.

Keywords: blood cell count, hematology, verification

S021

CALCULATION OF MEASUREMENT UNCERTAINTY OF SERUM IMMUNOGLOBULINS ACCORDING TO ISO/TS 20914 GUIDELINE

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Objectives: The aim was to calculate the measurement uncertainty (MU) of serum immunoglobulins (Ig) analyzed in Ankara Training and Research Hospital laboratory and to compare MU values with the maximum allowable measurement uncertainty (MAU) values published by European Federation of Clinical Chemistry and Laboratory Medicine (EFLM) in 2022.

Methods: Serum IgG, IgA and IgM were analyzed by immunoturbidimetric method and serum Ig E by sandwich immunoassay method on Roche Cobas 8000 analyzer. Relative expanded MU (%U_{rel}) values was calculated separately for each analyte based on two levels of internal quality control results according to the model in the ISO/TS 20914 document. The MU values obtained were compared with MAU values.

Results: The bias calculated from external quality control (EQQ) data for serum IgG, IgA and IgM (0.95%, 4.67% and 9.18%, respectively) was found to be lower than the desirable bias (4.4, 5.1 and 12.2, respectively) and was therefore neglected in the MU calculation according to the ISO/TS 20914. For the first and second level control levels, U_{rel} % was 4.0 and 4.1 for Ig G, 4.91 and 7.4 for IgA, 8.3 and 7.1 for IgM, respectively. EFLM MAU values for IgG, A and M are 5.3, 8.6, 8.9 respectively. The bias calculated from EQQ data for Ig E was 8.7%, %U_{rel} were 9.01% and 8.79%, however no comparison could be made because there is no MAU value in EFLM.

Conclusions: The measurement uncertainty for serum immunoglobulins were found to be within acceptable limits.

Keywords: Measurement uncertainty, ISOTS 20914, Serum immunoglobulins

S022

EVALUATION OF THE DIAGNOSTIC USEFULNESS OF TRIGLYCERIDE GLUCOSE INDEX AS A GLYCEMIC CONTROL MARKER

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Objectives: Diabetes Mellitus (DM) continues to be the most common endocrine disease today. Easily accessible, accurate and reproducible markers are needed in addition to the accepted markers to evaluate insulin resistance (IR) and glycemic control. Therefore, our study aimed to evaluate the use of triglyceride glucose index (TyG Index) as an indicator for insulin resistance and glycemic control.

Methods: Tg, HDL-c, HbA1c, fasting blood sugar (FBG), and insulin values of 7518 samples studied simultaneously in our TOGU Faculty of Medicine Hospital Laboratory between March 2023 and August 2023 were retrospectively examined. The patients were divided into two groups according to their HbA1c values: good glycemic control (<7%) and poor glycemic control (≥7%). ROC analysis was performed to evaluate the ability of the TyG Index to discriminate between insulin resistance and glycemic control. Statistical significance level was accepted as p<0.05.

Results: TyG Index (p<0.001) was found to be significantly higher in individuals with insulin resistance. When we looked at the areas under the ROC curve (AUC) to evaluate the ability of this parameter to distinguish insulin resistance, TyG Index was found to be 0.720 (p<0.001). In case of poor glycemic control, Tg/HDL-c (p<0.001) was also significantly higher and AUC value was 0.810 (p<0.001).

Conclusions: According to the current results, we think that the TyG Index is a useful marker of glycemic control and insulin resistance, and it may be a useful parameter to detect metabolic changes due to T2DM in the early stages.

Keywords: Diabetes Mellitus, Insulin Resistance, Glycemic Control, Triglyceride, Glucose

S023

DETERMINATION OF MEASUREMENT UNCERTAINTY FOR ESTIMATED SERUM OSMOLALITY BASED ON DATA OBTAINED FROM DIFFERENT ANALYSERS (ISO/TS 20914)

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Objectives: We aim to determine of the measurement uncertainty (MU) for estimated serum osmolality using glucose, urea and sodium (Na) analytes measured on different devices in the Medical Biochemistry Laboratory of Ankara Bilkent City Hospital.

Methods: Serum glucose, urea and Na were analyzed on Siemens Atellica CH (Siemens Healthcare GmbH) (9 analyzers) and Advia Chemistry XPT (Siemens Healthcare GmbH) (1 analyzer) analyzers. Relative expanded MU (U_{rel} %) values were calculated separately for each analyte based on two lot and two-level internal quality control (IQC) results between 01.03.2023 and 01.09.2023, according to the model in the ISO/TS 20914 document. From the obtained u_{rel} % values for tests, (u_{rel} OSM %) was estimated for osmolality according to the formula ($\sqrt{(2^2(\%u_{rel-Na})^2+(\%u_{rel-Ure})^2+(\%u_{rel-Glikoz})^2}$).

Results: The u_{rel} % values for Na, urea and glucose for Atellica and Advia Chemistry were 1.05, 4.84 and 3.22 for level 1 and 0.88, 3.80 and 2.82 level 2, and were 1.55, 2.48 and 2.70 for level 1, L2. 0.89, 2.84 and 2.67 for level 2, respectively. The estimated serum osmolality combined U_{rel} % (K=2, 95 % confident interval) was determined as 11.29 (Atellica), 9.12 (Advia Chemistry).

Conclusions: Since there was no MAU value for estimated osmolality in EFLM, no comparison could be made. We think that our study will contribute to the literature in this sense.

Keywords: measurement uncertainty, ISO, serum osmolality, estimated

S024

METHOD VERIFICATION AND METHOD COMPARISON FOR ELECTROCHEMILUMINESCENCE AND LC-MS/MS METHODS FOR SALIVARY CORTISOL MEASUREMENT

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Objectives: This study aimed to perform method verification for the measurement of salivary cortisol with the CORTII reagent based on the principle of electrochemiluminescence in the RocheCobas8000e801 module and Obikrom brand salivary free cortisol determination reagents in the LC-MS/MS device. A method comparison study was also conducted.

Methods: The study followed the CLSI guidelines for the evaluation of limit of blank (LOB), limit of detection (LOD), limit of quantitation (LOQ), linearity, precision and reference interval. The method comparison study was performed based on the CLSI guidelines with a total of 433 samples, including 393 morning salivary cortisol samples collected from 41 healthy adults and 40 different high concentrations obtained by adding Roche Elecsys PCU1 (lot.no:558012) quality control material to the saliva pool.

Results: The LOB, LOD, and LOQ values of the LC-MS/MS method were 0.065 nmol/L, 0.087 nmol/L, and 0.276 nmol/L, respectively. The method was considered linear between 0.690-41.4 nmol/L. The within-run imprecision for 0.276 nmol/L and 27.6 nmol/L levels were 4.82% and 4.57%, respectively. The LOB of the ECLIA method was not evaluated; LOD and LOQ values of 1.5 nmol/L and 3 nmol/L were confirmed, respectively. Between 2.13-68 nmol/L, the method was considered linear. At 5.16 nmol/L, the within- and between-run imprecision were 3.85% and 5.5%, respectively; at 32.8 nmol/L, the within- and between-run imprecision were 1.37% and 2.54%, respectively. For both methods, all samples from 41 reference subjects were below the threshold reported in the kit insert. The regression equation was $y = -0.179 + 1.244x$ and $r = 0.988$ by the Passing and Bablok regression analysis. The bias of the ECLIA method

was 0.975 nmol/L in concentration (Q1:0.031 nmol/L, Q2:2.33 nmol/L) and 17.9% in percentage based on Bland-Altman analysis.

Conclusions: Under the laboratory conditions of the study, the claimed performance values for both methods were acceptable. The bias of the ECLIA method appears to increase with higher concentration; however, the minimum bias target of 19.3% for cortisol based on biological variation was achieved.

Keywords: method verification, method comparison, salivary cortisol, electrochemiluminescence, lc-msms

S025

EFFECT OF ANTIRETROVIRAL THERAPY ON LYMPHOCYTE SUBGROUP AND CD38 AND HLADR IN HIV PATIENTS

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Objectives: We aimed to investigate the effect of antiretroviral therapy on lymphocyte subgroups and T cell activation markers, CD38 and HLADR, in patients with HIV.

Methods: Thirty HIV patients, 30 follow-up patients who received 3 months of antiretroviral therapy, and 20 controls were included in the study. Whole blood samples were collected in EDTA containing tubes. The percentages of T and T lymphocyte subgroups and CD38 and HLADR expressions were estimated by flow cytometric method. Absolute counts were calculated by double platform method. IL-2 levels were studied by ELISA and viral load analyzed by PCR method.

Results: CD4+/CD8+T cell ratio and CD4+/CD38+T cell percentage were significantly lower (respectively, $p=0.022$, $p=0.026$), CD8+/CD38+T and CD8+/HLADR+T cell percentage were higher ($p<0.001$) in the newly diagnosed group compared with controls. CD4+/CD8+T cell ratio and CD4+/CD38+T cell percentage were significantly increased (respectively, $p<0.001$, $p=0.006$) but CD8+/CD38+T and CD8+/HLADR+T cell percentage were decreased ($p<0.001$, $p=0.003$, respectively), in the post-treatment group compared with newly diagnosed group. There was no change in the absolute number of CD8+T cells after treatment. There was a negative correlation between viral load and CD4+/CD38+T cell percentage and a positive correlation with CD8+/CD38+T cell percentage. Serum IL-2 values were significantly lower only in the treatment group.

Conclusions: CD38 expression on CD4+T and CD8+T cells has a potential as an additional marker together with CD4+T cell count in the evaluation of the efficacy of ART in patients with HIV.

This study was supported by Hatay Mustafa Kemal University Scientific Research Projects (project number:21.YL.050).

Keywords: HIV, AIDS, CD38, HLA-DR, immune activation

S026

IDENTIFICATION OF THERAPEUTIC MOLECULES THAT WILL INTERACT COVALENTLY AGAINST SARS-COV2 IN SILICO APPROACHES

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Objectives: In the COVID19 pandemic period, which affects the whole world and new solutions for the disease are being investigated in the world. It is aimed to determine the molecules to be covalently bound in drug screening for important target proteins

Methods: It was prepared at neutral pH by downloading FDA approved 2360

molecules from Drugbank.

Covalent reactions were performed for each target protein. The molecules with the best docking score for each covalent reaction are ranked. The structures with the best docking score were taken into molecular simulation and Molecular mechanics with generalised born and surface area solvation (MMGBSA) values are calculated.

Results: The molecules with the best docking score for each covalent reaction are ranked. 2D and 3D ligand interaction diagrams of target proteins of molecules with high docking scores were analyzed. The structures with the best docking score were taken into molecular simulation and MMGBA values are calculated. Main protease in the target molecules with a high docking score Octreotide (-9.710kcal/mol) for TMPRSS2 in the target Abarelix (-8.753) for Spike ACE2 in the target Leucovorin (-7.021) for RdRp in the target Candicidin (-7.817)

Conclusions: The method known as drug repurposing in different indications is remarkable as it becomes less costly in terms of both time and required resources. Non-covalent reversible binding in different target proteins is difficult and challenging and their therapeutic effects are limited. Molecules found to be active by in vitro testing will be recommended for further in vitro testing.

Keywords: Main Protease, TMPRSS2, SpikeAce2, RDRP, SarsCov2

S027

ADENOSINE DEAMINASE: AS AN INFLAMMATORY AND PROGNOSTIC MARKER IN THE EARLY PHASE OF THE DISEASE IN COVID-19 PATIENTS?

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Objectives: This study was made to investigate the usability of serum adenosine deaminase level as a biochemical and prognostic marker in COVID-19 patients and to compare it with some other hematological and biochemical parameters routinely used for this purpose.

Methods: Our study consisted of patients admitted to the Chest Diseases Hospital and diagnosed with COVID19, and a control group consisting of healthy volunteers. In serum samples taken within 48 hours after the first RT-PCR test that was found positive, serum ADA levels were studied in all groups and subgroups (the uncomplicated patient group (UPG), the mild-moderate pneumonia patient group (MMPPG), and the severe pneumonia patient group (SPPG)). Lymphocyte count in hemogram, neutrophil/lymphocyte ratio (NLR), C-reactive protein (CRP), D-dimer and ferritin level were measured with serum ADA level simultaneously. ADA levels were determined by modifying the colorimetric method developed.

Results: A total of 61 individuals were included in our study, and no significant difference was found between all groups and subgroups in terms of ADA levels. On the other hand, lymphocyte count, NLR, CRP, D-dimer and ferritin values were found to be significantly different between COVID19 and the control group ($p < 0.001$). This difference was also observed among the COVID19 subgroups. Again, a significant correlation was found between comorbidity, vaccination status hematological and biochemical values expressing risk in COVID19 patients and the UPG, MMPPG, SPPG patient subgroups (Sig. < 0.001).

Conclusions: Through the data we've collected by our study, it was concluded that serum ADA levels can not be used as an inflammatory and prognostic marker in COVID-19 patients during the initial period.

Keywords: COVID-19, Adenosine deaminase, immunity, SARS-CoV-2

S028

THE EFFECT OF TAURINE ON PRESEPSIN AND INTERLEUKIN-6 LEVELS IN A LIPO-POLYSACCHARIDE-INDUCED SEPSIS MODEL

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Objectives: Lipopolysaccharide (LPS), a cell wall component of Gram-negative bacteria, plays an important role in the pathogenesis of sepsis. Taurine, a metabolic product of L-cysteine, inhibits the secretion of proinflammatory cytokines. The aim of this study was to investigate the effect of taurine on presepsin and interleukin-6 levels in a lipopolysaccharide-induced sepsis model.

Methods: In this study, 24 Wistar albino female rats, weighing 250-300 gr were used. Rats were divided into 4 groups as control, taurine, LPS, taurine+LPS. The rats were given 300 mg/kg/day saline or taurine by gavage for 10 days. After the 10th day, saline or LPS was injected intraperitoneally at a dose of 1 mg/kg/day for once. Presepsin and interleukin-6 (IL-6) levels in liver, kidney and serum samples were measured by ELISA method. Kruskal-Wallis test was used for statistical analysis. $p < 0.05$ was considered statistically significant.

Results: Presepsin levels in serum, liver and kidney tissues increased in the LPS group compared to the control and taurine groups ($p < 0.05$). In kidney tissue, taurine significantly decreased the increase in presepsin levels caused by LPS ($p < 0.05$). When IL-6 levels were evaluated, a decrease was observed in the taurine+LPS group compared to the LPS group in serum, while an increase was observed in the LPS group compared to the control and taurine groups in the liver ($p < 0.05$). No significant difference was observed in renal IL-6 levels ($p < 0.05$).

Conclusions: Taurine may be effective in proinflammatory response by decreasing tissue damage, presepsin and IL-6 levels in LPS-induced sepsis model.

Ethics committee no: G.Ü.ET-23.045

Keywords: presepsin, sepsis, Interleukin-6, lipopolysaccharide, taurine

S029

RETURNED ASSESSMENT OF SERUM VITAMIN B12 LEVELS OF PATIENTS DIAGNOSED WITH COVID-19

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Objectives: It is known that vitamins have effects such as disrupting the viral replication of the Coronavirus disease (COVID-19), developing an anti-inflammatory response and increasing immunity. We aimed to see the relationship between Vitamin B12 (Vit B12) serum levels and the prognosis of the disease in COVID-19 patients in this study.

Methods: The study included 9600 participants, aged between 18-65 years, who applied to Ankara Provincial Health Directorate Laboratory for SARS-CoV-2 diagnosis between March 2020 and December 2022. Sociodemographic information, serum Vit B12 levels of the patients were analyzed retrospectively from the Laboratory System. Serum vitamin B12 level was grouped in which 200-2000 pg/mL is normal, 150-200 pg/mL is mild deficiency, 100-150 pg/mL is severe deficiency and less than 100 pg/mL is very severe deficiency.

Results: The median age of the participants was 46.51(18-65) and the median Vit B12 level was 179.50 ng/L (75-641). 5834 (60.78%) patients had Vit B12 deficiency. Cough, loss of taste and smell, headache and pneumonia rates were higher in patients with severe and very severe Vit B12 deficiency than other groups ($p<0.01$). Vit B12 levels were higher than the platelet count of patients with mild and severe levels compared to normal rates ($p<0.01$).

Conclusions: It was determined that the clinical progression of COVID-19 patients with vitamin B12 deficiency was worse than those without vitamin B12 deficiency. Therefore, we think that Vit B12 supplements may have a positive effect in COVID-19 patients. However, more comprehensive and longer duration studies with more patients are required.

Keywords: covid-19, pandemic, vitamin B12

S030

CHANGES OF PLATELET-RELATED BIOMARKERS IN PULMONARY TUBERCULOSIS

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Objectives: Tuberculosis (TB) is the second leading cause of death from infectious diseases in the world, after COVID-19. Studies have shown that people with TB or a history of TB have an increased risk of myocardial infarction, ischemic stroke, and peripheral arterial disease. This study suggests that these diseases may be associated with TB.

Methods: The Sysmex Blood Counting Device can measure specific parameters related to platelets, such as platelet large cell ratio (P-LCR), mean platelet volume (MPV), platelet large cell count (P-LCC), and plateletcrit (PCT). We plan to investigate the changes in these parameters in TB patients. 50 patients with TB and having first-line treatment were taken for the patient group. 50 patients without any chronic disease were selected as the control group. CBC parameters were analyzed retrospectively with SPSS. Parametric-nonparametric differences were compared using the One Sample KS test and 2 independent sample t-tests.

Results: The mean age was 57.36 years for the patient group and 54.78 years for the control group, $p=0.610$. PLT and MPV were 313.50/mm³ (118-711) and 252.50/mm³ (100-639); 9.15 fL (7.20-13.10) and 9.80 fL (7.60-11.9); $p=0.001$ and $p=0.005$ in the

patient and control groups, respectively. P-LCR and P-LCC were 20.85% (7.50-48.50) and 24.7% (11.30-40); 69/ μ L (19-155) and 61.5/ μ L (5-130); $p=0.013$ and $p=0.206$, respectively. PCT was 27% (13-66) for patients and 25% (2-59) for controls, $p=0.093$.

Conclusions: MPV, PLT and P-LCR, which can be easily measured together with CBC, may help predict vascular events that may develop in TB patients. Further studies in this field may shed light on how the disease leads to acute vascular events.

Keywords: MPV, PLT, P-LCC, P-LCR, Complete Blood Count

S031

DISCOVERY OF FIRST-IN-CLASS PLASMODIUM OTU INHIBITORS AND UNVEILING NOVEL PATHWAYS

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Objectives: Malaria, a deadly infectious disease, is a global concern, especially due to the rise of drug-resistant parasites, necessitating the development of innovative treatments. This study offers a groundbreaking perspective by comparing it to Crimean Congo Hemorrhagic Fever Virus, another intracellular parasite. Both rely on the viral OTU protease to disrupt NF- κ B signaling pathways for host cell invasion. Notably, our research revealed shared amino acid sequences between malaria and Neospora parasites, similar to CCHFV's OTU domain. This discovery suggests that malaria and Neospora parasites may use OTU proteins to manipulate the NF- κ B pathway. Our research suggests targeting OTU proteins is crucial for malaria treatment. We conducted comprehensive *in silico*, *in vitro*, and *in vivo* analyses.

Methods: We created 3D models of novel OTU deubiquitinases from malaria and

Neospora parasites, showing robust activity *in vitro* and *in vivo*. Our research reveals how these OTU proteins affect immune pathways and ubiquitination. We meticulously screened a library containing approximately 5.000.000 compounds, subjecting them to stringent selection criteria encompassing docking scores, druggability, ADME-tox attributes, IC50 values, DUB inhibitory characteristics, and their impact on gene and protein expression profiles.

Results: We have identified four small molecules with potent anti-malarial. This study is a milestone in malaria treatment, extending to viral OTU-like proteins in malaria types.

Conclusions: Our study, which includes structural modeling, small molecule screening, deconjugation assays, and subsequent inhibitor development, paves the way for revolutionary anti-malarial therapies targeting these malarial OTU-like proteases.

Keywords: Malaria, deubiquitinases, anti-malarial, drug discovery, small molecules

S033

THE ROLE OF MICROBIOTA AND OXIDATIVE STRESS IN FOOD ALLERGIES

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Objectives: Food allergies appear with an increasing picture in the world, especially due to changes in environmental conditions. It is known that many factors play a role in food allergies starting from infancy, from genetic factors to environmental factors, from

the mother's nutrition during pregnancy to the packaged foods that children consume more and more every day. Microbiota plays an important role in the fulfillment of many different body functions. It is known that oxidative stress plays a role in the pathogenesis of many diseases, especially allergic diseases. Especially in food allergy, the process becomes more complicated with the effect of agents such as inflammation and oxidative stress. Therefore, in our study, it was aimed to reveal the effect of intestinal microbiota and oxidative stress on the process in individuals with food allergy caused by various factors.

Methods: Twenty patients diagnosed and followed up with food allergy and 20 healthy volunteers as the control group were included in the study. Live intestinal microbiota in the stools of individuals and MDA and GSH levels as markers of oxidative stress in serum were determined spectrophotometrically.

Results: When the study group was evaluated, it was determined that the oxidant balance was impaired in individuals diagnosed with food allergy, and a decrease in the number and variety of probiotics, a permanent flora element in the intestinal microbiota.

Conclusions: As a result, the importance of antioxidant supplements and especially personalized probiotic supplements is gradually increasing in eliminating the effect of allergic diseases on metabolism, which has increased in recent years.

Keywords: Oxidative stress, Probiotics, Microbiota, Food Allergies

S035

PLASMA LIPID PROFILE IS ALTERED IN CHRONIC MIGRAINE PATIENTS AND CORRELATED WITH MIGRAINE RELATED DISABILITY

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Objectives: Chronic migraine (CM) is a disabling common neurologic disorder predominantly affecting women and its treatment is challenging. Understanding the confounding factors in chronic migraine will provide alternative approaches for the management. Lipids have important functions in energy storage and cell membrane structure and they are the source of inflammatory and pain signaling molecules. However, its relationship with chronic migraine has not yet been clearly explained.

Methods: This study enrolled 30 woman subjects (15 CM patients and 15 age matched healthy controls). Clinical features, disease duration, body mass index (BMI) were recorded and migraine related cognitive symptoms scale (MigScog), headache impact test 6 (HIT-6), hospital anxiety and depression scale (HAD) and biochemistry laboratory tests describing the lipid profile were evaluated.

Results: Serum VLDL, TG, levels were significantly higher and HDL levels were significantly lower in CM patients than controls while BMI values were comparable in 2 groups. Migraine duration was positively correlated with VLDL ($r=0,499$), TG ($r=0,609$), HbA1c ($r=0,435$) and negatively correlated with HDL ($r=-0,387$). MigScog scores were correlated with VLDL ($r=0,489$) and TG ($r=0,536$) levels. HIT-6 showed correlateion with VLDL ($r=0,435$) and TG ($r=0,518$). HAD depresssion was correlated with VLDL ($r=0,605$) and TG ($r=0,636$). HAD anxiety was correlated with VLDL ($r=0,444$), TG ($r=0,555$) and negatively correlated with HDL ($r=0,381$).

Conclusions: We demonstrated abnormal serum lipid levels in CM patients and serum levels showed correlation with migraine related disability. Management strategies to regulate and control lipid parameters may have an important role in the treatment and prevention of CM.

Keywords: Chronic migraine, serum lipids, Migs-cog, HIT-6, HAD

S036

INVESTIGATION OF THE EFFECTS OF WHITE TEA ON THE DEVELOPMENT OF ATHEROSCLEROSIS IN MICE FEED WITH ATHEROGENIC DIET

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Objectives: The aim of this study is to present comprehensive and up-to-date evidence on the possible anti-atherosclerotic activity of white tea, which is known for its antidiabetic, neuroprotective, anticancer, antimicrobial and antiobesity properties.

Methods: In our study, C57BL-6J mice (n=8) were used in the control group, while ApoE^{-/-} mice (n=32) were used in the sham, case, white tea (WT100) and white tea (WT500) groups. Case and sham groups were fed with control diet and all other groups were fed with atherogenic diet for 16 weeks. In the last 4 weeks of the 16-week feeding period, white tea was given by gavage to the WT100 (100mg/kg/day) and WT500 (500mg/kg/day) groups as a single daily dose. Animals were sacrificed, blood and aortic tissues were collected. Total cholesterol (TC), triglyceride (TG) and glucose (Glu) in serum were measured by enzymatic colorimetric method, while paraoxanase-1 (PON-1) were measured by ELISA. Tumor necrosis factor- α (TNF- α), myeloperoxidase (MPO) and interleukin-10 (IL-10) levels were measured in aor

tic arch tissue by ELISA. In addition, aortic root was examined histopathologically.

Results: Compared with the case group, in the WT100 and WT500 groups; It was determined that TC, TG, plaque burden, atherogenic cytokine TNF- α and oxidative stress marker MPO levels decreased (p<0.05), while the levels of anti-inflammatory cytokines IL-10 and PON-1 increased (p<0.05).

Conclusions: In our study, it was concluded that white tea reduced inflammation and dyslipidemia in atherosclerosis.

Keywords: Apo E^{-/-}, Atherosclerosis, Dyslipidemia, Inflammation, White tea

S037

INVESTIGATION OF BCL11A (rs1427407) and HMIP (rs9399137) SNPs ASSOCIATED WITH HIGH HbF LEVELS IN β -THALASSEMIA

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Objectives: To evaluate the effect of rs1427407 and rs9399137 single nucleotide polymorphisms (SNP), which improve the phenotype by increasing HbF synthesis in β -thalassemia major or sickle cell anemia, on fetal hemoglobin (HbF) levels.

Methods: 44 pediatric patients (<18) who applied to Çukurova University Balcalı Hospital Pediatric Hematology Department with the complaint of β -thalassemia major or sickle cell anemia and received blood transfusion were included in our study. rs1427407 SNP were evaluated by tetra primer ARMS method and rs9399137 SNP was evaluated by RT-PCR method.

Results: According to the results of rs1427407 SNP of BCL11A locus of patients, 23 of them (52%) have "C/C", 9 (20,45%) carries "T/C" and 12 (27,27 %) carries "T/T" allele. SNP results obtained for rs9399137 in β -thalassemia and sickle cell anemia patients show 44 (100%) "T/T" alleles.

Conclusions: As a result, “C” allele for rs1427407 polymorphism and “T” allele for rs9399137 polymorphism were found at high frequency. Significant differences were found related to HbF level at all two polymorphic points. When the rs1427407 and rs9399137 polymorphisms were examined together, it was determined that HbF synthesis was high ($p<0.001$) in individuals carrying the rs1427407 “C/T” and rs9399137 “T/T” alleles together. It was found that the rs1427407 polymorphism affected HbF levels more in patients with β -thalassemia with the “C/T” genotype compared to individuals with sickle cell anemia ($p<0.001$).

Keywords: SNP analyse, HbF levels, haemoglobinopathy

S039

THE IMPORTANCE OF PANEL DESIGN FOR FLOW CYTOMETRY

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Objectives: Flow-cytometry immunophenotyping is crucial, especially for the diagnosis of hematological disease. Mixed-phenotype acute leukemia (MPAL) consists of a heterogeneous group of leukemias that are genetically, immunophenotypically, and clinically, diverse. Since the rarity of the disease, the diagnosis and treatment of MPAL is extremely challenging. Besides morphologic criteria, setting the correct diagnosis depends on the identification of immunophenotype by flow cytometry, and well-designed panels are crucial. The purpose is to demonstrate the importance of the panel design for the diagnosis of MPAL.

Methods: A 48-year-old male's diagnosed with T-Lymphoblastic Lymphoma (T-ALL) in another hospital

bone marrow sample was evaluated with immunophenotyping. The cell count findings were bicytopenia, borderline (white-cell-count: $29,29 \times 10^9$ cell/L) leukocytosis. His bone marrow aspiration showed 53% of blasts. Immunophenotyping showed a population of blasts exhibiting positivity of two lineages, T-lymphoid lineage, and B-lymphoid lineage with strong positivity of CD34-cCD3-CD7-CD2-CD4-CD5-CD1a-CD3- cCD79a-CD10-CD19- terminal deoxynucleotidyl transferase (TdT)-Human Leukocyte Antigen-DR (HLA-DR), moderate positive of CD22 and negativity of CD8-CD13-CD33-CD117-Myeloperoxidase (MPO).

Results: Flow-cytometry is unique in its ability to measure, and analyze the cells with a gating strategy and well-designed panel. Acute leukemia orientation tube (ALOT) is the first step for evaluating leukemias. The ability of the panel to distinguish normal from pathological and the give information about the lineage may be established with the antibodies used in the panel. Although the patient was diagnosed with T-ALL, our ALOT tube findings showed two lineages. We performed multiple tubes for further information about the blasts and the patient's diagnosis switched from T-ALL to MPAL.

Conclusions: A systematic approach to designing multicolor flow cytometry panels is crucial for accurate diagnosis of acute leukemia diagnosis.

Keywords: flow cytometry, Mixed-phenotype acute leukemia

S040

FLOW CYTOMETRIC DIAGNOSIS OF MULTIPLE MYELOMA: A CASE REPORT

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Objectives: Multiple myeloma is a plasma cell neoplasm characterised by lytic bone lesions, hypercalcaemia, renal failure and immunodeficiency. This disease is especially seen in men aged 65-70 years. In multiple myeloma, tumour cells express CD38 and CD138 as detected by flow cytometry.

Methods: A 69-year-old male patient was admitted to the Hematology Outpatient Clinic of Etlik City Hospital with complaints of extreme fatigue, frequent infections and bone pain, especially in the back region. Laboratory tests revealed anemia (9.4 g/dL), leukocytosis (15.200/mm³), elevated creatinine (2.2 mg/dL) and elevated C-reactive protein (36.7 mg/L). The bone marrow sample of the patient who was ordered flow cytometry with a prediagnosis of multiple myeloma was received to our laboratory and multiple myeloma panel was studied from this sample after preliminary procedures.

Results: After analysing the dot graphs in flow cytometry, 0.12% of the cells were found to be CD38 and CD138 bright positive and located in the CD45 negative area. Monoclonal lambda light chain expression was observed in these cells after capturing. CD117, CD81, CD200, CD27 and CD28 positivity was observed in neoplastic cells.

Conclusions: The development of effective treatment modalities such as Daratumumab, a monoclonal antibody against CD38, will directly affect treatment planning and thus prognosis. In addition, the fact that multiple myeloma cases not expressing CD56 are associated with poor prognosis makes flow cytometry more important in the clinical evaluation of this neoplasm. In conclusion, this study once again emphasises the importance of flow cytometry in all stages of hematological malignancies.

Keywords: Flow cytometry, Multiple myeloma, CD38, CD138

S041

EVALUATION OF HEMOGLOBINOPATHIES WITH CAPILLARY ZONE ELECTROPHORESIS

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Objectives: Hemoglobinopathies are genetic disorders that cause abnormalities in the structure of the globin chains in the hemoglobin molecule. Capillary Zone Electrophoresis (CZE) is widely used to diagnose hemoglobinopathies.

Hemoglobinopathies are observed as quantitative abnormalities (thalassemia) and qualitative abnormalities (hemoglobin variants).

Methods: Hemoglobin electrophoresis was performed with the CZE method (Sebia Minicap) on 3238 whole blood samples at Istanbul Başakşehir Çam and Sakura Hospital between September 1, 2022 and August 31, 2023.

Results: Hemoglobin electrophoresis was evaluated according to electrophoretic patterns. Hemoglobinopathies (thalassemias and Hb variants) were observed in 12.66% of reports (410 samples). In the evaluation, 7.85% (254 samples) had beta thalassemia, 2.22% (72 samples) had alpha thalassemia, 1.76% (57 samples) had Hemoglobin S (Hb S) variant, 0.46% had Hemoglobin D (Hb D) variant in 15 samples, Hemoglobin F (Hb F) variant in 0.25% (8 samples), Hemoglobin C (Hb C) variant in 0.06% (2 samples), % Hemoglobin E (Hb E) variant was detected in 0.03% (1 sample) and Hemoglobin O-Arab (HbO-Arab) variant was detected in 0.03% (1 sample).

Conclusions: With CZE, both common (thalassemias and Hb S variant) and rare (Hb D, F, C, E, O-Arab variants) hemoglobinopathies are detected in a shorter time and at a lower cost. Advanced genetic analyses are recommended in electrophoresis reports to diagnose detected hemoglobinopathies definitively.

Keywords: Hemoglobinopathy, electrophoresis, thalassemia, hemoglobin variant

S042

THE IMPACT OF TRANSPORTING TUBES WITH A PNEUMATIC SYSTEM ON ROUTINE COAGULATION TESTS

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Objectives: In the field of Clinical Biochemistry laboratories, there are many preanalytical variables that need to be controlled to obtain

accurate results in coagulation tests. In 2008, CLSI published a document that addressed the preanalytical stages of coagulation testing. In this document, it was emphasized that coagulation samples transported in pneumatic tubes should be protected from sudden agitation, as it could lead to protein denaturation and platelet activation.

Methods: Our study included 30 participants, from whom blood was collected into two different citrated coagulation tubes each. One of the samples was transported to the laboratory using a pneumatic tube, while the other was transported to the laboratory without using a pneumatic tube. Prothrombin time (PT), activated partial thromboplastin time (aPTT), and fibrinogen tests were performed on both coagulation tubes simultaneously. The results were compared using paired sample t-tests, and the compatibility of the results was demonstrated using correlation analysis, Passing-Bablok regression analysis, and Bland-Altman analysis.

Results: In the coagulation tubes transported with a pneumatic tube, PT results were significantly lower compared to those not transported with a pneumatic tube ($p=0.006$), while fibrinogen results were significantly higher ($p<0.0001$). There was no significant difference in aPTT results between the two tubes ($p=0.719$). The correlation coefficients (r) for PT, aPTT, and Fibrinogen were determined as 0.776, 0.883, and 0.870, respectively.

Conclusions: Based on the obtained results, it is suggested that coagulation factors particularly associated with the extrinsic pathway may undergo changes in their activation during transportation with pneumatic tubes.

Keywords: coagulation tests, pneumatic system

S043

THE EFFECTS OF THE TRANSPORT CONDITION ON STEM CELLS

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Objectives: In the context of stem cell transplantation, hematopoietic progenitor cells (HPCs) are a critical component. Flow cytometric quantitation of CD34+ cells should provide a rapid, reliable, and reproducible assay. The best conditions for storing and transporting HPCs in a liquid state are not clearly defined or established in the current standards applied in stem cell transplantation. Our objective was to evaluate the optimal transportation conditions through courier and pneumatic tube systems (PTS) for peripheral blood and apheresis products, aiming to enhance CD34 recovery and thereby potentially improve the results of transplant procedures.

Methods: Samples were collected from the same group of patients, resulting in paired data. The collected samples were divided into two separate tubes - one tube was sent to our laboratory with PTS, while a courier brought the other. Samples were simultaneously tested on the Beckman flow cytometer and Sysmex hematology analyzer.

Results: We tested parameters such as CD34+, CD45+live, and leukocyte counts and found no clinically significant difference between the two transportation methods. For absolute CD34 counting, the mean bias was -1.7%, 0.001% for CD45live, and 1% for WBC count. There were no proportional and systematic differences in the Passing-Bablok analysis.

Conclusions: Based on our findings, it can be concluded that PTS can be selected as a transportation method for fast delivery of samples to the laboratory without affecting the flow cytometry results in the CD34 enumeration process.

Keywords: flow cytometry, CD34, Stem cell

S045

LINEAR REGRESSION MODELS CAN PREDICT THE DIRECT LDL-C TEST LEVELS WITH 74% ACCURACY: MACHINE LEARNING-BASED COMPUTING OF CHOLESTEROL

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Objectives: At levels below 400 mg/dl of triglyceride levels, LDL levels can be calculated computationally with equations such as Friedwald's equation and Martin Hopkins equation, but not at

levels above 400 mg/dl. This study aims to develop a model to differentiate LDL cholesterol measurement using machine learning methods in cases where LDL levels cannot be measured computationally at levels above 400 mg/dl but can be measured by direct LDL-c test.

Methods: This research includes data from a cohort of 24,000 data points and 2,000 cases. Cholesterol, LDL, HDL, and Glucose levels were evaluated within the scope of this study. Including Artificial Neural Network (ANN), K-Nearest Neighbor (KNN), Linear Regression (LR), Stochastic Variational Bayesian (SVR), Random Forest (RF), (XGB), Decision Tree (DT), Extreme Gradient Boosting Regressor Models were created using various machine learning (ML) methods. The models with the highest diagnostic accuracy were compared and then evaluated.

Results: The study found that linear regression models could predict LDL-C levels with 74% accuracy. The machine learning model was able to predict laboratory test results with 74% accuracy.

Conclusions: The algorithm, created using data from 2,000 cases, can directly predict LDL-C test results with 74% accuracy. The results of this study may make it easier for clinicians to measure LDL cholesterol levels in individuals with hypertriglyceridemia.

Keywords: Machine learning, Linear regression, Direct LDL-c, Artificial Neural Network ANN, K-Nearest Neighbor

S046

EVALUATION OF KNOWLEDGE LEVELS, ATTITUDES AND BEHAVIOURS OF MEDICAL BIOCHEMISTRY SPECIALISTS ABOUT GREEN AND SUSTAINABLE MEDICAL LABORATORY

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Objectives: Our aim in this study is to analyze the level of knowledge, awareness, attitudes, and behaviors of medical biochemistry specialists

in Turkey under green and sustainable medical laboratories guideline (GSMLG).

Methods: This research is a cross-sectional survey study. Medical Biochemistry specialists between 23 and 65 years, participated. The GSMLG was used as a reference. The survey questions are organized under five sections using the Google form (

https://docs.google.com/forms/d/e/1FAIpQLSed-LGF9FHVWkYkN27unXguIAmOeBknBGYyy-Yp-_uVSDLkm6pA/viewform?vc=0&c=0&w=1&flr=0&pli=1). Excel was used for analysis of the responses.

Results: A total of 130 people responded to the questionnaire. According to section 1, 28.5% of the participants were academicians, 48.1% were specialists and 23.1% were assistants. The average age of the participants was 39.2±10.8 years and the gender distribution was 60% female and 40% male. 76.1% of the participants stated that they had heard of the concept of sustainability before in section 2. In section 3, it was observed that the participants realized sustainable green laboratory practices (energy and water consumption, waste and chemical use) that can be done individually. In the 4th section, it was determined that 83.1% of the laboratories where the participants work have chemical substance management, 74.6% have waste management, 44.6% have energy consumption and 43.7% have water consumption practices. In section 5, 60% of the participants stated that they did not have information about GSMLG.

Conclusions: Individual laboratory professionals have high sensitivity towards the environment. However, there are deficiencies in energy and water consumption management as managerial infrastructure. Most participants are not familiar with GSMLG.

Keywords: Sustainability, Green Laboratory

S047

BLOOD COLLECTION TRAINING STATUS OF LABORATORY TECHNICIANS

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Objectives: The majority of laboratory errors occur at the phlebotomy stage during the preanalytical process. Phlebotomist is not defined as a profession in Turkey. This process is mostly carried out by laboratory technicians. The aim of our survey is to determine the educational status of those who perform this process by separating practical and theoretical aspects.

Methods: The survey was administered via Google forms. 262 valid responses were evaluated.

Results: It was determined that 7.2% performed phlebotomy without any theoretical training during school or post-school, and 6.1% did it without any practical training. Those who performed phlebotomy without any training during school or after school were 3.4%. Of those who performed phlebotomy without any training at school or after school 66.7% graduated before 2014, 22.2% graduated between 2014 and 2020, and 11.1% graduated after 2020. In Turkey blood collection was included in the job description of laboratory technicians with the regulation published in 2014. Technicians who graduated before 2014 constitute the majority of the untrained group. It can be thought that it will be supportive about the group that should be prioritized in terms of training requirements.

Keywords: phlebotomy, laboratory technician, training

S048

MICROBIOLOGICAL EVALUATION OF DISPOSABLE HOLDERS USED IN THE BLOOD COLLECTION UNIT IN MULTIPLE USES

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Objectives: Some of healthcare facilities reuse blood tube holders in order to reduce costs associated with device purchase and waste removal. However, removing contaminated needles and reusing the holders can pose multiple potential hazards. We aimed to evaluate the disposable holders used in the blood collection unit microbiologically in case of multiple use.

Methods: The disposable holders (450201 VACU-ETTE® Standard Tube Holder, Greiner Bio-One, Kremsmuenster, Austria) were distributed to ten blood collection cabinets, one for each. The holders used for five weeks without any disinfection. On the first (40 swab), second (10 swab) and third (10 swab) days of the first week, a total of 60 swabs from the inner surface of the holder in each cabin, were taken. On the fifth day of the next four weeks, a total of 40 swabs were taken and, inoculated and evaluated for bacteria.

Results: At the end of the 1st, 2nd and 3rd day, it was observed that 10,40,10% of the holders grew Coagulase negative staphylococcus (CNS), 30,20,50% grew Staphylococcus epidermidis, 10% grew Staphylococcus aureus and 10% grew yeast. 2nd, 3rd, 4th, 5th week, 30.8, 28.6, 21.4, 33.3% had CNS, 46.2,42.9,57.1,46.7% had Staphylococcus epidermidis, 7.7% had Corynebacterium Spp, Also, 3rd week, 7.1% had Micrococcus Spp, 4th week, 7.1% had yeast, 5th week, 6.7% had Enterobacter spp and 6.7% had Enterococcus spp reproduction was observed.

Conclusions: It should be noted that non-disposable holders may be contaminated with bacteria or blood, which may pose a risk to the staff, patients and samples.

Keywords: holder, multiple use, contamination, bacteria

S049

INVESTIGATION OF THE RELATIONSHIP OF OXIDATIVE STRESS, INFLAMMATION, AND CELL ADHESION MARKERS WITH CLINICAL PARAMETERS IN FABRY DISEASE

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Objectives: The aim of the present study was to determine the relationship of growth differentiation factor 15 (GDF15), leucine-rich α -2-glycoprotein-1 (LRG1), galectin-3 (LGALS3) and oxidative stress parameters, *i.e.* total antioxidant level (TAS) and total oxidant level (TOS) with Fabry disease in blood serum samples.

Methods: 25 Fabry patients who applied to Hatay Mustafa Kemal University Medical Faculty Nephrology Clinic and 28 healthy volunteers were included in the current study. LGALS3, GDF15 and LRG1 protein levels in blood serum samples were measured by ELISA method, TAS and TOS levels were measured by colorimetric method and oxidative stress index (OSI) values were calculated. In addition, routine biochemistry parameters (glucose, ALT, AST, BUN, creatinine, sodium, potassium, calcium, phosphorus, uric acid) of the patient and control groups were measured. Receiver operating characteristic (ROC) test was performed to analyze the distinctiveness of some parameters in diagnosis of Fabry disease.

Results: GDF-15, LGALS3 and TAS values were significantly higher in the patient group than in the control group ($p < 0.05$). Sodium was found to be significantly lower in the patient group compared to the control group ($p < 0.001$). No significant difference was observed in other biochemical parameters between the groups ($p > 0.05$). The area under the curve (AUC) values of the ROC analyses were 0.7821 ($p < 0.05$) for LGALS-3, 0.6957 ($p < 0.05$) for GDF15, 0.8879 ($p < 0.05$) for sodium, 0.6714 in TAS ($p < 0.05$),

0.5016 ($p > 0.05$) for TOS and 0.5699 ($p > 0.05$) for OSI.

Conclusions: As a result, LGALS3, GDF15, sodium and TAS can be promising parameters in differentiation of Fabry disease patients ($p < 0.05$).

Keywords: Fabry disease, Alpha-Galactosidase A, GLA gene mutation, Biochemical parameters, Biomarkers

S050

THE IMPORTANT ROLE OF MULTIPLEX PCR IN THE DIAGNOSIS OF DUCHENNE MUSCULAR DYSTROPHY

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Objectives: Duchenne muscular dystrophy (DMD) is a hereditary neuromuscular disease with X-linked recessive inheritance. It is caused by mutations in the gene *DMD* that codes for the dystrophin protein. Multiplex PCR allows the detection of 98% of rearrangements of the *DMD* gene in 70% of cases of dystrophinopathies. The objective of our work is to show the importance of this tool in the diagnosis of DMD.

Methods: We report 14 patients referred to the Laboratory of Medical Genetics of the University Hospital Mohammed VI of Oujda for myopathy. Patients' DNA was extracted from peripheral venous blood. Its quality and quantity were

controlled by spectrophotometry. We performed a multiplex PCR for promoter and exons ranging from 3 to exon 60 of the *DMD* gene. We used three mixtures of primers.

Results: The results obtained are observed and interpreted according to the presence or absence of the expected bands under UV and based on a size marker as a reference. Multiplex PCR revealed deletions of the *DMD* gene in 4 patients (28.57%), which are grouped in exon regions 43 to 52.

Conclusions: Multiplex PCR plays a crucial role in the early identification of *DMD* gene mutations and therefore enables diagnosis and genetic counseling in this pathology and will be important for future therapeutic strategies.

Keywords: Multiplex PCR, Duchenne Muscular Dystrophy, genetic counseling

S051

THE INVESTIGATION OF EXPRESSION LEVEL DIFFERENCES OF CARDIAC AQUAPORINS IN H₂O₂ INDUCED H9c2 CARDIOMYOCYTES

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Objectives: The aim of study is investigation of expression level differences of cardiac aquaporins (*AQP1* and 7) in H9c2 cardiomyocytes after H₂O₂ treatment which can cause increased stress level in H9c2 cardiomyocytes.

Methods: By performing MTT assay, non-toxic H₂O₂ concentration for H9c2 cells was determined. After inducing H9c2 cells with H₂O₂ for 2 hours, RNA isolation and cDNA synthesis were performed. Expression levels of *AQP1* and *AQP7* were measured via qPCR on basis of *Beta actin* as a reference, DDCT values were calculated and statistically analyzed. This study was supported by Hacettepe University (Project number: FHD-2022-20252).

Results: MTT assay results showed that 200 mM H₂O₂ was non-toxic concentration. After treatment of cells with 200 mM H₂O₂, we found that *AQP1* expression level was not changed while *AQP7* expression level was significantly changed (p: 0,0312).

Conclusions: Since *AQP1* is known as aquaporin and *AQP7* is known as aquaglyceroporin, *AQP1* involves in water transportation and *AQP7* mainly involves in glucose uptake. Expression level of *AQP1* might not be changed because cells were always in aqueous environment during experiments. It is assumed that in an aqueous system, cells might stabilize their osmotic pressure and *AQP1* expression level might remain as same as before. On the other hand, increased expression level of *AQP7* can be related with the fact that *AQP7* coordinates glucose uptake that affects regulation of contracting and water balance in cardiomyocytes.

Keywords: AQP1, AQP7, H9c2, H₂O₂

S052

INVESTIGATION OF HNF1A GENE POLYMORPHISMS AND THEIR METABOLIC EFFECTS ON MODY AND TYPE 2 DIABETES

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Objectives: We aimed to investigate the distribution of common hepatocyte-nuclear-factor-1A-(HNF1A)-gene variations and their effects on clinical features in patients with type 2 diabetes-(T2DM) and clinically-diagnosed maturity-onset-diabetes-of-the-young (MODY).

Methods: HNF1A-gene was sequenced in genomic-DNA samples of 41-patients with T2DM and 53-patients with MODY by Next Generation Sequencing-(NGS). Statistical analyses were performed by SPSS-software package-(version-20.0-SPSS Inc.,IL,USA). This study was supported by the Research Fund of Istanbul University (Project-No.TOA-2017-24194).

Results: The distribution of the HNF1A rs1169288-(A>C), rs1169289-(G>C), rs1800574-(C>T), rs56348580-(G>C) and rs55834942-(G>A) polymorphisms was similar in the study groups ($p>0.05$). T2DM patients with the rs1169289 and rs56348580 GG genotypes had lower C-peptide levels than non-carriers, while those with the rs1169288 rare-C allele had higher waist-circumference ($p<0.05$). In the MODY group, rs1169289 minor-C allele carriers (GC+CC genotypes) had higher ALT than GG genotype ($p<0.01$). In addition, serum triglyceride levels were significantly higher in MODY subjects with rs56348580 GG genotype than those with the C allele ($p<0.05$).

Conclusions: The association of HNF1A-gene polymorphisms with the decrease in C-peptide levels indicates that they affect endocrine-pancreas function in T2DM-patients. Also, the effects of these gene variations on ALT and triglyceride levels suggest that they affect liver function in MODY-patients. In conclusion, our findings show that HNF1A-gene polymorphisms may have different metabolic effects in T2DM&MODY patients. However, it cannot be excluded that the difference may be due to the onset of the two forms of diabetes at different ages, as in this study. Therefore, further studies with larger sample sizes are required for stronger findings.

Keywords: MODY, T2DM, NGS, HNF1A, single nucleotide polymorphism SNP

S053

IMMUNOGOLD LABELING OF MUTANT AVP PRECURSORS AT ELECTRON MICROSCOPY

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Objectives: The aim of this study is visualizing the aggregate structures formed by mutant arginine vasopressin hormone (AVP) precursors with mutations in the neurophysin II region 207_209delGGC, G88V, C98X, E108D-1, E108D-2, and R122H which are responsible with a rare disease autosomal dominant neurohypophyseal diabetes insipidus (ADNDI) via transmission electron microscopy.

Methods: Mutant AVP precursors were expressed in COS-1 cells. They were fixed, permeabilized, blocked and incubated with primary antibodies. The cells were then stained with 15nm Gold secondary antibodies. The cells were dehydrated, embedded in resin and polymerized. Araldite cell blocks were shaved and placed on copper-coated formvar and visualized at transmission electron microscopy (TÜBİTAK SGAB Project No: 118S688, Hacettepe University BAP Project No: 19929).

Results: Electron-dense aggregate structures were visualized within the intracytoplasmic and exocytosomal vesicles.

Conclusions: Protein misfolding due to AVP mutations leads to the formation of aggregate structures, causing Endoplasmic reticulum (ER) conformational distortion and potentially increasing intracellular toxicity. According to the results, mutant protein precursors labeled with immunogold were accumulated within the ER lumen at different densities, with disruption ER architecture and causing the structure to expand in a vesicular manner. This condition might have the potential to impair ER function. Some mutations showed both intracellular and extracellular aggregate structures. In addition, this study has also some updates in the imaging protocol for transmissi

Keywords: Aggregate, AVP, Transmission Electron Microscopy, ADNDI

S054

COMPARATIVE EVALUATION OF SILICA MEMBRANE AND PHENOL-CHLOROFORM DNA EXTRACTION TECHNIQUES FOR ANCIENT SAMPLES

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Objectives: Ancient DNA (aDNA) refers to DNA in severely degraded substances like teeth and bones retrieved from museum specimens or archaeological excavations. A key challenge in aDNA research is the scarcity of intact DNA in these samples. Also, the decay of aDNA complicates its extraction, severely limiting the recoverable DNA length. Hence, it's vital to design custom extraction methods to maximize DNA yield from specimens. However, the complexities of handling damaged DNA have led to innovative isolation techniques. Several methods exist, all aiming to optimize DNA production while reducing co-extraction of PCR inhibitors. This study aims to compare two extraction techniques in terms of efficiency in aDNA.

Methods: 5 femur, 5 talus specimens from Stratonikeia Ancient City, were subjected to both silica membrane and phenol-chloroform DNA extraction methods. Mitochondrial DNA was amplified using three distinct primer pairs, generating amplicons of 162 bp, 177 bp, and 218 bp. The success of each extraction method on different sample types was comprehensively evaluated. The study was supported by Hacettepe University BAP project number with FYL-2021-19646.

Results: We found that the phenol-chloroform extraction method exclusively yielded successful results for the shortest amplicon (162 bp) in femur and talus specimens. In contrast, the silica membrane approach consistently yielded successful outcomes for all three

amplicons in these samples.

Conclusions: This study underscores the significance of selecting appropriate DNA extraction methods for different sample types. The success of the silica membrane method in yielding amplifiable DNA fragments of varying lengths, even from severely damaged samples, signifies its utility for diverse research applications.

Keywords: Ancient DNA, DNA extraction, mtDNA

S055

AUTOPHAGIC CELL DEATH STUDIES LACK EVIDENCE OF CAUSALITY

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Objectives: Autophagy has been a topic of extensive interest for the last two decades due to its critical role in health and many diseases. Autophagic cell death (or type II cell death) is a popular yet controversial concept, and how it is measured may vary greatly from study to study. Here we examined the methodology of publications with autophagic cell death claims and investigated the indisputability of the provided evidence.

Methods: We retrieved all autophagic cell death studies published in 2022 via Web of Science and analyzed their experimental design and methods. We classified the evidence provided for autophagic cell death in three groups:

Proof of increased autophagy and no data on cell death

Proof of increased autophagy and increased cell death (correlation)

Proof of increased autophagy causing cell death (causal relationship)

Results: We have analyzed 50 articles and determined that the majority (78%) failed to present adequate evidence to demonstrate a causal relationship between

autophagy and cell death. The most common type of evidence was demonstrating a correlation between autophagy and cell death (66%). Surprisingly, some articles (20%) even failed to provide adequate evidence for increased autophagy itself.

Conclusions: Since it is a popular topic, the number of articles mentioning autophagic cell death is increasing exponentially. However, not all published work contains autophagic cell death evidence. Here we report that misinterpretation of the term and poor experimental design are common practices among autophagic cell death studies.

Keywords: Autophagic Cell Death, Experimental Design, Quality Control

S057

MEASURING THE INHIBITION ACTIVITY OF HYPERGLYCEMIC ENZYMES WITH ZnO NANOPARTICLES

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Objectives: Agents are required to decrease the activity of protein kinase C (PKC) and glyceraldehyde three phosphatase (GADPH) enzymes, which increase their activity in hyperglycemic conditions. These agents are available in inorganic or organic form. However, the natural origin of these agents that do not harm human health and the environment should be preferred.

Methods: In this study, PKC and GADPH enzyme inhibitors were used as positive controls in agarose gel electrophoresis. In addition, ZnO nanoparticles obtained by the green synthesis method and their separation effects and inhibition activities on pBR322 DNA were evaluated through gel images. Enzymes were incubated with ZnO nanoparticles overnight at 37°C before electrophoresis. Then mixture is put into the wells containing 1% agarose gel. It runs for 50 minutes at 80 volts. UV image results obtained from the trans illuminator and evaluated.

Results: In the UV images, it was observed that the supercoiled DNA Form 1 structure separated into Form 2 in the enzymatic environment. The separation was not seen when Nano ZnO was present. Thus, nanoZnO can also be used as a drug to control hyperglycemia-related oxidative- stress.

Conclusions: In addition, the presence of zinc in Nano ZnO can prevent oxidative stress caused by zinc deficiency and increase its role in treating Type 2 Diabetes Mellitus by providing the external zinc requirement.

Keywords: hyperglycemia, pBR322 DNA, Nano ZnO, diabetes mellitus

S059

IMPORTANCE OF ALPHA-1 ANTITRYPSIN DEFICIENCY IN CHRONIC LUNG AND LI-VER DISEASES

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Objectives: Alpha-1 antitrypsin (AAT) is the most abundant circulating serine protease inhibitor and an acute phase reactant. AAT deficiency can cause chronic lung and liver diseases. The aim of this study is to raise awareness about AAT deficiency, which can cause complications with high morbidity and mortality.

Methods: This study included patients applied to Selçuk University Medical Faculty Hospital with a history of chronic lung and liver disease. All patients between the ages of aged 1-97 were included in the study. Patients were divided into three groups according to AAT levels: <100 mg/dl (low group), 100-200 mg/dl (reference range group) and >200 mg/dl (high group). AAT concentration was measured by photo metric method in Roche Cobas c702.

Results: A total of 1950 patients were included in the study. The mean age of the patients in the low group (n=80) was 29.7 years (min:1 max:78), in the reference range group (n=1559) was 35.9 years (min:1 max:95) and in the high group (n=311) was 42.5 years (min:1 max:97). While AAT levels were not low in 95.9% of the patients, they were found to be low in 4.1%.

Conclusions: Considering the long-term mortality and morbidity of the disease, this rate (4.1%) is not low. In addition, considering that the mean age of the low patient group was 29.7 years, it is considered to be too late to start the treatment of the disease. Considering the family history and clinical symptoms, we think that AAT test, which is a non-invasive test, should be performed at an earlier age in these patients.

Keywords: Alpha-1 antitrypsin deficiency, Alpha-1 antitrypsin, Lung diseases, Liver diseases

S060

EVALUATION OF IMMUNOLOGICAL TESTS PERFORMED BEFORE KIDNEY TRANSPLANTATION

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Objectives: T lymphocyte can recognize antigen through Major Histocompatibility Complex (MHC) molecules: Human Leukocyte Antigen (HLA) Class 1 (HLA A, B and C) in all nucleated cells, and 2 antigens (HLA DR, DQ and DP) in antigen-presenting cells, macrophages and dendritic cells. HLA compatibility between the recipient and donor, the presence of anti-HLA antibodies in the recipient must be performed to ensure kidney transplant's success.

Methods: Panel reactive Antigen (PRA), Donor specific Antigen (DSA) and Complement-dependent cytotoxicity (CDC) are performed on each patient before kidney transplantation in our Hacettepe University Tissue Genotyping Laboratory. Our number of tests this year is 265. CDC is repeated 24 hours before kidney transplantation. If PRA is greater than 13% (in men) and 20% (in women), the recipient is donor's wife and her birth & miscarriage numbers are high, the patient's first transplant was unsuccessful, multiple mismatches in their DSAs, CDC positivity (more than 20% dead B and T lymphocytes) and blood transfusion history, results will be confirmed by flow cytometry (fc).

Results: HLA determination by PCR analysis using Sequence specific primers (SSO) and/or Sequence specific oligonucleotide probes (SSP), and anti-HLA determination by Luminex method (for PRA and single HLA antigen), CDC and fc results will be presented from our laboratory.

Conclusions: The methods we use, such as CDC and fc, SSO/SSP HLA analysis with PCR, and PRA and single HLA antigen determination with Luminex have been complementing each other in terms of specificity and sensitivity, and are vital in terms of survival and complications.

Keywords: kidney transplantation, sso, ssp, luminex, cross-match, flow cytometry

S061

PROTECTIVE EFFECT OF NEUROPEPTIDE-S ON A CELLULAR MODEL OF PARKINSON'S DISEASE

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Objectives: Oxidative stress, altered levels of monoamine oxidases (MAO) and catechol O-methyl transferase (COMT) enzymes involved in the catabolism of dopamine are held responsible for dopaminergic neuron damage in Parkinson's disease. We aimed to determine the effects of brain derived Neuropeptide-S (NPS) on lipid peroxidation, dopamine catabolizing enzymes and dopamine levels on a cellular model of Parkinson's Disease.

Methods: Cellular model of Parkinson's Disease was created by treating human neuroblastoma cells (SH-SY5Y) with paraquat and the effects of NPS and the NPS antagonist ML154 was evaluated in cells treated with or without paraquat. Six different experimental groups were formed, 1- Control; 2- NPS (cells treated with 0.5 µM NPS for 24 hours); 3- Paraquat (cells treated with 1mM paraquat for 24 hours); 4- Paraquat + NPS (cells treated with 1mM paraquat and 0.5 µM NPS for 24 hours); 5/6- Paraquat + NPS + ML154 (cells treated with 1mM paraquat, 0.5 µM NPS and 0.1 µM or 1 µM ML154 for 24 hours). MAOA, MAOB, COMT, and TBARS levels were determined by ELISA method, while dopamine levels were measured by LC-MS/MS.

Results: Paraquat significantly increased lipid peroxidation, MAOB and COMT levels, and significantly decreased MAOA and dopamine levels compared to other groups (p<0.05). NPS treatment decreased paraquat-induced lipid peroxidation, normalized MAOA, MAOB, COMT to control levels and significantly increased cellular dopamine content (p<0.05).

Conclusions: This study demonstrated that NPS increased dopamine levels in a cellular model of Parkinson's disease by regulating dopamine catabolism and protecting against lipid peroxidation. #220S745.

Keywords: Parkinsons Disease, Neuropeptide-S, Paraquat

S062

PROTECTIVE EFFECTS OF NEUROPEPTIDE-S IN A RAT MODEL OF PARKINSON'S DISEASE

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Objectives: Parkinson's disease is a neurodegenerative disorder characterized by the loss of dopaminergic neurons in the substantia nigra (SN). Dopaminergic neuron damage occurs due to oxidative stress and altered levels of monoamine oxidases (MAO) and catechol-O-methyl transferase (COMT) enzymes which are involved in the catabolism of dopamine. In this study, we aimed to investigate the effects of brain derived Neuropeptide-S (NPS) on lipid peroxidation, dopamine catabolizing enzymes and dopamine levels on an in-vivo experimental model of Parkinson's disease.

Methods: Parkinson's disease model was created in rats by administering paraquat (PK) (7 days; 10 mg/kg) via gavage. Intranasal NPS was applied at a daily concentration of 40 nmol/500 µl while an NPS antagonist ML154 (20 nmol/5 µl) was delivered via intracerebroventricular (icv) administration for 7 days. Six different experimental groups were formed, Control; NPS; PK; PK+NPS and PK+NPS+ML154. MAOA, MAOB, TBARS, and COMT levels were determined in SN by ELISA. Dopamine levels in SN were measured by LC-MS/MS.

Results: Paraquat significantly increased TBARS, MAOB and COMT levels, and significantly decreased MAOA and dopamine levels compared to NPS and PK+NPS groups ($p<0.05$). NPS treatment decreased MAOB and COMT levels and normalized TBARS and MAOA to control levels. NPS treatment also significantly increased dopamine concentrations ($p<0.05$).

Conclusions: This study demonstrated that NPS increased dopamine levels in an in-vivo experimental model of Parkinson's disease by regulating dopamine catabolism and protecting against lipid peroxidation. This study was supported by a grant from TÜBİTAK #220S745.

Keywords: Parkinsons Disease, Neuropeptide-S, Paraquat

S063

INVESTIGATION OF THE EFFECTS OF SPARSTOLIN B ON APOPTOTIC PATH ACTIVATION IN COLORECTAL CANCER CELLS

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Objectives: Colon cancer is an important oncological problem in developed countries. Sparstolonin B (SsnB) is a polyphenol derivative and has been reported to have anti-carcinogenic activity. This study investigated the outcome of SsnB treatment on apoptotic pathway activation in human colorectal cancer cells (HCT-116) and in human healthy fibroblasts (BJ).

Methods: Cell proliferation was stimulated in HCT-116 and BJ cells treated with 10 nM phorbol 12-myristate 13-acetate (PMA) for 12 hours, while SsnB (25 µM) was applied to both cell types to determine apoptotic activity. The optimal doses and incubation times of PMA and SsnB were determined by MTT cell viability assay. Activation of the apoptotic pathway was analyzed by evaluating quantitative protein levels of caspase-3 and cleaved caspase-3 via immunofluorescence method. The number of apoptotic cells were defined by TUNEL method.

Results: HCT-116 cells treated with SsnB showed a 2.7 fold increased in caspase 3 and a 1.5 fold increase in cleaved caspase 3 protein levels compared

to controls ($p < 0.05$). There was also a 1.9 fold significant increase in the number of apoptotic cells in colon cancer cell lines treated with SsnB compared to controls. BJ cells treated with the same doses of SsnB showed no significant change in caspase 3, cleaved caspase 3 and apoptosis.

Conclusions: Data obtained show that SsnB treatment activated the apoptotic cascade in HCT-116 cells and caused an increase in the amount of apoptotic cells. This supports the development of SsnB as a potential therapeutic agent in colorectal cancer treatment.

Keywords: Caspase 3, Cleaved Caspase 3, Colorectal Cancer, Sparstolonin B, Tunel

S065

INVESTIGATION OF THE EFFECT OF MANGOSTIN FRUITS ON BLADDER CANCER CELL LINE

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Objectives: Mangostin (Clusiaceae plant family, *Garcinia mangostana* L.) is a tropical tree native to Southeast Asian countries. The nutritional value of the fruit of the tree is quite high due to the high fiber, vitamins, minerals, flavonoids, folate, tannin, saponin, anthocyanin and terpenes it contains. However, the main phytochemicals found in the species are xanthenes, which have many biological effects such as antibacterial, antifungal, antimalarial, antioxidant, proapoptotic, antiproliferative and anti-inflammatory. The anticancer effects of different types of xanthenes have been evaluated from different perspectives in many types of cancer. However, there is not enough information about bladder cancer. Therefore, the study aimed to determine the effect of α - and γ -mangostin on the 5637 cell line.

Methods: The cytotoxic effect of α -/ γ -mangostin on cell line was determined by the MTT method, the effect on reproductive viability was determined by co-

lony formation assays, and the effect on cell migration was determined by wound healing assays.

Results: IC₅₀ values of α -/ γ -mangostin were determined as 9.7 and 7.5 μ M, respectively. Colony formation assays showed that both α -/ γ -mangostin reduced colony formation in a dose-dependent manner. In wound healing assays, it was determined that α -mangostin decreased migration, while γ -mangostin had the opposite effect and increased migration.

Conclusions: The opposing effects of α - and γ -mangostin on cell migration suggest that the substances act through different molecular mechanisms. Therefore, it is necessary to elucidate the molecular mechanism by examining the gene expression differences responsible for migration and invasion processes.

Keywords: Bladder cancer, $\pm$ -mangostin, γ -mangostin, migration

S066

INVESTIGATION OF THE RELATIONSHIP BETWEEN TRYPTOPHAN METABOLISM AND PD1/PDL-1 SIGNALING PATHWAY IN NON-SMALL CELL LUNG CANCER TUMOR MICROENVIRONMENT

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Objectives: The immunosuppressive effect of tryptophan (TRP) metabolism has begun to be demonstrated in solid organ cancers, and while high IDO1 enzyme activity-related T cell regulation is disrupted, simultaneous high expression of PD-1 has been reported in the literature.

Methods: TRP metabolites plasma levels were determined by High Pressure Liquid Chromatography (HPLC), IDO1 and PDL-1 gene expressions qPCR method in 70 Non-Small Cell Lung Cancer (NSCLC) patients and 72 healthy controls. Statistical analyses were performed using chi-square for categorical variables and Mann Whitney U, t-test and Spearman Correlation for numerical variables in spss program (IBM; 28,0).

Results: TRP and kynurenine (KYN) levels were found to be lower in NSCLC group compared to control ($p < 0.001$; $p < 0.001$, respectively). In patients with NSCLC with advanced tumor stage, TRP levels were found to be lower than in patients with early tumor stage ($p = 0.025$), and KYN/TRP ratio was found to be higher in patients with advanced tumor stage compared to early tumor stage ($p = 0.025$; $p = 0.042$, respectively). Moderate-good positive correlation was found between TRP/IDO1 ($r = 0.559$; $p = 0.02$), and moderate-good positive correlation between PDL1/KYN ($r = 0.566$; $p = 0.018$).

Conclusions: It was determined that TRP can distinguish NSCLC from control with high specificity/sensitivity in ROC curve analysis results ($p > 0.001$). We think that TRP may be an independent risk factor for NSCLC.

Keywords: Tryptophan Metabolism, Tumor Micro-environment, IDO1, PDL1

S067

SALVIA CADMICA BOISS. VAR. CADMICA RESIN ON PROLIFERATION AND APOPTOSIS LEVELS IN HUMAN COLON CANCER CELL LINE

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Objectives: Colon cancer is the third most common cancer in the world. A particularly rich source of phenolic compounds is the family Lamiaceae and its largest genus *Salvia* L. This genus contains about 1000 species distributed worldwide, providing a range of herbal substances used as medicines, dietary supplements, food additives and even as cosmetic and perfume ingredients. The aim of this study was to investigate the in vitro anticancer activity of *S. cadmica* bois. var. *cadmica* ethanol extract on HT-29 and HEK-293 cell lines.

Methods: *S. cadmica* boiss. var. c., which we used in our study, was collected from Konya province, ethanol extract was obtained and applied to HT-29 and HEK-293 cells. 8 different doses in the concentration range of 500- 1200 µg/ml were applied and proliferation analysis was performed by MTT method. Apoptosis analysis was performed on Cytoflex device.

Results: IC₅₀ dose of HT-29 cell line was calculated with the help of % cell viability/concentration graph and IC₅₀: 1188.77 µg/ml was found at 48 hours. The determined IC₅₀ dose was applied to HEK-293 cells and the viabilities at 24 hours and 48 hours were 95.86% and 85.73%, respectively. The IC₅₀ dose obtained for *S. cadmica* boiss. var. c. ethanol extract was applied to the cells for apoptosis analysis and HT 29 cells went to early apoptosis by 35.19% and late apoptosis by 22.27%.

Conclusions: Our study provides evidence that the ethanol extract of *S. cadmica* boiss. var. *cadmica* shows promise as a cytotoxic and pro-apoptotic agent against colon cancer cells.

Keywords: Colon cancer, Apoptosis, Proliferation, *Salvia Cadmica* Boiss Var *Cadmica*

S068

THE PROTECTIVE EFFECTS OF MORIN OR TARAXASTEROL AGAINST THE CYTOTOXIC EFFECTS OF CISPLATIN/DOXORUBICIN IN MOUSE GC-1 SPERMATOGONIA CELLS

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Objectives: Chemotherapeutic compounds which are used against several cancer types can affect male fertility. This study was designed to determine the protective effects of morin or taraxasterol on cisplatin/doxorubicin (DOX)-induced cytotoxicity in mouse GC-1 spermatogonia (spg) cells.

Methods: GC-1 spg cells were treated with different concentrations of morin (12.5–200 μ M) and taraxasterol (40–200 μ M), and then exposed to cisplatin (10 μ g/mL) and DOX (0.5 μ g/mL). Cell viability and cell cycle analysis were performed by MTT assay and flow cytometry using propidium iodide.

Results: Morin or taraxasterol at all concentrations had no cytotoxicity on GC-1 spg cells. Treatment with cisplatin between 0.1–10 μ g/mL or DOX between 0.075–0.5 μ g/mL decreased cell viability of GC-1 spg for 24h. Pretreatment with 200 μ M morin followed by cisplatin or DOX-treatment for 24h offered significant increase in cell viability compared to cisplatin and DOX treatment alone. Based on these results, morin demonstrated a greater effect on inhibition of chemotherapy-induced cytotoxicity compared to taraxasterol. 10 μ g/mL cisplatin and 0.5 μ g/mL DOX alone led to a significant decrease in the G1 phase of the cell cycle compared to control cells,

which was accompanied with the increase at sub-G1 population. Whereas GC-1 spg cells pretreated with morin or taraxasterol significantly reduced cisplatin or DOX-induced sub-G1 apoptosis.

Conclusions: Morin significantly decreased chemotherapy-induced cytotoxic effects. Cisplatin or DOX treatment caused an increase in sub-G1 cell population, which was reduced by morin or taraxasterol pretreatment. Morin or taraxasterol might protect GC-1 spg cells from the side effects of cisplatin/DOX.

Keywords: Morin, GC-1 spg cells, chemotherapeutic agents, taraxasterol

S069

THE IMPACT OF THE VITAMIN D AND RESVERATROL ADMINISTRATION T2DM RAT AORTA TRACE ELEMENT AND MINERAL LEVELS

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Objectives: In this study, our aim is to fill this critical gap in knowledge by investigating the potential synergistic and individual effects of Vit D and resveratrol on T2DM-related aortic health

Methods: Animals were divided into eight, each group having seven animals, as follows: the healthy control group, a healthy group treated with resveratrol, the healthy group treated with Vit D, healthy group treated with resveratrol and Vit D, diabetic group, diabetic group treated with resveratrol, diabetic group treated with Vit D and diabetic group treated with resveratrol and Vit D. After microwave digestion, aorta samples were diluted to 1/10 in the ultrapure water. Diabetic animals were administered with 10% fructose-supplied drinking water for three weeks and resveratrol (1 mg/kg/day, by i.p. injection) and VitD (170 IU/week, oral route) alone or in combination (resveratrol 1 mg/kg/day, i.p. + VitD 170 IU/week, oral) was administered to the rats

in the treatment groups for four weeks. At the end of 9 weeks, all rats were sacrificed. Then trace elements and minerals levels including Ag, Al, As, Ba, Be, Ca, Cd, Co, Cr, Cs, Cu, Fe, Ga, K, Li, Mg, Mn, Na, Ni, Pb, Rb, Se, Sr, Tl, U, V, and Zn were investigated in all aorta samples via ICP-MS following acidic digestion.

Results and Conclusions: We have found that there are very important differences between the groups in Na, Se, Zn, Fe, Rb, Sr, and Cu levels compared to the untreated healthy control rats.

Keywords: trace elements, minerals, Vitamin D

S071

INVESTIGATION OF NEUROTROPHIN LEVELS IN MULTIPAROUS WOMEN WITH STRESS URINARY INCONTINENCE

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Objectives: The aim of the study is to investigate serum neurotrophin (NT) levels to understand how those molecules were changed in premenopausal multiparous women who suffer from stress-related urinary incontinence namely stress urinary incontinence (SUI) and mixed urinary incontinence (MUI). Diagnostic and distinguishing capabilities of the NTs for those disorders is also evaluated in the study.

Methods: Pre-menopausal multiparous women underwent a urodynamic examination, stress cough test and ICIQ-SF questionnaire. Participants have divided into three groups: a control group of healthy women and two patient groups of women diagnosed with SUI

and MUI. Their venous blood was taken, and serum NTs were measured by ELISA. The data obtained from patients were compared between groups. ROC analysis was performed to determine the role of NTs in diagnosing urinary incontinence.

Results: The result showed that the serum NGF and NT-3 levels in both incontinence subtypes are significantly low compared to the control. BMI score and number of VD are higher in incontinence subtypes compared to control, and ICIQ-SF score is more elevated in MUI compared to SUI.

Conclusions: The differences in serum NT levels were observed in pre-menopausal multiparous patients with urinary incontinence. Serum NGF levels in MUI patients and serum NT-3 levels in SUI patients tend to be decreased. Although the significance in serum levels change of NGF and NT-3, their discriminatory potential was weak or moderate.

Keywords: Mixed urinary incontinence, multiparous, neurotrophin, pre-menopause, stress urinary incontinence

S072

EFFECTS OF VANILLIC ACID ON ACETAMINOPHEN-INDUCED ENDOPLASMIC RETICULUM STRESS, AUTOPHAGY AND CYTOTOXICITY IN AML12 CELLS

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Objectives: This study aimed to investigate the effects of vanillic acid on acetaminophen-induced endoplasmic reticulum stress, autophagy, and cytotoxicity in the AML12 mouse hepatocyte cell line.

Methods: Firstly, the effect of vanillic acid on cell viability in AML12 cells was investigated by treating cells with 0-500 µM vanillic acid concentrations for 24 hours. Secondly, cells were treated with 5, 50, and 500 µM vanillic acid together with 10 mM acetaminophen for 24 hours. Then cell viability was determined by 3-(4,5-Dimethyl-2-thiazolyl)-2,5-diphenyl-2H-tetrazolium bromide (MTT) assay, endoplasmic stress marker activating transcription factor 4 (ATF4) and autophagy marker microtubule-associated proteins 1A/1B light chain 3B-II (LC3B-II) were measured by western blot.

Results: Vanillic acid concentrations treated up to 500 µM concentration had no significant effect on cell viability of AML12 cells. 10 mM acetaminophen caused a significant increase in ATF4 and LC3B-II levels and cytotoxicity. All vanillic acid concentrations caused a significant increase in cell viability in acetaminophen-treated cells. 50 and 500 µM vanillic acid caused a significant decrease in ATF4 and LC3B-II levels in acetaminophen-treated cells.

Conclusions: Our study showed that vanillic acid decreases acetaminophen-induced endoplasmic reticulum stress, autophagy and cytotoxicity in AML12 cells.

Keywords: Acetaminophen, Vanillic acid, Endoplasmic

reticulum stress, Autophagy, Hepatotoxicity

S073

COMPOSITIONAL AND FUNCTIONAL DIVERSITY OF COLON MICROBIOTA IN PATIENTS WITH INFLAMMATORY BOWEL DISEASE

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Objectives: Although there is an uncertain relationship between inflammatory bowel disease (IBD) and colorectal cancer, previous studies have suggested that specific changes in the colon microbiota may be associated with these diseases. Therefore, we aimed to reveal the compositional and functional microbial diversity in IBD and evaluate the potential of specific changes in the microbiota as a potential disease biomarker.

Methods: Colon biopsies of 10 IBD patients and 18 healthy subjects were included in this work. The composition of colon microbiota was profiled by sequencing the V3-V4 region of the 16S rRNA gene and the V9 region of the 18S rRNA gene. Bioinformatic and statistical analyses were done by using R. Then, functional annotation was done using FAPROTAX dataset based on the 16S data.

Results: Our analysis revealed compositional diversity of colon microbiota in IBD biopsies which was different than in healthy tissues ($P = 0.001$ for prokaryotes and $P = 0.001$ for eukaryotes). We found the abundance of *Pseudomonas* genus was significantly high in IBD biopsies (13.2% vs. 0.6%). Additionally, *Malasseziales* was revealed as the most abundant fungal clade in IBD biopsies (68.1%), especially in ulcerative colitis (76.5%).

In addition, our analysis showed that only two functions were significantly different between IBD subtypes based on the predicted functions ($P < 0.001$): acetoclastic methanogenesis and sulfur respiration.

Conclusions: By contributing to the known diversity of colon microbiota in patients with IBD, this work may provide a basis for future studies that evaluate the potential marker taxa for early diagnosis of IBD and colon cancer.

Keywords: Crohns disease, Ulcreative colitis, Colon cancer, Amplicon sequencing, Next-generation sequencing, Biomarker, Microbiome

S074

EVALUATING THE BACTERIAL DNA LOAD IN BLOOD AS A POTENTIAL COLORECTAL CANCER BIOMARKER

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Objectives: Since colorectal cancer is a global threat with its high rates of incidence and mortality, it is a subject of special interest in cancer biomarker studies. Although there is several non-invasive biomarkers commonly applied for colorectal cancers (such as the fecal occult blood test), the search for better biomarkers with higher sensitivity and reliability is going on. Regarding this, our work aimed to compare the bacterial DNA load in blood in colon cancer patients versus healthy individuals and evaluate its potential as a tumor biomarker.

Methods: The peripheral blood samples obtained from 12 patients with colorectal cancer and 18 healthy individuals were included in this work. Quantitative Real-time polymerase chain reaction was performed using pan-bacterial primers which target the V3-V4 hypervariable regions of the bacterial 16S rRNA gene with high specificity and sensitivity. The analysis was performed in triplicate and normalized to the *E. coli* DNA standard. Results were calculated as the number of copies of the 16S rRNA gene per μL of blood.

Results: Based on the calculations for 16S rRNA gene copies, we found colorectal cancer patients have five times more bacterial load in their blood compared to healthy individuals (in average 778545 vs. 146270 copies per μL), and this result was statistically significant ($p < 0.1$).

Conclusions: Our results support the relationship between the leaky gut and colorectal cancer and may suggest that bacterial DNA load in the bloodstream may serve as a non-invasive biomarker for dysbiosis and tumor diagnosis.

Keywords: Colorectal cancer, qPCR, 16S rRNA, biomarker, bacteria

S075

DETERMINATION THE EFFECT OF BIOCHANIN A ON T98G CELLS THROUGH THE CHANGE OF INTRACELLULAR CALCIUM LEVEL

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Objectives: Glioblastoma is one of the most aggressive tumor among the brain tumors. Due to the negative effects of classical chemo/radiotherapy, new studies have been focused on flavonoids which are natural dietary compounds. Flavonoids can show their anti-carcinogenic effects in many ways and some of them either reducing or inducing Endoplasmic reticulum (ER) stress in the cell. Change of intracellular calcium level can effect ER stress. We aimed to understand whether Biochanin A which is a flavonoid shows its effect on T98G cells via changing intracellular calcium level.

Methods: T98G cells were treated with 50 and 100 μM Biochanin A for 24 and 48 hours, separately. Then, intracellular calcium levels were measured with Fluo-8 Calcium Flux assay kit. Fluorescence data were analyzed to determine the change of intracellular calcium level. This study was supported by Hacettepe University (Project no: FHD-2022-19959).

Results: Agonist-induced maximum calcium response of T98G cells was determined by stimulation with carbachol. Intracellular calcium levels of T98G cells after treatment with Biochanin A were compared to maximum calcium level. T98G cells did not show any significant change in terms of intracellular calcium level.

Conclusions: Understanding effects of dietary compounds on ER stress in cancer cells is important since these compounds can be targeted in an appropriate way to develop a treatment. Biochanin A did not show its effects on T98G cells through inducing ER stress. However, it can somehow reduce carcinogenic effect of tumors which is already known information. Therefore, reasearch about this mechanism can provide valuable knowledge to developing new treatment strategies.

Keywords: Biochanin A, T98G, intracellular calcium level, ER stress

S076

PROTEOMIC INVESTIGATION OF THE EFFECTS OF DINUTUXIMAB BETA IN INSULINOMA INS-1 CELLS

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Objectives: Insulinoma is a tumor originating from pancreatic beta cells. Dinutuximab beta (DB) is a monoclonal antibody used for the treatment of high-risk neuroblastoma. The study aimed to investigate the changing protein profiles after DB application to Insulinoma INS-1 cells.

Methods: 4 experimental groups were formed. DB for 1. group, DB solver for 2. group, STZ and DB for 3. Group, the solvers of 3. group for 4. group were applied. Protein profiles were analyzed using Thermo Scientific nano LC- Dionex Ultimate 3000 RSL & Q-Exactive quadrupole Orbitrap mass spectrometer (MS/MS). UBE2L6, PSMA4, TSMB10, ARF1, UBE2V2, ERP29, NUDCD2, and ARF3 proteins that showed fold increase or decrease as a result of evaluation were validated with Simple Wes.

Results: There is a high number of proteins that are common among proteins or specific only to that group. Only down-regulated proteins were observed when the 1st and 2nd Groups were compared. When groups 3 and 4 were compared, both up-and down-regulated proteins were observed. Many signaling pathways have been shown, in which the protein ubiquitination pathway is dominant. Proteins associated with cancer and gastrointestinal diseases, cell death and survival, cell-cell signaling and interactions, and tissue development have been identified.

Conclusions: In line with the identified and validated proteins, proteins that cause cell death or proliferation were found in the pancreatic tumor of DB. The administration of relevant proteins to pancreatic tumor cells may be important for tumor and cancer therapy. The study will be supported by in vivo experiments.

Keywords: Dinutuximab beta, Insulinoma INS-1 cells, Proteomic, Cancer therapy

S077

THE EFFECT OF TRANSURETHRAL RESECTION AND BCG THERAPY ON CYTOKINE LEVELS IN NON-MUSCLE INVASIVE BLADDER CANCER

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Objectives: The present study investigated the effect of treatment on interleukin (IL)-1, IL-6, IL-8, and neopterin levels in patients with non-muscle invasive bladder cancer (NMIBC).

Methods:: Thirty patients with NMIBC and 30 age-matched controls were included in the study. Preoperative, postoperative first control [at two weeks after second transurethral resection of bladder tumor (TURBT)] and the second control (at the end of intravesical immunotherapy) blood samples were analyzed using ELISA to determine IL-1, IL-6, IL-8, and neopterin levels. The mean cytokine levels of the patients were statistically compared and comparing the patients' and controls' levels.

Results: There were no statistically significant differences between the mean IL-1, IL-6, IL-8, and neopterin levels of the patient and control groups before initial TURBT. In the patient group, there were no statistically significant differences in the IL-6 and IL-8 levels after both TURBT and intravesical Bacillus Calmette-Guérin (BCG) therapy. The mean of preoperative IL-1 and neopterin levels significantly decreased after TURBT ($p < 0.05$). However, this reduction does not continue after intravesical BCG instillation.

Conclusions: The findings of this study showed that the IL-1, IL-6, IL-8, and neopterin levels of the patients with NMIBC were similar to the levels of healthy controls. IL-1 and neopterin levels significantly decreased after TURBT. But these reduction did not continue after intravesical BCG instillation. These findings demonstrate that IL-1 and neopterin levels decrease after TURBT due to the reduction in tumor weight or tumor removal.

Keywords: Bladder cancer, neopterin, IL-8, IL-1, IL-6

S078

6-HYDROXY-L-NICOTINE ACTS AGAINST AMYLOID BETA 1-42 AGGREGATION IN HUMAN CANCER CELLS

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Objectives: 6-hydroxy-L-nicotine (6HLN) is a nicotinic derivative from the nicotine metabolism within *Paenarthrobacter nicotinovorans* that possess cognitive-improving abilities and antioxidant properties, eluding the side-effects of nicotine, the parent molecule. This study aims to elucidate the capacity of 6HLN to fight against amyloid beta (A β) 1-42 aggregation and reduce its toxicity in human cancer cells.

Methods:: Lung cancer cell line A549 and breast cancer cells MCF-7 were used in this study. The effects of cell growth medium supplemented by cell growth factors on A β 1-42 aggregation were investigated. Moreover, the effects of 6HLN on intracellular A β 1-42 aggregation and mitochondrial activity of cell lines such as A549 (human lung cancer (adenocarcinomic alveolar basal epithelial tumor)) and MCF-7 (human breast cancer (invasive breast ductal carcinoma)) were investigated.

Results: 6HLN fight against aggregation of A β 1-42 used in the monomeric state and the disaggregation process of A β 1-42 used in the fibrillar state in human cancer cells and showed inhibitory effects on mitochondrial activity against A β 1-42-induced decreased of human cancer cell viability.

Conclusions: 6HLN could be considered a promising protective compound that could reduce A β 1-42-induced toxicity.

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Keywords: 6-hydroxy-L-nicotine, amyloid beta 1-42, cancer cells, aggregation, toxicity

S079

INDUCTION OF APOPTOTIC CELL DEATH IN HUMAN LUNG CANCER CELLS THROUGH ENHANCED OXIDATIVE STRESS CAUSED BY RUBUS TERETICAULIS LEAVES EXTRACTS

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Objectives: Since the conventional methods used in lung cancer treatment are insufficient, the search for alternative treatments continues. The aim of this study was to investigate for the first time the antiproliferative and apoptotic effects of the active ethanol (RTE) and chloroform (RTC) extracts of *Rubus tereticaulis* leaves in A549 lung cancer cell line.

Methods: Non-small cell lung cancer cell line, A549, was treated with RTE and RTC individually. Cytotoxic effects of RTE and RTC were quantitatively detected by 3-(4,5-dimethyl-2-thiazolyl)-2,5-diphenyltetrazolium bromide (MTT) assay. Cellular ROS production was analyzed by using the fluorescent signal indicator 2.7 dichlorodihydrofluorescein diacetate (H2DCF-DA). Apoptosis was evaluated by fluorescence microscope after AO/EB staining and flow cytometry after Annexin V and PI staining.

Results: Both RTE and RTC induced cytotoxicity in A549 cells in a dose-dependent manner, which was accompanied with induction of reactive oxygen species (ROS) accumulation. The dead cells and apoptotic cells showed typical apoptotic morphologies. Both early apoptotic and late apoptotic cells detected by flow cytometry were increased in RTE and RTC treated cells. In addition, results showed that RTC has higher anti-proliferative, ROS generation and apoptotic effect than RTE. Therefore, the polarity of the solvent used to exert the anti-cancer effect of *Rubus*

tereticaulis leaves is crucial.

Conclusions: These results suggest that *Rubus tereticaulis* leaves has an anti-cancer effect to lung cancer cells through ROS-mediated apoptosis, and RTC could be an effective therapeutic or adjuvant strategy in cancer treatment.

Keywords: Lung cancer, anti-cancer effect, oxidative stress, *Rubus tereticaulis*, apoptosis

S080

Pllans-II: A PROMISING PROTOTYPE FOR TARGETED THERAPY IN CERVICAL CANCER

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Since chemotherapy treatments against cervical cancer adversely affect the patient's life quality, new molecules with antitumor potential and few side effects are required.

Objectives: We proposed to evaluate the *Pllans-II* antitumoral activity, a phospholipase A₂ from *Porthidium lansbergii lansbergii* snake venom against cervical cancer cells, the protein's safety on healthy mice and the cytotoxic effect of the recombinant version-*rPllans-II*.

Methods: We evaluated *Pllans-II* antitumoral and antimetastatic effect against two cervical cancer cell lines - CaSki and HeLa - and determined the biochemical pathways affected by transcriptomic analysis. Besides, we verified the *Pllans-II* innocuous in healthy mice by intraperitoneal injection. Finally, we produced *rPllans-II* using *E. coli* BL21 (DE3) and evaluated the cytotoxicity effect by *in vitro* test.

Results: *Pllans-II* displayed cytotoxic, antiproliferative, anti-migratory, and antiadhesive effects against both cancer cell lines. The *Pllans-II* apoptotic effect in CaSki cells was related to the inability to resolve endoplasmic reticulum stress induced by sub-expression of genes such as PERK, ERO1, PDIs, HSP70, and CHOP. HeLa cell death

was associated with the junction blockage between $\alpha_5\beta_1$ integrins and fibronectin of the extracellular matrix. Additionally, *Pllans-II* was harmless in mice, evidenced by no hemorrhagic effect nor liver and kidney histological alteration, including no change in pro-inflammatory and liver damage markers. Finally, *rPllans-II* showed cytotoxic activity against both tumoral cervical cell lines.

Conclusions: The selective *Pllans-II* antitumor effects against cervical carcinoma cells suggest that it could be considered a promising prototype for therapy against cervical cancer.

Keywords: Bioprospecting, Snake venom, PLA2, Recombinant protein, Transcriptomic analysis, Antitumoral effect

S081

CYTOTOXIC EFFECT OF NEWLY SYNTHESIZED BENZIMIDAZOLE DERIVATIVES ON LUNG AND BREAST CANCER CELL LINE

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Objectives: Compounds with benzimidazole structure are important heterocyclic compounds used as drug active ingredients. The benzimidazole ring has a kind of privileged skeletal structure from which many important drugs used in different therapeutic fields are obtained. Benzimidazole-based heterocyclic compounds have a very important place in chemistry due to their different biological activity properties such as anticancer, antihypertensive, antibacterial, anthelmintic, antiviral, antidiabetic, antifungal, antihistaminic, antidiabetic, antiulcer, antituberculosis, antiepileptic, analgesic, antioxidant and anti-inflammatory. In this study, it is aimed to investigate the cytotoxic effect of a newly synthesized

series of benzimidazole derivatives on lung cancer cell line (A549) and breast cancer cell line (MCF-7). MTT test at 5 different concentrations was used to evaluate cytotoxic effects.

Methods: In MTT analysis, A549 and MCF-7 cells were seeded into 96-well plates. Increasing concentrations of benzimidazole derivative compounds were applied to the manipulated cells; It was treated for 24 and 48 hours. 10 uL of MTT solution (5 mg/mL in PBS) was added to each well and incubated for 4 hours at 37°C in a CO₂ incubator. Cell proliferation values were calculated with an ELISA reader at a wavelength of 570 nm.

Results: Compound number 14 had an IC₅₀ = 159.2 µg/mL. It was determined that it showed cytotoxic effects against MCF-7 cells with an IC₅₀ >100 µg/mL.

Conclusions: This remarkable selective cytotoxic effect of compound number 14 on the MCF-7 cancer cell line prompts further studies to reveal the effects of this substance at the cellular level, especially the mechanisms responsible for the inhibition of cell viability.

Keywords: cancer, benzimidazole, cytotoxicity, A549, MCF-7

S082

METABOLOMIC PROFILING IN DISTINCT TYPES OF LEUKEMIA

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Objectives: This study was conducted to reveal phenotypic footprints of acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL) and non-Hodgkin lymphoma (HL) patients identifying affected metabolites and their pathway-related implications.

Methods: For the global serum metabolome profiling, quantitative ¹H nuclear magnetic resonance spectroscopy (NMR) and untargeted high-resolution liquid chromatography mass spectrometry (HRMS) methods were applied. 2D NMR analyses were performed to validate metabolite annotations. Leukocyte isolates were examined with the HRMS platform under equal conditions to identify differentially expressed metabolites.

Results: The metabolome results revealed significantly altered amino acids with their catabolism products, TCA cycle intermediates and phospholipids while the leukocyte isolates showed elevated levels of long-chain fatty acids and acylcarnitines with low biotin levels. Group-based changes indicated glucogenic and branched-chain amino acids with choline oxidation pathway metabolites were affected in AML while fumarate was found most differential in CLL and NHL. Commonly increased metabolites produced in protein degradation pathways as methyl guanidine, urea and creatinine were recorded. Serum LCMS analysis showed the purine metabolism as the most affected pathway in all groups. Leukocyte isolates exhibited differential levels of spermine, long-chain fatty acids, acylcarnitines and coenzymes among groups.

Conclusions: Complementary use of NMR-MS methodologies expanding the metabolite spectrum in both matrixes allowed comprehensive profiling of leukemia patients. The current findings eliciting group-based changes provide essential tips about pathogenetic mechanisms commonly observed in distinct subclasses along with individual driving forces. Yet, emerging results need to be validated with wider cohorts and omics information for each patient within the frame of personalized medicine approach.

Keywords: acute leukemia, chronic lymphoma, metabolomics, nuclear magnetic resonance, mass spectrometry

S083

INVESTIGATION OF SERUM TRYPTOPHAN AND KYNURENINE METABOLITES IN BREAST CANCER PATIENTS

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Objectives: Breast cancer is one of the most common cancers in women around the world. Tryptophan (Trp) and its metabolites play an important role in a variety of physiological processes, but also play an important role in cancer by promoting tumor progression. Trp degradation in cancer patients is primarily mediated by increased activities of tryptophan 2,3 dioxygenase (TDO) and indoleamine 2,3 dioxygenase 1 (IDO1). Stimulation of IDO1 and Trp degradation leads to the accumulation of Trp metabolites such as kynurenines. The aim of this study is investigating the differences in serum tryptophan levels and kynurenine metabolites between patients with breast cancer and the control group.

Methods: 50 breast cancer patients and 50 control subjects were included in this study. Trp and its metabolites were analyzed by LC-MS/MS. Statistical analysis was performed using IBM SPSS Statistics 21.0.

Results: Our results showed that serum kynurenine levels [286.5 (139.5-695.0) ng/ml vs. 232.5 (109.5-418.0) ng/ml, p=0.019] were statistically significantly higher and tryptophan/kynurenine ratio [87.5 (13.2-207.1) vs. 114.7 (33.1-246.0), p=0.011] was statistically significantly lower in patients with breast cancer compared to the control group. Serum levels of tryptophan (p=0.751), kynurenic acid (p=0.677), 3-hydroxykynurenine (p=0.094), and 3-hydroxyanthranilic acid (p=0.254) in the control group were similar to those in the breast cancer group.

Conclusions: Our results show that there is an irregularity in the concentration of metabolites of the

kynurenine pathway in patients with breast cancer. Particularly elevated kynurenine levels were found in breast cancer patients. However, our results indicate that further studies with a larger patient population on this topic are needed.

Keywords: Tryptophan, Kynurenine, Breast cancer

S084

INVESTIGATION OF THE IN VITRO AND IN VIVO EFFECTS OF TELOMERE-TARGETED NEW DRUG CANDIDATE COMPOUNDS IN DIFFERENT CANCER CELL LINES

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Objectives: Telomerase-inhibiting therapies may have side effects due to varied cancer telomere lengths. Hence, there is a need for different molecules targeting cancer telomeres regardless of their length. A new phosphatidyl nucleoside conjugated molecule (L6) demonstrated lower IC₅₀ value in various cell lines compared to 6-thio-dG (THIO). Based on in vitro evaluations, we have selected HT29 colon cancer cell line for further mechanism of action and anticancer efficacy studies with L6.

Methods: For in vitro TIF assay, cells were plated in 24-well plates, treated with 1 μ M of 6-thio-dG (THIO), L6, MAIA-2022-013 and Ribo-thio for 96 hours. Cells were blocked with 5% BSA, incubated with g-H2AX and telomere probe. For in vivo xenograft model, 2x10⁶ HT29 cells were injected into CD1 nude mice flanks. Mice received L6 treatment with 3mg/kg and 6mg/kg doses twice a week for three weeks. For in vivo syngeneic model, 2x10⁶ CT26 cells were injected into BALB/c mice flanks. Mice were treated with L6, 3mg/kg twice a week for two weeks, with a two-day interval between administrations.

Results: Telomere Damage Induced Foci (TIF) method revealed significant telomeric DNA damage differences induced by L6 molecule in comparison with both the PBS control group and 6-thio-dG. In xenograft model, L6 dose was 3mg/kg with a treatment frequency of 4 times per week. Syngeneic model findings have demonstrated that L6 induces tumor regression, enhances survival, and elicits altered Treg and CD8⁺ cell counts.

Conclusions: Our promising findings may inform the development of enhanced and safer cancer therapeutics through clinical applications.

Keywords: Cancer, Telomere, Telomerase, TIF Assay, In vivo models

S085

THE EFFECT OF AUTOVERIFICATION ON TURNAROUND TIME FOR CLINICAL CHEMISTRY AND IMMUNOASSAY TESTS

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Objectives: Auto verification (AV) is an important tool for developing quality processes in clinical laboratories. In this study, it was aimed to evaluate the effect of the AV system used in our laboratory for clinical chemistry and immune analysis tests on turnaround time (TAT).

Methods: The study was conducted in Çanakkale Onsekiz Mart University Hospital Medical Biochemistry Laboratory. In our laboratory, where MIA-Med (MIA Technology, Turkey) laboratory information system was used, 35 biochemistry tests were analyzed on the cobas c702 autoanalyzer (Roche Diagnostics, Germany), and 29 immune analysis tests analyzed on the cobas e602 immune analyzer (Roche Diagnostics, Germany) were autoverified by the middleware program (cobas infinity, Roche Diagnostics, Germany). After validation lasted about six months, AV was first started on 06.02.2023 and completed on 18.05.2023 for all the indicated tests. The data of the tests performed for one month before and after AV were obtained from the laboratory information system. The rates of tests exceeding TAT were calculated, and a comparison was made between the groups before and after AV.

Results: 71% of tests and 21% of tubes based results were autoverified. TAT after AV was improved by 6 minutes for emergency tests and 12 minutes for routine tests. While 6.4% of the results before the AV exceeded the TAT, 5.8% of the results after the AV exceeded the TAT ($p < 0.001$).

Conclusions: AV contributes positively to the total testing process. With well-defined and validated rules, AV makes tests more reliable and results faster.

Keywords: autoverification, turnaround time

S086

DETERMINATION OF SIX SIGMA LEVEL OF SAMPLE REJECTION REASONS IN PUBLIC HEALTH LABORATORY IN A SIX MOUNTH PERIOD IN ANKARA

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Objectives: Ankara Provincial Health Directorate Public Health Laboratory, collects blood and urine samples from various departments of all across the city.This aboratory works with 1 an

integrated system.Thousands of samples from 5 different tube groups are collected every day (biochemistry, complete blood count, hbA1c, thalassemia and urine analysis). Our study was carried out to evaluate the rate and reasons for such rejections by the quality indicators and six sigma process, to determine the acceptability of the rejection reasons by improving the accuracy of the results and lowering pre-analytical errors.

Methods: The data were obtained from the laboratory information management system (LIS). The rejection reasons were grouped according to the sample types. The defects per million opportunities (DPMO) and six sigma levels were calculated.

Results: This cross-sectional comparative study was performed on 2048403 laboratory sample in a six mounth period in terms of the percentage and type of errors that occurred in Public Health Laboratory,ANKARA in 2023. Out of 2048403 blood and urine samples 11280 samples were rejected (%0,55). The types of studied errors included insufficient sample size (%51), hemolysis (%32), sample clotting (%12), and mistakes in centrifuge(%3).

Conclusions: In this study, the frequency of sample rejection on every department was found to be acceptable. To increase the overall quality of laboratory management by increasing the Sigma values; we think that clinical and cause based analysis of error rates should be done regularly.

Keywords: preanalytical error, sample rejection reasons, six sigma

S087

EVALUATION OF 25-HYDROXY VITAMIN D3 TEST REQUESTS IN THE CONTEXT OF RATIONAL LABORATORY PRACTICES

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Objectives: Unnecessary laboratory test requests place a significant workload and financial burden on the health system. This study aims to retrospectively analyze the 25-OH vitamin D₃ test requests from various medical departments for redundancy and associated costs.

Methods: Data from the university hospital in Konya were analyzed. Since the hospital adopted rational laboratory practices in September 2018, 25-OH vitamin D₃ data were retrieved from the hospital database for the period from September 2016 to 2020. Data analysis was conducted using formulas within MS Office Excel. Frequency and percentage distributions were calculated based on the 25-OH vitamin D₃ test requests from different clinics. The costs of unnecessary tests were estimated based on the health services price list of the Social Security Institution Health Implementation Community.

Results: Between 2016-2018, there were 54,732 25-OH vitamin D₃ test requests, totaling 1,992,148 TL. Between 2018-2020, there were 83,901 25-OH vitamin D₃ test requests, amounting to 2,757,516 TL. Faulty test requests, which are the primary focus of this study, totaled 5,062 and cost 194,876 TL between 2016-2018. Between 2018-2020, they numbered 3,710 with a cost of 119,734 TL. Post-2018, there was a 27% reduction in the number of erroneous test requests and a 39% reduction in their associated costs.

Conclusions: Conducting more studies nationwide is crucial to mitigate the adverse impacts of unnecessary test requests on patients and to ascertain the genuine costs

Keywords: Unnecessary Test Requests Cost of Unnecessary Test Requests Retrospective Analysis

S089

CALCULATION OF MEASUREMENT UNCERTAINTY OF CARBAMAZEPIN AND VALPROIC ACID TESTS

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Objectives: The uncertainty of measurement is a statistical parameter which characterises the distribution of the values reasonably attributed to the measurand. Carbamazepine and valproic acid are antiepileptic drugs and monitoring of their blood levels are crucial in the clinical assesment of patients. In this study, we aimed to calculate the uncertainty of carbamazepine and valproic acid measurements in Balıkesir State Hospital.

Methods: Carbamazepine and valproic acid tests were measured in Roche Cobas 6000 autoanalyzer. The uncertainty of measurement was calculated according to the Nordtest guideline. Intra-laboratory reproducibility (uRw) was calculated from the internal quality control results of these tests at two different levels between 01.11.2022 and 01.04.2023. Uncertainty of measurement (U_{bias}) calculated from 6-month external quality control data. The combined standard uncertainty value was calculated using the standard uncertainty value. Expanded uncertainty was calculated at 95% confidence interval (CI), including all components of uncertainty.

Results: At the %95 CI, expanded uncertainty of measurement for carbamazepine and valproic acid were 11.08 and 8.08, respectively. Carbamazepine internal quality control CV% for level 1 and level 2 were 3.16% and 5.97%, respectively. Valproic acid internal quality control CV% for level 1 and level 2 were 4.48% and 5.30%, respectively. Carbamazepine uRw value was calculated as 2.39%, RMS_{bias} 4.97%, uC_{ref} 0.56%, u_{bias} 5.00%, uC 5.54%, U 11.08%. Valproic acid uRw value was calculated as 2.46%, RMS_{bias} 3.14%, uC_{ref} 0.60, u_{bias} 3.20, uC 4.04%, U 8.08%.

Conclusions: The uncertainty of measurement for both tests was lower than the total allowable error (20%) determined by CLIA and Rilibak. Reporting of measurements with uncertainty values are important for clinical decision, patient safety and reliability of our measurement results.

Keywords: Uncertainty of measurement, Carbamazepine, Valproic acid

S090

CAN REFERENCE CHANGE VALUES FOR BIOCHEMISTRY ANALYTES BE ESTIMATED FROM EXTERNAL QUALITY ASSESSMENT AND AVAILABLE BIOLOGICAL VARIATION DATA?

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Objectives: Patients receive healthcare services from different hospitals for various reasons. This limits the medical evaluation of consecutive test results from different laboratories because the autoanalyzers, reagents or methods used by laboratories may differ. Based on this limitation, we aimed to estimate the interlaboratory reference change value (IL-RCV) for biochemistry analytes (albumin, ALT, AST, amylase, total bilirubin, calcium, chloride, total cholesterol, CK, glucose, HDL-cholesterol, iron, LDH, lipase, magnesium, phosphate, potassium, total protein, sodium, triglyceride, urea and urate) from external quality assessment (EQA) and current biological variation (BV) data.

Methods:Data from 3 different monthly biochemistry EQA samples submitted by the RANDOX (RIQAS, England) in 2022 were analyzed and median CV_A was calculated for each analyte. Within-subject BV (CV_I) values were obtained from the EFLM database. Positive and negative IL-RCV were calculated with these data.

Results: CV_A values for albumin, amylase, calcium, chloride, creatinine, iron, LDH, lipase, magnesium, total protein and sodium were higher than their CV_I values. CV_A values of the other analytes were smaller than their CV_I values. The number of methods used in EQA was at least 7(chloride) and at most 21(amylase).

Conclusions: In BV studies, CV_I and CV_A values are calculated from healthy individuals with a single method. CV_A values used in our study were taken

from EQA and were obtained using more than one method. EQA samples differ from human serum and analyte concentrations in these samples may not be compatible with those in healthy individuals. Nevertheless, RCV values obtained from these data can guide the evaluation of consecutive interlaboratory test results.

Keywords: reference change value, external quality assessment, biological variation

S091

EVALUATION OF UNNECESSARY CK-MB(MASS) TEST REQUEST ACCORDING TO CHANGES IN CURRENT GUIDELINES

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Objectives: Unnecessary testing is a common preanalytical error. For diagnostic purposes of acute coroner syndrome (ACS), it is not recommended to routinely measure of CK-MB(mass) in 2020 ESC guidelines. The aim of this study was to evaluate test numbers of CK-MB(mass) and high-sensitivity cardiac troponin T (hs-cTnT) and the short- and long-term changes observed with corrective-preventive action (CPA).

Methods: As part of CPA, the CK-MB(mass) test was replaced from under the heading of 'cardiac biomarkers' to under the heading 'markers' on the physician screen in July 2021, the relevant units were informed and the search button with the parameter name was active. The total and combined number of CK-MB(mass) and hs-cTnT tests requested by clinic-polyclinic distributions were determined for the short (6-months) and long (18-months) periods before and after CPA.

Results: The number and rates of CK-MB and hs-cTnT tests before CPA were 2449,16570,14.8 for the short term and 7210,40271,17.9 for the long term, respectively. After CPA, the numbers and rates were 475,16986,2.8 for the short term and 1310,54032,2.42 for the long term, respectively. These differences were statistically significant ($p < 0.01$)

Conclusions: It was determined that CK-MB(mass) requests were reduced in a short and long time after CPA, and this was achieved by reduction of unnecessary request with hs-cTnT. This reduction is also important for economically. We believe that it is important for all units to follow current guidelines and order tests in accordance with these guidelines.

Keywords: Unnecessary Testing, CK-MBMASS

S092

CALCULATED TRANSFERRIN: IS IT NECESSARY TO CALCULATE NEW FORMULA AND NEW REFERENCE INTERVAL?

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Objectives: Transferrin is a parameter measured (TrfM) and calculated (TrfC) in medical laboratories, used in conjunction with other markers such as iron, total iron-binding capacity (TIBC), and ferritin to assess the body's iron status. The aim of this study is to develop a new formula for calculated transferrin and calculate a laboratory-specific reference interval.

Methods: A new transferrin formula was calculated using multiple linear regression for turbidimetrically measured transferrin (Roche c6000) (n=259). Data from individuals < 60 years (n=878) and > 60 years (n=273) were extracted from the Laboratory Information Management System (LIMS) based on our currently used formula (TrfC_{Old}). Reference intervals for TrfC_{Old} and newly calculated (TrfC_{New}) values were determined using the indirect method with the nonparametric percentile estimation method. Outliers were excluded using the Tukey method. The TrfH values obtained with the old and new formulas were evaluated against the reference intervals we used and newly calculated. Furthermore, TrfC_{Old} and TrfC_{New} values were compared with TrfM values, and the concordance of the results was assessed.

Results: For TrfC_{New}, the formula obtained was $0.008 \times \text{Iron } (\mu\text{g/dL}) + 0.007 \times \text{Total Iron-Binding Capacity } (\mu\text{g/dL}) + 0.071$. Reference intervals for TrfC_{Old} were <60 years: 1.95-3.15 g/L; >60 years: 1.68-3.32 g/L, while for TrfC_{New} they were <60 years: 2.12-3.30 g/L; >60 years: 1.85-3.40 g/L.

Conclusions: It is important for each laboratory to calculate its own formula for calculated parameters and establish and use laboratory-specific reference intervals for calculated parameters, as is the case for all parameters.

Keywords: Measured Transferrin, Calculated Transferrin, Multiple linear regression, Indirect reference interval calculation

S093

USE OF ARTIFICIAL INTELLIGENCE FOR REFERENCE INTERVAL CALCULATION IN THYROID FUNCTION TESTS: FUZZIFICATION OF TRANSITIONS AND GROUPING

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Objectives: In this study, it was aimed to determine the most optimal grouping in calculating the reference intervals(RIs) of TSH and fT4 tests and to fuzzify the transitions between groups with artificial intelligence applications.

Methods: In our study, TSH and fT4 test data from individuals aged ≥18 years, studied on the Roche Cobas 8000 e801 autoanalyzer (Roche Diagnostic, U.S.A.) between January 2019 and December 2021, were used. Patients with diagnoses thought to affect thyroid function tests were excluded from the study. After filtering, 9455 reference individuals (5958 women, 3497 men) with no missing data were identified as the reference sample group. Groupings were made using age, gender, TSH and fT4 results as criteria in the Kmeans algorithm.

Accordingly, the groups obtained are: Group-I: 18-26 years, Group-II: 27-34 years, Group-III: 35-42 years, Group-IV: 43-52 years, Group-V: 53-65 years, Group-VI: 66-94 years. We used the Tukey's method to eliminate outliers. RIs were determined using the non-parametric percentile method. With the Fuzzy C Means algorithm, the membership degree of each individual in the reference sample group was calculated according to the above groups and personalized RI were obtained. Age-specific RIs were calculated by taking the average of the reference values of individuals of that age. The results were compared with the RIs currently used in our laboratory.

Results: In the data, generally higher limits were obtained for TSH compared to the currently used RIs (Group-I: 0.82-5.11 μ IU/mL, Group-II: 0.82-4.54 μ IU/mL, Group-III: 0.69-4.55 μ IU/mL, Group-IV: 0.69-4.87 μ IU/mL, Group-V: 0.68-4.78 μ IU/mL, Group-VI: 0.60-5.93 μ IU/mL). For fT₄, while a single RI (0.93-1.7 ng/dL) is currently used, 6 different RIs were obtained (Group-I: 0.98-1.60 ng/dL, Group-II: 0.96-1.57 ng/dL, Group-III: 0.93-1.52 ng/dL, Group-IV: 0.91-1.53 ng/dL, Group-V: 0.92-1.56 ng/dL, Group-VI: 0.91-1.58 ng/dL). A 22-years-old individual's membership degrees in the 6 groups obtained by the Fuzzy C Means algorithm were 68%, 16%, 7%, 4%, 3% and 2%, respectively.

The RI for this individual was 0.80-4.98 μ IU/mL for TSH and 0.97-1.59 ng/dL for fT₄.

Conclusions: In our study, we concluded that with the fuzzification of transitions and grouping by machine learning applications, RIs could be more personalized and realistic calculated.

Keywords: machine learning, reference interval, thyroid function tests, fuzzification, artificial intelligence

S094

RELIABILITY OF PROTEIN ANALYSIS IN COMPLETE URINE ANALYSIS

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Objectives: Proteinuria is defined as excess urinary excretion of any type of protein. However, the most excreted protein fraction in urine is albumin. Albuminuria can also be seen in some physiological conditions. Albuminuria can also be an early sign of kidney dysfunction. Albumin is measured semiquantitatively in urine strips because it provides early information about renal function. However, if a loss of renal function is suspected, it should be confirmed by quantitative methods. In this study, we aimed to investigate whether the screening method for renal function is compatible with the gold standard method.

Methods: The study included the results of 3739 patients who complete urine analysis and protein analysis in 24-hour urine.

Results: According to the gold standard method, the positive predictive value of the screening test was 93% and the negative predictive value was 51%. The specificity and sensitivity of the screening test were 95.3% and 40.8%, respectively.

Conclusions: According to the study data, the results of the screening test can be considered successful in identifying patients. However, it could not exclude non-patient individuals sufficiently. The high rate of false positives may be due to physiologic protein-losing conditions or low sensitivity of the method used. Under these data, we think that patients with proteinuria detected as a result of complete urine analysis should be confirmed by protein and albumin analysis in 24-hour urine.

Keywords: Complete urine analysis, proteinuria, albumin

S095

THE EFFECT OF URINE PH VALUE ON URINE BIOCHEMICAL ANALYSES

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Objectives: Urine analyses provide information about renal and urinary system as well as systemic and metabolic disorders. Normally, urine pH is around 5-6. Urine pH increases as a result of urine storage and contamination by microorganisms. The exact impact of these pH changes on urine biochemical analyses is not fully understood. The aim of our study is to investigate whether pH changes have an effect on urine biochemical analyses.

Methods: A urine pool was created from 24-hour urine and spot urine samples in our laboratory. Urine pH was measured using pH indicator strips (mColorp-Hast). Urine pH was adjusted to 7, 8, 9, 10, and 11. Protein, albumin, creatinine, sodium, chloride, calcium (Ca), magnesium (Mg), phosphorus, glucose, urea, uric acid, and amylase levels in urine samples were analyzed using the Beckman Coulter AU5800 auto-analyzer.

Results: In the pH range of 7-11, there was no significant change in protein, albumin, creatinine, sodium, chloride, glucose, and uric acid levels. A pH variation ranging from 3% to 17% was observed for urea, Mg, and phosphorus. In the case of Ca there was a 26.4% decrease at pH 7, 8, and 9 compared to pH 6 and a 22.2% increase at pH 11 compared to pH 10.

Conclusions: Our study has shown that pH changes affect some urine biochemical analyses. Particularly, there was an average of 25% variation observed in urine calcium analysis, even when pH was not at extreme levels. To mitigate variability in urine calcium analyses, we recommend measuring pH before conducting the analysis.

Keywords: urine biochemistry, urine pH, urine calcium

S096

DETERMINATION OF POTENTIAL DRUG TYPES FOR NERVOUS SYSTEM DISEASES USING MULTI-TASK LEARNING TECHNIQUE

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Objectives: Drug design is a complex and time-consuming process that often takes many years. The CORINA Symphony tool was utilized to calculate 760 molecular features for each drug molecule in the dataset. In this study, the Clus-Multi-Task Learning (MTL) algorithm was applied to the nervous system (NS) drug dataset to determine NS disease groups (from N02, N03, N04, N05, and N06 groups). AD and WD were collected from Drugbank, the KEGG DRUG, and the PubChem databases.

Methods: 213 drugs, including both AD and WD, from different disease groups were classified using the Clus-Multi-task Learning (MTL) algorithm. In the tabular form of the dataset, each row represents a drug molecule, and each column indicates one of the 760 molecular descriptors. The last two columns denoted the class label corresponding to the withdrawn (WD) or approved (AD) status and the disease groups (multi-target classes) of NS drugs. MATLAB was used for data preprocessing. MTL was used to classify drugs by means of molecular descriptors.

Results: According to the results, MTL represented higher performance for the dataset. These results demonstrate that the classification model is suitable for both separation of ADs and WDs and determination of the NS disease groups. Accuracy rate (AR) was 0.82 for the dataset to determine NS disease groups and 0.95 for the dataset to classify NS drugs into approved and withdrawn categories.

Conclusions: The developed model can truly classify the test sets into both NS disease groups and NS approved and withdrawn categories.

Keywords: Drug Discovery, Multi-Task Learning, ToxPrint Chemotypes, Nervous System Drugs, Clus

S099

DEVELOPMENT OF A DRUG TO PREVENT MASTITIS PATHOLOGY THAT REDUCES MILK YIELD IN DAIRY COWS

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Objectives: Mastitis is the most common disease of dairy cattle and is an inflammation of the mammary tissue and milk glands. Neutrophils entering the tissue cause DNA release by NETosis mechanism. The aggregates and thrombotic aggregates formed by NETosis prevent the blood supply to the glands and the milk secreted from reaching the ducts, significantly reducing milk quality and milk yield. The mechanism depends on the catalytic activity of the protein PAD4 enzyme. Our aim was to inhibit the NETosis mechanism of neutrophils to prevent inflammation of mammary tissue in cattle.

Methods: We obtained our chemical libraries of molecules from selleckchem database. Our library, which we created using the DSV tool, consists of a combination of FDA approved chemicals and phytotherapeutic chemicals. We obtained the structure file of the PAD4 enzyme using structure prediction and validation tools. We obtained the amino acid sequence of *Bos taurus* using the NCBI database. The similarity ratio was calculated by pairwise alignment of the amino acid sequence with the human PAD4 enzyme. We predicted the structure of the PAD4 enzyme from *Bos taurus* using SwissModel. The accuracy of the model was ensured by the refinement module of the GalaxyWEB tool. The DSV program was used to analyze the binding of molecules to the catalytic site in the correct conformation.

Results: We detected “Diperpamide E, Guaijaverin and Luteolin-3’-D-glucuronide” molecules with ΔG° values less than -9. These 3 molecules, which we think are potential inhibitors, were found to bind to amino acids with catalytic functions.

Conclusions: The molecules were proven to inhibit the PAD4 enzyme using in-silico conditions.

Keywords: Bovine mastitis, NETosis, PAD4, In-silico, Milk yield

S100

INVESTIGATION OF RE1-SILENCING TRANSCRIPTION FACTOR-COREST REPRESSOR COMPLEX BY MOLECULAR MODELING

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Objectives: The REST/NRSF repressor constrains the expression of a considerable array of genes to neuronal tissues, effectively dampening their expression within non-neural contexts. In gene repression, certain auxiliary repressors such as CoREST and MeCP2 can remain bound to methyl CpG regions following NRSF-DNA dissociation, aiming to maintain low neuronal gene expression levels in specific cell types. REST has been recognized as a pivotal transcriptional controller, and its deviant expression has the potential to precipitate neurodegenerative disorders (NDs).

Methods: This study aimed to investigate the protein-protein interactions associated with neurological disorders and potential isoform structures of REST through the application of molecular modeling techniques. The Protein Data Bank (PDB) and AlphaFold databases were utilized to screen for structural isoforms of REST. Molecular docking analyses were conducted employing AutoDock Vina 1.2.2, while Molecular Dynamics (MD) simulations were carried out using AMBER20. Data analysis was performed using the xmgrace and VMD 1.9 software programs.

Results: Our findings illustrate the role of hydrogen bonds and electrostatic interactions in the interaction between REST and CoREST. These results hold the potential to aid in the identification of

therapeutic target regions for the treatment of neurological diseases.

Conclusions: Consequently, unraveling the intricacies of REST's mechanism holds promise for enhancing the efficacy of contemporary ND therapies. The majority of the computational calculations were conducted utilizing the resources provided by TUBITAK-ULAKBIM Truba, with additional support for this study being granted through Ege University Research Funds (BAP, Project No. 24211).

Keywords: RE1-Silencing Transcription Factor, co-REST, Molecular Modeling

S101

HOW MACHINE LEARNING READS CLINICAL FEATURES: A FOCUS ON A1c

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Objectives: In modern healthcare, machine learning (ML) is a potent tool for processing and interpreting vast clinical datasets, enhancing diagnostic and predictive capabilities. In this study, we aimed to optimize the performance of various ML algorithms by analyzing clinical laboratory data and assessing the algorithmic accuracy and the importance of feature selection for clinical predictions.

Methods: A total of 3.913 patient results, which include age, triglyceride, HDL-C, Vitamin B12, cholesterol, insulin, folate, urea, creatinine, CRP, hemoglobin, MCV, RDW, and glucose measurements, were included in the study. Two data sets were created with (WGDS) and without glucose (WOGDS) levels. Python programming language with Pycaret and Numpy libraries was used for ML model development. Fifteen different ML models were created for each of the two datasets. The best model was selected according to the accuracy of the cross-fold validation.

Results: Xgboost and LightGBM algorithms showed the highest accuracy for WGDS and WOGDS datasets, respectively. WGDS has slightly higher accuracy than WOGDS dataset for training and test sets (0.90 vs. 0.81 for training and 0.89 vs. 0.80 for test sets). Glucose had the highest feature importance, followed by age and MCV for WGDS. Age, triglyceride, and HDL-C were the most important features of WOGDS.

Conclusions: The study demonstrated the essential role of careful feature selection in affecting the performance of clinical laboratory-related predictive models. This highlights the necessity of careful feature selection and understanding dataset composition in clinical ML applications.

Keywords: machine learning, A1c, Feature importance, Model performance

S102

CAN CHATGPT BE A “RELIABLE FACILITATOR” IN THE PREPARATION OF A BIOCHEMISTRY LABORATORY TECHNICAL SPECIFICATION?

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Objectives: This study aims to assess whether ChatGPT can be a reliable facilitator in clinical biochemistry and specifically in tender preparation processes.

Methods: Questions about the “most commonly used measurement method,” “analyzers capable of performing the measurement,” and “evaluation of analyzers based on their speeds and features” for frequently analyzed tests in biochemistry laboratories, namely complete blood count(CBC), creatinine, TSH, and HbA1c, were asked to ChatGPT4.0 in Turkish. The responses received were evaluated based on whether they covered the most commonly included systems in tenders. Analyzers were queried for features like “cap piercing” for CBC,”sample loading capacity” for creatinine, “continuous random access” for TSH, and “Cation Exchange Chromatography” for HbA1c.

Results: The most commonly used measurement methods for all markers were entirely consistent with the literature. ChatGPT introduced the Sysmex, Beckman, Mindray, and Abbott systems for CBC, and the Roche, Abbott, Siemens, and Beckman systems for both creatinine and TSH among the top four. For HbA1c analysis, Bio-Rad, Tosoh, Arkray, and Menarini systems were at the forefront. When querying device speeds by brand and model, results consistent with the information provided by the manufacturers were obtained. Device features were evaluated, and the answers to the questions asked for creatinine, TSH, and HbA1c were consistent with the information provided by the manufacturers. However, even though the Cell-dyn Sapphire and Cell-dyn Emerald systems have the “cap piercing” feature, they were not mentioned in ChatGPT’s response.

Conclusions: ChatGPT is poised to be a “reliable facilitator” in the initial phase of laboratory tender processes, which is the preparation of technical specifications, even if not perfectly so at present.

Keywords: ChatGPT, Laboratory tender processes, Technical specification

S103

INVESTIGATION OF THE EFFECT OF GEL USED IN SERUM SEPARATOR TUBES ON VITAMIN B12 ANALYSIS

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Objectives: It was aimed to examining, due to the fact that falsely high results were observed in some serum vitamin B12 analyses, the effect of separator gels on serum vitamin B12 values.

Methods: Blood samples were collected from 30 healthy volunteers into two different serum gel tubes (Pirmax, gel&clot activator, 5 mL; Vacusera, gel&clot activator, 5 mL) and a serum

non-gel tube (Vacuette, clot activator, 6 mL). Serum samples were analyzed for vitamin B12 in the Advia Centaur XPT immunoassay system. Results of assays of serum B12 in two different serum separator gel tubes and a plain serum tube were compared. An investigation of the effect of mixing serum separator tubes was also carried out.

Results: There was no difference between the measured initial vitamin B12 values in the samples taken into three different tubes ($p>0.05$). By mixing the serum gel tube samples, serum vitamin B12 results increased compared to the initial analysis ($p<0.05$). The results of samples collected into tubes with separator gels obtained by re-centrifugation of the samples were similar to the initial vitamin B12 analysis ($p>0.05$).

Conclusions: Mixing serum separator gel tubes can cause spuriously elevated B12 levels on the Advia Centaur XPT immunoassay systems. We believe that it is important for all laboratories, especially those accepting samples from outside their own institutions, to report the B12 results after re-centrifugation just in case the serum samples in the gel tube are mixed with the gel during transport.

Keywords: serum separator tube, vitamin B12, mixing

S104

IS TOTAL CHOLESTEROL CAUSE THE DIFFERENCE BETWEEN THE PAINT BINDING METHOD AND THE ALBUMIN CONCENTRATIONS MEASURED BY CAPILLARY ELECTROPHORESIS?

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Objectives: Differences have been observed between albumin concentrations measured on autoanalyzers and serum protein electrophoresis (SPEP) in some patients. The aim of our study was to investigate whether the difference between albumin measured on an autoanalyzer and by capillary zone electrophoresis (CZE) is associated with the total cholesterol concentration in the sample.

Methods: The study is a retrospective study and included 292 patients for whom simultaneous albumin, SPEP and lipid panel tests were requested between September 2019 and June 2023. Albumin, triglyceride and total cholesterol measurements were performed on the Roche cobas 8000 analyzer, while SPEP was conducted using the Minicap Flex-Piercing (Sebia) CZE device. The percentage difference values (PDV) between albumin measured on an autoanalyzer (S.Alb) and CZE (PE.Alb) were calculated using the formula $PDV = (PE.Alb - S.Alb) / S.Alb * 100$. Patient results were grouped as ≤ 150 mg/dL and ≥ 151 mg/dL for triglycerides, ≤ 200 mg/dL and ≥ 201 mg/dL for total cholesterol and ≤ 130 mg/dL and ≥ 131 mg/dL for LDL cholesterol. Differences in PDV between groups were evaluated using the Mann-Whitney U test.

Results: There was no significant difference in S.Alb-PE.Alb PDV between the ≤ 150 mg/dL and ≥ 151 mg/dL triglyceride groups ($p=0.164$). However, there were significant differences in PDV between the ≤ 200 mg/dL and ≥ 201 mg/dL total cholesterol groups and between the ≤ 130 mg/dL and ≥ 131 mg/dL LDL cholesterol groups ($p=0.011$ and $p=0.016$, respectively).

Conclusions: Studies have shown that an increase in cholesterol concentration leads to the expansion of albumin peptide chains, resulting in an increase in albumin absorption spectrum. We believe that laboratory specialists should provide appropriate warnings in their report interpretations for clinicians, especially in patients with high cholesterol levels, when evaluating SPEP results.

Keywords: capillary zone electrophoresis, albumin, cholesterol, LDL, triglyceride

S105

A PRELIMINARY STUDY ON INTERFERENCE OF THE URINARY PROTEIN ASSAY BY POVIDONE IODINE SOLUTION CONTAMINATION

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Objectives: Povidone iodine (PVP) solutions are commonly used before urinary catheterization and sample collection in order to prevent any infectious contagion. This study was conducted to investigate any interfering effect of commercially available %10 PVP containing solutions on one of the colorimetric urinary total protein assays, the Automated Pyrogallol Red-Molybdate (PRM) method.

Methods: Three urine pools were prepared containing different amounts of total protein (6,3 mg/dl, 45,7 mg/dl and 119,8 mg/dl). PVP solutions at six different concentrations (2,5%, 1,25%, 0,6%, 0,3%, 0,15% and 0,07%) were added to the aliquoted urine pool samples. Urinary protein levels of the PVP-added samples were measured on Beckman Coulter AU 5800 autoanalyzer (Beckman Coulter, USA) with PRM method. The biases from the baseline results were calculated.

Results: In the samples containing 6,3 mg/dl total protein, the biases of the results were greater than 10% at all of the different PVP concentrations. In the samples containing 45,7 mg/dl protein, the biases were all exceeded 10% except 0,07% PVP concentration. Finally, in the samples containing 119,8 mg/dl protein, the biases were greater than 10% at 0,3% and higher PVP concentrations.

Conclusions: We briefly showed the interfering effect of PVP solution on urinary protein assay with PRM method on Beckman Coulter AU 5800 autoanalyzer. Health professionals should keep in mind the PVP contamination in clinically inconsistent high urine total protein results. Also in this case, using a different antiseptic solution at sampling process or choosing a different urinary total protein assay method may be considered.

Keywords: analytical error, urinalysis, pyrogallol red

S106

EVALUATION OF LIPEMIA INTERFERENCE WITH NATURAL ULTRALIPEMIC MATERIAL AND INTRAVENOUS LIPID EMULSION IN HEMOGLOBIN VARIANT ANALYSIS

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Objectives: In the preanalytical stage, lipemia interference is a common problem that affects accurate results. In this study, we aimed to evaluate lipemia interference in high, normal, and low HbA2 results with natural ultralipemic material (NULM) and intravenous lipemic emulsion (IVLE).

Methods: NULM and IVLE solutions were used to investigate the effect of lipemia in Hb(hemoglobin) variant analysis. The study was carried out according to the EP7-A2 guideline published by the Clinical and Laboratory Standards Institute for interference studies. Whole blood pools with high ($\geq 5\%$), normal (2.5-5 %), and low ($\leq 2.5\%$) HbA2 results were diluted with both NULM and IVLE stock solutions to create sub-pools containing five different concentrations of triglycerides. UniCap capillary electrophoresis device (Shenzen YHLO Biotech Co., Ltd., China) was used in this study. The repeated ANOVA test was used for statistical analysis (SPSS ver. 22 IBM).

Results: The values of high, normal, and low main pools were 5.1 ± 0.0 , 2.6 ± 0.06 and 2.1 ± 0.0 for HbA2 %, 91.4 ± 0.0 , 96.0 ± 3.5 , and 97.1 ± 0.0 for HbA %, respectively. HbF % for the high pool was 1.90 ± 0.0 . No interference was observed for HbA2, HbA, and HbF in either DULM or IVLE, according to repeated ANOVA analysis in pools, depending on lipid concentration.

Conclusions: In this study, the effect of lipemia interference on Hb variant analysis was investigated. The interference effect was not detected in both DULM and IVLE pools.

Keywords: Hb variant analysis, lipemia, interference, natural ultralipemic material, intravenous lipemic emulsion

S107

DOES TURBIDITY CAUSE INTERFERENCE IN QUANTITATIVE URINE TOTAL PROTEIN MEASUREMENT?

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Objectives: In this study, the effect of turbidity on quantitative urine total protein, albumin and creatinine concentrations was investigated.

Methods: Urine samples were used in the study, where total protein and albumin were analyzed on the RocheCobas 6000 analyzer and visually categorized as turbid ($n=48$) and clear ($n=29$). Total protein (<150 mg/L and >150 mg/L) and albumin results (<20 mg/L and >20 mg/L) were taken into consideration when selecting samples. Turbid and clear urines were centrifuged at different speeds and times and divided into four groups Group I: Without centrifugation, Group II: Centrifugation at 500 g for 5 minutes, Group III: Centrifugation at 1000 g for 5 minutes and Group IV: Centrifugation at 1500 g for 5 minutes. Whether there was a significant difference between the groups was determined by the Repeated Measured ANOVA test. Additionally, percentage difference from the non-centrifuged group was calculated for each group.

Results: In turbid urine, the median (min-max) values for albumin, total protein and creatinine were 32.7 mg/L (2-1882 mg/L), 414 mg/L (83-2954 mg/L) and 122 mg/dL (38-303 mg/dL) while in clear urine they were 689 mg/L (3-1700 mg/L), 749 mg/L (108-1949 mg/L) and 76 mg/dL (36-215 mg/dL), respectively. Significant differences among groups were observed in turbid urine in both total protein and creatinine values, as well as in total protein/creatinine ratios (group differences from Group I, $p < 0.001$, $p < 0.05$ and $p < 0.001$, respectively). In clear urine, there were no significant differences among any of the groups

($p > 0.05$ for all groups). The percentage difference the groups from Group I for total protein in turbid urine was as follows: -44%, -54% and -54.89%, respectively. Similarly, the percentage differences for total protein/creatinine were -38%, -47% and -50%, respectively.

Conclusions: In turbid urine, centrifugation is essential for obtaining accurate quantitative results for total protein, creatinine and total protein/creatinine results. Our study has shown that centrifugation at 1000g for 5 minutes is sufficient for removing turbidity.

Keywords: urine, interference, total protein, centrifugation, albumin

S109

A CONDITION THAT CAUSES LOW HbA1C MEASUREMENT BY HPLC METHOD

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Objectives: The HbA1c test is used for diagnosis and monitoring of diabetes mellitus. Many different analytical methods are used for HbA1c measurements. Immunometry, high-throughput liquid chromatography (HPLC) and boronate affinity chromatography are the most widely used methods. In this case, we aimed to present a patient who was clinically incompatible with the HbA1c level measured by the HPLC method.

Methods: A 72-year-old female patient applied to the family health center, Routine examination was performed and laboratory analyzes were requested. When the desired fasting blood glucose level was determined as 121 mg/dL among the routine tests, the HbA1c test was added to the patient's laboratory panel by the clinician. HbA1c measurement was made in HPLC device (Tosoh G8; Tokyo, Japan) in our laboratory. The patient's HbA1c result was 2%. This result was shared with the clinician. There was a discordance between clinical situation and test result. So it was decided that the patient should also be evaluated in terms of hemoglobin

variant. As a result of the analysis, HbD was 83.6%, HbA 7.7% and HbA2 0.7%. The patient's HbA1c concentration was measured by the turbidimetric immuno-inhibition method (Beckman Coulter, AU480, USA) and HbA1c was found to be 5.7%.

Results: The presence of hemoglobin variants cause interference in HbA1c results. Low or high results may occur in HbA1c results due to abnormal peaks in measurements made with HPLC.

Conclusions: In the monitoring of diabetic patients, it should be known that hemoglobinopathies affect HbA1c measurement methods and cause false results.

Keywords: HPLC, HbA1c, Immunometry

S110

BENIGN TRANSIENT HYPERPHOSPHATASEMIA IN CHILDREN

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Objectives: Transient hyperphosphatasemia (TH) is benign condition in which serum alkaline phosphatase (ALP) is transiently elevated without underlying systemic diseases. Therefore, it is quite beneficial to detect cases of TH and report them correctly before any further interventions.

Methods: Total number of 28 patients' data of which serum ALP activity analyses and electrophoretic separation of ALP isoenzymes performed in between 01.06.2022–01.07.2023, were collected retrospectively. Patients with high intestinal isoenzyme activity ($n=4$) and normal liver isoenzyme activity ($n=2$) were excluded. Then, the rest of 22 patients' results with ALP electrophoretic gels having faster anodal migration of isoenzymes and serum

ALP>1000 U/L, were reported with a note defining the TH diagnosis.

Results: The study group comprised of 22 toddlers (10 M/12 F) aged from 4 months to 3 years having serum ALP activity of (2258 ; 1005-4609 IU/L), (Median ; IQR). The liver and bone isoenzyme activity levels were found (676 ; 175-1890 IU/L), (1581 ; 482-3718 IU/L), (Median ; IQR) respectively. A seasonal peak of the cases was observed in autumn-early winter, indicating an association with viral infections and TH; but also this might be a detection bias. Additionally, the clinical history of study participants could not be collected and evaluated with laboratory results because of the disadvantage of being a central laboratory, approving biological samples from other facilities.

Conclusions: The recognition of this phenomenon with elevated levels of serum ALP activity and typical electrophoretic isoenzyme migration pattern in pediatric ages (<5 years of age) resolving spontaneously is important to avoid wasting of time and resources in clinical laboratories for further diagnostic evaluations.

Keywords: hyperphosphatasemia, alkaline phosphatase, isoenzymes, viral infections

S111

PSEUDOHYPERKALEMIA CASE RELATED TO TROMBOSITOSIS

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Objectives: The primary aim of this case study is to underscore the pivotal significance of discriminating thrombocytosis-associated pseudo hyperkalemia from the hyperkalemia.

Methods: An 80-year-old male patient with a history of cerebrovascular disease, hypertension, and diabetes mellitus presented with weakness and was admitted to the Neurology department. During follow-up despite elevated potassium values in hemolysis-free serum, the blood gas analysis potassium level remained within the normal range. Urea and creatinine values were within the normal range, and there were no clinical or electrocardiogram (ECG) findings

consistent with hyperkalemia. A progressively rising thrombocytosis was detected in the complete blood count (CBC). With the suspicion of thrombocytosis-associated pseudo hyperkalemia, potassium level was measured in the plasma from the lithium-heparinized tube.

Results: The patient had elevated platelet count ($1101 \times 10^3 / \mu\text{l}$) serum potassium level (5.26 mEq/L), while blood gas analysis potassium level (4.46 mEq/L) was within the normal range. Meanwhile, the potassium level measured in heparinized plasma was found to be 4.68 mEq/L.

Conclusion: Elevated platelets lead to a greater release of intracellular potassium during clotting, resulting in higher serum potassium levels compared to plasma potassium levels. This condition is defined as thrombocytosis-associated pseudo hyperkalemia. Early recognition of this condition will prevent the patient from receiving inappropriate hyperkalemia treatment and reduce confusion among healthcare professionals.

S112

WHAT IS A NON-REFRIGERATED CENTRIFUGE CAPABLE OF?

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Objectives: The preanalytical phase significantly impacts laboratory outcomes, especially in remote centers where control is challenging.

Methods: Our secondary state hospital laboratory also served the Family Health Center (FHC). A patient with elevated FT4, FT3, and suppressed TSH was referred from FHC for suspected primary hyperthyroidism to Internal Medicine clinic in our hospital. However, subsequent tests at our hospital revealed normal values. To ensure that blood is drawn from the correct patient, we contacted FHC and confirmed that the barcodes were double-checked. Since blood was drawn into two separate tubes for biochemistry and hormone analysis, FHC samples were analyzed on cross analyzers.

Results: FT4, FT3, and TSH results were normal upon reanalysis. Yet, significant discrepancies in ALP, ALT, amylase, LD, HDL-C, and UIBC were observed in biochemistry analyses. Lower enzyme values and higher FHC sample density indicated a temperature-related error. FHC staff revealed that the centrifuge worked without cooling, and some samples sent without centrifugation. In the afternoon, it was requested to run the centrifuge without samples under the same conditions and it was learned that the temperature reached 63°C. The patient's hyperthyroidism diagnosis was incorrect due to the high-temperature centrifugation, leading to specimen rejection.

Conclusions: Poor control of centrifuge temperatures can cause misdiagnosis with primary hyperthyroidism due to TSH and thyroid-binding globulin denaturation. Liver diseases and iron deficiencies may also be overlooked due to erroneously low ALT, ALP, and UIBC results.

Keywords: Centrifugation, Enzymes, Hormones, Preanalytical Phase, Temperature

S113

THE PLACE OF FLOW CYTOMETRY IN DIAGNOSIS OF MYELOYDYSPLASTIC SYNDROME IN A PATIENT WITH PANCYTOPENIA: A CASE REPORT

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Objectives: Myelodysplastic syndrome (MDS) is diagnosed morphologically. In addition, flow cytometry is a valuable and rapid diagnostic method in evaluation of increase in myeloblasts which is the most important factor determining prognosis of MDS and in estimation of dysplastic changes in bone marrow.

Methods: A 50-year-old male patient was admitted to Internal Medicine clinic with weakness and fatigue for last 2 weeks. He was followed up by Hematology department because of pancytopenia in hemogram. In peripheral blood smear, erythrocytes were anisocytic, leukocyte formula was consistent with hemogram, no atypical cells were seen. Since pancytopenia persisted in follow-up hemograms, bone marrow aspiration was performed.

In flow cytometry, approximately 6% of CD45 cells were observed in CD45 dim area, and when these cells were examined, approximately 3% CD34 negative, CD33 and CD117 positive myeloblasts were determined. It was observed that granulocytes were divided into two groups with low and high granularity. There was significant loss of granularity in granulocytes. It was observed that maturation properties of granulocytic series were also impaired. With these findings, pre-diagnosis of MDS was considered. Bone marrow aspiration pathology result was also evaluated as MDS, which was consistent with flow cytometry result. In pathological examination MDS was evaluated as RAEB-II according to WHO classification, since 11% blasts were found and dysplastic changes were observed in myeloid and erythroid series, and treatment was planned accordingly.

Results: It was observed that bone marrow aspiration flow cytometry result and pathology result were compatible in diagnosis of MDS.

Conclusions: Although flow cytometry does not provide clear classification information for morphologically diagnosed MDS, it is a valuable and rapid diagnostic method that predicts whether the diagnosis is MDS and at what risk level it is in the classification.

Keywords: flow cytometry, myelodysplastic syndromes

S114

CAN REFLEX TESTING UTILIZE THE HEMATOLOGY ANALYZER FLAG?

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Objectives: Reflex testing is the automatic addition of tests by analyzers based on algorithms established by laboratory professionals. We aimed to demonstrate that preliminary diagnoses of patients can be made using the reflex test that can be utilized on the hematology analyzer in this case series.

Methods: Patient #1 is a 70-year-old female who has Alzheimer's, hypertension, and osteoporosis. She admitted to a hematology outpatient clinic with fatigue. Chronic anemia and mild thrombocytopenia were found to be present in the patient's history. During the physical examination, she appeared pale and tachycardic. Abnormal lymphocyte/lymphoblast?, neutropenia, and pancytopenia flags have been observed on the hematology analyzer (Mindray, BC 6800, China). On peripheral smear (Mindray, Slide Maker&Stainer, China), immature myeloblasts were present. The patient was diagnosed with acute myeloid leukemia after obtaining a bone marrow biopsy.

Patient #2, an 82-year-old female who has hypertension, atrial fibrillation, and mild dementia, has been admitted to the hematology outpatient clinic. She was referred from an internal medicine clinic due to anemia. She had difficulty walking, skin pallor, and hepatosplenomegaly during physical examination. On hematology analyzer, blast? abnor. lymphoblast? immature granulocyte, lymphocytosis and leukocytosis flags appeared. Peripheral smear revealed leukocytosis, mature lymphocytosis, and smudge cells in almost every high-power field. Flow cytometry showed B-cell chronic lymphocytic leukemia in peripheral blood.

Conclusions: The hematology analyzer flags should be considered when performing reflex testing in our case series to avoid delays in diagnosis and treatment, particularly in hematological diseases.

Keywords: Hematology, Reflex testing, B-cell chronic lymphocytic leukemia, Acute myeloid leukemia

S115

FALSELY HIGH FREE TRIIODOTHYRONINE VALUE DUE TO MONOCLONAL ANTIBODY THERAPY

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Objectives: Compatibility of thyroid function test results with each other and with the patient's clinic is important in diagnosis and follow-up. We reported a woman who had a false high free triiodothyronine value (fT3) due to monoclonal antibody therapy. The aim was to emphasize that oncology patients may encounter inappropriate results due to the use of monoclonal antibodies and to share the laboratory process we experienced in this case.

Methods: In a 64-year-old woman; fT3, free thyroxine (fT4), and thyroid stimulating hormone (TSH) values were found 10.4pg/mL, 1.03ng/dL, and 10.8μIU/mL, respectively. The patient was receiving thyroid hormone and monoclonal antibody therapy. Free triiodothyronine measurement was repeated in alternative platforms. The serum of the patient was treated with a heterophile antibody blocking tube (HBT). In addition, the patient sample was transferred to two separate tubes. While PEG was added to one, distilled water was added to the other at the same rate. Free triiodothyronine values in serum with PEG were compared with serum which was added distilled water. The same procedures were applied to the control serum.

Results: In the alternative platform, the fT3 value was found 3.18ng/mL. When the patient serum treated with PEG was compared to the serum that was added distilled water, a decrease (from 6.94ng/mL to 3.55ng/mL) was detected in fT3. No decrease in fT3 was observed in the control serum to which the same procedure was applied. Incubation of the patient sample with HBT showed 97% of recovery for fT3.

Conclusions: Inappropriate results may occur in

patients using monoclonal antibodies.

Keywords: monoclonal antibody therapy, free triiodothyronine

S116

CAN GLUCOSE, AND ELECTROLYTES OBTAINED ON BLOOD GAS ANALYSER BE USED INSTEAD OF BIOCHEMISTRY ANALYSER RESULTS IN ADULT PATIENTS?

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Objectives: A blood gas analysers are vital equipment frequently used in emergency departments and intensive care units. The aim of this study was to determine the agreement in glucose, sodium, potassium and chloride parameters that measured both biochemistry auto-analyser and blood gas analyser.

Methods: In the present study, 120 patient's test results of glucose, and electrolytes measurements simultaneously in blood gas and autoanalyzer were evaluated retrospectively for about 1-months period.

Results: While the potassium, and chloride values measured on the auto-analyser were significantly higher ($p < 0.01$), sodium significantly lower than those on the blood gas analyser ($p < 0.01$). There was no statistically significant difference for glucose between the two analysers ($p > 0.05$). In the Spearman correlation analysis between the two measurements, correlation coefficients (r) were found as 0.924, 0.942, 0.862, and 0.983 ($p < 0.001$) for sodium, potassium, chloride, and glucose respectively. According to the Bland-Altman analysis, the mean differences between the two methods were not statistically significant for glucose (mean difference 0.01 mg/dL, 95% CI -1.254–1.635, $p = 0.796$), sodium (mean difference 1.891 mmol/L, 95% CI -0.729–4.512, $p = 0.155$), and potassium (mean difference -0.719 mmol/L, 95% CI

-2.674–1.235, $p = 0.467$), however, there was statistically significant for chloride (mean difference 1.356 mmol/L, 95% CI 0.059–2.652, $p = 0.04$).

Conclusions: The results of our study suggest that glucose results measured by both analysers can be used interchangeably, but care should be taken when interpreting electrolyte values.

Keywords: autoanalyser, blood gas analyser, electrolytes, glucose

S117

COMPARISON OF ADVANCED GLYCATION END PRODUCT (AGE) AND ZINC LEVELS IN PATIENTS WITH DIABETES MELLITUS AND DIABETIC NEPHROPATHY

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Objectives: Diabetes is a metabolic disease characterized by hyperglycemia. Diabetic nephropathy (DN) is the leading cause of kidney disease. Zinc is required for the processing and storage of insulin in the pancreatic β -cell. Zinc metabolism has been shown to be associated with an increased risk of diabetes. Advanced glycation end products (AGEs) are proteins or lipids that become glycated. It is a biomarker that plays a role in the development of diabetes. The aim of this study is to evaluate serum Zn and AGE levels in patients with diabetes and diabetic nephropathy.

Methods: Our study included 37 diabetes mellitus (DM) patients, 46 DN patients

and 27 healthy individuals between the ages of 18-75. Serum AGE and serum zinc levels were measured from the blood taken from these individuals. The biochemical data obtained from the study were analyzed with the SPSS 26.0 statistical analysis package program.

Results: In our study, HbA1c values were found to be significantly higher in the DM and DN groups compared to the healthy group ($p<0.001$), while creatinine values were found to be significantly higher in the DN group compared to the other two groups ($p<0.001$). While serum AGE levels were found to be significantly higher in the DN group compared to the other two groups ($p=0.012$), zinc levels were found to be significantly higher in healthy individuals than in patients with disease ($p=0.039$).

Conclusions: These data we obtained should be supported by further studies with larger participant groups.

Keywords: AGE, Zinc, Diabetic nephropathy, Diabetes Mellitus

S118

INVESTIGATION OF APELIN, ELABELA, ENDOGLIN AND IMA BLOOD LEVELS IN ACUTE MYOCARDIAL INFARCTION

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Objectives: Acute myocardial infarction (AMI), one of the leading causes of mortality and morbidity, is a disease characterized by cardiac myocyte loss caused by long-term ischemia. The aim of this study was to determine the blood levels of apelin, elabela, endoglin and IMA in AMI and to investigate the relationship of these parameters with HsTn-I, which is the gold standard biomarker in the diagnosis of AMI.

Methods: The study population consisted of 45 patients with AMI and 45 healthy individuals. Plasma apelin, elabela, endoglin and

serum IMA levels were measured by ELISA method. Serum levels of routine biochemical markers were withdrawn from the hospital automation system.

Results: In the study, HsTn-I and endoglin levels were higher in the group with AMI (904.44 ± 875.92 ng/L and 22.14 ± 5.24 ng/mL) compared to the control group (11.57 ± 4.11 ng/L and 11.44 ± 5.40 ng/mL) ($p<0.001$); apelin and elabela levels were found to be statistically significantly lower in the group with AMI (220.62 ± 69.13 ng/L and 1036.51 ± 139.31 ng/L) compared to the control group (279.28 ± 109.67 ng/L and 1386.08 ± 139.00 ng/L) ($p<0.001$). IMA levels were found to be higher in the patient group compared to the control group, but it was not significant. In addition, there was a significant negative correlation between serum HsTn-I and plasma apelin and elabela levels; a positive and significant correlation was determined between plasma endoglin levels.

Conclusions: Finally, while apelin and elabela from plasma adipokine levels were decreased in the group with AMI, endoglin was found to be high. Finally, these adipokines may have roles in the etiopathogenesis, diagnosis and treatment of AMI.

Keywords: acute myocardial infarction, HsTn-I, apelin, elabela, endoglin, IMA

S119

WNT SIGNALING INHIBITORS FOR INCREASING OSSEOINTEGRATION

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Objectives: Sclerostin (Scl) is a primary inhibitor controlling the Wnt signaling pathway. It can directly bind to LRP5/6 and inhibit the activation of LRP5-6 related signaling. This study aimed to evaluate the effect of targeted inhibition of Scl and to create a balanced stimulation of bone formation in tooth extraction sockets by suppressing the bone resorption mechanism. Secondly, we explored the regulatory interaction of Scl and bone during local administration.

Methods: New Zealand male rabbits (3-month-old, weight 2.5-3 kg) were fully randomized to ensure bias. Experiments were done in 3 groups (control, graft, Scl-Ab). Calculated doses of Scl-Ab were applied together with the graft material to extraction sockets, and results were obtained at two and 4-week intervals. Volumetric tomography slice imaging, histomorphologic analysis, and radiologic measurements were performed.

Results: Volumetric tomography analysis of a defined mandibular region of interest demonstrated that experimental animals treated with Scl antibody had higher average mandibular bone volume than graft and control groups. The Scl antibody of Group 3 had increased trabecular thickness of alveolar bone, a clinically relevant measure of bone quality related to bone formation.

Conclusion: A therapeutic composition of Scl antibodies supports early bone formation around dental implants and graft materials in extraction sockets. The local inhibition of Scl secreted within the bone microenvironment targets Wnt/beta-catenin pathway modulation that enhances the potential bone formation.

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Keywords: Bone healing, Sclerostin, Bone formation-resorption, Osseointegration

S120

GOJIBERRY POTENTIATES THE EFFECT OF L-CARNITINE IN THE TREATMENT OF CHRONIC MYELOID LEUKEMIA IN VITRO

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Objectives: In our study, we targeted to investigate the effect of gojiberry (GB) and L-carnitine (LK) in combination on chronic myeloid leukemia (CML) with the underlying mechanism.

Methods: Antioxidant capacity-determined GB extracts were applied to K562 leukemia cells for 72 h. Groups were determined as control 1 (no treatment), control 2 (Gleevec), LK, GB, and GB combined with LK (GB+LK). Their effects were determined by cell number, cell viability and apoptotic cell rate (Flow cytometry), the levels of apoptotic (Caspases-3,8,9, Bax) and anti-apoptotic (Bcl-2) proteins (ELISA), and the ultrastructure (TEM). Anova test was applied, and $p < 0.05$ was accepted as statistically significant.

Results: The highest cell number and viability decrease was found in the combination group (PG-B+LK<0.05). The combination group led to the highest increase in apoptotic cell rate in concomitant with the highest increase in the levels of caspases-3,8 (PGB+LK<0.05). In addition, the highest number of apoptotic cells was also determined in the combination group during TEM evaluation.

Conclusions: In the current study, it's detected firstly that GB combined with LK shows a synergistic effect through the induction of extrinsic apoptosis.

Keywords: Gojiberry, L-Carnitine, Chronic Myeloid Leukemia, Phytotherapy, Apoptosis

S121

THE EFFECT OF ENRICHMENT OF BLACK TEA AND YOGHURT DRINK WITH VITAMIN D3 ON SERUM 25(OH)D3 LEVELS IN RATS

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Objectives: Various measures are being taken by health authorities to prevent vitamin D deficiency in the world. One of these measures is to add vitamin D to some foods that are frequently consumed in the society which are easily available and economically appealing to the general public. We aimed to investigate the effect of adding vitamin D to yoghurt drink with the purpose of increasing serum vitamin D levels, thus causing less lactose intolerance compared to tea and yoghurt drink, which are the most frequently consumed drinks after water in the world.

Methods: The control (C) group was fed only with a purified diet. In addition to the purified diet, each of the other groups were fed with yoghurt drink (Y), yoghurt drink fortified with fat-soluble vitamin D (YF); yoghurt drink fortified with water-dispersible vitamin (YW), tea (T), tea fortified with fat-soluble vitamin D (TF), tea fortified with water-dispersible vitamin D (TW) for 40 days.

Results: Serum 25(OH)D₃ levels of the YW group were 161%(P<0.001), 124%(P<0.001) higher than those of the control, yoghurt drink groups, respectively. The 25(OH)D₃ levels of the TF group were 71%(P=0.001), 80%(P=0.001) higher than those of the control, tea groups, respectively. The 25(OH)

D₃ levels of the TW group were found to be 185%(P=0.001), 200%(P=0.001) higher than those of the control, tea groups, respectively.

Conclusions: Fortifying black tea with water-dispersible vitamin D₃, yoghurt drink with water-dispersible or fat-soluble vitamin D can be applied as an effective way to reduce vitamin D deficiency in the population.

Keywords: Yoghurt drink, Water-dispersible vitamin D, Fat Soluble vitamin D, Supplementation

S122

THE PROGNOSTIC NUTRITIONAL INDEX (PNI) USED TO PREDICT OUTCOMES IN ISCHEMIC STROKE PATIENTS BY ASSESSING THEIR NUTRITIONAL STATUS

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Objectives: Malnutrition has been reported to be related to adverse prognosis in acute ischemic stroke (AIS) patients. Unfortunately, traditional nutritional assessment tools usually increase the workload of neurologists, which makes them unfeasible in clinic work. We aimed to elucidate the association between the prognostic nutritional index (PNI), an easily obtainable baseline nutritional marker, and outcomes in AIS patients.

Methods: The present study retrospectively included 1405 patients. PNI was calculated as 5*lymphocyte count (10⁹ /L) + serum albumin concentration (g/L), and the good prognosis was defined as modified Rankin Scale score of 0-3. The relationship between PNI and clinical parameters was evaluated.

Results: We found that the patients in the low PNI group had a higher frequency of anemia (12.9 vs. 2.3%, P<0.001) and a higher level of the Controlling nutritional status (CONUT) score (P<0.001). The relationship between PNI and nutrition-related factors, such as body mass index (r = 0.208, P = 0.001), age (r = -0.329, P<0.001), total cholesterol

($r = 0.268$, $P < 0.001$) and hemoglobin concentration ($r = 0.328$, $P < 0.001$), was significant. Low PNI value (adjusted odds ratio: 2.250, confidence interval: 1.192-4.249, $p = 0.012$) stayed as an independent predictor for the poor outcome.

Conclusions: The PNI was independently associated outcomes in AIS patients. As an easily obtainable nutritional marker, PNI may be a useful nutritional assessment tool in the clinic work.

Keywords: ischemic stroke malnutrition prognostic nutritional index

S123

EFFECT OF NUTRITIONAL DISORDER ON SERUM TRYPTOPHAN-KYNURENINE PATHWAY METABOLITE LEVELS

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Objectives: The Tryptophan-Kynurenine pathway (KY) plays a critical role in cellular energy production in the form of nicotinamide adenine dinucleotide. KY is a key regulator of the immune system as energy requirements increase significantly during the immune response. Nutritional disorders cover a broad spectrum, including malnutrition and overnutrition leading to obesity. Our aim in this study was to evaluate the effect of malnutrition on the tryptophan-kynurenine pathway, a novel pathway associated with inflammation.

Methods: Materials and Methods: In this study, serum quinurenine levels were analyzed by LC-MS/MS in 54 participants aged 18-65 years with BMI between 25-30 (Group 1), 31 participants with BMI below 18 (Group 2) and 74 participants with BMI above 30 (Group 3). The study procedure was based on protein precipitation followed by concentration of the samples under nitrogen and subsequent analysis by tandem mass spectrometry.

Results: Statistical analysis showed that serum tryptophan levels were lower in Group 2 compared to Group 1 and Group 3 ($p < 0.05$). Serum quinurenine, quinurenic acid, quinolinic acid levels and quinurenine/tryptophan ratio were significantly higher in Group 3 compared to Group 1 ($p < 0.05$). In Group 2, serum kynurenine, kynurenic acid levels and kynurenine/tryptophan ratio were statistically significantly higher and serum 3-hydroxyquinurenine levels were statistically significantly lower compared to Group 1 ($p < 0.05$).

Conclusions: Our findings suggest that quinurenine pathway metabolite levels are altered in individuals with eating disorders. Further studies in a larger population are needed.

Keywords: Eating disorders, Tryptophan, Kynurenine pathway

S124

USING DIFFERENT BLOOD SAMPLES HAS A SIGNIFICANT EFFECT ON AMINO ACID CONCENTRATIONS OBTAINED BY LC-MS/MS

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Objectives: Newborn screening programs enable the detection of newborn errors by analyzing amino acids from a dry blood spot. Although capillary blood obtained from a heel prick is the recommended sample, it has become a common occurrence for phlebotomists to drop blood from other tubes onto filter paper instead of heel blood because of the easy application. The aim of this study is to investigate amino acid levels from different sample types collected from the same individuals and compare the results with capillary blood samples.

Methods: 30 healthy individuals were included in this study. Blood samples collected to the citrate tubes (group 1), gel tubes (group 2), plain tubes (group 3), heparin tubes (group 4), ED-

TA tubes (group 5), and compared with fingertip samples (group 6). Amino acid levels (valine, leucine/isoleucine, methionine, phenylalanine, tyrosine, aspartic acid, alanine, arginine, citrulline, glycine, glutamine, glutamic acid) were analyzed by using Liquid chromatography-mass spectrometry.

Results: Highest mean/median values were obtained from capillary blood samples. Most of the amino acids were found to be different ($p < 0.05$) from peripheral blood results (except for valine in groups 3 and 5, leucine in groups 3, 4, and 5, and aspartic acid in group 5, methionine and glutamine in all the groups, citrulline in group 3).

Conclusions: The significant difference obtained from the results can be explained by the low concentrations of major amino acids within cells. Therefore, a different sampling method should not be used in newborn screening, or the laboratory should be informed about the sample type.

Keywords: LC-MS/MS, BLOOD, NBS, AMINO ACID

S125

TRIMETHYLAMINE-N-OXIDE AND UNCOUPLING PROTEIN-1 LEVELS IN GESTATIONAL DIABETES MELLITUS

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Objectives: Gestational Diabetes Mellitus (GDM) is a disorder of glucose tolerance that begins or is first detected during pregnancy, leading to serious complications. Trimethylamine-N-oxide (TMAO) levels, a short-chain amine obtained by oxidizing Trimethylamine (TMA), have been reported to

have a positive association with the risk of diabetes. Uncoupling Protein-1 (UCP-1) is a protein recognized as a marker for the thermogenic activity of brown and beige adipose tissues. Activation of brown adipocytes increases UCP-1 levels and stimulates glucose uptake into brown adipose tissue. This study aimed to determine whether TMAO and UCP-1 levels in the first trimester are associated with the development of GDM.

Methods: 6-12 weeks pregnant women were followed up until the oral glucose tolerance test (OGTT) performed at 24-28 weeks and TMAO and UCP-1 were analyzed from their sera at these two stages. TMAO levels were measured by LC/MS-MS and UCP-1 levels were measured by sandwich ELISA. GDM group ($n=30$) and control group including healthy pregnant women ($n=30$) were compared according to gestational periods.

Results: The GDM group showed higher serum TMAO levels than the control group both at 6-12 weeks ($118,73 \pm 14,09$ vs. $98,89 \pm 31,23$, $p=0,003$) and 24-28 weeks ($206,73 \pm 90,69$ vs. $79,33 \pm 37,01$, $p < 0,001$). At weeks 24-28, lower serum UCP-1 levels were found in the GDM group compared to the control group ($8,32 \pm 1,71$ vs. $9,73 \pm 1,77$, $p=0,047$).

Conclusions: The analysis concluded that serum TMAO measurement in the first trimester can be used as a biomarker for the risk of developing GDM in the future, but UCP-1 cannot be used for this purpose. Further studies are needed to elucidate the relationship between GDM and TMAO and UCP-1.

Keywords: Gestational Diabetes Mellitus, Trimethylamine-N-Oxide, Uncoupling Protein-1, Brown Adipose Tissue

S126

EVALUATION OF TRISOMY 21 RISK WITH DOUBLE AND TRIPLE SCREEN TESTS: A CASE REPORT

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Objectives: The double screen test is performed in the first trimester of pregnancy using a

computer programme to assess maternal age, gestational week, maternal weight, presence of nasal bone, nuchal translucency (NT), pregnancy-associated plasma protein-A (PAPP-A) and free beta-human chorionic gonadotropin (β -hCG). Triple screen test is performed in the second trimester of pregnancy with β -hCG, alpha-fetoprotein (AFP) and unconjugated oestriol-3 (uE3) tests.

Methods: A 23-year-old woman with no history of previous pregnancy and delivery was admitted to Etlik City Hospital at the 12th gestational week. The values obtained from the patient's blood and radiological results were entered into the Prisca package programme and risk assessments were made.

Results: The free β -hCG and PAPP-A values were found to be 63.1 ng/ml and 1.16 mIU/ml, respectively. Trisomy 13, 18 and 21 risks calculated using Prisca package programme based on these values and patient information were found to be below the cut-off value ($<1:10000$). AFP 15.9 IU/ml, uE3 0.14 ng/ml and 29335 β -hCG mIU/ml were determined after analysis of the sample received for triple screen. The risk for trisomy 21 was calculated as $>1:50$. This ratio was found to be above the cut-off value.

Conclusions: Implementation of prenatal testing reduces the incidence of interventional procedures that can lead to serious complications such as preterm birth, haemorrhage and fetal death. Therefore, it is of great importance to implement double, triple and quadruple screen tests, to improve their performance and to calculate the risks in the most accurate way.

Keywords: Trisomy 21, Down syndrome, Double screen test, Triple screen test

S127

OXIDATIVE DNA DAMAGE OF ACETHAMIPRID IN ZEBRAFISH (DANIO RERIO), VERTEBRATE MODEL ORGANISM

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Objectives: Pesticides are used globally to protect agricultural crops against damage by insects, diseases, or weeds. Acetamiprid (ACE) is one of the widely used commercial neonicotinoids in agricultural production and causes serious health problems of environmental pollution, aquatic organisms, and humans. DNA damage caused by sublethal concentrations of acetamiprid (24 and 72 hours) was studied in zebrafish (*Danio rerio*), which can be used as a model organism in ecotoxicological studies.

Methods: The fish used in the experiment were obtained from commercial suppliers in Ankara and experiments were carried out in Gazi University Department of Biology Education. Zebrafish have become an extensively used model organism for exploring the adverse impacts of pollutants in aquatic environments. The fish were placed in 10 L aquariums and adapted to laboratory conditions for 15 days. Zebrafish were exposed to 10 and 100 mg/L acetamiprid for 24 and 72 h. 8-hydroxydeoxyguanosine (8OHdG, ng/100 mg tissue) is a biomarker of oxidative DNA damage that was detected by LC-MS/MS.

Results: There was a significant difference between groups ACE-10-24h and ACE-10-72h exposure. The whole-body tissue 8-OHdG values were significantly increased in the ACE-24 h (10,00-13,17 ng/100 mg tissue) group compared to the control group (1,91-7,90 ng/100 mg tissue). These results suggest that ACE could lead to oxidative DNA damage by causing an increase in 8-OHdG levels.

Conclusions: The results of the study showed that exposure to acetamiprid had effects on the DNA damage of zebrafish. This study provided valuable in-

formation on the toxicity of ACE on zebrafish.

Keywords: Zebrafish, Acetamidrid, DNA damage, 8-OhdG, Toxicity

S128

EFFECT OF STORAGE PERIOD ON BLOOD ETHANOL LEVELS

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Objectives: In ethanol analysis, a back up sample is taken simultaneously in addition to the test sample and stored at -20 °C for 6 months according to the guideline of the Ministry of Health's 'Procedures and Principles of Ethanol Analysis Procedures in Blood Samples'. The first plasma sample studied with ethanol was also stored with the back up sample. If officially requested by legal authorities, the back up sample is sent to the Forensic Medicine Institute. Otherwise, samples are disposed of as medical waste after 6 months. Our study aimed to compare ethanol levels of 114 samples stored for 6 months with those initially measured.

Methods: The plasma of the test sample was used because it was not possible to dissolve and separate the plasma of the back up sample stored as whole blood. Ethanol analysis was performed using the enzymatic method with alcohol dehydrogenase on Roche Cobas-6000. SPSS version V21.0 was used for statistical analysis. The distribution of variables was evaluated by Kolmogorov-Smirnov test and the data were compared by paired sample-t test. The significance level was determined as $p < 0.05$.

Results: Only 51 of the stored samples had an initial measured ethanol level of >10 mg/dL. The ethanol levels of these samples were statistically significantly lower than the first measured ethanol levels ($p < 0.001$).

Conclusions: We confirmed that the ethanol verification test cannot be performed by storing the plasma of the initial sample and should be performed using a back up sample stored as whole blood in confirmation laboratories.

Keywords: Ethanol, analysis, Refrigeration

S129

EVALUATION OF MONOCYTE COUNT TO HIGH-DENSITY LIPOPROTEIN CHOLESTEROL RATIO IN AMPHETAMINE USERS

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Objectives: Amphetamine is a widely abused psychotropic compound due to its stimulant effects. It damages peripheral organs by causing oxidative stress and the inflammatory process. Monocyte count to high-density lipoprotein cholesterol ratio (MHR) has been believed to be a new marker of inflammation and oxidative stress. The aim of the study is to investigate the relationship between MHR and amphetamine.

Methods: Amphetamine users on probation ($n=31$, male) and healthy individuals ($n=31$, male) were included in the study. Complete blood count was measured by Mindray BC-6800 hematology analyzer. HDL cholesterol and amphetamine were measured by Abbott C8000 automatic biochemical analyzer. Data were analyzed by SPSS for Windows version 22.0 for statistical analysis.

Results: The MHR was significantly higher in amphetamine users ($p < 0.001$). There were no statistically significant differences in monocyte count, HDL cholesterol, other complete blood count parameters, and inflammatory indicators such as CRP, neutrophil to lymphocyte ratio (NLR), and platelet to lymphocyte ratio (PLR).

Conclusions: The result of the study indicated that MHR can be an early indirect marker of oxidative stress and inflammation in amphetamine users.

Keywords: MHR, monocyte to HDL ratio, amphetamine

S130

METABOLIC EFFECTS OF ORAL TITANIUM DIOXIDE IN JUVENILE RATS: INSIGHTS FROM NMR-BASED METABOLOMICS ANALYSIS

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Objectives: Nuclear magnetic resonance (NMR) spectroscopy in metabolomics allows comprehensive metabolite analysis. Titanium dioxide (TiO₂), commonly referred to as E171, is widely used as a food additive. We conducted NMR-based metabolomic analyses at the tissue level in juvenile rats after oral administration of E171-TiO₂.

Methods: Female Sprague–Dawley rats were divided into control and E171-TiO₂-treated groups (n=9). TiO₂ was orally administered at 100 mg/kg/day for 6 weeks. Metabolomic analysis was performed using a 500 MHz NMR instrument with homogenized kidney and liver tissue.

Results: 32 and 52 metabolites were detected in liver and kidney tissue samples, respectively. Alterations were found as 4 metabolites in the liver and 5 in the kidney, using the t-test. PLS-DA and pathway enrichment analyses were conducted. In the liver tissue samples from the E171-TiO₂-treated group, levels of N-acetylglucosamine, fumarate, serine were increased while uracil level was decreased compared to control group (p<0.05). Conversely, in the kidney tissue samples of E171-TiO₂-treated group, there was reduction in N-methylhydantoin, 1-methylhistidine,

alanine, fumarate and methylamine levels comparing to controls (p<0.05). Pathway analysis revealed alterations in pyrimidine metabolism; alanine, aspartate, and glutamate metabolism in liver tissue. In kidney tissue, the affected pathways included the citrate cycle, pyruvate metabolism, glyoxylate and dicarboxylate metabolism.

Conclusions: Emerging evidence suggests a potential link between aberrant metabolite profiles in hepatic tissues and the development of insulin resistance and hepatotoxicity. Similarly, perturbed metabolite patterns in renal tissues have been associated with adverse impacts on renal function, resembling characteristics reminiscent of kidney cancer.

Keywords: Nuclear magnetic resonance spectroscopy, Metabolomics analysis, Titanium dioxide TiO₂ exposure, Metabolic pathway alterations

S131

THE IMPORTANCE OF URINE INTEGRITY TESTS IN DRUG SUBSTANCE ANALYSIS USING LC/MS-MS:AN EVALUATION OF REJECTED SAMPLES

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Objectives: The aim of this study is to assess the necessity of rejecting initial samples from individuals who fail integrity tests(creatinine,density,pH,nitrite) before conducting drug substance analyses.This evaluation includes cases where new samples were collected from individuals who initially failed the integrity tests.

Methods: A total of 53patients were included in the study,which involved toxicology tests conducted using the SCIEXQTRAP-5500-Triple Quadrupole-LC-MS/MS system and integrity tests performed on the Beckman-Coulter-AU480 device. Results were categorized based on rejection reasons,and the values of analytes were evaluated before and after resampling.Negative results from both the initial and subsequent samples were excluded.Microsoft-Excel was used for data analysis.

Results: Among the 53 patients, 42 were rejected due to creatinine, 27 due to density, and 1 due to pH issues. Out of the 53 patients, 20 were excluded because both the rejected and resampled samples yielded negative results. Of the remaining 33 samples, 1 was rejected due to pH, 4 due to density, 16 due to creatinine, and 12 due to both creatinine and density issues. When analyzing based on analyte values, 52 out of 65 negatives turned positive according to LOQ values. While 56 positives remained unchanged, 4 results turned negative. Using cut-off values, 60 out of 88 negatives became positive, with 24 positives remaining unchanged, and 2 positives turning negative. Considering patient status, 10 out of 12 negative patients turned positive based on LOQ values, while 21 positive patients remained unchanged. Using cut-off values, 10 out of 14 negative patients turned positive, and 2 out of 19 positive results turned negative.

Conclusions: When comparing analyte values, it is observed that positives remained unchanged. It is suggested that, for LC/MS-MS analysis, evaluation based on the LOQ value may be more accurate than the threshold value. Additionally, re-sampling is recommended for false-negative patients, while re-sampling for patients with positive results may be unnecessary.

Keywords: Urine integrity test, toxicology, LC-MS-MS, drug analysis, urine

S133

INVESTIGATION OF THE EFFECTS OF KRILL OIL ON TESTICULAR TISSUE IN HIGH FAT DIET-INDUCED OBESE RATS

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Objectives: New sources of dietary components continue to be identified for the amelioration of obesity and obesity-related diseases. Antarctic krill is a recognized as a new alternative source

of Ω -3PUFA. Krill oil is derived from krill and contains about 40% phospholipids and Ω -3 fatty acids. This study aimed to investigate the effects of krill oil on testicular tissue in high-fat diet-induced obese rats.

Methods: In this study, a total of 3 groups (n=24) were formed as control (control diet), case (High-fat-diet) and Krill Oil (HFT+Krill oil 600 mg/Kg/day). The groups were given a daily diet ad libitum for 12 weeks. Krill oil was given by oral gavage. Rats were weighed weekly. The animals were sacrificed when 20% weight gain was detected in the case group compared to the control group as an obesity criterion. TBARS and Total SH levels in testicular tissues and TNF- α levels in serum were analyzed. Testicular tissue was examined immunohistochemically with hematoxylin-eosin (H&E) staining.

Results: TBARS, Total SH and TNF- α levels were significantly increased in the control group (p<0.01) compared to the case and krill oil groups. As a result of H&E staining was observed that the difference between groups was not significant.

Conclusions: It is thought that the low TBARS, Total SH and TNF- α levels in the case group compared to the control group is due to the high-fat diet content (casein, vitamins and aromatic compounds). Therefore, although the given diet provided weight gain, it is thought to have a protective effect against inflammation and oxidative damage.

Keywords: Krill oil, obesity, testis

S134

INVESTIGATION OF THE TREATMENT EFFECTIVENESS OF SIMULTANEOUS INHIBITION OF TRPC3/6 ION CHANNELS IN THE MOUSE LIVER FIBROSIS MODEL

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Objectives: Liver fibrosis is a pathological condition characterized by the formation of fibrotic tissue as a result of excessive accumulation of extracellular matrix (ESM) components such as collagen in the liver in response to inflammation or direct toxic damage. The aim of this study is to investigate the possible therapeutic effects of blockade of Transient Receptor Potential Cation Channels (TRPC3/6 ion channels) and the inflammatory pathways mediating this therapeutic effect at the biochemical, histological and molecular level in the liver Carbon Tetra Chloride (CCl₄) fibrosis model created in mice.

Methods: BALB/c strain mice were injected with CCl₄ to induce liver fibrosis. Expression levels of anti-inflammatory and inflammatory cytokine genes in liver and spleen tissues of all animal groups were investigated, histological and biochemical analyzes were performed in liver tissues.

Results: Our analysis data by qRT-PCR revealed that Peroxisome Proliferator Activated Receptor (PPAR) beta/NFATC1/NFATC3 (Nuclear factor of activated T-cells) expressions were significantly increased in mice exposed to CCl₄, and that both colchicine and TRPC3/6 inhibition suppressed this pathway. In terms of PPARs, it was observed that only PPARbeta expression increased significantly, but PPAR alpha and PPAR gamma expressions did not change significantly.

Conclusions: In the study, it was shown that TRPC3/6 inhibition plays an important therapeutic effect in alleviating hepatic toxicity in CCl₄-induced liver injury and can improve hepatic dysfunction and prevent histopathological changes. In addition, its mechanism is to reduce oxidative stress and inflammation.

Keywords: Trpc36, ppar, nfat, liver fibrosis, fibrosis

S135

ISCHEMIA MODIFIED ALBUMIN LEVELS IN MIGRAINE PATIENTS

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Objectives: The aim of the study is to investigate the serum Ischemia Modified Albumin (IMA) levels in migraine patients. Ischemia is caused by modification of albumin caused by reactive oxygen derivatives formed as a result of ischemia. It is also related to diseases associated with oxidative stress and inflammation. The pathophysiology of migraine bases on the effect of neurogenic inflammation and oxidative mechanisms.

Methods: The study population consisted of forty patients and forty control subjects. IMA measurements from serum were made with the albumin cobalt binding test described by Bar-Or et al. The difference between the absorbance values of the samples and the blanks at 470 nm were recorded as IMA values.

Results: There was no statistically significant difference between two groups for the age and the genders. (p>0.05). The IMA value of migraine group was found to be statistically significantly higher than control group (p=0.001; p<0.01). There wasn't any correlation between disease duration, attack duration, Visual Analogue Scale (VAS score) with IMA values (p>0.05). A weak correlation was found to be statistically significant (r=0.358; p=0.023; p<0.05) between the IMA values and the frequency of attacks. Receiver operator curve (ROC) analysis showed that the cut-off point for IMA was 0.389. Sensitivity was 70%, specificity was 80%, positive predictive value was 77.8% and negative predictive value was 72.7%. The area under the ROC curve obtained was determined as 80.4% with a standard error of 4.8%.

Conclusions: As a result of this study, elevated IMA levels in migraine patients support the presence

of ischemia, hypoxia and oxidative damage. The IMA level may be a predictive biomarker in migraine patients.

Keywords: migraine, IMA, Hypoxia, oksidative stress

S136

THE EFFECT OF EUGENOL ON PARAOXONASE-1 AND PARAOXONASE-3 LEVELS IN AML12 MOUSE HEPATOCYTES

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Objectives: Eugenol is a substance primarily extracted from clove plants and has medicinal use. Paraonase-1 and paraonase-3 are bound to high-density lipoprotein in circulation and have antioxidant and anti-atherogenic properties; the liver mainly synthesizes them. The effect of eugenol on paraonase enzymes is unknown. We aimed to investigate the effect of eugenol on paraonase-1 and paraonase-3 protein levels in AML12 mouse hepatocytes.

Methods: First, AML12 cells were treated with 25, 50, 100, 250, 500, and 1000 μ M eugenol for 24 hours, and the effect of eugenol on cell viability in AML12 cells was evaluated by MTT assay. Then, cells were treated with 5, 50, and 500 μ M eugenol for 24 hours, and paraonase-1 and paraonase-3 were measured by western blot.

Results: 25, 50, 100, 250, and 500 μ M eugenol did not cause a significant change, but 1000 μ M eugenol caused a significant decrease in the cell viability of AML12 cells. Eugenol caused a significant increase in paraonase-1 levels at 500 μ M without affecting paraonase-1 levels at 5 and 50 μ M concentrations. 5, 50, and 500 μ M eugenol did not cause a significant change in paraonase-3 levels in AML12 cells.

Conclusions: Our study showed that eugenol increases paraonase-1 levels and does not change

paraonase-3 levels in AML12 mouse hepatocytes.

Keywords: Eugenol, Paraonase-1, Paraonase-3, Liver, AML12 cells

S137

INVESTIGATION OF THE L-ARGININE-NITRIC OXIDE-ASYMMETRIC DIMETHYL ARGinine PATHWAY IN AUTISM

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Objectives: Autism spectrum disorder (ASD) is a neurodevelopmental disorder characterized by stereotypical behaviors that begin early in life and continue throughout life. Serum levels of oxidative molecules such as Asymmetric Dimethyl Arginine (ADMA) pathway metabolites and Nitric Oxide (NO) were measured to investigate the levels and pathophysiological role of some molecules involved in neurodegeneration in neurodegenerative diseases such as ASD.

Methods: Fifty newly diagnosed and followed-up patients, aged 0-6 years, who met the DSM-IV ASD classification criteria, who applied to the Child and Adolescent Psychiatry Outpatient Clinic of the Republic of Turkey Ministry of Health Konya City Hospital, were included in the study. A control group consisting of healthy children, 45 volunteers aged 0-6 years, who applied to the Ministry of Health Konya City Hospital Health Board and were not diagnosed with any autism or other medical disease, were selected. The levels of ADMA, SDMA, L-NMMA, L-arginine, homoarginine, citrulline and ornithine, which are metabolites in the ADMA pathway, in the serum samples of the participants were analyzed by LC-MS/MS method. Serum NO, NOS and DDAH1 enzyme levels were determined by ELISA method.

Results: Serum ADMA, L-NMMA, arginine and citrulline levels were statistically significantly higher in the patient group than in the control group, serum SDMA, homoarginine, ornithine, NO, NOS, DDAH1 levels were found to be statistically signi-

ificantly lower in the patient group compared to the control group.

Conclusions: It is understood that ADMA pathway metabolites and NO may be biomarkers in the early diagnosis and treatment of children with ASD.

Keywords: Nitric oxide, Oxidative stress, Autism

S138

EVALUATION OF THE EFFECT OF LITHIUM USE ON THYROID HORMONES AND INFLAMMATORY MARKERS

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Objectives: Lithium therapy is main prophylactic treatment for bipolar disorders. Lithium affects normal thyroid functioning through multiple mechanisms. Therapy with lithium often produces granulocytosis in psychiatric patients which creates inflammatory response. The aim of our study was to investigate the effect of lithium on thyroid hormone levels and systemic immune inflammation index.

Methods: Patient data who received lithium treatment for bipolar disorders were retrospectively collected from Hospital Information System. There were 41 patients who received lithium treatment for more than 3 months and with a therapeutic drug monitoring more than twice. Systemic immune inflammatory index is calculated using platelet, neutrophil and lymphocyte counts (P*N/L). The tests were performed on the Cobas 8000 Modular Analyzer System using serum samples. The data were evaluated by Kolmogorov-Smirnov, One-way ANOVA, Friedman, paired sample-t tests using Statistical Package for the Social Sciences V22.0. The significance level was determined as $p < 0.05$.

Results: There was a slight TSH and systemic immune inflammatory index increase which was not

significant statistically ($p > 0.05$). At the 4th-8th months of the treatment, neutrophil, leukocyte and free T4 levels increased compared to those in 16th-20th months of the treatment but again not statistically significant ($p > 0.05$).

Conclusions: No statistically significant difference was obtained in short-term follow-up in our study. Since it is predicted that lithium may alter the tests by different mechanisms, longer-term follow-up should be performed for such patients.

Keywords: Lithium, Thyroid, Marker

S139

RELATIONSHIP BETWEEN SERUM EMPAGLIFLOZIN AND METFORMIN LEVELS AND HEMATOLOGICAL PARAMETERS

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Objectives: Metformin and empagliflozin are drugs used in the treatment of Type-II-Diabetes Mellitus (T2DM). Some hematological parameters are associated with endocrine stress, diabetic complications, and systemic inflammation. Studies show that neutrophil-to-lymphocyte ratio (NLR), platelet-to-lymphocyte ratio (PLR), and monocyte-to-lymphocyte ratio (MLR) are new potential markers of inflammatory response. This study aims to investigate the relationships between empagliflozin-metformin drug levels and hematological parameters.

Methods: Drug levels were measured with LC-MS/MS in serum taken from 43 T2DM patients using empagliflozin and 34 T2DM patients using metformin. The hemogram parameters of these patients were scanned retrospectively and statistical analysis was performed with the SPSS

Statistics 22.

Results: Metformin blood levels positively correlated with lymphocyte levels ($r=0.484, p=0.004$); and negatively correlated with NLR ($r=-0.386, p=0.024$), PLR ($r=-0.466, p=0.005$), MLR ($r=-0.343, p=0.047$), PCT ($r=-0.378, p=0.028$) levels. Empagliflozin blood levels positively correlated with lymphocyte levels ($r=0.307, p=0.045$); negatively correlated with hematocrit ($r=-0.377, p=0.013$), plateletcrit ($r=-0.301, p=0.05$), NLR ($r=-0.31, p=0.043$), PLR ($r=-0.436, p=0.003$) levels. When the hemogram findings of patients using empagliflozin and metformin were compared, the MPV value of patients using empagliflozin was statistically significantly higher than those using metformin ($p=0.028$). The two groups had no significant difference regarding other hemogram parameters ($p>0.05$).

Conclusions: In our study, serum empagliflozin and metformin levels were found to be associated with hematological parameters that may be indicative of diabetic complications, inflammation, endocrine stress. The limited number of patients and lack of clinician follow-up and evaluation of the patients are the main disadvantages of our study. Studies conducted in a larger population with clinicians are needed.

Keywords: Drug level, Hematological parameters, Type II Diabetes, Empagliflozin, Metformin

S140

DEVELOPMENT OF A LIQUID CHROMATOGRAPHY TANDEM MASS SPECTROMETRY METHOD FOR OPIPRAMOL

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Objectives: Opipramol is a tricyclic antidepressant that does not inhibit neuronal uptake of norepinephrine and/or serotonin. It is considered a weak dopaminergic, histaminergic and serotonergic antagonist and binds to sigma receptors in the brain.

Recent data in the literature also reveal some of the dangers and side effects that may be associated with the use of opipramol. Therefore, our aim was to develop a rapid, specific and reproducible sensitive method for the quantitative determination of opipramol in serum.

Methods: 200 μ L of sample was taken into eppendorf tubes and 800 μ L methanol were added. The mixture was then vortexed for 30 seconds and centrifuged at 2000xg for 10 minutes. Supernatants were taken into clean glass tubes and dried at 40°C under nitrogen gas. The dried residues were dissolved in 150 μ L of methanol:water (10:90% v/v) 30 μ L was injected into LC-MS/MS system.

Results: Linearity for opipramol is in the range of 0.1-2000 ng/ml. Total working time is 5 minutes. Therecision value was less than 7.5% and the accuracy results ranged from 95.3% to 103.4%. Extraction recovery ranged from 95.8% to 98.4%, and matrix effect values were less than 10% for all analytes.

Conclusions: A rapid, cost-effective, reproducible LC-MS/MS method for the quantitative determination of opipramol has been developed.

Keywords: Mass spectrometry, adverse effect, therapeutic drug monitoring

S141

BIOLOGICAL EFFECTS OF 6-HYDROXY-L-NICOTINE AND COTININE IN VARIOUS EXPERIMENTAL MODELS OF DEMENTIA: IN SILICO AND IN VIVO STUDY

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Objectives: The impact of two structurally related nicotinic derivatives, namely cotinine (COT) and 6-hydroxy-L-nicotine (6HLN), was evaluated on memory impairment, anxiety-like behavior and oxidative stress in two animal models of Alzheimer's disease (AD): a rat model induced by brain infusion of beta-amyloid peptide 25-35 ($A\beta_{25-35}$) and a zebrafish model induced by scopolamine (SCOP).

Methods: COT and 6HLN were administered to A β_{25-35} -treated rats and SCOP-treated zebrafish and their performances were evaluated using specific *in vivo* tasks. The oxidative stress parameters and acetylcholinesterase activity were measured from the brain samples of the animals. Using *in silico* tools, we attempted to associate behavioral outcomes with the theoretical binding potential of these compounds into two different allosteric binding sites of $\alpha 4\beta 2$ nAChRs.

Results: A β_{25-35} and SCOP decreased the memory performances and increased the anxiety-like behavior in the *in vivo* assays and increased the oxidative stress and acetylcholinesterase activity in the brain of rats and zebrafish, respectively. As compared to nicotine, COT and 6HLN ameliorated, more effectively, the memory deficits and anxiety caused by A β_{25-35} or SCOP. Also, the nicotinic derivatives significantly reduced the oxidative stress and acetylcholinesterase activity in the brain of A β_{25-35} - or SCOP-treated animals. Furthermore, we showed that COT and 6HLN indeed bind to $\alpha 4\beta 2$ nAChRs with similar or even higher energy than nicotine and that the $\alpha 4\beta 2$ binding site is preferred over the $\alpha 4\alpha 4$ binding.

Conclusions: COT and 6HLN might improve memory and anxiety-like behavior by modulating cholinergic activity and thus might represent new neuropharmacological agents in AD.

Keywords: Alzheimers disease, cotinine, 6-hydroxy-L-nicotine, nicotine, animal model

S142

QUERCETIN REDUCES AXL LEVELS, AN IMPORTANT THERAPEUTIC TARGET, IN LX2 CELL LINE

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Objectives: Liver fibrosis is a prevalent condition caused by various forms of chronic liver diseases. Recent studies have reported that AXL, a receptor belonging to the tyrosine kinase family and expressed in various tissues, is significantly released into the bloodstream during the development of liver

fibrosis and hepatocellular carcinoma. Interleukin 6 (IL-6) is a versatile cytokine with a four-stranded structure that plays multiple roles within the body. In the liver, IL-6 serves as a crucial inducer of the acute phase response and contributes to the body's defense against infections. Quercetin is recognized for its diverse biological and pharmacological activities, encompassing antioxidant, antiviral, anti-inflammatory, antiproliferative, and antifibrotic effects. Indeed, the favorable impacts of quercetin on liver injury and fibrosis have been substantiated through numerous animal models. In this study, it was aimed to investigate the effect of quercetin on AXL and IL-6 levels in HSC line (LX2).

Methods: Quercetin IC₅₀ value was determined as 125 μ M according to the literature. AXL and IL-6 levels were determined by ELISA method.

Results: We found that quercetin statistically decreased the levels of AXL and IL-6 in LX2 ($p < 0.001$, $p < 0.001$).

Conclusions: The reduction in AXL and IL-6 levels suggests a notable anti-fibrotic effect of quercetin. Several studies have demonstrated that AXL inhibition leads to a decrease in IL-6 levels. In our study, quercetin may have exerted its anti-fibrotic effect through the AXL-IL-6 mechanism. However, more research is needed to investigate the potential use of quercetin in the treatment of fibrosis.

Keywords: Liver fibrosis, quercetin, AXL, IL-6

S143

THE ROLE OF DOXORUBISINE-LOADED MESENCHYMAL STEM CELLS IN ANAPLASTIC THYROID CANCER TREATMENT

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Objectives: Mesenchymal stem cells(MSCs) are adult stem cells capable of self-renewal and multi-generation differentiation. It can be isolated from many tissues such as bone marrow and adipose tissue. It has been demonstrated by studies that isolated MSCs are promising drug delivery vectors for treating of cancer and other diseases.

Methods:: MSCs were obtained from the patient lipoaspyrate with approval. Isolated MSCs were confirmed with Flow cytometrics. In the cell line CAL-62(Anaplastic Thyroid Cancer-ATC), Doxorubicine (DOX) IC50 and IC25 concentrations were determined by the MTT method. After DOX was loaded into MSCs with these doses, MSCs were called Conditional Media(CM). Wound healing analysis was performed to evaluate the effect of CM on migration and metastasis. The oxidative stress index(OSI) was examined in cell homogenates.

Results: In the analysis performed by flow cytometric method, it was identified as MSC by confirming CD73+, CD90+ and CD105+. According to the time of closure in the Control and DOX50 groups in the Wound Healing Analysis, the percentage of clearance of CM50, and CM25 was 37.7%, and 23.1% respectively. When the OSI was evaluated; Significant statistical differences were detected between the control group and other groups($p < 0,005$).

Conclusions: It was observed that CM groups obtained by loading DOX to MSCs reduced the migration rate in ATC cells according to DOX groups. When the effectiveness of CM50 and CM25 doses were compared between the groups, it was understood that there was no statistical difference. In the analyses carried out; It was observed that MSCs could be loaded with drugs and were as effective as standard chemotherapeutics at lower doses.

Keywords: Mesenchymal stem cells, Anaplastic Thyroid Cancer, Adipose tissue, Lipoaspyrate

S146

ANALYTICAL PERFORMANCE VALIDATION OF THE NEONATAL IRT FEIA KIT DEVELOPED FOR NEWBORN CYSTIC FIBROSIS SCREENING

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Objectives: The analytical performance properties of the Trimaris Neonatal IRT FEIA kit, which was developed to measure IRT levels in dried blood spots (DBS) quantitatively for use in newborn Cystic Fibrosis screenings, were examined via method comparison analyses.

Methods:: Two different methodologies were applied for the method comparison studies using DBS samples of IRT levels within the analytical limits. First, IRT measurements were performed in 130 DBS samples in parallel with Trimaris Newborn IRT FEIA and its equivalent kit, and the results were examined by regression analysis and Bland–Altman analysis. Additionally, IRT values of 52 external quality control samples obtained from CDC were measured by Trimaris Neonatal IRT FEIA, and the results were examined by regression and Bland–Altman analyses.

Results: In the first analysis, the correlation(R) value was found to be 0.96, with slope:1.044 (95%CI: 0.992 – 1.096) and intercept:5.497 (95%CI: 0.404 – 10.591); Bland–Altman analysis indicated that the bias was 9.004ng/ml(11%). In the second analysis, the correlation(R) value was found to be 0.99, with slope:1.097 (95%CI: 1.061 – 1.163), and intercept:0.37 (95%CI: -4.67 – 5.41); Bland–Altman analysis indicated that the bias was 10.15ng/ml (10%).

Conclusions: As the total allowable error in newborn screenings assays using DBS is 30%, the bias values obtained in method comparison studies conducted both using the equivalent kit, and external quality control samples lie within the acceptable range.

Slope and intercept values within acceptable limits, and high correlation coefficients show that Trimaris Neonatal IRT FEIA performs quantitative IRT measurements from DBS samples accurately.

Keywords: neonatal screening, Dried Blood Spots DBS, IRT, Cystic Fibrosis, FEIA

S147

EFFECT OF SILYMARIN ON ACRYLAMIDE-INDUCED APOPTOSIS AND CYTOTOXICITY IN MOUSE HEPATOCYTE CELL LINE

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Objectives: Although previous studies reported the hepatoprotective effects of silymarin, its effect on acrylamide-induced hepatotoxicity is unknown. The present study aimed to determine the effect of silymarin on acrylamide-induced apoptosis and cytotoxicity in AML12 cells.

Methods: We treated AML12 cells with 12.5, 25, 50, 100, 200, and 400 µg/ml silymarin for 24 hours to determine the effect of silymarin on cell viability. AML12 cells were treated with 12.5, 25, and 50 µg/ml silymarin simultaneously with 10 mM acrylamide for 24 hours to determine the effect of silymarin on acrylamide-induced cytotoxicity. Cell viability was evaluated by MTT assay. AML12 cells were treated with 12.5 and 25 µg/ml silymarin simultaneously with 10 mM acrylamide for 24 hours to determine the effect of silymarin on in acrylamide-induced apoptosis. Then, procaspase-3 and cleaved caspase-3 levels were measured by immunoblotting.

Results: 400 µg/ml silymarin caused a significant decrease in cell viability in AML12 cells, and 100 and 200 µg/ml silymarin-treated cells were below 90% of the control group. Acrylamide caused a significant increase in cleaved caspase-3 levels and a significant decrease in cell viability. 12.5 and 25 µg/ml silymarin

caused a significant increase, but 50 µg/ml silymarin did not change cell viability in acrylamide-treated cells. Procaspase-3 levels were not significantly different between groups. 12.5 and 25 µg/ml silymarin caused a significant decrease in cleaved caspase-3 levels in acrylamide-treated cells.

Conclusions: This study showed that silymarin caused a significant decrease in acrylamide-induced apoptosis and cytotoxicity in mouse hepatocyte cells.

Keywords: Acrylamide, Silymarin, Apoptosis, Cytotoxicity, AML12 cells

S148

POTENTIAL BENEFICIAL EFFECTS OF BROMELAIN AGAINST OXIDATIVE DAMAGE CAUSED BY METHOTREXATE IN RAT TESTICULAR TISSUE

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Objectives: Methotrexate is an antiproliferative folic acid antagonist used in the treatment of various types of cancer. However, the clinical use of methotrexate in cancer treatment is limited due to some side effects. Bromelain, obtained from of the unripe pineapple plant, is a mixture of proteolytic enzymes. Antioxidant effects of bromelain have been shown in many studies. This study aimed to investigate the potential beneficial effects of bromelain against male reproductive system oxidative damage caused by methotrexate administration.

Methods: Twenty eight rats were randomly divided into 4 equal groups. The rats in the first group were kept as the control group. The rats in the second group were given bromelain by gavage at a dose of 200 mg/kg once a day for 14 days. The rats in the third group were administered a single dose of 20 mg/kg methotrexate intraperitoneally on the third day. Bromelain and methotrexate were administered together in the same dose and manner to the rats in the fourth group.

Results: Methotrexate administration did not cause any significant change in MDA and GSH levels



and SOD and GPx activities compared to the control group, but caused a significant decrease in CAT activity ($p=0,005$). Administration of bromelain along with methotrexate caused a significant decrease in GPx activity ($p=0,015$) and a significant increase in CAT activity ($p<0,001$) compared to the group administered methotrexate alone.

Conclusions: In this study, methotrexate administration caused a partial oxidative damage, depending on the number of doses and duration of administration probably. Co-administration of bromelain with methotrexate showed limited protective effect.

Keywords: Methotrexate, Bromelain, Reproductive Damage, Oxidative Stress, Testicular Tissue