Congress Abstracts

62nd National Congress of the Hungarian Society of Laboratory Medicine

Szeged, Hungary, August 28–30, 2025

President of the Congress
Imre Földesi

Scientific Organizing Committee
János Kappelmayer

Contents

Abstracts

Oral Communications

These abstracts have been reproduced directly from the material supplied by the authors, without editorial alteration by the staff of this Journal. Insufficiencies of preparation, grammar, spelling, style, syntax and usage are the authors' responsibility.

ORAL PRESENTATIONS

Abstr. Nr. SE1.1

Applicability of laboratory algorithms at a university laboratory in anemia and body fluid analysis

Hevessy Z., Kürti G.-Szabó E., Baráth S., Bartha-Tatár A., Tóth G., Kappelmayer J.
Department of Laboratory Medicine, Faculty of Medicine, University of Debrecen, Debrecen, Hungary

Background: We have developed previously a complete and efficient algorithm for laboratory medicine physicians for the differential diagnosis of anemia. We have also introduced an algorithm for cell counting in body fluids (BF) recently. We aimed to test the applicability of these algorithms in the routine workflow.

Methods: We collected the HGB and RETI% results measured at the Department of Laboratory Medicine of the University of Debrecen in 2023 from the laboratory information system (LIS) database. Last year 297 samples were investigated for thalassemia, their laboratory results were collected from LIS. Turnaround time (TAT) was calculated from LIS data in a period before and after the introduction of the new BF algorithm.

Results: We found that 16.7% of men (5,495), 16.9% of non-pregnant women (NPW) (7,261), and 27.4% of pregnant women (PW) (825) had HGB levels below the WHO-defined anemia threshold. The number of anemic patients who had RETI% ordered was low, with only 19.9% of anemic men (1,096), 18.9% of anemic NPW (1,371), and 1.45% of anemic PW (12). On the other hand, 51% (944) tests in NPW and 76% (1359) RETI% tests in men were carried out in non-anemic individuals. In case of thalassemia investigation, low MCV was detected in 54% of samples, iron panel could be performed in 30% of patients and those patients having HbA2>3.5% had *HBB* gene alteration in 90%. With the new BF algorithm routine TAT median of WBC in CSF decreased to 31 min from 84 min and emergency TAT median to 33 min from 78 min ($p<0.001$) and percentage of outliers decreased dramatically.

Conclusion: Most anemic patients do not have a RETI% result, on the other hand, a significant proportion of RETI% measurements were performed in non-anemic individuals. Pop-up windows in the clinical medical system could aid clinicians in navigating the next step in the anemia investigation based on the algorithm. The new BF algorithm decreased the number of samples that need to be counted by microscopy and TAT decreased drastically.

Abstr. Nr. SE1.2

Quality control on hematology cell counters by accreditation requirements and guidelines

Szakony S., Szurovecz M., Zemplenyi M.
Central Laboratory, South Buda Central Hospital, St Imre University Teaching Hospital, Budapest, Hungary

Background: The ISO 15189 accreditation standard pays special attention to ensuring the validity of examination results. Accomplishing this in hematology cell counters is not as simple as in clinical chemistry. The International Council for Standardization in Hematology (ICSH) published a guideline in 2024 to help laboratories develop quality control (IQC) policies. Our laboratory has previously used several methods in hematology IQC, and we have refined these by the guidelines.

Methods: We have determined the manufacturer's commercial control's measurement frequency, target value, and action limits. We also employ other forms of IQC: retained fresh patient specimens, patient moving averages, delta-checking with previous patient results, and verification of cell counter results by blood film examination. The results are recorded partly in the IQC program, an Excel spreadsheet, and a laboratory information system (LIS).

Results: The clinically important parameters of the commercial control are plotted on a Levey-Jennings graph at 3 levels (WBC, RBC, Hb, MCV, PLT) and evaluated using a trend analysis or rule-based system. However, this is not sensitive enough, so we use retained fresh patient specimens daily to assess imprecision and weekly for inter-instrument comparison. The patient moving averages detect drift between control runs. Delta-check helps to detect pre-analytical errors. Abnormal

hematological parameters are evaluated through blood film examinations. Hematology supervisor periodically reviews documentation.

Conclusion: The IQC policy developed based on the ICSH guideline enabled the continuous coordination of the two hematology automated systems, used in the laboratory, operating on different principles, the early detection of emerging problems and the timely initiation of troubleshooting, the daily verification of the precision limits specified by the manufacturer, and the fine-tuning of the blood film examination algorithm.

Abstr. Nr. SE1.3

False-Positive HIL Index: How It Can Lead to the Diagnosis of a Malignant Hematologic Disorder

Batik D., Babarczy E., Gőcze P.
Győr-Moson-Sopron-County Petz Aladár University Teaching Hospital, Győr, Hungary

Background: Hemolysis, icterus, and lipemia (HIL) are the most common sample integrity issues that can interfere with laboratory testing. They may lead to erroneous results and, ultimately, inappropriate medical decisions. In automated systems, visual HIL index verification is often omitted, and reliance is placed solely on the automated results.

Method: We present two case studies demonstrating how falsely elevated lipemia or hemolysis indices can lead to the diagnosis of hematologic disease. The first case involved a 45-year-old female patient admitted to the emergency department with splenic rupture, while the second case involved a 75-year-old female patient with a wrist fracture. Blood samples were sent to the emergency laboratory. Complete blood count analysis was performed on a Sysmex XN-1000 analyzer, and chemical testing was conducted on a Siemens Atellica CH 930 module.

Results: The chemical analyzer's HIL index indicated two crosses (++) for lipemia in one case and three crosses (+++) for hemolysis in the other, yet visual inspection revealed both samples to be completely homogeneous. Due to the discrepancy in HIL indices, the laboratory ordered additional tests, including total protein, immunoglobulins, and serum protein electrophoresis. After consulting with the attending surgeon, preliminary suspicion of a malignant hematologic disorder was raised.

Conclusion: The discrepancy between the HIL index and visual serum inspection may reveal an underlying malignant hematologic condition. A simple observation can quickly raise suspicion of a hematologic malignancy. Thus, even a central laboratory in a hospital can provide crucial support to clinicians in early detection.

Abstr. Nr. SE1.4

Challenges in the Evaluation of Variants of Unknown Significance in Hematological Malignancies

Andrikovics H., Csabán D., Benedek-Szabó F., Bors A., Őrfi Z.
Laboratory of Molecular Genetics, Central Hospital of Southern Pest – National Institute of Hematology and Infectious Diseases, Budapest, Hungary

In the field of oncohematology, there are currently no universally accepted international guidelines regarding including variants of unknown significance (VUS) in diagnostic reports generated by next-generation sequencing (NGS). This study reevaluates previous NGS findings using consensus reference variant lists derived from large-scale studies and compares them to automated classification algorithms designed to evaluate somatic mutations. The 59-gene consensus myeloid NGS panel was utilized (CLC Genomics Workbench 21, Golden Helix - VSClinical). The ClinGen/CGC/VICC, WHO, ComPerMed Expert Panel, and NCCN guidelines were used to determine the clinical significance of identified variants. Clinical samples (n=467) from 443 patients with suspected or confirmed oncohematological diseases involved 17,102 variants (755 oncogenic/

likely oncogenic; 471 variants of unknown significance, and 15876 benign by the Golden Helix – VSClinical automated variant classification). Classification remained unchanged for 98% of variants (n = 16,687). A total of 120 variants initially classified as VUS were reclassified as clinically significant, 91 of them based on evidence reported by WHO and NCCN guidelines (e.g., frameshift variants in *ASXL1*, *CEBPA*, *BCOR*, and *NPM1* genes). Classifying somatic variants can be challenging. In response, the UK NEQAS launched the *"Pathogenicity of Hematological Neoplasia Variants"* pilot survey and external quality control program in 2023, aiming to standardize the interpretation of genetic variants in hematological malignancies. While the 98% concordance rate is reassuring, reclassifying even a small percentage of VUS to clinically relevant findings highlights the importance of periodic data reevaluation. Continuous monitoring of comprehensive clinical and functional research studies is essential for reclassifying variants of unknown significance.

Abstr. Nr. SE1.5

Laboratory evaluation of glucose-6-phosphate dehydrogenase enzyme activity in Hungary

Fejes Z.[1], Kürti G.-Szabó E.[1], Nagy O.[1,2], Balogh I.[1,2], Hevessy Z.[1], Kappelmayer J.[1]
[1]Department of Laboratory Medicine, Faculty of Medicine, University of Debrecen, Debrecen, Hungary. [2]Divison of Medical Genetics, Faculty of Medicine, University of Debrecen, Debrecen, Hungary

Background: Glucose-6-phosphate dehydrogenase (G6PD) enzyme deficiency is one of the commonest enzymopathies worldwide (over 500 million people are affected). In G6PD deficiency, less NADPH are generated in red blood cells making them more vulnerable to oxidative stress induced by antimalarial drugs (*e.g.* primaquine) or other medications (*e.g.* antibiotics, NSAIDs), that may trigger acute hemolytic anemia (AHA) in such patients. Our goal was to evaluate the results of G6PD measurements and estimate the prevalence of G6PD deficiency in Hungary.

Methods: G6PD activity was measured spectrophotometrically using an enzymatic quantitative assay in a total of 96 patients (54 males, 39 infants and 57 adults) with suspicion of non-immune mediated anemia, malaria infection or intravascular hemolysis. *G6PD* gene variants were retrospectively investigated by bioinformatic reanalysis of a 5-year period of sequencing data.

Results: Based on the enzyme activity results, out of the 96 clinical samples we detected 2 patients with G6PD deficiency (<10%) and 2 others showed decreased G6PD level (58 and 60%, respectively). Among the 701 genetically tested patients, we found 3 patients with a Class-II pathogenic *G6PD* variant in exon11 (p.Arg454Cys), which may trigger AHA after oxidative stress. A 19-year-old Nigerian male patient with fever, abdominal pain, and weakness was diagnosed with *Plasmodium ovale* infection. Due to the markedly reduced G6PD enzyme activity (6%), he received extended administration of reduced dose of primaquine, and drug induced AHA was not developed during the observation period.

Conclusion: Although G6PD deficiency is a rare genetic disease in Hungary (estimated prevalence is <1%), the increasing number of affected ethnic groups makes it reasonable to measure enzyme activity as a screening laboratory test.

Abstr. Nr. SE1.6

Autoimmune Hemolytic Anemia caused by *Streptococcus pneumoniae* Infection – A Case Report

Tomán A[1], Csapody M.[2], Szabó C.[2], Bekő G.[1]
Bethesda Children's Hospital, Central Laboratory[1], Intensive Care Unit[2], Budapest, Hungary

Background: Autoimmune hemolytic anemia (AIHA) is a rare, acquired condition caused by antibodies targeting antigens on red blood cells. In the cold type, these antibodies become active at lower temperatures. Diagnosis is based on clinical history, symptoms, and laboratory findings consistent with hemolysis.

Methods and Results: We report the case of a 1-year-old girl admitted to our intensive care unit due to respiratory failure. Her illness began five days before with upper respiratory symptoms and followed by fever three days later. *Streptococcus*

pneumoniae antigen was detected in the pleural fluid. Laboratory tests revealed anemia, moderate thrombocytopenia, elevated acute phase proteins and LDH, prolonged APTI, low albumin and total protein. Due to rapid deterioration, she required invasive respiratory support. Her blood count showed a drastic decrease in hematocrit and platelet count within 12 hours, and cold agglutinins appeared in the blood smear. Neurological symptoms, the fact of pneumococcal infection, and anemia raised the possibility of p-HUS. The presence of cold agglutinins, absence of schistocytes, normal renal function, and hepatosplenomegaly supported the diagnosis of AIHA. An unusual aspect of the disease course was that, despite suspected intravascular hemolysis, serum bilirubin levels remained within the normal range throughout. High-dose methylprednisolone therapy was initiated as treatment. The *Mycoplasma* IgM titer was initially elevated; however, based on the subsequently low IgG levels, an acute *Mycoplasma* infection was ultimately ruled out as the underlying cause.

Conclusion: Our patient showed a progressive clinical and laboratory improvement on intravenous therapy and was successfully extubated on the seventh day of treatment. At another hospital she underwent decortication and lung resection, after which the air leak resolved. Due to her hematologic condition, she remains under hematology follow-up.

Abstr. Nr. CS1.2

Investigation of blood biomarkers for the management of traumatic brain injury (TBI)

Bencze D.[1], Bíró L.[2], Sütő R.[3], Pócsi M.[1], Kappelmayer J.[1], Nagy B. Jr.[1]
[1]Department of Laboratory Medicine, [2]Gyula Kenézy Campus, Emergency Medicine Unit and [3]Intensive Care Unit, Faculty of Medicine, University of Debrecen, Debrecen, Hungary

Background: Assessment of blood biomarkers represents a relevant approach to identify patients at risk for intracranial injury requiring computed tomography (CT) examination. Protein S100 beta (S100B) is a well-known TBI biomarker but has a relatively short half-life. Combined measurement of astrocytic glial fibrillary acidic protein (GFAP) and neuroaxonal marker ubiquitin carboxyterminal hydrolase L-1 (UCH-L1) has recently been introduced to aid the clinical diagnosis of mild TBI within 12 hours of trauma.

Methods: In this study, 41 TBI patients having Glasgow Coma Scale (GCS) score of 3-15 were enrolled at the age of 59.1 ± 21.3 years (11 females and 30 males). Serum GFAP, UCH-L1 and S100B at admission were analyzed on an Architect® i1000SR (Abbott) and a Liaison® XL (DiaSorin) instrument, respectively. Diagnostic characteristics of these biomarkers were statistically evaluated, and their levels were correlated with TBI severity based on CT positivity and GCS scores.

Results: Significantly ($p<0.001$) higher concentrations of GFAP (2896 [161-8455] vs. 36 [20-71] ng/L), UCH-L1 (3398 [386-8079] vs. 446 [285-682] ng/L), and S100B (2.38 [0.42-4.90] vs. 0.22 [0.11-0.35] µg/L) were measured in patients with positive CT scan compared to those with negative result. A significant inverse correlation was found between GFAP and GCS values ($r=-0.405$, $p=0.010$). According to ROC-curve analysis, baseline GFAP was the most effective among these biomarkers to indicate clinically significant TBI with a substantial AUC value of 0.928 ($p=0.0009$). Using the official GFAP cut-off value of 35 ng/L, 100% sensitivity and 48.6% specificity was determined.

Conclusion: Based on our preliminary data, GFAP and UCH-L1 can routinely contribute to accelerated diagnosis of TBI.

Abstr. Nr. SE2.1

Macro-TSH screening in daily practice

Szurovecz M., Szűcs J., Szakony S.
Central Laboratory, South Buda Central Hospital, St Imre University Teaching Hospital, Budapest, Hungary

Background: The issue of macro-TSH has been raised in the scientific literature for the past two decades, but only recent reviews have been published to investigate it. Hormone replacement therapy for subclinical hypothyroidism is usually started when the TSH level is above 10 mIU/L, therefore, it is crucial to identify cases of elevated TSH levels due to macro-TSH

or other potential laboratory interferences such as heterophile antibodies (HeAbs) and human anti-mouse antibodies (HAMAs).

Methods: Among the possible investigation steps, we have chosen two that can be performed in any laboratory: dilution test and precipitation with polyethylene glycol (PEG). In the latter, serum samples are incubated at a 1:1 ratio with a solution of 12.5% PEG. In the case of dilution, a deviation above the measurement uncertainty was considered positive. In the case of PEG precipitation, a PEG-precipitable TSH value above 75% was considered positive.

Results: In the first four months of 2025, out of 3300 TSH measurements (Abbott Architect i2000SR), we found 52 cases with results above 10 mIU/L, of which 24 cases had subclinical hypothyroidism. Sample dilution and PEG precipitation was performed in 8 cases. There was no difference in sample dilution. All but one of the TSH results that could be precipitated with PEG were above 80%.

Conclusion: The laboratory workflow for investigating unusual TSH results should, at a minimum, include a dilution test and PEG precipitation. PEG precipitation is a dependable diagnostic method for identifying macro-TSH. Nevertheless, effective communication between clinicians and laboratory professionals is essential to reduce the likelihood of inaccurately reported thyroid function test results.

Abstr. Nr. SE2.2

A methodology for assaying cortisol and cortisone in serum and dried blood microsamples in cooled asphyxiated newborns

Csöndör É[1], Farkas R.[1], Kovács K.[2], Dobi M.[2], Kerekes R.[2], Zsolnai H.[2], Vásárhelyi B.[1], Szabó M. [2], Karvaly G.B.[1]
[1]Department of Laboratory Medicine, Semmelweis University, Budapest, Hungary, [2] Department of Neonatology, Pediatric Center, Semmelweis University, Budapest, Hungary

Background: Perinatal asphyxia is a life-threatening event, and whole-body hypothermia combined with intravenous hydrocortisone sodium succinate therapy has proved to be important for the survival of the neonates with hemodynamic instability. As part of a study conducted by the Pediatric Center, Semmelweis University (IF-56-7/2016/EKU), a method was developed to quantitate cortisol (F) and cortisone (E) with the aim to meet the special clinical demands related to the assessment of the glucocorticoid status of these newborns.

Methods: F and E levels were evaluated in 50 µL serum or 10 µL capillary dried blood obtained using volumetric absorptive microsampling (VAMS) technology and liquid chromatography–mass spectrometry. Following method validation, assay results were compared in serum and in dried blood technically (n=25), as well as in arterial serum and capillary blood obtained by heel prick *in vivo* (n=80).

Results: In serum, within-run and between-run accuracy were 102-110% and 97-105.6% for F, as well as 97-101% and 96-108% for E. Assay precision was <15%. In VAMS samples, F and E recoveries were 119-143% and 77-109%, respectively, on the day of sample drying (day 0). After keeping samples at room temperature for 7 days, the recoveries were 89-99% and 84-99%. On days 0 and 7, assay reproducibility was 7,2-17,0% and 5,5-5,8% for F and 1,9-17,0% and 5,1-6,9% for E. Strong correlation was observed between serum and dried blood levels (r=0.9075), but, in samples collected from asphyxiated neonates, with large random differences in the case of F, and random as well as systematic differences in the case of E.

Conclusion: The method is suitable for assessing cortisol and cortisone concentrations in serum and capillary dried blood microsamples collected from cooled neonates.

Abstr. Nr. SE2.3

Our experiences with pancreatic elastase measurement in suspected exocrine pancreatic insufficiency among children

Meláth M., Mezei E, Nagy I., Párniczky A.
Heim Pál National Pediatric Institute, Budapest, Hungary

Background: Pancreatic elastase (PE) concentration measured in faeces is a reliable marker for the evaluation of pancreatic exocrine function. It supports diagnosis and helps to determine the severity in many chronic pancreatic diseases, such as cystic fibrosis (CF), chronic pancreatitis (CP) and other malabsorption syndromes. It is considered to be normal over 200 µg/g of stool.

Methods: We performed 745 PE test on the faecal sample of children hospitalized at Heim Pál National Pediatric Institute from September 2020. Tests were based on ELISA method and patients taking pancreatic enzyme replacement therapy (PERT) were not excluded as the used monoclonal antibodies show no cross-reactivity with animal derived elastase-1. There, 685 sample of 745 samples were collected from children previously diagnosed with CF whose PE is under control twice a year. 31 tests were carried out on samples from children with CP or other suspected exocrine pancreatic insufficiency (EPI). We performed 29 measurements due to CF biomarker abnormalities based on newborn screening.

Results: We measured pathological PE values in all CF patients except for one. We detected increasing PE levels during the administration of modulator therapy. 2 patients with suspected EPI showed abnormal PE. Of newborns 1 patient was found to have CF diagnosis which was confirmed by PE test.

Conclusion: Based on our results, the non-invasive faecal PE test is a reliable and easily accessible diagnostic tool that can contribute to the early detection of EPI and development of an appropriate therapeutic strategy in pediatric patients. Our data show that results should also be considered when evaluating values are between 200-500 µg/g.

Abstr. Nr. SE2.4

Analysis of platelet transcripts as potential diagnostic biomarkers for the early detection of lung cancer

Balla G.J.[1], Pócsi M.[1], Lieber A.[2], Matolay O.[3], Szilárd S.[4], Fejes Z.[1], Kappelmayer J.[1], Nagy B. Jr.[1]
[1]Department of Laboratory Medicine, [2]Department of Pulmonology, [3]Department of Oncology, [4]Department of Biochemistry and Molecular Biology, Faculty of Medicine, University of Debrecen, Debrecen, Hungary

Background: Despite the recent development of diagnostic and therapeutic interventions, the incidence of lung cancer remains high. Platelets can advance tumor progress via transferring tumor cell-derived RNAs. Consequently, the RNA content of human platelets is modified in cancer, which is known as tumor-educated platelets.

Methods: RNA isolated from leukocyte-depleted platelet samples of newly diagnosed early-and advanced stage lung tumor patients prior to any treatment was analyzed using next-generation RNA sequencing (Illumina). We compared these results to age- and gender-matched healthy controls and COPD patients (n=3/group). Genes showing significant expression changes (FC > or < 1.5) were analyzed by ClueGO (gene ontology). We compared the correspondence of genes with abnormal expression in the histopathological lung and platelet samples of a patient with early-stage lung cancer.

Results: In early-stage lung tumors, the level of 524 platelet transcripts increased (e.g. *MALAT1*), while 119 genes decreased significantly (e.g. *GATA3*) compared to controls. In advanced stage, 757 genes were elevated (e.g. *TP53I3*) and 198 showed decreased levels (e.g. *RUNX3*). Platelet genes with abnormal expression are involved in the regulation of intracellular processes, such as cell activation, vesicle secretion, cytoskeletal rearrangement and transcription regulation. Finally, we identified 65 tumor-derived pathological transcripts (e.g. *SERPINE2*) in platelets, detectable in both lung biopsy and platelet samples. These genes are involved in stress processes.

Conclusion: RNA expression in human platelets is significantly altered in lung tumor acting as a potential new diagnostic test for the detection of pulmonary cancer.

Abstr. Nr. SE2.5

The role of molecular genotyping in the differential diagnostic workflow of hydatidiform mole

Böjtös I., Tardy E.P., Sarkadi E., Simon J., Fülöp V.
Central Hospital of Northern Pest-Military Hospital, Budapest, Hungary

Background: Hydatidiform mole (HM) is an abnormal gestational disease with elevated β-hCG level, specific ultrasound, histopathologic and genetic alterations. HM can be classified as complete mole (CHM), with an empty ovum fertilized by diploid or two haploid sperms, and partial mole (PHM) being triploid with one maternal and two paternal genomes. HM can progress into gestational trophoblastic neoplasia, so differentiating HM from hydropic abortion (HA) is of utmost importance in further clinical management. As specific histopathologic markers can give discordant results, defining the genetic background provides the most reliable outcome. Ploidy pattern can be defined by conventional karyotyping, fluorescence in situ hybridization or microsatellite analysis (MS-STR), while specifying the number of the paternal chromosome sets is achieved by analysing the methylation pattern of imprinted genes with methylation specific multiplex ligation-dependent probe amplification (MS-MLPA). The latter two require DNA isolated from fresh or paraffin embedded tissue (FFPE).

Methods: 291 cytogenetic analyses were done on fresh products of conception (POC) by standard methods. The introduction of MS-STR and MLPA broadened the diagnostic workflow, facilitating the identification of the paternal genome. 8 FFPE samples were analysed because of ambiguous hystopathology finding.

Results: 140 POC sample gave abnormal results. From the 19 HM samples 10 were identified as CHM, 9 were classified as PHM. The analysis of 7 FFPE specimens resulted in clear-cut HM diagnosis, one sample was classified as HA.

Conclusion: The most optimal workflow for the differential diagnosis of HM starts with karyotyping fresh POC specimen to distinguish between HA and HM. MS-MLPA enables to define the quantity of the paternal genome. Lacking fresh tissue, genotyping FFPE samples with molecular genetic methods is a highly accurate and integral part of the differential diagnosis in our center.

Abstr. Nr. SE3.1

Ethical challenges of innovative medical interventions in the face of artificial intelligence

Fodor B.[1,2]
[1] Borsod-Abaúj-Zemplén County Hospital and University Teaching Hospital, Department of Laboratory, Miskolc, Hungary
[2]University of Miskolc, Faculty of Healthcare Studies, Miskolc, Hungary

The rapid advancement of innovative medical technologies is fundamentally transforming cell-level therapeutic and diagnostic possibilities. Theranostics are opening new horizons in precision medicine, while organoids are becoming indispensable in pharmaceutical research as reliable models mimicking human tissues. The use of quantum dots enables in situ visualization of surgical areas, and lab-on-a-chip systems along with next-generation sequencing technologies are challenging traditional scientific paradigms. The digital revolution and the era of big data have inundated physicians and healthcare professionals with an unprecedented volume of information, presenting significant processing challenges.

Regenerative medicine now allows for the growth of organs and even embryonic gene manipulation, with the CRISPR-Cas9 system playing a key role. In parallel, biohackers are developing gene therapy agents in non-traditional, even home-based environments, while research into the digitization of consciousness is intensifying. These technological breakthroughs raise serious ethical concerns. The spread of cyberchondria - health anxiety driven by online information - alongside the tension between technological capabilities and the foundational principles of medical ethics (autonomy, non-

maleficence, beneficence, and justice), is becoming increasingly evident. Artificial intelligence-based medical algorithms are gaining a greater role in diagnostic and therapeutic decision-making, prompting a re-evaluation of ethical norms and professional responsibilities. This presentation aims to explore key ethical aspects of modern medical procedures in the face of artificial intelligence.

Abstr. Nr. SE3.2

Admission D-Dimer Levels Combined With Artificial Intelligence-Supported Imaging Can Help Predict Outcomes in Acute Ischemic Stroke Patients Treated with Intravenous Thrombolysis

Kis B.[1,2], Orbán-Kálmándi R.[2,3], Lóczi L.[2,4], Bomberák D.[2,3], Hodossy-Takács R.[2,3], Szegedi I.[2,5], Nagy A[6], Kádár A.Z.[2,3], Vasas N.[1], Berényi E.[1], Harston G.[7], Csiba L.[4,5], Oláh L.[5], Bagoly Z.[2,3]
University of Debrecen, [1]Department of Radiology, [2]Lendület "Momentum" Hemostasis and Stroke Research Group of the Hungarian Academy of Sciences, [3]Division of Clinical Laboratory Sciences, [4]HUN-REN-DE Cerebrovascular Research Group, [5]Department of Neurology, [6]Department of Preventive Medicine, Debrecen, Hungary; [7]Brainomix Ltd., Oxford, UK

Background: In acute ischemic stroke (AIS), early prognostic markers are crucial to guide treatment decisions. We aimed to assess whether admission D-dimer levels and artificial intelligence (AI)-supported imaging analysis can serve as predictive tools in AIS patients treated with thrombolysis.

Methods: In this prospective observational study, 423 AIS patients receiving i.v. rt-PA were included. Admission, post-lysis (n=132) and 24-hour D-dimer levels were measured. Alberta Stroke Program Early CT Scores (ASPECTS) and cerebral atrophy were assessed with AI-based software on admission and in 24-hour CT scans. Primary outcomes included 90-day functional status (modified Rankin Scale, mRS), mortality, and hemorrhagic transformation (HT).

Results: In multivariable logistic regression analysis, increased admission D-dimer levels (>0.5 mg/L) were independently associated with poor outcome (mRS 3–6; OR:1.41, 95%CI:0.92–2.14) and mortality (OR:2.37, 95%CI:1.19–4.74). A 24-hour ASPECTS ≤7 showed strong association with unfavorable outcomes. Cerebral atrophy also independently predicted poor functional outcome and mortality. Kaplan-Meier analysis confirmed better survival among patients with lower D-dimer levels at admission ($p<0.001$).

Conclusion: In AIS patients, admission D-dimer levels and AI-based assessment of cerebral atrophy are readily available markers at admission that may support early risk stratification and help individualized treatment decisions in AIS care.

Abstr. Nr. SE3.3

Translating in vivo sensory glucose data into Hemoglobin A1c

Nagy T.[1], Nagy Z.[1], Kátai E.[1], Molnár G.[2], Wittmann I.[2], Miseta A.[1]
[1]Department of Laboratory Medicine, University of Pécs, Medical School, Pécs, Hungary, [2]2nd Department of Internal Medicine and Nephrological Center, University of Pécs, Medical School, Pécs, Hungary

Background: Glycation index is the discrepancy between measured and estimated (from average glucose levels) HbA1c that have an impact on the effectiveness of diabetes therapy. Previously we have demonstrated that glycation index can be quantified by the Michaelis constant on a population level. The aim of our present study was to test the accuracy of this method on the level of individual patients.

Methods: We have collected *in vivo* sensory glucose concentrations' data from 36 patients equipped with continuous glucometers for the duration of 6 months or longer. Glucose data were aggregated to obtain daily average values and from these values, daily HbA1c formation was calculated using the Michaelis-Menten (MM) equation. The effect of red blood cell (RBC) turnover was also integrated into the calculations and was assumed to last for 120 days. HbA1c levels measured in the laboratory were used to refine the personalized Michaelis constant.

Results: We have found that HbA1c levels calculated by MM equation approximated the measured HbA1c values within the uncertainty limit of the laboratory HbA1c test. Our method also produced a more realistic curve describing the dynamic change of HbA1c over time than the conventional glucose management indicator that is used by *in vivo* sensory instruments.

Conclusion: Daily HbA1c calculations refined by the MM equation and incorporation of RBC turnover into the calculations is an improvement on current methods to determine the glycation index. Our method also allows for the quantitative re-assessment of the calculations in anemic conditions when RBC lifespan is altered.

Abstr. Nr. SE3.4

Fifty years of newborn screening for inherited disorders in Hungary

Monostori P.[1], Baráth Á.[1], Galla Z.[1], Grecsó N.[1], Lénárt I.[1], Bereczki C.[1]
[1]Metabolic and Newborn Screening Laboratory, Department of Paediatrics, University of Szeged, Szeged, Hungary

Background: Screening is the systematic examination of an asymptomatic population, in order to identify individuals at high risk for a given disease. Newborn screening (NBS) allows a simultaneous detection of several inherited disorders from dried blood spots (DBSs) with the aim to avoid irreversible damage and reduce mortality. NBS in Hungary started in 1968 in Szeged, while Budapest joined as the 2nd centre in 1972. From 1975, the Hungarian NBS is being performed nationwide from DBSs, currently obtained 48-72 of age.

Methods: NBS is a comprehensive system involving birth institutions, laboratories, clinical, dietetic and social care and many others. Analytical techniques in NBS include tandem mass spectrometry, liquid and gas chromatography, immuno-assays and molecular biological tests. We provide an overview of the past 50 years of NBS, the present situation and future directions in Hungary.

Results: The screening panel in Hungary has been extended several times and now contains 27 inherited disorders, being among the broadest panels in Europe. We have developed multiple additional diagnostic assays to allow the detection and follow-up of further rare diseases. Thus, the NBS centres offer high-throughput, quality assurance-certified and comprehensive service for the patients.

Conclusion: Hungary celebrates the 50th anniversary of the implementation of the nationwide NBS. The centres in Szeged and Budapest use highly specialized assays in screening and diagnostics with in-depth know-how. Their work contributes to an improved life quality and helps saving lives among patients with a large number of inherited disorders. Both NBS centres are ready for a further extension of the offered services, as well as international collaborations.

Abstr. Nr. SE3.5

Spinal Muscular Atrophy (SMA) Laboratory Challenges – Case Report

Bekő G.[1], Tomán Á.[1], Mikos B.[2]
Central Laboratory[1], SMA Center[2], Bethesda Children's Hospital, Budapest, Hungary

Background: Spinal muscular atrophy (SMA) is a severe neuromuscular disorder caused by a defect in the *survival motor neuron 1 (SMN1)* gene. The severity of the disease is primarily determined by the number of *SMN2* gene copies; the more copies present the slower its progression. In Hungary, all three approved drugs—nusinersen, risdiplam, and onasemnogene abeparvovec—are currently state-funded. It is now well established that the best therapeutic outcomes are achieved when treatment is initiated early, ideally before the onset of symptoms. This is feasible in Hungary, where newborn SMA screening is available through a research program. One of the challenges of gene replacement therapy in infancy is the high baseline

serum high-sensitivity troponin I (hs-cTnI) levels prior to administration, as onasemnogene can also induce cardiotoxicity. Hs-cTnI is widely used to monitor potential cardiac contraindications or side effects of GRT, but reference data in healthy newborns are limited.

Methods: A male infant born in September 2024 was diagnosed with SMA type 1 at 14 days of age. He had two copies of *SMN2*. At diagnosis, he exhibited resting tachypnea and generalized muscle hypotonia, which did not worsen following gene replacement therapy administered at 28 days of age.

Results: Before gene therapy, hs-cTnI was 94.7 ng/L, CK 216 U/L. One week after therapy, hs-cTnI decreased to 26.9 ng/L, CK to 144 U/L. After three weeks, hs-cTnI was 8.1 ng/L, CK at 229 U/L. Despite the initially elevated myocardial necroenzyme levels, comprehensive cardiac monitoring did not reveal any structural abnormalities or hemodynamic side effects. The elevated values resolved spontaneously.

Conclusion: Elevated myocardial necroenzyme levels in newborns may reflect a physiological aspect of postnatal hemodynamic adaptation. However, such elevations can rarely be attributed to the cardiotoxic effects of onasemnogene. Therefore, it is crucial to monitor the patient's cardiac status closely until enzyme levels normalize.

Abstr. Nr. SE3.6

Neonatal gene replacement therapy in spinal muscular atrophy: age-specific characteristics, the importance of collaboration between laboratory specialists and clinicians

Keszthelyi V., Trifán V., Tomán Á., Bekő G., Mikos B.
Bethesda Children's Hospital of the Hungarian Reformed Church, Hungary

Background: The criterion for gene replacement therapy of spinal muscular atrophy (SMA) is a low anti-AAV9 titer. Due to the T-cell mediated immune reaction, it can mainly cause hepatopathy, thrombocytopenia, myocardial involvement, and rarely thrombotic microangiopathy. The cooperation of the clinician and laboratory specialist is essential for their early recognition.

Method: Retrospective study of SMA patients who received gene replacement therapy.

Group I: n = 28, SMA was recognized based on clinical symptoms, the patients' average age at the start of therapy was 1.66 years. In group II (n = 5), gene replacement treatment was performed at an average age of 32 days in presymptomatic patients through SMA screening. Complex laboratory tests were performed before therapy and then weekly for 12 weeks to monitor cardiac, hepatic, and renal organ involvement, steroid side effects, and inflammatory reaction.

Results: The anti-AAV9 titer in the blood before administration was lower than 1:12.5 in all patients. Transaminases showed a biphasic peak in group I, were asymptomatic in 89.3%, and were reversible symptomatic with steroid intensification in 10.7%. Thrombocytopenia was 71.4% in group I and 16.6% in group II, with a trough value: group I: 121.8 G/L, group II: 286.6 G/L, hs-cTn-I was abnormally high in group II before therapy (mean: 40.8 ng/L vs. group I: 12.02), reaching its peak value 1 week after administration (group I: 38 vs. group II: 109). Organ-specific therapy was not necessary in any patient due to side effects.

Conclusion: The gene replacement treatment of SMA requires close clinical and laboratory cooperation. Among the tests, the determination of anti-AAV9 titer before administration, which is not available in our country, requires special preparations and organization. The presymptomatic use of the product is a unique opportunity for motor development similar to healthy peers, and technology independence, and to minimize side effects.

Due to atypical initial clinical symptoms of unwanted effects, complex laboratory follow-up is crucial for the correct management of immunosuppressive therapy, the prevention of thrombotic microangiopathy and definitive organ damage.

Abstr. Nr. SE4.1

Novel hemophilia treatments require novel approach by the clinical laboratory; case-reports of hemophilia A patients on emicizumab

Bereczky Z.,[1] Zombori M.,[2], Diaconu A.,[3], Nagy E.[4], Horváth Elek D.[4], Molnár É[1], Katona É.[1]
[1]Division of Clinical Laboratory Science, Department of Laboratory Medicine, Faculty of Medicine, University of Debrecen, [2]Heim Pál Children's Hospital, Budapest, [3]Pediatric Department, "Carol Davila" University of Medicine and Pharmacy, Bucharest, [4]Department of Laboratory Medicine, Faculty of Medicine, University of Debrecen

Background: The novel, bi-specific antibody, emicizumab (EMI) has markedly improved hemophilia A (HA) therapy. EMI is currently administered mostly in HA with inhibitors and it requires special skills in terms of monitoring its plasma levels, determining factor VIII activity and inhibitors to FVIII in the presence of EMI and detecting anti-drug antibodies (ADA).

Aim: We present the cases of two children with severe HA and demonstrate the role of the laboratory in their clinical management.

Case-reports: Both children were treated initially with recombinant FVIII. They showed the development of inhibitor to FVIII very early and immunotolerance induction (ITI) was unsuccessful. EMI prophylaxis was initiated with satisfactory plasma level (46.5 and 49.2 μg/mL) after the loading period. Clinical outcome of the first boy was excellent, however, in the second, unexpected bleeding started after the 15th maintenance dose.

Methods: EMI was monitored by modified one-stage assay, FVIII activity and inhibitor were detected by chromogenic assays with bovine components. A specific Bethesda assay and an ELISA were developed for the detection of ADA.

Results: Both children showed significant amount of anti-FVIII inhibitor even upon their latest examination (1.7 BU and 3.5 BU) with undetectable FVIII level. In case of the second child APTT was prolonged (132.5 sec) and EMI level was <2 μg/mL, ADA titer was 3.47 BU, which was confirmed by ELISA. After diagnosis of ADA on-demand rFVIIa treatment was initiated.

Conclusion: Clinical laboratory has an essential role in effective and safe treatment of HA in the new era.

Abstr. Nr. SE4.2

Pharmaceutical effects and side effects in laboratory reports

Dolman V., Peterfalvi A.
Department of Laboratory Medicine University of Pécs, Medical School Clinical Centre, Pécs, Hungary

Pharmaceuticals and dietary supplements are major components of any therapeutic regimen. The desired effects of medicines are often monitored with routine laboratory tests (e.g. coumarins – INR, antidiabetics – HgA1c, levothyroxine – TSH), or the drug level is directly determined in case of a narrow therapeutic window (e.g. chemotherapeutic agents). Several pharmaceuticals might cause such preanalytical or analytical interferences that can precipitate misleading laboratory test results. Here, we present a literature overview of possible drug effects on any lab test results, as well as some real-life cases focusing on electrolyte imbalances, leading to either incorrect results, or analytically valid but – sometimes extremely – abnormal results due to unsuitable drug administration or the overlooking of certain accompanying medical conditions, which thus result in side effects displayed also in the laboratory reports.

Abstr. Nr. SE4.3

When Medicines Turn Lethal: A Retrospective Study of Suicide-Related Substances

Vén B.[1], Lajtai A[1], Lakatos Á.[1], Csabai D.[1], Hesszenberger D.[1], Mayer M[2], Kuzma M.[2], Nagy T.[1]
[1]Department of Laboratory Medicine, University of Pécs, Clinical Centre, Pécs, Hungary, [2]Department of Forensic Medicine, University of Pécs, Medical School, Pécs, Hungary

Background: Hungary has had one of the highest suicide rates in Europe for decades. While there have been positive changes in mortality rates in recent years, helped by early detection of psychiatric disorders, increased treatment options and an improved socio-economic environment, the problem remains significant. The rate of suicide attempts with medication is particularly notable and remains a common modality due to the easy availability of drugs. A deeper understanding of this phenomenon is essential to improve the effectiveness of health care and prevention.

Methods: The study was based on data collected at the Toxicology Department of University of Pécs Clinical Centre. The analytical processing of the analysed serum and whole blood samples was performed by high performance liquid chromatography, coupled with diode array detector (HPLC-DAD). In many cases, primary analyses were preceded by immunochemical screening methods to help determine the direction of the targeted analysis.

Results: Based on data for the period of January 1, 2020 to April 1, 2025, the most commonly identified substances in drug intake with suicidal intent were alprazolam, amlodipine, quetiapine, clonazepam and zolpidem. The results of post-mortem toxicology studies confirm that these drugs were also the most frequent in fatal cases.

Conclusion: Our study has shown that certain agents, in particular alprazolam, amlodipine, quetiapine, clonazepam and zolpidem, play a major role in suicidal drug use. Our results may provide useful guidance for rapid identification and targeted treatment in emergency care, as well as highlight the need for closer control of prescribing and education of patients at risk. The data can contribute to the further development of prevention strategies and drug safety measures.

Abstr. Nr. SE4.4

Supporting precision dosing of vancomycin by using online pharmacokinetic calculators in the clinical laboratory

Lovász B., Kunz S., Köllő Z., Karvaly G.B.
Department of Laboratory Medicine, Semmelweis University, Budapest, Hungary

Background: Precision vancomycin therapy supported by online pharmacokinetic calculators is gaining interest. An insight into the preanalytical and postanalytical phases with the help of these applications can improve the performance of clinical laboratories. We aimed to establish a workflow to provide a pharmacokinetics-based evaluation of vancomycin concentrations that can be integrated into clinical infrastructure.

Methods: Based on clinical experience gained at Semmelweis University, the performance of online pharmacokinetic calculators (VancoPK, VancoCalc, and the Sanford Health Care Adult Vancomycin AUC Calculator) and online tools relying on professional pharmacokinetic software (TDMx and BestDose™) was compared. A clinical laboratory team was formed to advise clinicians and evaluate the results of vancomycin assays using suitable software. A format of interpretative laboratory reports was created, and the communication of these reports via the medical information system was implemented.

Results: Pharmacokinetic evaluation has been integrated into a multidisciplinary workflow, with the clinical laboratory participating in management of the pre- and post-analytical phases. All freely available online calculators have limitations, while those relying on professional pharmacokinetic software are flexible and allow keep comprehensive electronic records. Interpretative laboratory reports uploaded to the medical information system support evidence-based clinical judgment and decision-making.

Conclusion: In the era of precision therapy and integrated healthcare, supporting intravenous vancomycin treatment with therapeutic drug monitoring, pharmacokinetic evaluation, and the generation of interpretative laboratory reports offers a novel competence and the opportunity to work as a part of multidisciplinary in-hospital teams to clinical laboratories.

Abstr. Nr. SE4.5

Escalating doses of intravenous APAC demonstrate anticoagulant effect in pigs

Bomberák D[1,2,3], Orbán-Kálmándi R.[1,2], Lóczi L.[2,5], Z. A. Kádár Z. A.[2], Hodossy-Takács R[1,2,3], Németh N.[6], Kappelmayer J.[4], Jouppila A.[7], Lassila R.[7] and Bagoly Z.[1,2]
University of Debrecen, [1]Division of Clinical Laboratory Science, [2]Lendület "Momentum" Hemostasis and Stroke Research Group of the Hungarian Academy of Sciences, [3]Kálmán Laki Doctoral School, [4]Department of Laboratory Medicine, [5]HUN-REN-DE Cerebrovascular Research Group, [6]Department of Operative Techniques and Surgical Research, Debrecen, Hungary,[7] Aplagon OY, Helsinki, Finland

Background: Locally acting antiplatelet and anticoagulant (APAC) is developed as a novel antithrombotic agent for administration during vascular interventions. We aimed to assess safety and escalating intravenous (i.v.) doses of APAC on hemostasis using a large animal model.

Methods: We studied escalating APAC boluses (0.15-1.5 mg/kg; n=11) and their reversal in anesthetized pigs for pharmacodynamics using functional coagulation testing. In some experiments, aspirin (500 mg) was co-administered with APAC, and protamine sulfate for reversal. Blood was repeatedly sampled for blood cell counts, activated partial thromboplastin time (APTT), prothrombin and thrombin time (PT, TT), thrombin generation (TG), activated clotting time (ACT), rotational thromboelastometry (ROTEM), and collagen-induced platelet aggregation (CIPA).

Results: APAC modestly inhibited CIPA at high doses, while APTT, TT and ACT, unlike PT, prolonged dose-dependently. The anticoagulant ED_{50} doses of APAC and UFH showed similar range (0.54 vs 0.43 mg/kg), but UFH lasted longer and was less reversible by protamine. At 0.75 mg/kg of APAC, TG was abolished, InTEM coagulation and clot formation times were prolonged $\geq$2.8-fold, maximum clot firmness was reduced to 8-45%, and amplitude to 35-80%. APAC effects were transient ($T_{1/2}$ APAC=30 min), and reversible by protamine.

Conclusion: Escalating i.v. doses of APAC were safe and provided modest platelet inhibition. Our results indicate that the dose-dependent anticoagulation effects of APAC can be easily monitored using conventional laboratory assays.

Abstr. Nr. CS5.1

Improving Prostate Cancer Risk Stratification: Diagnostic and Economic Impact of the Prostate Health Index (PHI)

Hajas T.[1]
[1]Beckman Coulter Hungary Ltd.

Background: Prostate cancer is a significant public health concern in Hungary, with high incidence and mortality rates. While early detection is essential, current PSA-based screening methods suffer from limited specificity and sensitivity, often leading to unnecessary biopsies and MRI scans. The growing demand for diagnostic imaging, coupled with restricted MRI availability, places additional strain on the healthcare system. There is a pressing need for a more accurate and cost-effective diagnostic strategy.

Methods: The Prostate Health Index (PHI), which combines total PSA (tPSA), free PSA (fPSA), and [-2]proPSA (p2PSA), offers 3 times enhanced risk stratification compared to traditional PSA testing. PHI scores, derived from serum samples, help distinguish between benign conditions or indolent tumors and clinically significant prostate cancer (csPCa), particularly those with Gleason Score >7.

Results: Incorporating PHI into diagnostic models improved predictive accuracy from 72.14% to 76.09%. When combined with mpMRI, PHI further improved csPCa detection. Limiting biopsies to patients with PI-RADS 5 or PI-RADS 3/4 and PHI ≥ 30 could reduce biopsy rates by up to 50%. PHI also showed strong correlation with Gleason Grades, supporting its role in pathological risk stratification. As per findings from the PRIM study, a strategy using mpMRI for all patients and biopsying only positive lesions reduced unnecessary biopsies by 35% but missed 9% of ≥GG2 and 5% of ≥CPG3 cancers. In contrast, using PHI ≥ 30 to exclude referrals missed 8% and 5% of ≥GG2 and ≥CPG3 cancers, respectively, while reducing unnecessary biopsies by 40% and requiring 25% fewer mpMRIs. PSAd-based pathways missed fewer cancers but led to more unnecessary biopsies. The PHI-based strategy had the lowest mean costs, with decision curve analysis (DCA) demonstrating net clinical benefit across a range of thresholds.

Conclusion: PHI significantly enhances prostate cancer risk assessment and serves as an effective triage tool to reduce unnecessary imaging and biopsies. Its integration into clinical workflows may lower healthcare costs and ease diagnostic burdens without compromising the detection of clinically significant disease. These findings support the broader implementation of PHI in Hungary's prostate cancer screening protocols.

Abstr. Nr. CS5.2

The place and role of proPSA and the PHI index in prostate cancer screening and follow-up - prospective clinical study at the University of Pécs

Damásdi M.
Department of Laboratory Medicine, University of Pécs, Medical School, Pécs, Hungary

Background: Prostate cancer incidence in Hungary is below the European average, but mortality is above the EU average. Timely detection and treatment can lead to nearly 100% 5-year survival rates, while metastatic prostate cancer survival rates are much lower (5-28%). Hungary lacks an organized prostate cancer screening program, leading to a high proportion of histologically negative biopsies and insignificant prostate cancer cases. Effective screening requires organ-specific biological markers like PSA, which alone lacks sufficient sensitivity and specificity.

Methods: This clinical trial at the University of Pécs included 116 patients meeting risk-adapted prostate cancer screening criteria between February and November 2021. Suspected prostate carcinoma necessitated TRUS-guided prostate biopsies. Data and samples (histology, blood, urine) were collected from these patients. The study examined proPSA and PHI values alongside other markers to identify parameters with the best diagnostic potential for significant prostate cancer.

Results: ProPSA and PHI values were significantly higher in histologically proven significant prostate cancer cases (>ISUP 2) (62%) compared to histologically negative cases (38%). In risk-adapted screening, proPSA assays and PHI calculations with elevated PSA values (4-10 ng/ml total PSA or PSAD ≤0.1-0.15 ng/ml/cm^3) could reduce unnecessary biopsies and increase the detection of significant prostate cancer.

Conclusion: The study highlights the need for additional biological markers to improve prostate cancer screening and follow-up. ProPSA and PHI values show promise in enhancing diagnostic accuracy and reducing unnecessary biopsies.

Abstr. Nr. CSE5.3

Our first experience on the analysis of -2proPSA and determination of Prostate Health Index (PHI) for the management of prostate cancer

Nagy B. Jr.[1], Kalina E.[1], Bálint R.[1], Pócsi M.[1], Flaskó T.[2], Kappelmayer J.[1]
[1]Department of Laboratory Medicine, [2]Department of Urology, Faculty of Medicine, University of Debrecen, Debrecen, Hungary

Background: The total level of prostate-specific antigen (tPSA) has been used as a tumor marker for screening prostate cancer (PC), however, it has a limited specificity causing an excessive number of prostate biopsies, while its low sensitivity may lead to decreased detection of low-grade PC. Hence, the recent introduction of -2proPSA assay and especially the determination of the Prostate Health Index (PHI) has led to improved clinical PC detection. Our aim was to introduce this biomarker at our Clinical Center to facilitate the clinical decision on active surveillance or radical prostatectomy.

Methods: In total, 176 male patients were enrolled from the Department of Urology. The level of tPSA and fPSA were measured and compared on two platforms (Liaison XL, DiaSorin and DxI 9000, Beckman Coulter), while -2proPSA and PHI were newly determined. These data were correlated with each other, and their utility was evaluated in cancer stratification based on the Gleason score and other clinical parameters.

Results: Values of tPSA ($r=0.965$, $p<0.0001$), fPSA ($r=0.945$, $p<0.0001$) and PHI ($r=0.805$, $p<0.0001$) significantly correlated with each other on distinct platforms. Interestingly, despite these facts, PHI substantially differed in one third of all patients with a mean score difference of 5.28 when tPSA and fPSA were determined by Liaison test. When patients showing 'grey zone' tPSA levels of 2-10 µg/L were separately analyzed, the PHI showing 47.7 [31.3-65.8] values was effective to decide whether a biopsy was needed.

Conclusion: -2proPSA and related PHI can be helpful approach for the differential diagnosis of PC, and all forms of PSA are suggested to be parallelly analyzed on the same BC platform.

Abstr. Nr. SE5.1

Introducing a novel educational platform for learning karyotyping in cytogenetic laboratories

Andrikovics H.[1], Szegedi Z.[2], Kozma A.[1],Tankó L.[1], Farkasné Hamenda G.[1], Heincz Z.[1], Petro P.[1], Antali F.[1], Matula Z.[1], Borsy A.É.[1]
[1]Laboratory of Molecular Genetics, Central Hospital of Southern Pest – National Institute of Hematology and Infectious Diseases, Budapest, Hungary; [2]Bioinformat-X Bt., Budapest, Hungary

Background: Current guidelines recommend chromosome banding analysis to diagnose infertility, prenatal/postnatal abnormalities, and (hemato)oncological conditions. However, karyotyping requires highly specialized skills that require significant time and practice. We aimed to develop an educational software that facilitates fast, engaging learning of karyotyping without constant expert supervision.

Methods: We compiled high-resolution, anonymized images of normal metaphases and corresponding karyograms, validated by two independent cytogenetic experts. Metaphases were obtained from PHA-stimulated peripheral blood cultures (n=297) and spontaneous bone marrow cell cultures (n=430).

Results: The cloud-based platform is currently available in Hungarian and English. It offers a user-friendly, gamified learning experience structured into progressively challenging levels. Each level includes interactive tasks using randomly selected chromosome images. Learners are guided by built-in assistance and receive continuous feedback. The software trains users to distinguish chromosomes based on centromere position, size, shape, and banding pattern—first in smaller tasks (e.g. pairs, subgroups), then in full 46-chromosome human karyotyping. The program takes learners from basic terminology to advanced proficiency. Training ends with a final exam and issuance of a certificate indicating the result.

Conclusion: The online educational platform enables users to acquire basic karyotyping skills within 2–3 weeks of consistent use, without requiring direct supervision. Future development will focus on expanding the platform to include structural chromosomal abnormalities. This valuable tool accelerates cytogenetic training, which addresses an unmet need.

Abstr. Nr. SE5.2

Effect of hemostasis polymorphisms on the outcome of acute ischemic stroke thrombolysis

Hodossy-Takács R.[1,2], Kádár A.Z.[1,2], Bomberák D.I.[1,2], Gindele R.[1], Orbán-Kálmándi R.[2], Lóczi L.[2], Oláh L.[3], Szegedi I.[2,3], Csiba L.[3], Bagoly Z.[1,2]
University of Debrecen, [1]Division of Clinical Laboratory Sciences, Department of Laboratory Medicine, [2]Lendület "Momentum" Hemostasis and Stroke Research Group of the Hungarian Academy of Sciences, [3]Department of Neurology, Debrecen, Hungary

Background: Predicting the outcome of thrombolysis in acute ischemic stroke (AIS) is challenging, and ~6–8% of patients will develop hemorrhagic transformation (HT) after treatment as side-effect. Genetic factors may influence thrombus lysability and treatment response. We aimed to evaluate the effect of selected hemostasis polymorphisms on thrombolysis outcomes.

Methods: In this single-center, prospective cohort study, AIS patients receiving intravenous thrombolysis by recombinant tissue plasminogen activator were tested for FII G20210A, FVLeiden mutation, and 12 single-nucleotide polymorphisms in the genes of protein C, protein S, protein C receptor and antithrombin III genes (PROC, PROS1, PROCR, and SERPINC1). Thrombin generation assay was assessed using an admission platelet poor plasma. HT was diagnosed via CT 24 hours post-lysis. Favourable outcome was defined as ≥4-point NIHSS improvement by day 7.

Results: A total of 118 AIS patients were divided into groups based on outcomes (28 HT, 40 favourable, 50 unfavourable), matched by age, sex, and baseline NIHSS. FVLeiden mutation, PROS1 IVS11+54 T>C and PROC IVS1-1476 A>T were more common in AIS patients compared to the European reference population. The PROC IVS1-1641 G>A variant was more frequent in HT patients, increasing the risk of hemorrhage 3.96-fold in heterozygous (95% CI: 1.19–13.19) and 5.55-fold in homozygous carriers (95% CI: 1.59–19.31). This variant was associated with decreased endogenous thrombin potential in carriers vs. wild types (1629±429 vs. 1926±489 nM*min, respectively, p=0.0148).

Conclusion: FVLeiden mutation, PROS1 IVS11+54 T>C and PROC IVS1-1476 A>T may contribute to AIS susceptibility. PROC IVS1-164 G>A is associated with hypocoagulability and elevated HT risk following thrombolysis.

Abstr. Nr. SE5.3

Difficulties caused by hemoglobin variants in the assessment of hemoglobin A1c

Derzsi N.[1], Czégeni A.[2], Konderák J.[1], Mezei Z.[3] , Tatár A.[3]
[1]SYNLAB Budapest Diagnostic Centre Clinical Chemistry Laboratory, Budapest, Hungary
[2]North-Buda St. John Hospital Department of Internal Medicine and Diabetology II, Budapest, Hungary
[3]University of Debrecen Clinical Centre Laboratory Medicine, Debrecen, Hungary

Background: In hemoglobinopathies, HbA1c measurements can yield inaccurate results, complicating diabetes monitoring. In addition to hemoglobinopathies with clinical symptomps there are "silent" Hb variants, which do not alter blood counts and are undetectable by HPLC or electrophoresis.

Methods: EDTA plasma samples from two patients were analyzed for HbA1c using both HPLC (Tosoh G11) and immunoturbidimetry (Beckman Coulter). Hemoglobin electrophoresis (Sebia Hydrasys 2 Scan Focusing) and beta-globin gene sequencing were also performed.

Results: In the first case HbA1c by HPLC was unmeasurable due to an abnormal chromatogram. In the second case, an elevated HbA1c result conflicted with the patient's clinical profile. Following consultation between the clinician and the laboratory Hb electrophoresis and immunochemical HbA1c testing were performed in both cases. Neither patient showed abnormal fractions via electrophoresis. Regarding the first patient, HbA1c was measurable using the immunochemistry method. Genetic testing revealed a beta-globin mutation known as Graz hemoglobin – linked to falsely high or undetectable

HbA1c by HPLC, without clinical symptoms. In the second patient, HbA1c was normal via the immunochemistry method, aligning with clinical findings. This patient had a genetic mutation known as the Rainier haemoglobin variant, which is associated with familiar erythrocytosis and likely responsible for falsely elevated HbA1c measured by HPLC.

Conclusion: These cases emphasize the importance of alternative HbA1c methods and genetic testing when HbA1c results conflict with clinical data. Close collaboration between clinicians and laboratories is essential for accurate diagnosis and monitoring.

Abstr. Nr. SE5.4

Cases of combined disorders of hemoglobin composition in Hungary

Szirmay B., Kiss G.
Department of Laboratory Medicine, University of Pécs Medical School, Pécs, Hungary

Background: The occurrence of hemoglobinopathies is quite rare among the Hungarian population. However, especially in university towns, we can encounter such cases from time to time due to the presence of foreign students.

Methods: Herein, we demonstrate the cases of two patients with combined hemoglobin diseases who were treated at the Clinical Centre, University of Pécs, Hungary. Patient 1: A 25-year-old Nigerian man with sickle cell trait was presented to the emergency department with pain in his legs. Patient 2: A 10-day-old newborn of a Sierra Leonean mother was examined in the neonatal unit due to decreasing hemoglobin level. CBC was measured by Sysmex XN-9000 analyzer and a peripheral blood smear was also prepared. Hemoglobin composition was analyzed by capillary zone electrophoresis (Sebia Capillarys 2). Hemoglobin level of Patient 1 was 145 g/L with a mean corpuscular volume (MCV) of 68.7 fL. Besides HbS (52.2%), a prominent fraction of HbC (43.3%) and the absence of HbA were detected accompanied by target cells, irregularly contracted and angular cells in the blood smear. Consequently, Patient 1 was diagnosed with hemoglobin SC disease. In case of Patient 2 we found a hemoglobin level of 99 g/L and an MCV of 78 fL. Hemoglobin electrophoresis showed that the main fraction was HbF (84.9%) furthermore HbA (9.9%), HbS (4.2%) and hemoglobin Bart's (1%) were also detected. In the blood smear target cells, dacryocytes, sickle cells and schistocytes were observed. Based on the findings, the combination of sickle cell trait and alpha-thalassemia minor was concluded.

Conclusion: Our cases point out that microscopic assessment of red blood cell morphology is still essential in the differential diagnostics of hemoglobin disorders. Furthermore, the laboratory should be prepared to recognize rare abnormalities adapted to the local population.

Abstr. Nr. SE5.5

Investigation of the interplay between hemostasis and inflammation in acute hemorrhagic stroke patients

Péter-Pakó H.[1,2], Lóczi L.[2], Hodossy-Takács R.[1,2], Orbán-Kálmándi R.[1,2], Singh P.[3], Baráth S.[3], Hevessy Z.[3], Árokszállási T.[4], Szegedi I.[2,4], Héja M.[4], Csiba L.[4], Bagoly Z.[1,2]
University of Debrecen, [1]Division of Clinical Laboratory Science, [2]MTA-DE Lendület "Momentum" Hemostasis and Stroke Research Group, [3]Department of Laboratory Medicine, [4]Department of Neurology, Debrecen, Hungary

Background: Non-traumatic intracerebral hemorrhage (ICH) accounts for ~15% of all strokes but it has the highest mortality. Pre-clinical studies have identified inflammatory cytokines as contributors to ICH outcome.

Aims: To find out whether inflammatory cytokines measured at admission could predict outcomes in ICH patients, and to explore their association with the imbalance of hemostasis, as measured by the thrombin generation assay (TGA).

Methods: In this prospective, observational study, 87 consecutive ICH patients were enrolled. Hematoma evolution was recorded on admission, day 14, and 90 (CT scans). Stroke severity and long-term outcomes at day 90 were assessed by the National Institutes of Health Stroke Scale (NIHSS) and the modified Rankin Scale, respectively. Flow cytometric cytokine profiling (LEGENDPlex: IL1-β, IFN-α2, IFN-γ, TNF-α, MCP-1, IL-6, IL-8, IL-10, IL-12p70, IL-17A, IL-18, IL-23, IL-33) and TGA was performed from platelet poor plasma at admission.

Results: IL-6, IL-10, IL-12p70, and IL-18 levels were increased in all patients. Admission stroke severity and bleeding volume were associated with IL-6 levels. MCP-1 levels were elevated in patients who died by day 90 vs. to those who survived (median: 454, IQR: 262-526 vs. 313; 251-411 pg/mL, p=0.0261). TGA parameters were not associated with the studied cytokine levels.

Conclusion: Elevated IL-6, IL-10, IL-12p70, and IL-18 levels suggest a systemic inflammatory response. Elevated IL-6 levels, associated with stroke severity, and increased MCP-1 levels, associated with mortality suggest that studies on inflammatory cytokines in ICH may provide valuable information on the pathomechanism and outcomes.

Abstr. Nr. SE5.6

Advances and clinical implications of molecular genetic diagnostics in acute myeloid leukaemia

Csabán D., Bors A., Meggyesi N., Kozma A., Őrfi Z., Borsy A., Tankó L., Szabó F., Tisza K., Hardi A., Harasztdombi J., Szalai L., Bátai Á., Dolgos J., Gopcsa L., Lakatos V., Mikala G., Vályi-Nagy I., Reményi P., Andrikovics H.
Central Hospital of Southern Pest, Budapest, Hungary

Background: The therapeutic landscape of acute myeloid leukemia (AML) has undergone considerable transformation in recent years. In clinical practice, comprehensive characterization of the patient's genetic profile is fundamental to optimal therapeutic decision-making.

Methods: Between 2019 and 2024, our laboratory implemented several advanced diagnostic platforms, including a targeted myeloid next generation sequencing (NGS) panel, whole exome sequencing, fragment analysis for *CEBPA* and *UBTF*, and droplet digital PCR for *NPM1* and *IDH1/2* mutations. Our study includes 706 AML patients under 65, years of age diagnosed and treated with curative intent at our institution between 2001 and 2024.

Results: Among the cohort, 44 cases with core-binding factor (CBF) translocations (6.2%), 21 cases harbouring *CEBPA* (2.9%), 218 cases with *NPM1* (30.9%), 9 with UBTF mutations (1.3%), 59 cases with other fusion genes (8.4%), and 149 cases with myelodysplasia-related cytogenetic abnormalities or mutations (21.1%) were identified. In 131 *NPM1*-mutated cases analyzed by NGS, co-mutations were observed in *DNMT3A* (55%), *FLT3*-ITD (48%), and *WT1* (11%) genes.

Conclusion: Karyotyping, supported by FISH and myeloid NGS profiling, effectively identifies recurrent genetic changes and myelodysplasia-associated genetic alterations in adult AML. Detecting co-mutations and measurable residual disease can refine the European LeukemiaNet 2022 risk stratification. Additionally, *UBTF* partial tandem duplications - previously reported predominantly in pediatric AML - were also detected in adult patients and may delineate a subgroup associated with an unfavorable prognosis.

Abstr. Nr. SE6.1

Indirect reference interval determination for an anti-dsDNA autoantibody test

Földesi R., Nagy G., Antal-Szalmás P.
University of Debrecen, Department of Laboratory Medicine, Debrecen, Hungary

Background: Accurate reference intervals (RI) are essential for the interpretation of laboratory test results. Direct RI determination requires control samples from healthy individuals, is rather expensive and time-consuming and the development of RIs for pediatric samples can generate ethical problems, too. Definition of RIs based on “real-life” data stored in laboratory information systems - the indirect RI determination - can circumvent several of these issues.

Methods and Results: We collected anti-dsDNA data generated between 2014-2023 from the GLIMS database. Altogether 57.905 values were downloaded, from which 54.627 belonged to outpatients. We used different approaches for selecting a single measurement for each tested individual. Two different mathematical algorithms – kosmic and refineR – were used for classification of the downloaded anti-dsDNA values to negative and positive categories and for the definition of the cut-off between them. RIs for males/females and different age groups were also determined.

Conclusion: Our data show that – using optimal data selection, data size and mathematical algorithms – indirect reference interval determination can provide similar cut-offs to the direct method in the case of autoantibodies, too.

Abstr. Nr. SE6.2

Effects of changing methods in the determination of phospholipid autoantibodies

Huszár K., Mező-Géresi K., Tajti B. T., Simon J.
Central Department of Laboratory Diagnostics, North-Pest Center Hospital – Military Hospital, Budapest, Hungary

Background and Metholds: Two methods are currently used for the detection of anticardiolipin (aCL) and anti-beta2 glycoprotein I (aB2GPI) antibodies: enzyme-linked (ELISA) and chemiluminescence immunoassay (CLIA). In our laboratory, the CLIA was adapted in May 2023, which was intended to replace the ELISA tests. At the same time, the ELISA method was used as a screening test, then only selected samples were further tested on isotype-based (GAM) CLIA assays. Therefore, the detection of autoantibodies was determined by combining both techniques. In this study, we present our experiences to the following topics: 1. Patient follow-up and comparison of chemiluminescence unit (CU) vs. U/ml units, 2. The correlation between prognostic diagnosis and positive results which were determined by only one assay. 3. Verification of discrepant results in a third test. 4.Sustainability of the combined use of the two techniques.

Results: A total of 6223 patients samples were analysed during the examined period. In 1055 cases (16.9%) additional isotype-specific CLIA tests were performed. Among these, 411 (38.9%) samples showed concordant positivity in both assays, while 91 (8.2%) were positive only in ELISA, and 62 (5.9%) only in CLIA. 54 (19.6%) samples with discrepant results were verified in second ELISA tests manufactured by other company. Our results suggested: 1. The results of CLIA show correlation between the isotype distribution of the previous results in patient’s history. 2. There is no correlation between isolated technical positivity and the suspected clinical diagnoses. 3. Performing a third test could not provide additional information. 4. Samples are near to the cut-off should also be further examined to minimise false negative results; the risk should be less than 1%.

Conclusion: In our hands CLIA assays are suitable for detecting aCL and aB2GPI autoantibodies, however we will intend to use ELISA screening test in the future based on both professional and economic considerations.

Abstr. Nr. SE6.3

Investigation of plasma level of circulating miRNAs in patients with ANCA-associated vasculitis

Nagy B. Jr.[1], I. File[2], Póliska S.[3], Pócsi M.[1], Fejes Z.[1], Kappelmayer J.[1], Balla J.[2]
[1]Department of Laboratory Medicine, [2]Department of Internal Medicine, [3]Department of Biochemistry and Molecular Biology, Faculty of Medicine, University of Debrecen, Debrecen, Hungary

Background: Antineutrophil cytoplasmic antibody (ANCA)-associated vasculitis (AAV) is characterized by destruction of small- and medium-sized blood vessels. Serologic classification of AAV into PR3- and MPO-ANCA disease correlates with disease characteristics, as relapse rate is larger in PR3-ANCA, while mortality ratio is higher in MPO-ANCA. Non-coding miRNAs have a function of post-transcriptional gene silencing, and abnormal level of circulating miRNAs can act as potential diagnostic and prognostic disease biomarkers, however, only limited data on miRNAs is available in AAV.

Methods: Sixteen PR3-positive and 11 MPO-positive AAV patients (mean age of 58.9 ± 17.1 years) were enrolled with 7 age-matched clinical controls with non-AAV chronic kidney disorder. Na-citrate-anticoagulated plasma samples were obtained at AAV diagnosis and follow-up specimens were also available from some patients. Extracellular miRNA was extracted, and next generation sequencing (NGS) was used to analyze the level of circulating miRNAs, which were compared between each serology patient subgroup and controls as well as among ANCA individuals.

Results: Compared to controls, several significantly elevated (e.g. miR-15a; miR-181a) and decreased (e.g. miR-874; miR-30d) miRNAs were found in PR3- and MPO-positive AAV patients, respectively, while induced miR-199a, miR-199b, and miR-151a differentiated the two serology subcohorts from each other. During recovery, miR-223 (in the PR3 group) and let-7d-3p (in the MPO group) were downregulated (FC > -2, $p < 0.05$) in the follow-up samples.

Conclusion: Circulating miRNAs may be applied as new biomarkers for the diagnosis, classification and monitoring of AAV.

Abstr. Nr. SE6.4

Severe haemagglutination interfering with automated blood counting: a diagnostic challenge in cold agglutinin disease

Farkas K.L.[1], Lengyel Z.[2], Kárpáti K.[2], Modok S.[2], Fődi É.[3], I Földesi I.[1]
[1]Institute of Laboratory Medicine, [2]Center of Hematology, University of Szeged, [3]Hungarian National Blood Transfusion Service, Szeged, Hungary

Background: Cold agglutinin disease (CAD) is a rare form of haemolysis mediated by cold-reactive IgM autoantibodies that induce red blood cell (RBC) agglutination and complement activation. In vitro agglutination can interfere with automated blood count measurements, thus delaying the diagnosis.

Methods and Results: A 73-year-old woman was referred to hematology in March 2025 with the gangrene of both index fingers. In the past her rheumatoid arthritis was treated with corticosteroids. Over the last year she developed cold-induced acrocyanosis and livedo reticularis. The laboratory findings were consistent with haemolysis (high levels of bilirubin and LDH, low haptoglobin), but the automated blood count analysis failed repeatedly due to the significant agglutination of the RBCs. Even samples transported in a hot water bath at 37°C remained unsuitable for analysis. Thus, the patient herself was transported to the laboratory and her blood was collected on-site using preheated blood collection devices and analysed immediately. With this method her haemoglobin was finally measurable, and the full blood count revealed her severe anaemia (Hb: 67 g/l). Blood group serological tests were also performed in a similar way, i.e. using 37 °C blood samples, and all reagents, gel cards and test cells required several hours of warming. Serological testing confirmed cold agglutinins with a broad thermal amplitude, and the diagnosis of CAD was established. Bone marrow examination revealed chronic lymphocytic leukaemia, which was treated initially with rituximab and then with venetoclax and obinutuzumab.

Conclusion: This case illustrates how strong cold agglutination can compromise laboratory tests and pose a diagnostic challenge in CAD. This case highlights the importance of the pre-analytic phase of laboratory tests for accurate assessment of results and appropriate clinical management of patients.

Abstr. Nr. SE6.5

Increased thrombin generation in kidney transplant recipients with donor-specific antibodies directed against human leukocyte antigens

Lóczi L.[1,2,3], Singh P.[4], Bomberák D.[1,3], Nemes B.[5], Z. Bagoly Z.[1,2,3]
University of Debrecen [1]Division of Clinical Laboratory Sciences, [2]HUN-REN-DE Cerebrovascular Research Group, [3]Lendület "Momentum" Hemostasis and Stroke Research Group of the Hungarian Academy of Sciences, [4]Department of Laboratory Medicine, [5]Department of Surgery, Debrecen, Hungary

Background: The development of anti-HLA donor specific antibodies (DSAs) may lead to antibody-mediated rejection (ABMR), a common cause of graft loss with unknown underlying pathomechanism in kidney transplant recipients. We hypothesized that in kidney transplant patients the presence of DSAs induce endothelial damage and hemostasis alterations, including hypercoagulability, as assessed by the thrombin generation assay (TGA) that may contribute to ABMR.

Methods: In this observational study, 27 kidney transplant recipients with DSAs (DSA+ group) and 16 without DSAs (DSA– group) were enrolled. Venous blood samples were obtained, and besides TGA, von Willebrand factor antigen (VWF), FVIII activity, soluble E selectin (sEsel), soluble P selectin (sPsel), and inflammatory cytokine profiling were carried out. To correlate results with potential changes in DSA status over time, patients were followed and reassessed 6±1.5 months later.

Results: Endogenous thrombin potential (ETP) was significantly higher in DSA+ vs. DSA– patients (median:1666; IQR:1438-2012 vs. 1230; IQR:1097-1659 nM*min, p=0.0019). TNF-α and IL-6 were significantly increased in the DSA+ vs. DSA– group. VWF and sPsel were increased in the majority of patients. Follow-up measurements indicated that the observed alterations were not transient. The extent of anti-HLA II DSA positivity correlated positively with ETP, while tacrolimus levels negatively correlated with ETP, VWF and FVIII levels.

Conclusion: The presence of DSAs lead to hypercoagulability in kidney transplant patients, and TGA may be a useful test during follow-up, the timing of graft biopsy and the assessment of antibody-mediated graft injury.

Abstr. Nr. SE6.6

Evaluation of viability tests as readout of lymphocyte transformation test in drug hypersensitivity diagnostics

Gyovai A.[1], Metzler G.[1], Papp K.[1,2], J. Prechl J.[1]
[1]K+F Laboratórium, Diagnosticum Zrt, Budapest, [2] Department of Physics of Complex Systems, ELTE, Budapest

Background: In vitro cell-based assays can support the diagnostics of drug hypersensitivity reactions. Because of the diversity of pharmacological mechanisms, clinical symptoms, genetic components, and laboratory tests involved in adverse drug reactions, it is important to understand how a particular test performs in the diagnostic procedure.

Methods and Results: We retrospectively analyzed more than 6000 measurements of numerous drug compounds tested in 738 serum samples over the past 6 years. Our cell viability-based lymphocyte transformation test had a coefficient of variation of 10% and showed similar performance over the whole range of tested patients' ages (18-91 years). With an adequate number of parallel measurements, the test can identify modest increases in stimulation indices with high confidence. Similar percentages of analytically positive responses (11.4%, 13.5%, and 9.7%) were observed for the three most frequently tested drug groups, namely, antibiotics, non-steroid anti-inflammatory agents, and anesthetics.

Conclusion: Our results confirm that cell viability tests are suitable alternatives for proliferation assays in drug allergy testing.

POSTER PRESENTATIONS

Abstr. Nr. PS1.1

Newborn screening of the SMA in Hungary

Lénárt I.[1], Hegedűs K.[2], Baráth Á.[1], Bereczki C.[1], Szabó A.[2], Szatmári I.[2], Monostori P.[1]
[1]Metabolic and Newborn Screening Laboratory, Department of Paediatrics, University of Szeged, Szeged, Hungary, [2]Paediatric Centre, Semmelweis University, Budapest, Hungary

Background: Spinal muscular atrophy (SMA) is a rare genetic motor neuron disorder caused by the mutation of the *SMN1* gene. The copy number of the *SMN2* gene modifies the severity of phenotype and determines which type will develop. By the appearance of targeted therapies, the SMA met the criteria for implementing to the international newborn screening (NBS) programs giving an opportunity to the early diagnosis.

Methods: Internationally the NBS of SMA is based on the detection of the homozygous deletion of the *SMN1* exon 7. The isolated DNA from dried blood spots is processed by quantitative real-time polymerase chain reaction (qPCR) technology. Screen positive infants were referred to assigned clinical geneticists to provide the pre-, and post-test genetic counselling for the family. The determination of the copy numbers of the genes *SMN1* and *SMN2* was performed by multiplex ligation-dependent probe amplification assay (MLPA).

Results: The SMA screening test was performed in 155,985 cases nationwide during the 26 months of the pilot study corresponding to 87% of all newborns who participated in the regular NBS program in this period. The test result was positive in 19 cases. In all of 19 infants the MLPA was performed and the median age at this time was 14.5 days. The *SMN1* copy number was 0 in all cases which confirmed the result of the screening test and the diagnosis of SMA. The copy numbers of *SMN2* ranged from 2 to 4 according to the severity of the disease.

Conclusion: The pilot study was considered successful as all 19 positive cases were confirmed by MPLA and received appropriate therapies. There were no known missed cases. The incidence of the disorder was 1:7,799, similar to that expected. Our future aim is to extend the regular NBS program with the SMA to improve the participation rate to 100%, i.e. a complete coverage of all Hungarian newborns.

Abstr. Nr. PS1.2

Early experiences with Alzheimer's disease risk assessment

Ölveczky-Hajszán A., Pintér E.
Synlab Budapest Diagnostic Center, Immunology Laboratory, Budapest, Hungary

Background: Alzheimer's disease is a major cause of dementia, affecting around 50 million people worldwide. According to the World Health Organization, this number may triple by 2050. Age, genetic predisposition - particularly the apolipoprotein E epsilon 4 allele - and various cardiovascular and lifestyle-related factors contribute to its development. Pathophysiological changes, such as amyloid-β and tau protein aggregation, begin years before clinical symptoms emerge. Early diagnosis is essential for timely intervention.

Methods: We applied a novel plasma-based amyloid-β ELISA method as a less invasive, cost-effective alternative to imaging and lumbar puncture. Risk assessment was based on plasma levels of oligomerized amyloid-β, and these results were evaluated.

Results: Between November 2024 and March 2025, we tested 142 patients at the Synlab Immunology Laboratory. Participants were grouped by age (0–39, 40–59, 60–89 years), and we analyzed positivity rates and gender distribution. In the youngest group (n=5), no positives were found. Notably, 11 individuals (22%) in the 40–59 group showed elevated values, highlighting the need for early detection. In the 60–89 group, 25 individuals (28.7%) tested positive. Among positive cases, 24 were female (64.9%) and 12 male (35.1%), supporting previous findings on gender differences. Positivity increased with age. Patients with

medium or high risk were informed about when to repeat testing and advised on lifestyle changes. They were also offered the option to register with a neurocognitive research center.

Conclusion: This plasma-based Alzheimer test enables early detection of neurodegenerative changes during the asymptomatic stage. It shows strong potential for preclinical Alzheimer's screening, supports differential diagnosis, and informs treatment decisions. We are actively monitoring positive cases for follow-up. Additional data are needed to improve result interpretation and support wider clinical use.

Abstr. Nr. PS1.3

Interferences in complete blood count analysis in severely burned patients – case studies

Papp I., Kiss G., Szirmay B.
Department of Laboratory Medicine, University of Pécs, Medical School, Pécs, Hungary

Background: In Hungary, 4-5000 cases of burn injuries need hospital treatment every year. Complete blood count (CBC) analysis is essential in the care of burned patients; however, certain results can be misleading. When exposed to strong heat, the deformability of red blood cells (RBCs) decreases, which can lead to the formation of spherocytes, schistocytes and microvesicles. These particles can cause interference during analysis, depending on the principle used. Since hematology analyzers generally apply the impedance method to count RBCs and platelets, in some cases, pseudothrombocytosis can be seen in patients with severe burns. The presence of small-sized damaged RBCs can be confirmed by examining the peripheral blood smear, which has an appearance similar to hereditary pyropoikilocytosis. Our study aimed to demonstrate this phenomenon through the cases of 3 patients with extensive (>50% of body surface) grade II-III burns.

Methods and Results: CBC measurement and blood smear preparation were performed by the XN-9000 analyzer and SP-10 unit of Sysmex. Platelet count was determined based on 3 different principles (impedance, optical and specific fluorescent staining). Marked thermal poikilocytosis was detected in the blood smears in 2 out of 3 cases and striking differences were seen between platelet values measured by different methods. In the smear of the third patient only a few microvesicles were observed and platelet values did not differ substantially.

Conclusion: Our results suggest that severe burn injuries are not necessarily associated with the development of thermal poikilocytosis, it may depend on the type of heat exposure. Our study also shows the advantage of CBC analyzers having a channel for specific platelet counting and the importance of smear examination in the absence of that. We also emphasize the importance of consultation between clinicians and the laboratory.

Abstr. Nr. PS1.4

Developing an artificial intelligence-supported automated karyotyping software: the KAYRA

Borsy A.É.[1], Kozma A.[1], Farkas Hamenda G.[1], Brucsi-Molnár A.[1], Tankó L.[1], Pintér A.[2,3], Répai A.[2], Cserey G.[3], Andrikovics H.[1]
[1]Laboratory of Molecular Genetics, Central Hospital of Southern Pest – National Institute of Hematology and Infectious Diseases, Budapest, Hungary; [2]Jedlik Innováció Kft., Budapest, Hungary; [3]Faculty of Information Technology and Bionics, Pázmány Péter Catholic University, Budapest, Hungary

Background: A karyotyping software (called KAYRA) capable of identifying human chromosomes was trained by deep learning neural networks based on several hundred pictures of metaphase-chromosome pairs. The cloud-based software can automate chromosome segmentation and arrange chromosomes into karyograms from uploaded metaphase images.

Methods: Karyotyping was performed on the same 10 normal metaphases (derived from PHA-stimulated peripheral blood or spontaneous cell cultures of bone marrow) using both KAYRA and two reference software programs widely applied in diagnostics.

Results: Investigating the segmentation capabilities revealed that KAYRA was 98.9% efficient for solitary, contiguous, or intersecting chromosomes, compared to 40.5% for reference software1 and 78.2% for the AI-supported reference software2 ($p<0.0001$). KAYRA identified 89.1% of chromosomes in comparison to 54.5% ($p<0.0001$) and 86.9% ($p=0.36$) for the reference software 1 and 2. KAYRA's superiority was more evident for identifying large and medium-sized chromosomes ($p<0.0001$). Regarding the vertical orientation of chromosomes, the software exhibited an efficiency of 89.8%, 78.4% ($p<0.0001$), and 94.5% ($p=0.0095$), respectively.

Conclusion: The AI-based karyotyping software *KAYRA* represents a promising advancement for cytogenetic laboratories, offering substantial improvements in segmentation and identification accuracy. However, as none of the current karyotyping solutions - including those supported by AI - offer 100% performance, validation by trained cytogeneticists and the continued education of cytogenetics professionals remain essential. Supported by NKFIH 2021-1.1.4-GYORSÍTÓSÁV-2022-00054).

Abstr. Nr. PS1.5

Serum gelsolin as a complementary marker for intensive care unit-acquired weakness among critically ill patients

Horváth-Szalai Z.[1], Rostás I.[1], Szirmay B.[1], Ragán D.[1], Kustán P.[1], Huber T.[2], Papp I.[1], Miseta A.[1], Mühl D.[3], Kőszegi T.[1], Molnár T.[3]
[1]Department of Laboratory Medicine, [2]Department. of Biophysics, [3]Department of Anaesthesiology and Intensive Therapy, UPECS, Pécs, Hungary

Background: Intensive care unit-acquired weakness (ICUAW) is a complex and severe complication among critically ill patients, characterized by prolonged muscle weakness. Its diagnosis requires a multidimensional approach where predominantly clinical (e.g. neurological and radiological) examinations are recommended however the resources are often limited. Blood biomarkers have not been investigated deeply for this purpose. Serum gelsolin (GSN) is synthetized by skeletal muscle cells. It primarily functions as an actin-binding protein, the level of which can decrease in severe systemic inflammation. We investigated the potential predictive capacity of GSN regarding ICUAW in critically ill patients.

Methods: We recruited ICU patients (n=73) in our follow-up study. Based on their clinical characteristics, patients were retrospectively categorized into ICUAW (n=47) and non-ICUAW (n=26) groups. Clinical and laboratory parameters were collected from the medical health records. Healthy individuals (n=34) served as controls. Serum GSN levels were measured by our previously developed automated immunoturbidimetric assay (Roche Cobas c502 module).

Results: Admission serum GSN levels were significantly reduced in both ICU patient groups when compared to controls. ICUAW patients had lower 1st day GSN levels than non-ICUAW patients (median levels: 8.1 vs. 14.3 mg/L, $p<0.05$) and similar tendency was observed during follow-up. Based on ROC analysis, GSN showed potential predictive capacity regarding ICUAW (ROC AUC: 0.711, $p<0.01$).

Conclusion: GSN might serve as an intriguing and additional marker in the prediction of ICUAW.

Abstr. Nr. PS1.6

Serum actin-binding proteins with potential predictive value in traumatic brain injury patients

Horváth-Szalai Z.[1], Szirmay B.[1], Rostás I.[1], Szekeres Z.[1], Dobos Á.[1], Nagy Z.[1], Amrein K.[2], Huber T.[3], Péterfalvi Á.[1], Gombos K.[1], Nagy T.[1], Tóth P.[2], Kőszegi T.[1], Czeiter E.[2]
[1]Department of Laboratory Medicine, [2]Department of Neurosurgery, [3]Department of Biophysics, UPECS, Pécs, Hungary

Background: Traumatic brain injury (TBI) is a frequent cause of death and disability both in young and elderly patients affecting approximately 1400 individuals/year in Hungary. Besides radiological findings and clinical scores, blood biomarkers could also play a role in assessing injury severity. In severe tissue damage, levels of serum actin-binding proteins could rapidly fall which might indicate the severity of injury. We aimed to assess the predictive capacity of serum gelsolin (GSN), Gc-globulin and Flightless-I (Fli I) in TBI patients.

Methods: We included TBI (n=42) and control (n=30) patients in our study. Clinical and classical laboratory parameters were collected from the hospital information system. GSN and Gc-globulin levels were investigated by our previously developed immunoturbidimetric methods (Roche Cobas c502 module), while Fli I concentration was determined by automated Western blot.

Results: Serum GSN, Gc-globulin and Fli I levels were all depleted in TBI patients at admission when compared to controls (median levels in TBI vs. control: GSN: 48.30 vs. 82.94 mg/L; Gc-globulin: 283.94 vs. 406.83 mg/L; Fli I: 4.07 vs. 5.12 mg/L; $p<0.001$). After stratifying patients according to injury severity, moderate + severe TBI patients exhibited lower GSN (42.01 vs. 60.47 mg/L, $p<0.01$) and Gc-globulin levels (270.18 vs. 310.24 mg/L, $p<0.05$) than mild TBI patients. ROC analysis indicated possible predictive capacity of GSN (ROC AUC: 0.74, $p<0.05$) and Gc-globulin (ROC AUC: 0.71, $p<0.05$) when assessing TBI severity.

Conclusion: Serum actin-binding proteins might serve as potential complementary predictive markers when assessing TBI severity.

Abstr. Nr. PS1.7

Comparison of the effect of CFTR modulators via human epididymis protein 4 (HE4) serum level in p.Phe508del-CFTR homozygous cystic fibrosis (CF) patients

Pócsi M.[1], Szántó T.G.[2], Péterfia C.[3], Halász A.[4], Mészáros B.[2], Laki I.[5], Szabó H.[6], Panyi G.[2], Nagy B. Jr.[1]
[1]Department of Laboratory Medicine, [2]Department of Biophysics and Cell Biology, University of Debrecen, Debrecen, Hungary; [3]Department of Pediatrics, University of Pécs, Pécs, Hungary; [4]National Korányi Institute for Pulmonology, Budapest, Hungary; [5]Törökbálint Institute for Pulmonology, Törökbálint, Hungary; [6]Department of Pediatrics, Albert Szent-Györgyi Medical School, University of Szeged, Szeged, Hungary

Background: Serum HE4 is elevated in CF that negatively correlates with lung function (ppFEV1). Here we investigated if serum HE4 was decreased in CF patients homozygous for the p.Phe508del-CFTR in response to CFTR modulators (CFTRm) *lumacaftor/ivacaftor* (LUM/IVA) and *elexacaftor*/*tezacaftor/ivacaftor* (ETI).

Methods: HE4 serum levels were measured in total 69 CF subjects before treatment and at 1-2 and 3-6 months after the administration of ETI or LUM/IVA. In parallel, HE4 was quantified in the supernatant of p.Phe508del-CFTR CFBE 41o– cell cultures before and after such treatment. The effect of both CFTRm on CFTR function was monitored by whole-cell patch clamp.

Results: HE4 levels were significantly reduced already after 1-2 months of CFTRm therapy (-20.7 vs. -18.5 pmol/L) when the mean change of ppFEV1 was 4.0 vs. 1.6% and remained decreased throughout the treatment. Significant inverse correlation between HE4 and ppFEV1 was observed in both study cohorts ($r=-0.537$ and $r=-0.575$, $p<0.0001$; respectively). The effect on p.Phe508del-CFTR was more pronounced by ETI than LUM/IVA in CFBE cells showing restored F508del-CFTR function and a larger reduction in HE4 levels in their supernatant after 24 hours compared to untreated cells.

Conclusion: Serum HE4 levels negatively correlate with lung function improvement and monitor drug efficacy in CF patients under ETI or LUM/IVA treatment.

Abstr. Nr. PS1.8

The relationships between triglycerides, lipemic index, and LDL cholesterol on the Beckman Coulter analyzer

Altmann Á., Sipos L.
Synlab Hungary Kft, Székesfehérvár, Hungary

Background: In alignment with the accreditation requirements outlined in the ISO 15189:2023 and to satisfy the quality assurance in our laboratory, the analytical methods applied to clinical chemistry parameters, the verification of performance characteristics, and the determination of measurement uncertainties are performed in accordance with the instructions for use provided by the manufacturers.

Methods and Results: In our current work, we analyzed the interfering effect of triglyceride (TG) levels >11.3 mmol/L in determination of low-density lipoprotein cholesterol (LDL cholesterol), and the correlations with the lipemia index automatically determined by the Beckman Coulter AU5800 chemical analyzer. Serum samples were collected from 62 patients in BD Vacutainer tubes. Significance tests were performed using linear regression within a 95% confidence interval, using MedCalc software. TG levels ranged from 11.3 mmol/L to 48.72 mmol/L. LDL cholesterol measurements were performed on primary (Group A) and 50%-saline-diluted (Group B) samples. Results were evaluated based on the following performance specification: LDL = 0.012–1.57 mmol/L concentration range with total CV% = 2.71%; LDL = 1.57–2.63 mmol/L with total CV% = 2.34%; LDL = 2.63–3.70 mmol/L with total CV% = 2.68%. The coefficient of variation (CV%) values for LDL cholesterol measurements in Group A and Group B ranged from 9.84% to 68.04%, demonstrating a significant correlation with TG levels measured from primary samples ($p<0.0001$).

Conclusion: Based on our current findings TG concentrations >11.3 mmol/L significantly distort LDL cholesterol results. Continuous monitoring of manufacturer test protocol recommendations is essential for maintaining patient safety.

Abstr. Nr. PS1.9

One year's success of improved angiotensin-converting enzyme activity measurement: A comprehensive overview

Szabó A.Á., Enyedi E.E., Tóth Z.B., Pintér T.B., Siket I.M., Fagyas M.
Division of Clinical Physiology, University of Debrecen, Debrecen, Hungary

Background: Angiotensin-converting enzyme (ACE) activity plays a pivotal role in diagnosing and monitoring sarcoidosis, but ACE inhibitors (ACEI) can falsely lower activity levels. Since 2024, the University of Debrecen Clinical Centre has been using an advanced measurement method capable of objectively detecting the presence of any ACEI in serum samples. Results are reported only for ACEI-negative samples, while ACEI-positive cases are flagged to inform clinicians. Our aim was to evaluate the efficiency of the improved laboratory procedure. We sought to observe changes in clinician practice and the proportion of samples containing ACEI.

Methods and Results: The results of patients were analysed who underwent diagnostic ACE activity measurements in 2022-2023 and in 2024. The statistical analysis was performed using the chi-square test. In 2022-2023, 1167, while in 2024, 561 measurements were performed, of which 1 result from each period was not evaluated due to missing data. Contrary to expectations, the proportion of samples containing ACEI was slightly higher in 2024 compared to the previous years (20.7% vs. 18.6%). Measurement requests were predominantly received from the pulmonology department (pulm group) in both periods, although several requests also came from other departments (non-pulm group). Between 2022-2023 ACEI effect was significantly higher in pulm group than in non-pulm group (19.7% vs. 13.8%; $p<0.05$). In 2024, ACEI effect decreased by 1.2% in the pulm group, while it significantly increased in the non-pulm group compared to 2022-2023 (25.3% vs. 13.8%; $p<0.005$). The proportion of non-pulm originated measurement requests significantly increased in 2024 compared to previous years (32.5% vs. 19.2%; $p<0.0001$). These changes collectively likely contributed to the increased proportion of ACEI-positive samples.

Conclusion: Our overview highlights that further improvements have to be implicated to increase the efficiency of ACE activity measurement.

Abstr. Nr. PS1.10

The introduction of the correction of the sodium concentration in our Laboratory for hyperglycaemia

Pákozdi C., Dávid E.V., Orosz A., Simon Á.
Central Laboratory, Hetényi Géza Country Hospital, Szolnok, Hungary

Background: According to the recommendation of the Health Professional Guideline on the Diagnosis and Treatment of Hyponatraemia (2018), a corrected sodium concentration should be given in the case of hyperglycaemia. High blood glucose levels increase the osmolality of the blood plasma, resulting in a falsely low sodium value during measurement, which needs to be corrected.

Methods: Since 2025 our laboratory has been using corrected sodium concentrations. Of the glucose concentrations measured in one week (n=3345), 1157 were above the upper limit of the reference range (6.1 mmol/L). Three groups were created according to serum glucose concentrations: I: 6.1-10.0 mmol/L, (n=988); II: 10.1-15.0 mmol/L, (n=140); III: ≥15.1 mmol/L, (n=29).

Results: Acute hyperglycaemia decreased the serum sodium concentration in all cases. The correction was performed according to the formula given in the technical guideline. The mean decrease in serum sodium concentration averaged 2.4 mmol/L for every 5.5 mmol/L increase in glucose concentration. 14 cases were found with sodium concentrations below the lower limit of the reference range (ref.: 132-146 mmol/L). This was corrected to be within the normal reference range.

Conclusion: By providing a corrected sodium concentration due to hyperglycaemia, it is possible to reduce unnecessary sodium supplementation due to falsely low sodium concentrations. This would further increase plasma osmolality and even can cause serious neurological complications.

Abstr. Nr. PS1.11

Verification of quantitative examination methods according to guidelines

Szűcs J., Szurovecz M., Szakács J., Szakony S.
Central Laboratory, South Buda Central Hospital, St. Imre University Teaching Hospital, Budapest, Hungary

Background: According to ISO 15189:2022, the laboratory shall have a procedure to verify examination methods before introducing them into use, by ensuring that the required performance, as specified by the manufacturer, can be achieved, and the extent of the verification is sufficient to ensure the validity of results pertinent to clinical decision making. The standard does not specify precise requirements; therefore we have compiled our procedure based on the Clinical and Laboratory Standards Institute (CLSI) guidelines (EP06, EP09, EP15, EP28).

Methods: Before introducing the urine albumin test, we performed the verification between 10/01/2024 and 11/24/2024. The precision and bias (EP15) determination was performed over five days, with five parallel measurements per day, on samples with three different concentrations, and the results were recorded in the EP15-Ed3-WB Excel table. Linearity was performed based on EP06, and the results were recorded in the EP-Ed2-WB table. The specified reference range was verified based on EP28.

Results: The within-run precision for sample 1 and the within-lab precision for sample 3 differed from the manufacturer's data but were within the target value (7.4%). The bias was within the target value (8.2%) calculated based on biological variability at all three concentrations. In the linearity tests, all data points and all confidence intervals except one of the 6

concentrations fell within the indicated area. 2 out of 20 reference person results fell outside the specified range. According to the ISO 15189 standard, the verification report includes the performance specifications to be achieved, the results achieved, and a statement that the performance specifications were met.

Conclusion: The verification process for urine albumin allowed us to demonstrate that the examination's performance characteristics meet expectations, and the test can be integrated into daily practice.

Abstr. Nr. PS1.12

Sweat chloride testing in pediatric cystic fibrosis diagnosis: Opportunities and limitations. Experiences with Macroduct® and Chlorochek® Systems

Czingolya-Fodor V.[1], Gilányi I.[1], Szegedi H.[1], Soltész P.[1], Kretovics J.G.[1], Fodor B.[1,2]
[1]Department of Laboratory Medicine, Borsod-Abaúj-Zemplén County Central Hospital and University Teaching Hospital, Miskolc, Hungary, [2]Faculty of Healthcare Studies, University of Miskolc, Miskolc Hungary

Background: Cystic fibrosis (CF) is a common autosomal recessive disorder caused by *CFTR* gene mutations. Early diagnosis is essential to initiate targeted therapy, improving patient outcomes. Sweat chloride measurement is the gold standard for CF diagnosis, offering a cost- and time-efficient alternative to genetic testing, though not a replacement. We aim to present our institutional experience with sweat chloride testing, highlight the applied systems, and discuss diagnostic value and limitations.

Methods: Sweat samples were collected using the Macroduct® Advanced Sweat Collection System, which induces sweating via pilocarpine iontophoresis and collects it in capillary tubing. Chloride concentration was measured using the Chlorochek® Chloridometer, an automated colometric titration system providing fast, accurate results from minimal volumes.

Results: From April 2022 to May 2025, 245 samples were processed; 222 yielded valid results, while 23 were insufficient. Elevated chloride levels (≥60 mmol/L) were found in 7 patients, indicating suspected CF. Macroduct® enabled efficient collection, while Chlorochek® ensured precise analysis. Challenges included insufficient sweating or inadequate stimulation. Although CF is typically diagnosed in childhood, one adult case (born 1965) highlighted that testing may be relevant later in life, supporting extended diagnostic consideration in select cases.

Conclusion: Sweat chloride testing is a reliable, quick, and practical method for CF screening, particularly in pediatric respiratory or gastrointestinal presentations. The combined use of Macroduct® and Chlorochek® supports high-quality testing in our institution. For milder phenotypes, diagnosis may be relevant even beyond childhood. Reducing pre-analytical errors and ensuring patient follow-up are key to improving diagnostic accuracy.

Abstr. Nr. PS1.13

Lipoproteins and apolipoproteins as cardiovascular risk factors

Domokos-Taró T.[1,2], Jost K.[2], Nikodémusz E.[2], Földesi I.[2]
[1]Division of Central Laboratory, Hódmezővásárhely – Makó Health Care Centre, Hódmezővásárhely, Hungary, [2]Institute of Laboratory Medicine, Albert Szent-Györgyi Health Centre, University of Szeged, Szeged, Hungary

Background: Lipids are essential sources of energy, fundamental components of cell membranes and hormones. They play an important role in the pathogenesis of atherosclerotic cardiovascular diseases, but the exact relationship between hyperlipidaemia and cardiac events is still controversial.

Methods: In our experimental work, we processed 102 serum samples from neurological patients. The samples were primarily from two groups of patients: those who had stroke and those who were cardiovascularly healthy. The results were compared between the two groups using different statistical tests. In addition, the correlation between the different lipid

fractions (HDL cholesterol – apolipoprotein-AI and LDL cholesterol – apolipoprotein-B) and the concordance between LDL cholesterol values measured by colorimetry and calculated by the Friedewald formula were investigated. Our study also included a comparative analysis of three parameters on two nephelometers (Siemens Atellica NEPH 630 and Binding Site Optilite).

Results and Conclusion: Statistical analysis of the results showed that (1) among the analytes measured, only triglyceride levels showed a significant difference between the stroke and the control group. (2) The relationship between HDL cholesterol and apolipoprotein-AI and between LDL cholesterol and apolipoprotein-B was linear. (3) The correlation between the measured and calculated LDL cholesterol was linear with significant agreement. (4) Statistical analysis of the three parameters on the two nephelometers [apolipoprotein-AI, apolipoprotein-B, lipoprotein (a), apolipoprotein-B / apolipoprotein-AI ratio] indicates that the values measured by the two instruments are correlated, but there are significant differences between them. However, these differences do not appear to be clinically relevant.

Abstr. Nr. PS1.14

Analytical performance evaluation of the ECL-100 immunochemistry analyser

Joó P., Berbécs Prescsák A., Ajzner É.
Szabolcs-Szatmár-Bereg County Hospital and University Teaching Hospital, Nyíregyháza, Hungary

Background: The ECL-100 (Epitope Diagnostics, USA) is a chemiluminescent immunoassay analyser that uses capture antibodies on magnetic particles to measure various analytes in human serum.

Methods: Analytical performance of ECL-100 using PCT, NSE, CA 72-4 and HGH assays (Epitope Diagnostics) was evaluated. Each one of the ECL-100 assays (New Tests) were compared by the assays that are used actively in our laboratory (Old Tests): PCT on Advia Centaur XPT (Siemens, Germany), NSE on Liason XL (Diasorin, Italy), HGH on Immulite 2000 Xpi (Siemens) and CA 72-4 ELISA (IBL, Switzerland), respectively.

Results: Repeatability and reproducibility were tested using assayed quality control materials of the manufacturers on clinically important levels by 10 repetitive measurements and were found CV≤ 2,6% with the New Tests and CV≤ 5,65% on Old Tests, respectively. The results corresponded well with the specifications given by the manufacturers. Excellent correlations were found between New Tests and Old Tests using 50 patient serum samples with R^2 values as follows: PCT=0,97; NSE=0,99; CA 72-4=0,97; HGH=0,98.

Conclusion: Analytical performance of the ECL-100 analyser using PCT, NSE, CA 72-4 and HGH assays was found excellent. The ECL-100 tests showed good correlation with the assays that are used actively in our laboratory. Despite not being fully automated, the ECL-100 was easy to use. The cost-effective and compact ECL-100 analyser can be perfect choice in smaller scale laboratories for testing PCT, NSE, CA 72-4 and HGH parameters.

Abstr. Nr. PS1.15

Analysis of proinflammatory cytokines in cerebrospinal fluid (CSF) samples of patients with subarachnoid hemorrhage (SAH)

Nagy B. Jr.[1], Pócsi M.[1], Szántó D.[2], Bodnár F.[3], Molnár C.[2], Fülesdi B.[2], Kappelmayer J.[1]
[1]Department of Laboratory Medicine, [2]Department of Anesthesiology and Intensive Care Unit, [3]Department of Infectious Diseases, University of Debrecen, Debrecen, Hungary

Background: SAH is an acute cerebrovascular event which represents 5% of all stroke cases and invasion of red blood cells with their subsequent lysis result in pronounced immune responses with overexpression of proinflammatory cytokines in the subarachnoid space. However, the diagnostic potential of these mediators measured in CSF is still under investigation.

Methods: Interleukin-6 (IL-6), procalcitonin (PCT) and tumor necrosis factor-α (TNF-α) levels were determined in CSF samples by automated immunoassays (Cobas® e411 and Maglumi® X3, respectively) at admission and during the follow-up of SAH patients (n=14). Disease severity was evaluated by Hunt-Hess score (HHS). As controls, other non-SAH neurosurgical cases were enrolled (n=8). These cytokines were correlated with clinical data, C-reactive protein (CRP) and other routinely available CSF parameters.

Results: Only baseline IL-6 CSF levels were significantly elevated in SAH compared to controls which highly correlated with TNF-α and absolute MN cell counts. Importantly, CRP and PCT were substantially related to the albumin ratio but not WBC counts in contrast to IL-6 and TNF-α indicating the distinct source of these cytokines. Degree of SAH severity was inversely associated with higher baseline IL-6 (r=-0.5956, p=0.0366) and PCT (r=-0.5796, p=0.0322) values. Finally, IL-6 in CSF reliably monitored the clinical condition and remained highly elevated in those SAH cases with early death.

Conclusion: Based on our preliminary data, among the four cytokines, CSF IL-6 demonstrated the most promising characteristics in the diagnosis of SAH suggesting its regular measurement in the daily clinical practice.

Abstr. Nr. PS2.1

Really that much?

Szabó T., Szabó S., Vass L., Seres E.
Bács-Kiskun County Teaching Hospital, Kecskemét, Hungary

Background: In the case of a 12.5-year-old girl, an oral glucose tolerance test (OGTT) and other laboratory tests were requested by the referring physician due to migraine headaches and obesity (BMI 28.3 kg/m^2). In addition to blood glucose, insulin levels were also measured at 0 and 120 minutes. The 120-minute insulin value was extremely high, >1000 µU/mL. During consultation with the attending physician, a possible interference affecting the measurement method was considered. To rule this out, the OGTT and additional laboratory tests were repeated. The second test again showed extremely high insulin levels. After another consultation, a thorough anamnesis revealed the presence of acanthosis nigricans.

Methods: Insulin and hormone determinations were performed on serum samples using a Cobas e immunochemistry analyzer (ECLIA method); other laboratory tests were performed on a Cobas c chemistry analyzer (photometric method), and thyroid hormone tests were performed using a LIAISON analyzer (ECLIA method).

Results: Relevant laboratory measurements: 1st test: 0-minute insulin: 56.87 µU/mL,
0-minute glucose: 4.1 mmol/L, 120-minute insulin: >1000 µU/mL, 120-minute glucose: 9.1 mmol/L. Additional parameters: C-peptide: 5.53 ng/mL, Cortisol: 499.8 nmol/L. Thyroid hormones: TSH 3.37 mIU/L, FT4 10.9 pmol/L, FT3 4.5 pmol/L, anti-TPO 18 IU/mL. Electrolytes, liver function values, lipid profile parameters, and blood counts were within age-appropriate reference ranges. 2nd test (OGTT): 0-minute insulin: 71.18 µU/mL, 0-minute glucose: 4.6 mmol/L, 120-minute insulin: >1000 µU/mL, 120-minute glucose: 8.8 mmol/L. Rheumatoid factor and immunoglobulins (IgG, IgA, IgM) were within the reference ranges for her age.

Conclusion: After excluding potential diagnoses such as insulinoma, acromegaly, Cushing's syndrome, hypothyroidism, liver disease, and interfering measurement factors, the final diagnosis was insulin resistance, which in this case was accompanied by unusually extreme insulin levels likely due to pancreatic hypersecretion.

Abstr. Nr. PS2.2

The importance of gastropanel markers

Kádár K.B., E. Pintér E.
SYNLAB Diagnostic Center, Immunology Laboratory, Budapest, Hungary

Background: Due to the increasing frequency of gastrointestinal complaints, metabolic disorders, immunological and autoimmune diseases, increasing attention is being paid to the examination of the state of the gastric mucosa. The aim of this study was to evaluate the usefulness of a non-invasive test, the GastroPanel, which provides an opportunity to assess gastric acid secretion, *Helicobacter pylori* infection and the presence of atrophic gastritis.

Methods: 1024 patients (mean age 44.5 ± 14.4 years; 679 women, 345 men) were examined. The detection of antibodies against *H. pylori*, the determination of pepsinogen I and II, and gastrin-17 concentrations were determined using the GastroPanel ELISA test, from serum samples. The distribution by age group and gender (0–17 years: 17 females, 12 males; 18–50 years: 433 females, 239 males; 51–95 years: 229 females, 94 males) showed female dominance.

Results: Symptoms associated with acid hyperproduction were observed by 36.72% of women, while 15.6% of men. Taking acid-suppressing medication occurred in 6.8% of women and 3.8% of men. *H. pylori* infection prior to the study was reported by 9.4% of women and 4.3% of men, and eradication treatment was received by 7.3% of women and 3.3% of men. In the 18–50 age group, high levels of *H. pylori* antibodies were measured in 7.6% of women and 4.8% of men. Elevated gastrin-17 levels occurred in 4.9% of women and 2.3% of men, while decreased gastrin-17 levels occurred in 9.2% of women and 6.3% of men. Higher levels of gastrin-17 (5.1%) and pepsinogen II (4.5%) were detected among women aged 51–95. Atrophic gastritis was found in 2.1%, mainly in women aged 30–70.

Conclusion: It can be stated that significant gender and age differences can be observed in the distribution of GastroPanel biomarkers and the occurrence of symptoms, which supports the importance of an individualized gastroenterological evaluation. Atrophic gastritis represents an increased risk of developing gastric cancer, so its timely recognition is very important.

Abstr. Nr. PS2.3

Parathyroid hormone washout as complementary diagnostic tool

Király T.[1], Deák V.[2] Rucz K.[3], Solymosi T.[4], Peti A.[1]
[1]Central Laboratory, Hospital of Siófok, Siófok, Hungary, [2]Internal Medicine, Somogy County Kaposi Mór Teaching Hospital, Kaposvár, Hungary, [3]Internal Medicine - Endocrinology, Hospital of Siófok, Siófok, Hungary, [4]Internal Medicine, Bugát Pál Hospital, Gyöngyös, Hungary

Background: The measurement of parathyroid hormone assay in the washout fluid (PTHw) obtained by ultrasound-guided fine-needle aspiration can be used for clarifications of etiology of lesions. In the diagnosis and follow-up of different thyroid and parathyroid diseases, this approach can be a very useful complementary diagnostic tool until surgery. The aim of this study was to present our experience with PTHw assessment.

Methods: This retrospective, comparative study conducted in several hospitals includes adult patients who underwent endocrinological treatment for primary hyperparathyroidism. After preliminary sample preparation, the measurements were carried out on the Beckman Coulter UniCell DXI-600 immunological automated analyzer. The patient's laboratory results between 2022 and 2024 years with measurements of PTHw were statistically analyzed in SPSS 24.

Results: In this study 33 patients with suspected parathyroid lesions were enrolled, 5 men / 28 women, age: 58 ± 15 years, adenoma diameter: 17.1 ± 6.96 mm and volume: 2004.3 ± 2616.66 mm^3, serum PTH (PTHs): 16.4 ± 15.81 pmol/L and PTHw: 1922.5 ± 9219.36 pmol/L. The size of adenoma was in significant correlation to age (-0.487, $p<0.01$) but without statistical associations to PTHw (0.234) or the rate of PTHw/PTHs (0.242). The average time until surgery was 13.1 ± 18.93 months.

Conclusion: We think that the PTHw measurement is a reliable method in parathyroid adenoma localization, the ultrasound-guided fine-needle aspiration procedure is adequately safe, therefore patients should benefit with fewer tests and reduced healthcare expenses. Using PTHw could lead to a faster diagnosis and surgery treatment if needed.

Abstr. Nr. PS2.4

Reference intervals for Anti-TPO and Anti-TG biomarkers in children, pregnant women and adults

Kecskeméti G[1,2], Szabó Z.[3], Sallay K.[4], Nagy I.[5], Nagy B.[1], Shemirani A.H.[1,6]
[1]Department of Laboratory Medicine, University of Debrecen, Debrecen, Hungary, [2]Gróf Tisza István Hospital, Berettyóújfalu, Hungary, [3]Gynecology, Tatabánya, Hungary, [4]Children's General Practitioner, Tatabánya, Hungary, [5]Corden International, Budapest, Hungary, [6]Central Integrated Laboratory, Tatabánya, Hungary

Background: Accurate reference intervals (RI) for anti-thyroglobulin (Anti-TG) and anti-thyroid peroxidase (Anti-TPO) antibodies are critical for diagnosing autoimmune thyroid disorders. We aimed to determine appropriate RIs for Anti-TPO and Anti-TG autoantibodies (UniCel, DxI 800 Access, Beckman Coulter).

Methods: Stored serum samples from 836 individuals were included in the study, consisting of 677 adults and 159 children. Data were subdivided into adults and children, with further stratification by gender, pregnancy status, age group, and trimester. Outliers were excluded using the Tukey method (IQR × 1.5). RIs were calculated as the 2.5th and 97.5th percentiles according to the Clinical and Laboratory Standards Institute guidelines.

Results: Reference intervals for Anti-TG were 0.1–0.76 IU/mL (males) and 0.1–0.7 IU/mL (non-pregnant females); for Anti-TPO, 0.25–2.3 IU/mL (males) and 0.25–2.48 IU/mL (non-pregnant females). Children's RIs were stratified by age (1-5, 6-10, 11-14, 15-17 years), showing stable Anti-TG (0.1-0.89 IU/mL) and Anti-TPO (0.25-1.35 IU/mL) ranges. Pregnant women's RIs were established across trimesters, with upper limits for Anti-TPO reaching 1.7 IU/mL and for Anti-TG reaching 0.84 IU/mL in the second trimester.

Conclusion: Our findings provide precise Anti-TPO and Anti-TG reference values, crucial for reliable autoimmune thyroid diagnostics in diverse Hungarian populations.

Abstr. Nr. PS2.5

Not all tumors that appear to be tumors or diagnostic challenge of systemic lupus erythematosus

Varga R.[1], Fodor B.[1,2]
[1]Borsod-Abaúj-Zemplén County Central Hospital, Miskolc, Hungary
[2]Institute of Clinical Methodology, Faculty of Healthcare Studies, University of Miskolc, Miskolc, Hungary

Background: Systemic lupus erythematosus (SLE) is one of the most common systemic autoimmune diseases, in which pathological immune complexes and autoantibodies together cause the patient's complaints. In 90% of cases, young women between the ages of 18 and 40 are affected. Clinical symptoms are very diverse, and any organ or organ system can be affected through its inflammation or immune-mediated damage. Both genetic and environmental/lifestyle factors may play a role in its development.

Methods and Results: In our case studies, we present the diagnostic difficulties of SLE through the medical histories of a 71-year-old female patient and a 50-year-old male patient. Both of them had symptoms of weakness and weight loss, one of them had fever, and the other patient also had joint and abdominal pain. From their first laboratory tests, high CRP with accelerated erythrocyte sedimentation rate, anemia and proteinuria should be highlighted. Both patients underwent weeks of tumor research with a multitude of additional laboratory and imaging tests, as well as endoscopic examinations. After all of these ended with negative results, immunoserological tests were performed, which were performed "urgently". Low C3 and C4 levels, homogeneous ANA positivity and anti-dsDNA positivity were described in both patients. Based on the clinical picture and immunoserological tests, the diagnosis of SLE was confirmed, so high-dose corticosteroid therapy was started, which resulted in a significant improvement in their condition.

Conclusion: The two presented cases are good examples of how even a well-known disease such as SLE is not always an easy task to diagnose, if it does not affect the most typical age group and gender. We would like to emphasize that immunoserological tests, which are otherwise classified as non-urgent tests, should be performed urgently in well-defined clinical situations.

Abstr. Nr. PS2.6

Life or death? A versatile biomarker: neuron-specific enolase (NSE)

Kiss I.[1], Hankovszky P.[2], Bukva M.[3], Telkes M.[1], Babik B.[2], Földesi I.[1]
[1]Institute of Laboratory Medicine, University of Szeged, Szeged, Hungary, [2]Institute of Anaesthesiology and Intensive Care, University of Szeged, Szeged, Hungary, [3]Faculty of Science and Informatics, University of Szeged, Szeged, Hungary

Background: Heart failure can occur for a variety of reasons, from illness to accidents. However, the possibility of reversing this seemingly permanent condition through rapid and effective intervention reduces the number of deaths. Therefore, it is important to make the most of the existing knowledge and diagnostic capabilities to assess prognosis. Neuron-specific enolase (NSE) as a marker of neurological status changes is of importance in this context. NSE is an enzyme in the neurons. Elevated levels are found in tumours differentiated in the neuroendocrine direction, such as neurobastoma and neuroendocrine metastases, and is a specific marker of small cell lung cancer (SCLC). In view of this knowledge, we use it as a tumour marker. However, several studies have shown that its presence in nerve cells makes it suitable for monitoring neurological events: depending on the degree of brain hypoxia, its level indicates neurological status changes or the likelihood of death.

Methods: In our study, we examined the NSE results of 50 patients who had successfully undergone resuscitation after cardiac arrest for any reason, looking for variations of levels in samples taken on 2 and 3 consecutive days. Patients were men and women, between 18-90 years. We used NSE results of patients from the Institute of Anaesthesiology and Intensive Care at the University of Szeged. The samples were analysed by a COBAS 8000 analyser (ROCHE) with NSE reagent.

Results: The study is still ongoing; the results will be evaluated using appropriate statistical methods.

Conclusion: From the results obtained, we expected that as the NSE level increases over time, the patient's condition would progress, whereas the marker level decreases, the patient's condition would improve. The proof of this is ongoing.

Abstr. Nr. PS2.7

Screening of colorectal cancer by qualitative and quantitative determination of human haemoglobin in faeces

Tóbiás Á.[1#], Lukács A.[1#], A. Hoffmann A.[1], Bartucz H.[1], Gálóczi I.[1], Czakó L.[2], Gieszinger G.[2], Földesi I.[3], Gao P.[4], Varga C.[1]
[1]HR-Pharma LTD, Szeged, Hungary; [2]First Department of Medicine, University of Szeged, Szeged, Hungary; [3]Institute of Laboratory Medicine, University of Szeged, Szeged, Hungary; [4]Epitope Diagnostics Inc, San Diego, USA; [#]: contributed equally

Background: Despite the Hungarian Screening Programme, colorectal cancer presents a large public health burden, it is the second most common cause of cancer-related death in Hungary. In the first step of colorectal cancer screening a rapid immunochemical test is carried out as a qualitative detection of human haemoglobin in the stool. Patients with a positive test result are referred to colonoscopy for diagnosis. Immunological-based rapid test has been developed to detect human haemoglobin in faeces, but it does not measure the exact level of it. Because of false-positive results many patients are unnecessarily sent to colonoscopy.

Methods and Results: In this study, first, haemoglobin is measured by rapid test in approximately 100-150 stool samples in the First Department of Medicine, University of Szeged. Then, from the same stool samples, Chemiluminescence

Immunoassay (CLIA) kit (q-FOB™ assay) is applied for the quantitative determination of human haemoglobin in faeces using the ECL100 Immunoassay analyser at HR-Pharma.
The q-FOB™ assay utilizes a two-site "sandwich" technique with two antibodies that bind to different epitopes of haemoglobin. Since highly specific human haemoglobin antibodies are used, false-positive results are practically excluded. To avoid false-negatives, q-FOB™ assay detects human haemoglobin levels in much lower concentrations than rapid test. To standardize the collection process, a special Fecal Sample Collection Device is used. Colonoscopy data are also collected in the First Department of Medicine, University of Szeged.
The aim of our study is to compare the colonoscopy data with qualitative and quantitative haemoglobin detection results and adjust a cut-off level for fecal haemoglobin detection to decide who should undergo colonoscopy.

Abstr. Nr. PS2.8

Peripheral arterial disease (PAD) as a marker of altered thyroid hormone metabolism in patients with diabetic foot ulcers – A retrospective analysis

Dávid E.V.[1], Pákozdi C.[1], Barta G.[2], Simon Á.[1]
[1]Central Laboratory, Heténi Géza County Hospital, Szolnok, Hungary
[2]Department of Internal Medicine, Heténi Géza County Hospital, Szolnok, Hungary

Background: Peripheral arterial disease (PAD) is a common manifestation of systemic atherosclerosis and is frequently underdiagnosed. Recent studies suggest that alterations in thyroid hormone metabolism, particularly the ratio of free triiodothyronine (FT3) to free thyroxine (FT4), may reflect systemic disease and predict cardiovascular outcomes. International data indicate that low triiodothyronine (T3) levels or a low FT3/FT4 ratio are associated with worse cardiovascular prognosis. Some studies have linked a lower FT3/FT4 ratio to atherosclerosis and the presence of PAD.

Methods: In our study, we reviewed the medical histories of patients with diabetic foot ulcers treated at our hospital to explore the association between type 2 diabetes mellitus (T2DM), foot ulceration, and the FT3/FT4 ratio.

Results: By retrospectively analyzing our hospital database for the years 2023–2024, we identified 4,305 patients under diabetic care and 156 patients with documented foot ulcers. Of these, only 342 had recorded FT3 and FT4 measurements. Based on the inclusion criteria, we were able to analyze 9 cases (T2DM) in detail, each with varying complications, HbA1c levels, thyroid status, and comorbidities. Six of these cases involved lower limb ulcers. Among them, 3 had thyroid disorders, while the other 3 did not. In five cases, the FT3/FT4 ratio was below 0.368, which may indicate inflammation, metabolic imbalance, or impaired tissue hormone utilization. A lower FT3/FT4 ratio could contribute to the persistence of chronic ulcers.

Conclusion: Considering both metabolic control (HbA1c) and hormonal balance may be important in assessing ulcer risk and prognosis. Routine monitoring of the FT3/FT4 ratio may be advisable in diabetic patients with ulcers, especially when thyroid involvement is suspected.

Abstr. Nr. PS2.9

The role of laboratory medicine in the diagnostics of Cushing's syndrome: a retrospective review of cases of patients undergoing bilateral inferior petrosal sinus catheterization

Kurunczi M.[1], Telkes M.[1], Kupai K.[2], Valkusz Z.[2], Földesi I.[1]
[1]Institute of Laboratory Medicine and [2]Department of Internal Medicine and Cardiology Center, Albert Szent-Györgyi Clinical Center, University of Szeged, Szeged, Hungary

Background: Cushing's disease is a rare disorder caused by an adrenocorticotropic hormone (ACTH)-secreting pituitary adenoma. Differentiation between Cushing's disease and ectopic ACTH syndrome is challenging, because clinical

presentation, biochemical profiles (basal ACTH and cortisol levels), dexamethasone suppression tests and imaging techniques are often insufficient for accurate diagnosis. Bilateral inferior petrosal sinus sampling (BIPSS) is widely regarded as the gold standard for distinguishing between these conditions. During BIPSS, ACTH is collected directly from the inferior petrosal sinuses, which drain blood from the cavernous sinuses surrounding the pituitary gland. Significant central-to-peripheral ACTH gradient confirms the pituitary origin of ACTH overproduction.

Methods and Results: Between 2021 and 2024, four patients underwent BIPSS at our Center. Specimens were taken from three venous locations at time points of -5 or -3, 0, and +3 or +5, +10, and +15 minutes relative to corticotropin-releasing hormone (CRH) stimulation. Sandwich ECLIA was performed to determine ACTH levels from EDTA plasma and competitive ECLIA to measure serum cortisol. This work presents three patients briefly and one in detail. While post-procedural data were not available for one individual, the remaining three patients subsequently underwent transsphenoidal pituitary surgery based on the BIPSS results.

Conclusion: This study highlights the key role of laboratory medicine in Cushing's diagnostics. Collaboration between the interventional team and clinical laboratory professionals is crucial for the success of BIPSS. Accurate timing of sample collection, appropriate handling of specimens - especially of ACTH due to its instability - and fast turnaround time of results are essential for proper interpretation and optimal patient management.

Abstr. Nr. PS2.10

Reward dependence and „Flow" state appearance in sport performance

Nagy Z.[1, 2], Karsai I.[3], Nagy T. [1], Kátai E.[1], Miseta A.[1], Fazekas G.[4], Láng A.[5], Kocsor F.[5], Kállai J.[6]
[1]Department of Laboratory Medicine, University of Pécs, Hungary,
[2]Sport and Medicine Research Group, Regenerative Science, Szentágothai Research Centre, University of Pécs, Hungary, [3]Sports and Physical Education Center, University of Pécs, Hungary, [4]Department of Vascular Surgery, University of Pécs, Hungary, [5]Institute of Psychology, University of Pécs, Hungary, [6]Department of Behavioural Sciences, Medical School, University of Pécs, Pécs, Hungary

Background: In this research, we sought to answer whether neurobiological markers could be associated with personality traits, such as reward dependence and the experience of the "flow" state.

Methods: 22 healthy, non-medicated, regularly exercising men (mean age: 40.27 years, SD: 5.4) participated in the study. Participants completed a shuttle run test, then repeated it two weeks later in a competitive situation. Prior to and after the runs, they completed several psychological tests. Blood and urine samples were taken immediately before and after the exercise. Blood was analyzed for routine laboratory parameters including testosterone and cortisol, while urine was tested for catecholamines, homovanillic acid (HVA) and vanillylmandelic acid (VMA).

Results: Catecholamines, testosterone, cortisol and VMA levels increased after physical exercise, whereas HVA levels decreased. The increase of testosterone levels was smaller in the competitive- than in the non-competitive condition, while cortisol levels were inversely related. In addition, noradrenaline levels during non-competitive physical exertion showed a correlation with the degree of reward dependence. Higher flow state values were associated with significantly lower catecholamine levels.

Conclusion: For male runners, noradrenaline and testosterone levels measured during physical exercise in competitive and non-competitive situations correlate with reward dependence. Our study supports the transient hypofrontality theory that lower prefrontal/frontal activity is required to achieve flow reward, to which the release of catecholamines may contribute in a synchronized manner.

Abstr. Nr. PS2.11

Unexpectedly high free T4 level without clinical symptoms

Szabó B., Zsjak K., Nagy M., Szellő O.
Budai Irgalmasrendi Hospital, Budapest, Hungary

Background: A 63-year-old male patient was admitted to the Cardiology Department by ambulance (OMSZ) due to leg swelling and progressively worsening exertional dyspnea, which later also occurred at rest. In cases of acute heart failure, the laboratory diagnostic protocol includes TSH and fT4 tests to rule out thyroid dysfunction. The laboratory results - elevated TSH along with high fT4 - did not match the clinical presentation. In cases where laboratory results are inconsistent with the clinical picture, the possibility of interfering factors must be investigated.

Methods: Hormones were determined using the ECLIA method on the cobas e 602 immunochemistry analyzer.

Results: TSH: 5.38 mIU/L (ref.: 0.27–4.2 mIU/L); fT4: 63.33 pmol/L (ref.: 11.9–21.6 pmol/L); fT3: 4.69 pmol/L (ref.: 3.1–6.8 pmol/L). The elevated TSH and high fT4 values were inconsistent with the clinical picture. A repeated sample taken 4 hours later showed: TSH: 2.61 mIU/L; fT4: 24.74 pmol/L. These results raised the possibility of drug interference. The discrepancy between the clinical condition and laboratory results suggested potential method interference. Upon detailed evaluation of the main causes of interference, intravenous furosemide therapy was identified as interfering factor.

Conclusion: Furosemide (the most commonly used loop diuretic) can cause a falsely elevated free thyroxine (fT4) level in laboratory tests. This does not reflect a true increase in thyroid hormone but rather a methodological interference. In high doses (usually >80 mg/day), furosemide can displace T4 from plasma proteins or compete for binding sites, thereby increasing the measured free T4 (fT4) concentration artificially. Furosemide may interfere with the binding between antibodies and fT4 in the assay, resulting in falsely elevated fT4 values.

Abstr. Nr. PS2.12

Circulating cell-free DNA methylation profiling for early detection of colorectal cancer

Lukász P.[1], Mészáros A.[2], Szakács O.[2], Serdült A.[2], Hunyadi P.[2], Virág L.[2], Kis D.[2], Szijártó A.[1], Biró O.[2], Bánky B.[1]
[1] Department of Surgery, Transplantation and Gastroenterology, Semmelweis University, Budapest, Hungary, [2]Clinomics Europe Ltd., Budapest, Hungary

Background: Early screening for colorectal cancer (CRC) is a crucial public health challenge worldwide. Detecting pre-cancerous lesions or less advanced stages of CRC can significantly improve patient survival rates. DNA methylation is considered an early event in cancer development and progression. This report presents preliminary results on the clinical applicability of ColonAiQ®, a cell-free DNA (cfDNA) methylation profiling assay. The sensitivity rates were compared with routinely used tumour markers CEA and CA19-9.

Methods: The histopathologically classified patient group (n=123) was recruited at Semmelweis University: 10.6% non-neoplastic gastrointestinal disorders (GI), 14.6% adenomas and polyps (A), 17.1% CRC stage 0–I, 20.3% CRC stage II, 26.8% CRC stage III, and 10.6% CRC stage IV. Age- and sex-matched healthy donor samples were included as controls (n=60). cfDNA samples were analyzed by multiplex methylation-specific qPCR targeting 5 gene regions.

Results: Elevated CEA/CA19-9 levels were compared to ColonAiQ positivity in the different patient groups: GI: 7.7/15.4% vs. 15.4%; A: 0.0/5.6% vs. 44.4%; CRC 0-I: 0.0/9.5% vs. 66.7%; CRC II: 20.0/32.0% vs. 84.0%; CRC III: 9.1/39.4% vs. 87.9%; CRC IV: 38.5/69.2% vs. 92.3%. Co-methylation of 4-5 targets was found mostly in advanced CRC samples, while 1-3 methylated regions were found in patients with non-advanced CRC, A, and GI cases. The healthy control group had a false positive rate of 5.0%.

Conclusion: The non-invasive blood-based ColonAiQ test was shown to be more sensitive than commonly used tumor markers for CRC, especially in precancerous and early stages. Preliminary results suggest that ColonAiQ could aid in the early detection of colorectal cancer patients, potentially reducing morbidity and mortality.

Abstr. Nr. PS3.1

Evaluation of two automated capillary electrophoresis and immunofixation systems for human serum protein analysis

Mező-Géresi K., Huszár K., Tajti B.T., Simon J.
Central Department of Laboratory Diagnostics, North-Pest Center Hospital – Military Hospital, Budapest, Hungary

Background: The diagnosis of patients with monoclonal gammopathies, such as multiple myeloma, depends on accurate identification and characterisation of monoclonal proteins. Serum and urine protein electrophoresis and their immunological characterisation are the most important methods for diagnosing and assessing patients' response to treatment. The aim of the study was to obtain equivalent results for patient samples between the Helena V8 Nexus and Sebia Capillarys 2 systems. The SAS Vitrési instrument was compared to the Sebia Hydrasys 1 for serum and urine immunofixation.

Methods and Results: A total of 216 serum samples were analysed on the Helena V8 Nexus and Sebia Capillarys 2 instrument. Overall, the serum protein samples which were screened on Helena and Sebia capillary analysers, demonstrated comparable results. All normal and abnormal results were identified and the relative area percentage (%) and band values were also comparable. As the Helena V8 Nexus and Sebia Capillarys 2 Serum protein capillary zone electrophoresis methods use different equipment and buffer chemistries for analysis, the trace morphologies and relative area percentage values are not expected to be identical, however equivalent results are expected, which has been demonstrated in the study performed. A total of 45 serum and urine samples were analysed for immunofixation, and we could demonstrate comparable and concurrent results.

Conclusion: Overall, the samples analysed using both Helena and Sebia gel and capillary electrophoresis methods demonstrated equivalent results with no discrepancies, including comparable fraction % values. However, it was also recommended while on site, that the customer should create their own local reference range. Advantages were seen on several samples when tested using Helena methods in comparison to Sebia; improved banding resolution and clearer peak definition were noted on the Helena systems

Abstr. Nr. PS3.2

Early detection of the *BCR::ABL1* T315I mutation in Philadelphia-positive acute lymphoid leukemia and chronic myeloid leukemia

Meggyesi N.[1], Varga L.[1], Antali F.[1], Harasztdombi J.[2], Hardi A.[2], Lakatos V.[2], Gopcsa L.[2], Reményi P.[2], Andrikovics H.[1]
[1]Laboratory of Molecular Genetics, [2]Department of Haematology and Stem Cell Transplantation, Central Hospital of Southern Pest, National Institute of Hematology and Infectious Diseases, Budapest, Hungary

Background: Mutations in the *BCR::ABL1* may confer resistance to tyrosine kinase inhibitors (TKIs) in Philadelphia-positive acute lymphoid leukemia (Ph+ ALL) and chronic myeloid leukemia (CML). Recently, international guidelines have recommended a switch from Sanger sequencing to more sensitive techniques such as next-generation sequencing (NGS) and droplet digital PCR (ddPCR), as the mutation detection rate can be increased from 25% to 50%. Detection of *BCR::ABL1* T315I is critical due to its association with resistance to first- and second-generation TKIs.

Methods and Results: Between 2017-2024, our laboratory monitored ~400 CML and ~40 Ph+ ALL patients annually. Since 2005, we have performed 660 Sanger sequencing (with a sensitivity of 10-20%) to identify TKI resistance mutations. Recently, a new ddPCR-based test was established for the detection of T315I (achieving a sensitivity of 0.5% T315I/*BCR::ABL1*). We identified TKI resistance-mutations using Sanger sequencing analysis in 22.4% of cases (148/660). The most frequently detected mutations affected *BCR::ABL1* T315, F317, E255, F359, and Y253 codons. Retrospective analysis of 15 T315I-positive patients demonstrated that the novel ddPCR method enabled the detection of the T315I mutation a median of 3.53 months earlier than by Sanger sequencing.

Conclusion: As the presence of specific mutations can influence TKI selection and the therapeutic response, early detection of the T315I mutation facilitates the timely implementation of appropriate treatment strategies, such as ponatinib, asciminib, or allogeneic hematopoietic stem cell transplantation. The targeted detection of T315I mutation with ddPCR allows faster and more sensitive method for mutation analysis compared to Sanger and next-generation sequencing.

Abstr. Nr. PS3.3

Verification during the preanalytical phase of hemostasis

Sipos L., Szabó M., Brumbauer M., Farkas M., Kiss B.
Synlab Hungary Kft, Székesfehérvár, Hungary

Background: Regarding the storage and transport conditions of hemostasis samples, the CLSI H21 ED6:2024 guideline provides guidance for both manufacturers and medical laboratories. In alignment with the accreditation expectations outlined in ISO 15189:2023, it emphasizes the importance of internal laboratory control over preanalytical processes.

Methods: In our study, we examined the temperature dependence of factor VII (FVII) through changes in prothrombin time (PT). Four plasma samples were collected from each of 20 volunteers in 3.5 mL Greiner Vacuette tubes containing 3.2% trisodium citrate anticoagulant. PT and FVII assays were performed using the Siemens BCS XP analyzer. Measurements were conducted from plasma samples labeled I (primary) and III/a (secondary) stored at 25°C, and from plasma labeled II (primary) and III/b (secondary) stored at 4°C, at the following time points: immediately after sample preparation (0 minutes), then after 8, 12, 16, 20, 24, 32, 36, 40, and 44 hours of storage. Secondary plasma samples labeled IV were frozen at -20°C, and ongoing measurements were performed and evaluated after various storage periods: 1 day, 1 week, 1 month, 2 months, 3 months, and 4 months.

Results and Conclusion: For data evaluation, the performance specification for reproducibility: PT CV% <5%, FVII CV% <9% were provided by the manufacturer. Significance tests were conducted using linear regression with a 95% confidence interval, applying MedCalc software. Based on our results, it can be concluded that for primary samples, in accordance with the guideline recommendations, PT and FVII are stable for up to 24 hours at room temperature. However, in our experiment, PT measurements from secondary plasma were reliably reproducible up to 16 hours at room temperature and up to 20 hours when stored cooled. Interestingly, FVII in secondary samples was less stable at 25°C than at refrigerated temperature, highlighting the importance of proper sample preparation.

Abstr. Nr. PS3.4

Acquired autoimmune hemolytic anemia – a case report

Varga R., László K.
Synlab Laboratory, Székesfehérvár, Hungary

Background: Autoimmune hemolytic anemia (AIHA) is a rare hematologic disorder characterized by the production of autoantibodies against red blood cells, leading to premature erythrocyte destruction. The bone marrow attempts to compensate via increased erythropoiesis, resulting in reticulocytosis; however, if this compensatory mechanism is insufficient, anemia ensues. AIHA can be classified as either idiopathic or acquired and autoantibody thermal activity allows further subdivision into warm and cold types.

Methods and Results: An 83-year-old female patient presented to the Emergency Department with fatigue, pallor, and significant unintentional weight loss over the preceding three months. Laboratory results were white blood cells (WBC) 33.4 G/L, red blood cells (RBC) 1.33 T/L, hemoglobin 63 g/L, mean cell volume (MCV) 113 fL, and elevated mean cell hemoglobin concentration (MCHC) 417 g/L. Reticulocyte count was also high (83‰). Marked red blood cell agglutination was observed on the wall of the collection tube. Due to suspicion of cold agglutinins, the sample was incubated at 37°C for 30 min prior to

repeat analysis. After incubation, results were RBC 2.03 T/L, MCV 106 fL, MCHC 287 g/L. Because of leukocytosis and lymphocytosis (23.6 G/L), peripheral blood smear evaluation was performed. Atypical lymphoid cells with irregular, lobulated nuclei were found, raising the possibility of an underlying lymphoproliferative disorder. Elevated lactate dehydrogenase (1,535 U/L) and reduced haptoglobin (<0.3 g/L) levels were also observed. Based on our results, AIHA was strongly suspected. Flow cytometric analysis revealed mantle cell lymphoma. Correlating clinical presentation with diagnostic findings, AIHA associated with lymphoproliferative disease was established.

Conclusion: Prompt interpretation of relevant laboratory results, along with targeted diagnostic testing, is critical in establishing the diagnosis and guiding the management of acquired AIHA.

Abstr. Nr. PS3.5

Impact of different platelet counts on the results of lupus anticoagulant tests

Pető O., László K.
Synlab Laboratory, Székesfehérvár, Hungary

Background: Lupus anticoagulant (LA) is one of the antiphospholipid antibodies, alongside anti-cardiolipin and anti-beta2-glycoprotein I antibodies. The presence of these antibodies can be observed in various autoimmune diseases, such as antiphospholipid syndrome (APS) and is strongly associated with thrombosis. LA is measured by functional coagulation assays. For reliable LA testing, it is essential to obtain platelet-poor plasma (PPP: PLT<10 G/L) because high platelet counts can interfere with LA tests. Since platelet membranes contain phospholipids, high number of platelets can lead to excess phospholipids in the samples, potentially affecting test accuracy. Coagulation test results heavily rely on proper sample handling such as collection and centrifugation. This work aimed to investigate how different platelet counts affect LA test results.

Methods and Results: 200 samples were collected from 40 patients and tested for LA with two test systems [dRVVT-based (Russell's viper venom time) and APTT-based clotting assays (Siemens)]. Blood samples were collected into 3.2% trisodium citrate tubes (five tubes from every patient). One sample of each patient was double centrifuged for 15 minutes at 3500 rpm, while the others were centrifuged only once at 800, 1200, 1500, and 2000 rpm, respectively. Platelet counts were measured in every plasma by Sysmex XN-1000 analyzer, and each plasma was frozen at -20°C until further analysis. LA tests were performed on Siemens BCS XP system according to the ISTH 2020 guideline. Eight PPP samples were positive for LA; however, LA was not detected in the platelet-rich plasma samples of the same patients. Moreover, clotting times were consistently shortened in proportion to increasing platelet counts.

Conclusion: In conclusion, obtaining PPP is essential for accurate LA results, because high platelet count can significantly shorten clotting times, potentially leading to false-negative results.

Abstr. Nr. PS3.6

Identification of pathogenic hybrid genes in patients with atypical hemolytic uremic syndrome

Takács B.[1], Szabó E.E.[1], Marossy K.[1], Prohászka Z.[1], Szilágyi Á.[1]
[1]Department of Internal Medicine and Haematology, Research Laboratory, Semmelweis University, Budapest, Hungary

Background: Hemolytic uremic syndrome (HUS) is a rare thrombotic microangiopathy characterized by hemolytic anemia, thrombocytopenia, and renal impairment. The atypical form (aHUS) of the disease is mainly caused by genetic abnormalities in regulators of the complement alternative pathway (AP) leading to uncontrolled complement activation and endothelial injury. Pathogenic alterations of complement factor H, a key regulator of the AP, are identified in most cases. The gene of factor H (*CFH*) is located on chromosome 1q32 in the regulators of complement activation (RCA) gene cluster, adjacent to five

highly homologous genes encoding five factor H-related proteins (CFHRs). Due to the high homology of these genes non-allelic homologous recombination resulting in large deletions or duplications are quite frequent in this region.

Methods: To reveal structural variants in *CFH, CFHR1-5* genes multiplex ligation-dependent probe amplification (MLPA) was performed in aHUS patients. Breakpoints of the suspected hybrid genes were detected by Sanger sequencing of long-PCR products.

Results: Three patients with two different hybrid genes encoding fusion proteins were identified in the 460 patients studied. A large duplication involving part of *CFH*, the whole *CFHR3* and part of *CFHR1* gene was detected in two patients. Sanger sequencing revealed that these patients carry a previously reported, aHUS associated *CFHR1-CFH* hybrid gene. In the third patient a large heterozygous deletion was detected by MLPA and sequencing verified the lack of an 84 kb long region on one allele resulting in a *CFH-CFHR1* hybrid gene.

Conclusion: The identification of pathogenic hybrid genes in three aHUS patients indicates the importance of using techniques such as MLPA and long-range PCR in patients with this rare, life-threatening disorder, as large rearrangements are usually not detected by conventional sequencing methods.

Abstr. Nr. PS3.7

Identification of the underlying genetic variants in a case with hereditary thrombotic thrombocytopenic purpura

Miklós J.[1], Sinkovits G.[1], Prohászka Z.[1], Szilágyi Á.[1]
[1]Department of Internal Medicine and Haematology, Research Laboratory, Semmelweis University, Budapest, Hungary

Background: Thrombotic thrombocytopenic purpura (TTP) is a rare, life-threatening thrombotic microangiopathy (TMA) primarily caused by a severe deficiency of the ADAMTS13 enzyme, responsible for cleaving ultra-large von Willebrand factor (ULVWF) multimers. In congenital (hTTP) cases, this deficiency results from homozygous or compound heterozygous pathogenic variants in the ADAMTS13 gene. Genetic analysis by Sanger sequencing enables the identification of small variants; however, in some patients, persistent ADAMTS13 deficiency is observed without detectable inhibitors or pathogenic mutations in both alleles, raising the suspicion that these individuals may carry genetic alterations not detectable by routine sequencing methods.

Methods: In routine diagnostic workup of hTTP patients, Sanger sequencing of all 29 exons of the ADAMTS13 gene is performed to screen for pathogenic mutations. By this strategy, only one likely causative variant was identified in one of the suspicious hTTP cases. In order to detect large deletions or structural rearrangements not captured by standard sequencing methods, we introduced long-range polymerase chain reaction (long-PCR) assays.

Results: By applying the newly developed long-PCR methods, we successfully identified a deletion in heterozygous form in the studied patient. The detected 483 bp long deletion involves the entire exon 1, including the initiation site of the canonical transcript, indicating that no ADAMTS13 protein could be translated from the affected allele. Family screening confirmed that the two likely causative variants identified in the patient are located on different chromosomes.

Conclusion: Our results underscore the importance of complementing routine Sanger sequencing with long-PCR or similar methods when standard approaches fail to explain persistent ADAMTS13 deficiency. In the future, the application of these novel genetic methods may substantially improve the classification and management of patients with atypical or genetically unresolved forms of TTP.

Abstr. Nr. PS3.8

Paraprotein interference: a hidden challenge in laboratory diagnostics – case studies

Menrát-Fazekas D., Méri A., Galasz V., Simon J.
Central Department of Laboratory Diagnostics, North-Pest Center Hospital – Military Hospital, Budapest, Hungary

Background: Paraproteins are pathological monoclonal immunoglobulins produced by a single clone of B-cells or plasma cells. Their presence is most commonly associated with plasma cell disorders, such as multiple myeloma, Waldenström's macroglobulinemia, or other lymphoproliferative diseases. These abnormal proteins can interfere with laboratory analyses through various analytical and pre-analytical mechanisms. Their presence in the blood can lead to significant distortions in the results of numerous laboratory tests, thereby complicating the diagnostic process. Paraprotein-related interference may lead to both false-positive and false-negative results, thereby affecting the reliability of hematological, hemostasis, chemical, and immunoserological assays. Analytical systems operating on photometric and turbidimetric principles are particularly sensitive to these effects.

Methods and Results: In this work, we present case studies that clearly demonstrate the impact of paraprotein-related laboratory interferences on test results and their clinical importance. These case studies highlight the crucial role of laboratory professionals in supporting the diagnostic process: early recognition of suspicious results, identification of analytical problems, and prompt communication with clinicians are essential. Such actions are important to ensure an accurate diagnosis, to initiate appropriate further testing, and to avoid unnecessary interventions.

Conclusion: Recognizing the interferences caused by paraproteins, along with close collaboration between laboratory and clinical professionals, plays a key role in ensuring the timely diagnosis of hematological diseases. Through this, laboratory practice can have a direct and significant impact on patient outcomes.

Abstr. Nr. PS3.9

Germline-focused tumor analysis in hematological malignancies

Varga L., Csabán D., Őrfi Z., Bors A., Tankó L., Borsy A.É., Harasztdombi J., Hardi A., Reichardt J., Fábián J., Várkonyi A., Lakatos V., Gopcsa L., Reményi P., Andrikovics H.
Central Hospital of Southern Pest, Budapest, Hungary

Background: Germline-focused tumor analysis represents the re-evaluation of routinely performed next-generation sequencing (NGS) data on tumor or leukemia tissue, originally intended for detecting somatic mutations, based on specific germline-oriented criteria. This approach enables the identification of potentially hereditary, pathogenic genetic variants in genes associated with hereditary hematologic malignancies (HHMs), even without a suggestive personal or family history.

Methods: The present study aimed to perform germline-focused tumor analysis on 23-68 myeloid gene panel NGS tests between 2019 and 2024. The study included patients diagnosed with myelodysplastic syndrome (n=209), acute myeloid leukemia (n=268) and other hematologic malignancies (n=3). The NGS panel comprised genes known to harbour both somatic and germline mutations (e.g. *RUNX1*, *TP53*).

Results: In 69 patients, germline-focused tumor analysis indicated the possibility of an underlying hereditary predisposition. The germline origin was ruled out (n=33, 75%) or confirmed (n=11, 25%) by testing remission samples, hair follicles, or family members in 44 out of 69 cases. The confirmed, unrelated HHM cases (11/480, 2.3%) had germline alterations in the *DDX41*, *RUNX1*, *TP53*, *TERT*, and *PTPN11* genes. Specifically, *DDX41* variants were confirmed in over 75% of suspected cases (4/5, with one case lost to follow-up among 362 tested), *RUNX1* in 11.5% (3/26), and *TP53* in 8.3% (1/12) of tested individuals (all from the 480-patient cohort).

Conclusion: Our findings suggest that HHM may be more prevalent in adult patients with myeloid malignancies than previously recognised, even in the absence of classical clinical or familial indicators. Germline-focused tumor analysis

represents a viable approach for uncovering hereditary predisposition. However, current guidelines for its application in hematological malignancies based on large-scale studies are lacking.

Abstr. Nr. PS3.10

Inflammatory biomarkers predict outcome after thrombolysis in acute ischemic stroke

Éles Z.[1,2], Lóczi L.[1,2], Bomberák D.[1,2], Orbán-Kálmándi R.[1,2], Szegedi I.[2,3], Csiba L.[3], Oláh L.[3], Nagy A.C.[2,4], Dénes Á.[5], Bagoly Z.[1,2]
University of Debrecen; [1]Division of Clinical Laboratory Science, [2]Lendület "Momentum" Hemostasis and Stroke Research Group of the Hungarian Academy of Sciences, [3]Department of Neurology, [4]Department of Health Informatics, Debrecen, Hungary
[5]"Momentum" Laboratory of Neuroimmunology, Budapest, Hungary

Background: Tissue plasminogen activator (t-PA) treatment does not always lead to improved outcome in acute ischemic stroke (AIS). As inflammation plays a key role in stroke pathophysiology, we aimed to assess inflammatory cytokine/chemokine levels in t-PA treated AIS patients at admission, their association with acute phase hemostasis parameters and their predictive value.

Methods: In this prospective observational study, 132 AIS patients receiving t-PA therapy were enrolled. Routine chemistry tests, CRP, blood count, hemostasis screening tests, fibrinogen, D-dimer, von Willebrand factor (VWF) antigen, FVIII and ADAMTS13 activity were determined from blood samples at admission. Inflammatory cytokine/chemokine levels (CD54, IL-6, MCP-1, CD62P, CCL5, IL1R1, IL1R2, angiogenin) were measured using a cytometric bead array. Stroke severity was determined by the National Institutes of Health Stroke Scale (NIHSS). Long-term clinical outcome was defined 3 months post-event according to the modified Rankin Scale (mRS).

Results: Severe strokes (admission NIHSS>15) were associated with increased D-Dimer, IL-6, CCL5 and IL1RI. A positive correlation was identified between CCL5 and FVIII levels, while IL-6 concentrations correlated positively with CRP, FVIII, VWF levels and negatively with ADAMTS13 activity. In a multiple logistic regression analysis, CCL5 and ADAMTS13 emerged as independent predictors of poor (mRS 3-6) outcome, alongside NIHSS and age.

Conclusion: Stroke severity is associated with enhanced inflammatory response, potentially contributing to poor outcomes. CCL5 and ADAMTS13 were found to be independent predictors of unfavorable outcome.

Abstr. Nr. PS3.11

Case report of acquired dysfibrinogenemia

Réger B.[1], Kátai E.[1], Pál S.[2], Faust Z.[2]
[1]Department of Laboratory Medicine, [2]Department of Transfusion Medicine, University of Pécs, Pécs, Hungary

Background: Dysfibrinogenemia is a rare coagulation disorder, which can be hereditary or acquired. In some cases, it is asymptomatic but can often lead to bleeding or bleeding and thrombosis. The etiology of acquired dysfibrinogenemia includes liver dysfunction, multiple cancer types and could also be associated with monoclonal immunoglobulin production. The latter bind to fibrin, decreasing fibrin polymerization.

Methods and Results: We present the case of a 68-year-old male patient prior to elective Transcatheter Aortic Valve Implantation (TAVI). The routine laboratory assessment of hemostasis revealed prolonged prothrombin time (PT: 29.9 s), activated partial thromboplastin time (APTT: 92.3 s), thrombin time (TT) - no clot formation under extended measure time (300 s) and low level of fibrinogen by Clauss method (1.5 g/L; reference range: 2-4 g/L). Serum protein electrophoresis was performed, showing 2 extra fractions between α2 and β (4.9%, 2.96 g/L) and between β and γ fractions (4.9%, 2.96 g/L), respectively. Further examination using immunofixation electrophoresis detected IgA monoclonal immunoglobulins with λ

light chains. The laboratory analyses revealed a bleeding tendency, with low levels of fibrinogen. Further examinations detected monoclonal immunoglobulin synthesis as the etiology of the dysfibrinogenemia.

Conclusion: This case highlights the importance of timely recognition of this rare hemostatic disorder.

Abstr. Nr. S3.12

The effect of road transport on the results of routine blood coagulation tests

Harsányi M.,[1] Jakab É.[1], Csernák Z.[1], Pintér E.[2], Hideg T.[3]
[1]SYNLAB Budapest Szent János Hospital Laboratory (JKH), [2]SYNLAB Hungary Immunology Laboratory of Budapest Diagnostic Center, [3]SYNLAB Hungary Clinical Chemistry Laboratory of Budapest Diagnostic Center (SBDK), Budapest, Hungary

Background: The aim of our study is to investigate how routine coagulation test results are affected by the transport of primary samples on road.

Methods: Blood samples were collected into 3.2% trisodium citrate tubes from 170 patients at the outpatient clinic of JKH. The samples were centrifuged at 1500g for 15 min, then PT was measured using a Siemens BCS XP system, and APTT was performed on 80 samples, too. The primary samples were transported to SBDK within 4 hours at room temperature, where measurements were repeated on a Siemens BCS XP system after repeated centrifugation. In order to compare the two measurement systems, secondary samples (500-500 µl plasma) were also prepared from 88 primary samples and PT and APTT measurements were also performed at the SBDK laboratory. The distance between the two laboratories was 11 km and the transport time ranged from 28 min to 1 hour 37 min.

Results: We have found no significant difference between the results of the primary samples and the re-centrifuged primary samples in terms of PT ($p<0.0001$) and APTT ($p<0.0001$). Median PT results of primary samples was 8.4 sec (JKH) and 8.2 sec (SBDK), respectively. In the case of APTT, the median was 29.2 sec (JKH) and 28.8 sec (SBDK). To compare the measurement systems of the two sites, our results are as follows: for PT, median of JKH primary samples is 8.3 sec while SBDK secondary plasma median is 8.0 sec ($p<0.0001$), APTT: median of JKH primary samples is 29.6 sec; median of SBDK secondary plasma samples is 28.87 sec ($p=0.0004$).

Conclusion: The sample transport on road by vehicles does not have negative effect on measured haemostasis test results (PT and APTT) in case of re-centrifuged primary samples.

Abstr. Nr. PS3.13

Development of a new ELISA assay for the quantitative determination of anti-emicizumab antibodies

Katona É.[1], Uj E.A.[1,2], Diaconu A.[3], Bereczky Z.[1]
[1]Division of Clinical Laboratory Science, Department of Laboratory Medicine, University of Debrecen, [2]Kálmán Laki Doctoral School, University of Debrecen, Debrecen, Hungary, [3]Pediatric Department, “Carol Davila” University of Medicine and Pharmacy, Bucharest, Romania

Background: Emicizumab, a humanized bispecific monoclonal antibody, has been approved for treating patients with hemophilia A. However, a minority of patients have developed anti-drug antibodies (ADAs) that compromise its efficacy. Our objective was to create an ELISA method to quantify anti-emicizumab antibodies.

Methods: We confirmed the presence of anti-emicizumab antibodies with a neutralizing effect in the plasma of a hemophilia A patient who experienced ineffective treatment with emicizumab. We used a modified Bethesda assay and a home-made ELISA to detect the anti-emicizumab antibodies. In our bridging type of ELISA, we used unlabeled emicizumab to capture the

anti-emicizumab antibodies from the sample. The bound ADAs were detected using biotinylated emicizumab and streptavidin-HRP.

Results and Conclusion: A plasma dilution of 1:42 demonstrated a half-maximal absorbance in the ELISA. Emicizumab-specific antibodies were affinity-purified from the patient's plasma using emicizumab coupled to Sepharose 4B gel. Immunofixation electrophoresis of the purified Ig displayed a polyclonal IgG-type antibody pattern. The Ig fraction was purified further with Protein G affinity chromatography. We used the purified anti-emicizumab IgG to calibrate the bridging ELISA. In the original plasma sample of the patient, we measured an anti-emicizumab antibody concentration of 581 µg/mL. This anti-emicizumab concentration was more than 10 times higher than the emicizumab level measured in the patient after the loading period of treatment (49.2 µg/mL). Since the emicizumab level in the investigated plasma of the patient was below the detection limit, this anti-emicizumab level proved to be sufficient to clear the therapeutic antibody from the circulation.

Abstr. Nr. PS3.14

Beta-antithrombin levels in patients with venous thromboembolism

Uj E.A.[1,2], Molnár É.[1], Miklós T.[1,2], Gindele R.[1], Shemirani A.H.[1], Bereczky Z.[1], Katona É.[1]
[1]Division of Clinical Laboratory Science, Department of Laboratory Medicine, University of Debrecen; [2]Kálmán Laki Doctoral School, University of Debrecen, Debrecen, Hungary

Background: Antithrombin (AT) is a critical inhibitor of the coagulation cascade and exists in two isoforms: alpha-antithrombin (α-AT) and beta-antithrombin (β-AT). These isoforms differ in their glycosylation pattern. β-AT comprises 5-10% of total AT in the normal plasma. β-AT has a higher affinity for heparin than α-AT, making it a more effective inhibitor. There is no data about how β-AT activity levels change in thrombotic disorders. This study aimed to determine total and β-AT activity levels in patients with venous thromboembolism (VTE) compared to age-matched healthy controls.

Methods: We analysed citrated plasma samples from controls (n=208) and patients with VTE (n=208) collected at least 3 months after the acute event. Total antithrombin heparin cofactor activity was measured using a chromogenic anti-factor Xa assay in the presence of heparin. To measure β-AT, we modified this test by increasing the NaCl concentration of the reagent to 1.1 M to inhibit the heparin binding of α-AT.

Results: The total AT activity (%) level [median (IQR)] did not show a significant difference between the control and VTE groups [100.0 (92.0-109.0)% and 99.0 (92.0-108.75)%, p=0.541]. The β-AT activity levels showed a significant elevation in the VTE group compared to controls [93.3 (89.3-97.3)% vs. 89.2 (83.5-95.0)%; p<0.001]. The ratio of β-AT within total AT (%) was also significantly elevated in the VTE group compared to controls [9.3 (8.8-9.8)% vs. 8.9 (8.3-9.4)%; p<0.001)].

Conclusion: In our study, plasma levels of β-AT and its ratio within total AT were elevated in VTE patients. Since total AT levels did not differ from those of the controls, a decrease in the α-AT form can be presumed. Further studies are needed to clarify the pathophysiological significance of these changes.

Abstr. Nr. PS3.15

Monoclonal gammopathy detected through an atypical D-dimer profile

Ivanciuc A., Sárközi-Pál E.G., Hurják B., Szoboszlay I.
Markhot Ferenc County Hospital, Eger, Hungary

Background: Paraproteinemias are characterized by the production of monoclonal immunoglobulins that can cause analytical interference in various laboratory assays, particularly in immunoassay-based measurements. Falsely elevated D-dimer levels may mislead the diagnostic evaluation of thromboembolic diseases, especially when the underlying paraproteinemia is previously undiagnosed. Recognizing such analytical discrepancies is crucial for accurate diagnosis and patient management.

Methods: We analyzed the serum sample of a 60-year-old female patient with no relevant prior medical history. The routine laboratory panel included estimated glomerular filtration rate (eGFR), cardiac troponin T, and D-dimer quantification using an immuno-turbidimetric method. Due to the markedly elevated D-dimer level (9464 µgFEU/L), a 1:10 dilution was performed, revealing a disproportionately low value (1110 µgFEU/L). This finding suggested analytical interference, prompting targeted additional investigations, including serum protein electrophoresis and immunofixation electrophoresis.

Results: The patient exhibited impaired renal function (eGFR: 36 mL/min) and an elevated cardiac troponin T level (48.05 ng/L). The extreme D-dimer elevation and the disproportionate dilution response raised suspicion of an analytical problem. Serum protein electrophoresis revealed a distinct monoclonal spike in a concentration of 8.14 g/L, and immunofixation identified an IgG kappa monoclonal gammopathy. The analytical discrepancy observed during D-dimer measurement by immunoturbidimetry guided the diagnostic process towards the identification of a previously unknown paraproteinemia.

Conclusion: This case highlights that disproportionate D-dimer reduction upon dilution may serve as an important clue for the presence of paraproteinemia, even in patients without a prior history of monoclonal protein detection. Accurate laboratory interpretation requires the application of dilution studies, targeted protein analyses, and an understanding of assay-specific interferences.

Abstr. Nr. PS3.16

Clinical symptoms, genetic findings, and pregnancy outcomes in patients with low plasminogen activator inhibitor-1 levels

Hodossy-Takács R.[1,2], Orbán-Kálmándi R.[2], Molnár É.[1], Tóth[3] E.L., Deli T.[3], Lóczi L.[2], Molnár S.[1], Schlammadinger Á.[4], Boda Z.[4], Rázsó K.[4], Brúgós B.[4], Kerényi A.[5], Bereczky Z.[1], Krasznai Z.T.[3], Bagoly Z.[1,2]
University of Debrecen, [1]Division of Clinical Laboratory Sciences, [2]MTA-DE Lendület "Momentum" Hemostasis and Stroke Research Group, [3]Department of Obstetrics and Gynaecology, [4]Department of Internal Medicine, [5]Department of Laboratory Medicine, Debrecen, Hungary

Background: Plasminogen activator inhibitor-1 (PAI-1) deficiency is associated with bleeding and pregnancy complications. While the p.Ala15Thr variant reduces PAI-1 levels, the overall genetic background remains unclear. We aimed to assess the prevalence of low PAI-1 levels in symptomatic individuals, identify genetic variants, and monitor two pregnancies in p.Ala15Thr heterozygous women.

Methods: We retrospectively analysed PAI-1 levels (2022-2024) in patients assessed for bleeding with no other hemostatic disorder. Symptoms were categorized using the ISTH BAT. PAI-1 levels were measured via ELISA; Sanger sequencing was performed. Pregnancies in p.Ala15Thr heterozygous women were followed from preconception to postpartum, with laboratory testing every 3-6 weeks (PAI-1, FVIII, FXIII, α2-plasmin inhibitor, plasminogen, von Willebrand factor levels, Clot-Pro, ROTEM).

Results: Among 95 patients investigated for bleeding diatheses, common symptoms included menorrhagia (38%), ecchymosis (23%), and postoperative bleeding (17%). Although 73% had low PAI-1 levels, genetic testing (n=38) showed 60% were wild type (n=23); 29% p.Ala15Thr heterozygous (n=11) and 11% p.Val17Ile heterozygous (n=4). In two monitored p.Ala15Thr heterozygous pregnancies, PAI-1 levels normalized by the third trimester. Both delivered at term without complications.

Conclusion: Low PAI-1 levels were mainly linked to menorrhagia and surgical bleeding. Genetic mutations were not always detectable, possibly due to limited test sensitivity. No obstetric complications occurred in p.Ala15Thr heterozygotes.

Abstr. Nr. PS4.1

A truly quantitative immunoassay for the characterization of antigen specific serum antibody response

Prechl J.[1], Kovács Á.[2,3], Papp K.[1,4], Hérincs Z.[1], Pfeil T.[5]
[1]K+F Laboratórium, Diagnosticum Zrt, Budapest, [2]Department of Applied Analysis and Computational Mathematics, ELTE, Budapest, [3]Department of Biostatistics, University of Veterinary Medicine Budapest, [4]Department of Physics of Complex Systems, ELTE, Budapest, [5]HUN-REN–ELTE Numerical Analysis and Large Networks Research Group, Budapest, Hungary

Current assays for the measurement of specific antibody levels are not quantitative in the biochemical sense. The quantitative characterization of humoral immune responses on the systemic level requires a universal, quantitative, comparable measurement method of antigen specific serum antibodies of selected immunoglobulin classes.
Here we describe a fluorescent immunoassay, which provides the biochemical parameters that are both necessary and sufficient to quantitatively characterize the humoral immune response. For proof-of-concept, we used the recombinant receptor binding domain of SARS-CoV-2 as antigen on microspot arrays and varied the concentration of both the antigen and the serum antibodies from infected persons to obtain a measurement matrix of binding data. The two titration curves were simultaneously fitted using an algorithm based on the generalized logistic function and adapted for analyzing biochemical variables of binding. We obtained equilibrium affinity constants and concentrations for distinct antibody classes. These variables reflect the quality and the effective quantity of serum antibodies, respectively.
The proposed fluorescent dual-titration microspot immunoassay generates truly quantitative serological data that is suitable for immunological, medical and systems biological analysis.

Abstr. Nr. PS4.2

Frequency of mono- and polysensitization in food and respiratory allergies in Budapest and Debrecen

Varjú O.[1], Pintér E.[1], Sipka S.[2]
[1]Synlab Budapest Diagnostic Center, Immunology Laboratory, Budapest, [2]Department of Internal Medicine, Clinical Center, University of Debrecen, Debrecen, Hungary

Background: People living in highly allergenic regions are at higher risk of sensitization; therefore, the incidence of mono- and polysensitized patients is higher in these areas.

Methods: The aim of the current study was to determine the incidence of mono- and polysensitization in individuals living in Budapest (N=1343) and Debrecen (N=1526), where the agricultural area is also larger. In Budapest, measurements were performed at the Synlab Central Immunology Laboratory using the Immulite 2000Xpi chemiluminescent immunoassay method, while in Debrecen, the ADALTIS Personal Lab Allergy “capture” ELISA was used. The patients were divided into different age groups: children under 1 year, children 2-6 years old, and then those over 7 years old and adults.

Results: Food sensitization was more prevalent in Budapest across all age groups. In Budapest, mono-sensitization to egg was characteristic in children (91%), while polysensitized individuals often reacted to multiple allergens including milk (64%) and peanut (29%). Respiratory sensitization was rare in infants but polysensitization dominated among older children in both cities, particularly to dust mites (Debrecen 31%, Budapest 44%) and household dust, with higher prevalence in Budapest. Monosensitization to conidial fungi (Debrecen 20%, Budapest 32%) was more frequent than polysensitization (Debrecen 4%, Budapest 25%) in both locations. Ragweed and tree pollen sensitizations were also more prominent in Budapest (36%). In rural settings, cow hair was often involved in polysensitization, while feather allergens more commonly triggered monosensitization.

Conclusion: These results suggest that a metropolitan environment may result in sensitization to multiple allergens, while in a smaller city with a larger agricultural area, a dominance of single allergens can be observed.

Abstr. Nr. PS4.3

Fully automated indirect immunofluorescence test processing

Jakab M., Pintér E.
SYNLAB Budapest Diagnostic Center, Immunology Laboratory, Budapest, Hungary

Background: Indirect immunofluorescence tests remain widely used for the detection of autoimmune diseases even today. However, the preparation and evaluation of the test slides are time-consuming and labor-intensive. Various factors can influence the results, including subjective visual reading, serum dilution, substrate manufacturing, microscope components and conjugate quality.

Methods: Several automated systems for autoimmune pattern recognition are now available on the market. In this study, the applicability of the Euroimmun Sprinter and microscope was evaluated in routine daily practice. The aim was to determine the diagnostic accuracy of the EUROLabOffice 4. 0 software. The IF Sprinter automated system was used for fully automated processing of immunofluorescence tests. Image acquisition was performed using the EUROPattern Microscope Live IF, and image evaluation was conducted with the EUROLabOffice 4.0 software.

Results: Between December 1, 2024, and March 31, 2025, a total of 629 endomysium (EMA) IgA and IgG autoantibody, 316 antineutrophil cytoplasmic antibody (ANCA) and 503 nuclear and cytoplasmic anti-nuclear antibody (ANA) patterns were examined. In each case, the evaluation given by the software was compared with the results of the visual evaluation. For EMA IgA autoantibody tests, the sensitivity was 94.6%, while for the IgG type it was 95.6%. The specificity exceeded 99%. In the case of atypical ANCA patterns, sensitivity was 70% and specificity was 92%. For cANCA and pANCA patterns, sensitivity was 50% and specificity was 98%. For ANA samples, sensitivity was 79% and specificity was 92%.

Conclusion: The results provided by the Euroimmun software agree well with the results reported by the observer, making indirect immunofluorescence evaluation of automated autoimmune tests an objective and time-efficient tool for routine testing. For clinicians, faster evaluation also contributes to a streamlined workflow in daily practice. However, to achieve optimal diagnostic accuracy, it is essential to combine automated and visual evaluation methods.

Abstr. Nr. PS4.4

Investigation of the genetic background of properdin deficiency in two families

Szabó E. E., Tóth A., Prohászka Z., Szilágyi Á.
Department of Internal Medicine and Haematology, Research Laboratory, Semmelweis University, Budapest, Hungary

The complement system is a key part of innate immunity that consists of three activation pathways. Properdin is a positive regulator of the alternative pathway (AP) C3 convertase, stabilizing this enzymatic complex on target surfaces.
Two male patients with a history of severe meningococcal sepsis were investigated in our laboratory. Complement measurements revealed AP deficiency with normal levels of C3, C4, C1q and factor B in both patients and normal classical pathway activity. These findings indicated a complement deficiency, most likely X-linked properdin deficiency, prompting genetic testing of the patients.
DNA sequence of the whole coding region of the *CFP* gene encoding properdin was determined by Sanger sequencing of PCR products amplified from total genomic DNA of both patients. In addition, family screening was also conducted.
In the first patient, a previously not reported hemizygous frameshift variant (p.R220Kfs*8) was identified and classified as likely pathogenic. Family screening showed that this variant was maternally inherited. The patient's brother and nephew are also hemizygous for the variant, while the mother's sister is a heterozygous carrier.
In the second patient, a hemizygous cysteine-to-tyrosine substitution (p.C296Y) was detected. As this variant has not been previously reported or characterized, it is classified currently as a variant of uncertain significance. However, its functional significance is supported by the fact that the variant is co-segregated with AP deficiency in the hemizygous brother and heterozygous mother, while normal AP activity was detected in the father and another brother not carrying the variant.

Properdin deficiency is a severe immunodeficiency associated with an increased risk of infection by encapsulated bacteria. Confirming the diagnoses by identifying the underlying genetic variant is essential in these patients as preventive measures, including vaccination (accompanied by monitoring of antibody titers) and/or antibiotic prophylaxis are recommended and may prevent further infections.

Abstr. Nr. PS4.5

Comparison of Gram-positive and Gram-negative bloodstream infections based on routine laboratory parameters

Bodri M.[1], László K.[2], Barna K.T.[1]
[1]SYNLAB Laboratory Dunaújváros, Dunaújváros; [2]SYNLAB Laboratory Székesfehérvár, Székesfehérvár, Hungary

Background: Sepsis is an excessive host inflammatory response to infection, leading to organ damage. It is predominantly of bacterial origin, and a significant proportion of cases are associated with bloodstream infection (BSI). The role of pathogen type in the pathomechanism of sepsis remains incompletely understood. The aim of this study was to compare Gram-positive (GP) and Gram-negative (GN) bacterial BSIs associated with sepsis based on laboratory parameters.

Methods: In 317 septic cases with a positive haemoculture, we examined the difference in laboratory results and their variation over time between the GP, GN and other pathogen-specific BSIs and determined their predictive value for differentiating the selected groups. Prognostic estimates were also calculated for outcome, in terms of organ failure and mortality.

Results: Significant differences were observed in the values and temporal variation of procalcitonin (PCT), platelet count to PCT ratio (PLT/PCT), mean platelet volume to PCT ratio, neutrophil granulocyte count to PCT ratio, and direct bilirubin parameters between GP and GN BSIs. The predictive value of the PLT/PCT was AUC = 0.741 (95% CI = 0.683-0.799 [$p < 0.001$]), with a sensitivity of 73%, specificity of 70%, positive and negative predictive values of 86% and 50%, respectively, for discriminating GP cases. In GN BSIs, the risk of kidney failure was OR = 1.946 (95% CI = 1.186-3.193 [$p = 0.008$]) and the risk of liver failure was OR = 4.029 (95% CI = 1.822-8.906 [$p = 0.001$]) compared with GP cases. Thirty-two-day survival rates did not differ between GP and GN BSIs. For pathogen-specific BSIs, PLT/PCT had an AUC of 0.832 (95% CI = 0.782-0.881) predictive value for staphylococcal BSIs, with a sensitivity of 77% and specificity of 80%.

Conclusion: Our results suggest that in sepsis associated with BSI, the type of pathogen plays a significant role in the host's inflammatory response, which may provide a basis for exploring alternative diagnostic and prognostic markers.

Abstr. Nr. PS4.6

Investigation of interference between homogeneous and centromere indirect immunofluorescence antinuclear antibody patterns

Szabó L., Kovalcsik A., Földesi R., Török Sőrés G., Antal-Szalmás P., Nagy G.
Department of Laboratory Medicine, University of Debrecen, Debrecen, Hungary

Background: Detection of antinuclear antibodies (ANA) is crucial in diagnosing systemic autoimmune diseases. ANA screening is performed using the HEp-2 indirect immunofluorescence assay. Pattern interpretation becomes particularly challenging in the presence of multiple autoantibodies. By mixing dilutions of samples with single, confirmed patterns, interference of homogeneous and centromere patterns-commonly co-occurring in SLE and scleroderma or AIH and PBC overlap syndromes-can be evaluated.

Methods: Different dilutions of samples with either homogeneous or centromere pattern were mixed to model varying pattern intensities. Centromere pattern effect on homogeneous pattern recognition was investigated and vice versa. Three evaluation methods were used: conventional microscopy, on-screen reading and EuroPattern (EPa) automated analysis.

Results: Conventional and on-screen evaluations consistently identified homogeneous pattern with high accuracy (up to 100%), even when centromere titers were equal or higher. EPa efficiency declined due to interference from 85% to 78,6%, then to 36,2% as centromere titers increased, though correlations between expected and observed homogeneous titers remained relatively stable. In contrast, homogeneous interference markedly impaired detection of centromere pattern: samples with only centromere antibody were recognized in 97–100% of cases, detection dropped to 3–15% if homogeneous pattern dominated. Correlation between expected and observed centromere intensities decreased substantially because of homogeneous interference.

Conclusion: Centromere pattern reduced accuracy of homogeneous pattern recognition minimally, while interference of homogeneous pattern on centromere pattern was remarkable. EPa performance deteriorated markedly, revealing limitations of current automated systems in interpreting mixed ANA patterns.

Abstr. Nr. PS4.7

Comparative evaluation of indirect immunofluorescence methods for the detection of anti-smooth muscle antibodies

Demeter S.[1], Nagy G.[1], Földesi R.[1], Török Sőrés É.[1], Papp M.[2], Antal-Szalmás P.[1]
[1]Department of Laboratory Medicine, University of Debrecen; [2]Division of Gastroenterology, Department of Internal Medicine, University of Debrecen, Debrecen, Hungary

Background: Smooth muscle antibodies (SMA) are important serological markers in the differential diagnostics of autoimmune liver diseases, particularly autoimmune hepatitis. The reference method for SMA detection is indirect immunofluorescence (IIF) using composite rodent tissue sections (liver, kidney, stomach - LKS). However, methodological differences can make interpretation difficult.

Methods: To compare assay performance, 45 serum samples (25 SMA-positive, 20 SMA-negative) were tested using rodent tissue IIF kits from EUROIMMUN and INOVA Diagnostics. Analyses were performed at serum dilutions of 1:40 and 1:160, while interkit concordance was assessed at endpoint titers of 1:40 and 1:80. SMA subtypes (V, VG, VGT) were determined by renal staining patterns. Results were analyzed using contingency tables and Cohen's kappa (κ). F-actin reactivity was also evaluated by immunoblotting and correlated with kidney staining patterns.

Results: The highest overall agreement between the two kits was observed at the 1:80 titer cut-off, particularly in stomach and kidney tissues, with 86.7% concordance and $\kappa = 0.734$. On these tissues the 1:40 titer cut-off showed higher rate of positivity using the Werfen kit (80.0 vs. 55.6%), since the lower dilution resulted in - probably - higher, non-specific background fluorescence and more false positives. Liver tissue showed stable performance at both titers and in both kits. Combining tissues slightly improved interkit agreement but did not outperform single tissue evaluation. VG and VGT SMA patterns were more frequently associated with F-actin positivity than V-type, moreover higher SMA end-point titers were associated with these combined patterns.

Conclusion: These results support the importance of harmonization of dilution protocols and pattern-based interpretation in clinical IIF testing.

Abstr. Nr. PS4.8

Identification of a new hypervirulent CC17 *Streptococcus agalactiae* strain in unusually rapid and fatal newborn meningitis

Kovács D.[1], Sacheli R.[2], Meex C.[2], Melin P.[2], Tóth Á.[3], Papp K.[1], Ajzner É.[1]
[1]Szabolcs-Szatmár-Bereg County Hospital and University Teaching Hospital, Nyíregyháza, Hungary; [2]National Reference Center *Streptococcus agalactiae*, University Hospital Centre of Liège, Belgium; [3]National Center for Public Health and Pharmacy, Budapest, Hungary

Streptococcus agalactiae (GBS) plays a prominent role in perinatal and neonatal infections. Nearly 30% of neonatal infections are GBS infections. According to the Centers for Disease Control and Prevention, the incidence of early infections in 2022 was 0.17/1000 and late infections were 0.23/1000 worldwide. 80-95% of all neonatal meningitis cases were caused by strains belonging to the hypervirulent CC17 clonal complex. In the autumn of 2024, a 1-month-old baby was admitted to the emergency unit of our institution and was lost within an hour despite intensive treatment. Laboratory tests of the patient's cerebrospinal fluid indicated meningitis, the antigen rapid test result was GBS positive, GBS was cultured within 24 hours. Since the course of the disease was found unusually rapid, we decided to transfer the GBS isolates to the National Reference Laboratory for genotyping. The multilocus sequence typing resulted in a previously unidentified sequence therefore the strain was sent to the Belgian GBS National Reference Laboratory for further testing. The strain was found to belong to the high-risk CC17 clonal complex group with virulence genes coding hyper-virulency. This previously unknown GBS strain with sequence type ST2396 explains the extreme fast, fatal meningitis course in our patient. Identification and recording in international MLST database of this novel hypervirulent GBS-ST2396 strain was only possible due to the close collaboration between professionals of the neonatal intensive center and microbiology laboratory of our institute.

Abstr. Nr. PS4.9

Human recombinant RNase7/Fc fusion protein – a possible opsonin

Földesi R.[1], Nagy G.[1], Vereb G.[2], Majoros L.[3], Antal-Szalmas P.[1]
[1]Department of Laboratory Medicine, University of Debrecen, Debrecen, Hungary; [2]Department of Biophysics and Cell Biology, University of Debrecen, Debrecen, Hungary; [3]Department of Medical Microbiology, University of Debrecen, Debrecen, Hungary

Background: Antibiotic resistance is a serious, global threat. The improper use of existing antibiotics and the lack of development of new ones have led to the emergence of (multi)resistant bacteria. To enhance the effectiveness of our defense against infections, we need to broaden the range of therapeutic interventions. In this study, we tested a novel fusion protein with antimicrobial activity. One part of the molecule consists of the active domain of the well-characterized antimicrobial protein RNase7, while the other half is the Fc region of the immunoglobulin G (IgG) molecule.

Methods and Results: Using flow cytometry, we demonstrated that the RNase7/Fc protein bound to Gram-negative bacteria (*E. coli, S. typhimurium, S. hartford, S. minnesota*) in a time- and dose-dependent manner, and to a lesser extent to Gram-positive species (*L. monocytogenes, S. pneumoniae*). The association was particularly strong when we tested Re and Ra Gram-negative microbes. Binding was inhibited in a concentration-dependent manner by free LPS that binds RNase7, or by LBP+sCD14 molecules, which bind to LPS on the surface of Gram-negative bacteria. The association of RNase7/Fc to Gram-negative bacteria promoted their phagocytosis. The proportion of bacteria-engulfing neutrophil granulocytes increased by 1.5- to 2.5-fold in the presence of 10 µg/mL RNase7/Fc. This process was primarily mediated by FcRγIII (CD16). Using confocal fluorescence microscopy, we showed that RNase7/Fc-opsonized, fluorescently labeled bacteria were localized intracellularly.

Conclusion: The tested RNase7/Fc molecule acts as an opsonin, binds dominantly to Gram-negative bacteria and enhances the phagocytosis of these microbes by isolated neutrophil granulocytes via the FcRγIII receptor.

Abstr. Nr. PS4.10

Kinetics of humoral immune reactions to the SARS-CoV-2 mRNA vaccine

Farkas K.L.[1], Szilasi J.T.[1], Araczki Á.[1], Márki Á.[2], Szűcs M.[2], Bánhalmi A.[3], Földesi I.[1]
[1]Institute of Laboratory Medicine, [2]Institute of Medical Physics and Informatics, [3]Department of Software Engineering, University of Szeged, Szeged, Hungary

Background: The coronavirus (SARS-CoV-2) pandemic caused a global health crisis. Although it had a negative impact on everyday life, it also catalyzed revolutionary innovations, such as the introduction of mRNA-based vaccines. Shortly thereafter, automated tests became available on the market to determine the antibody levels in response to infection and/or vaccination.

Methods: In parallel with the introduction of these tests, a long-term clinical study was launched at our Institute to investigate the immune response to infection and vaccination among healthcare workers (N=546). From this cohort, a subgroup of vaccinated but previously uninfected persons was selected (n=95) to study the humoral immune response to mRNA-based vaccination. Antibody levels against two relevant SARS-CoV-2 proteins - the nucleocapsid and spike - were measured before the first and second vaccine doses and monthly thereafter for six months, until administration of the third dose. The spike antibody levels were used to monitor the humoral immune response over time. The aim of this investigation was to describe the kinetics of the immune response to vaccination in this group.

Results: Based on the average slopes between the clusters we confirmed that the antibody response of healthy population can be classified into three groups: rapid rise-rapid fall (RR-RF), rapid rise-slow fall (RR-SF), slow rise-slow fall (SR-SF). There was no significant difference in slopes between the first two measuring points among the clusters. In RR-RF, the slope between the second and third measurement points and between the third and fourth points was significantly different from the other two groups ($p<0.001$). Between the fifth and sixth measurement points, only the RR-RF and SR-SF groups showed significant difference ($p=0.001$).

Conclusion: Our data suggests that there are individual variations in humoral immune responses among patients vaccinated with mRNA-based anti-SARS-CoV-2 vaccines.

Abstr. Nr. PS4.11

Comparative analysis of autoantibody positivity during the COVID-19 pandemic and the non-COVID period

Kopasz Á., Marossy A., Pintér E.
Synlab Diagnostic Center, Immunology Laboratory, Budapest, Hungary

Background: Various viral infections may act as triggering factors in the development of autoimmune diseases. In susceptible individuals, immune dysregulation can lead to the production of autoantibodies, impairing the function of specific target organs.

Methods: We analyzed changes in the occurrence of anti-neutrophil cytoplasmic antibodies (ANCA) in samples tested at the Synlab Immunology Laboratory between 2019 and 2022 to assess potential autoimmune responses influenced by SARS-CoV-2 infection. The years 2019 and 2022 were considered non-COVID periods, while 2020 and 2021 represented the pandemic phase. Indirect immunofluorescence was used to detect cytoplasmatic ANCA (cANCA), perinuclear ANCA (pANCA), atypical ANCA patterns, as well as anti-nuclear antibodies (ANA) on HEp-2 cells. Conventional enzyme-linked immunosorbent assay (ELISA) was performed to detect elastase, lactoferrin, cathepsin G, bactericidal permeability-increasing protein (BPI), and lysozyme. Myeloperoxidase (MPO) and proteinase 3 (PR3) were assessed using a modified ELISA.

Results: The number of patients was nearly equal in both periods, with a consistent female-to-male ratio of approximately 2:1 (females: 10750 and 11162, males: 5130 and 5126). The positivity rate was 48% during the pandemic and 52% in the non-

COVID period. Atypical ANCA and HEp-2 patterns showed increased positivity during the pandemic. However, this difference was not statistically significant (p = 0.317). MPO positivity during the pandemic was slightly higher among women (44 cases) than men (42 cases). No further antibody types were analyzed.

Conclusion: Our results suggest no significant difference in the number of patients with autoantibodies indicative of autoimmune vasculitis between the two periods, in contrast with several previously published studies.

Abstr. Nr. PS4.12

24/7 with Passion: Saving Time, Saving Lives?

Móra-Oravecz D., Käfer M., Simon J.
North-Pest Central Hospital – Military Hospital, Budapest, Hungary

Background: The incidence of sepsis is rising globally, including in Hungary, due to various factors. Prompt microbiological diagnostics and collaboration between microbiologists and clinicians are essential in the management of sepsis. In response to this growing need, the Microbiology Laboratory of the North-Pest Central Hospital – Military Hospital has been operating continuously, 24 hours a day, 7 days a week, since the beginning of 2024. Our aim is to support clinical decision-making with timely and accurate results, thereby contributing to improved outcomes for critically ill patients.

Methods: In 2024, we processed, stained, microscopically evaluated, and tested 2084 positive blood culture bottles, performing direct antimicrobial resistance tests, bacterial and fungal identification. In alignment with professional guidelines, laboratory processes were optimized to reduce diagnostic turnaround times. Microbial identification was performed using MALDI-TOF MS from early-phase colonies. Clinicians were continuously informed of the results to enable rapid therapeutic interventions.

Results: The continuous laboratory service significantly reduced the time to reporting preliminary smear results, microorganism names, and resistance profiles. Although some departments have yet to fully utilize our services' benefits, overall clinician feedback has been positive, particularly regarding the acceleration of microbiological diagnostics and its potential clinical benefits.

Conclusion: There is currently no direct evidence linking faster diagnostics to reduced antibiotic use, shorter hospital stays, or faster recovery. However, ongoing collaborative studies aim to improve antibiotic stewardship. Promoting awareness of our activities and the value of collaboration through internal forums supports our key priority of strengthening cooperation between clinicians and microbiologists.

Abstr. Nr. PS4.13

The role of gender and age in the development of iron overload and anemia in patients with chronic kidney disease

Potó S., Korponai H., Hemrik H.
Corden Hungary Ltd., Flór Ferenc Hospital, Kistarcsa

Background: In dialysis patients, iron-deficiency anemia is frequently observed, which is partly a complication and partly a symptom associated with chronic kidney disease. These patients receive iron supplementation. Monitoring anemia is possible through laboratory testing of iron metabolism. In our current study, we aim to observe the occurrence and progression of iron-deficiency anemia and possible iron overload in dialysis patients treated at Flór Ferenc Hospital.

Materials and Methods: Data were collected from 100 dialysis patients at Flór Ferenc Hospital between September 2024 and March 2025. The analyzed parameters included ferritin, transferrin, serum iron (Fe), hemoglobin (Hgb), reticulocyte count, red blood cell count (RBC), mean corpuscular volume (MCV), and transferrin saturation. Data were grouped by sex and age (<60 years and ≥60 years).

Results: In September 2024, ferritin levels were significantly higher among older women (average 959 ng/ml), while they were lower in younger men (average 710.5 ng/ml). Hemoglobin levels were higher in younger men (average 121.3 g/l), whereas transferrin saturation was higher in older women (average 35.5%). By March 2025, both hemoglobin and iron levels had decreased, while transferrin saturation remained elevated in older patients, suggesting possible iron overload. Despite iron supplementation, anemia persisted.

Conclusion: Our study found that anemia persisted in older patients despite treatment. Iron store saturation was also observed, as indicated by high ferritin levels and transferrin saturation. Iron overload may lead to hemochromatosis, which is a worsening factor in patients with chronic kidney disease. It is important to apply treatment protocols in a patient-centered manner with regular monitoring. Further research is necessary to improve patient quality of life and survival.

Author index

(continued)

(continued)

(continued)

Konderák, J.	SE5.3
Kopasz, Á.	PS4.11
Korponai, H.	PS4.13
Kovács, Á.	PS4.1
Kovács, D.	PS4.8
Kovács, K.	SE2.2
Kovalcsik, A.	PS4.6
Kozma, A.	SE5.1, SE5.6, PS1.4
Köllő, Z.	SE4.4
Kőszegi, T.	PS1.5, PS1.6
Krasznai, Z.T.	PS3.16
Kretovics, J.G.	PS1.12
Kunz, S.	SE4.4
Kupai, K.	PS2.9
Kurunczi, M.	PS2.9
Kustán, P.	PS1.5
Kuzma, M.	SE4.3
Kürti G.-Szabó, E.	SE1.1, SE1.5
Lajtai, A.	SE4.3
Lakatos, Á.	SE4.3
Lakatos, V.	SE5.6, PS3.2, PS3.9
Laki, I.	PS1.7
Láng, A.	PS2.10
Lassila, R.	SE4.5
László, K.	PS3.4, PS3.5, PS4.5
Lengyel, Z.	SE6.4
Lénárt, I.	SE3.4, PS1.1
Lieber, A.	SE2.4
Lóczi, L.	SE3.2, SE4.5, SE5.2, SE5.5, SE6.5, PS3.10, PS3.16
Lovász, B.	SE4.4
Lukács, A.	PS2.7
Lukász, P.	PS2.12
Majoros, L.	SE6.1, PS4.9
Márky, Á.	PS4.10
Marossy, A.	PS4.11
Marossy, K.	PS3.6
Matolay, O.	SE2.4
Matula, Z.	SE5.1
Mayer, M.	SE4.3
Meex, C.	PS4.8
Meggyesi, N.	SE5.6, PS3.2
Meláth, M.	SE2.3
Melin, P.	PS4.8
Menrát-Fazekas, D.	PS3.8
Méri, A.	PS3.8
Mészáros, A.	PS2.12
Mészáros, B.	PS1.7
Metzler, G.	SE6.6
Mezei, E.	SE2.3
Mezei, Z.	SE5.3
Mező-Géresi, K.	SE6.2, PS3.1
Mikala, G.	SE5.6
Miklós J.	PS3.7
Miklós, T.	PS3.14
Mikos, B.	SE3.5, SE3.6
Miseta, A.	SE3.3, PS1.5, PS2.10
Modok, S.	SE6.4

(continued)

(continued)

Reichardt, J.	PS3.9
Reményi, P.	SE5.6, PS3.2, PS3.9
Répai A.	PS1.4
Rostás, I.	PS1.5, PS1.6
Rucz, K.	PS2.3
Sacheli, R.	PS4.8
Sallay, K.	PS2.4
Sarkadi, E.	SE2.5
Sárközi-Pál, E.G.	PS3.15
Schlammadinger, Á.	PS3.16
Serdült, A.	PS2.12
Seres, E.	PS2.1
Shemirani, A.H.	PS2.4, PS3.14
Siket, I.M.	PS1.9
Simon, J.	SE2.5, SE6.2, PS3.1, PS3.8, PS4.12
Simon, Á.	PS1.10, PS2.8
Singh, P.	SE5.5, SE6.5
Sinkovits, G.	PS3.7
Sipka, S.	PS4.2
Sipos, L.	PS1.8, PS3.3
Soltész, P.	PS1.12
Solymosi, T.	PS2.3
Sütő, R.	CS1.2
Szabó, A.	PS1.1
Szabó, A.Á.	PS1.9
Szabó, B.	PS2.11
Szabó, C.	SE1.6
Szabó, E.E.	PS3.6, PS4.4
Szabó, F.	SE5.6
Szabó, H.	PS1.7
Szabó, L.	PS4.6
Szabó, M. (Budapest)	SE2.2
Szabó, M. (Székesfehérvár)	PS3.3
Szabó, S.	PS2.1
Szabó, T.	PS2.1
Szabó, Z.	PS2.4
Szakács, J.	PS1.11
Szakács, O.	PS2.12
Szakony, S.	SE1.2, SE2.1, PS1.11
Szalai, L.	SE5.6
Szántó, D.	PS1.15
Szántó, T.G.	PS1.7
Szatmári, I.	PS1.1
Szegedi, H.	PS1.12
Szegedi, I.	SE3.2, SE5.2, SE5.5, PS3.10
Szegedi, Z.	SE5.1
Szekeres, Z.	PS1.6
Szellő, O.	PS2.11
Szijártó, A.	PS2.12
Szilágyi, Á.	PS3.6, PS3.7, PS4.4
Szilárd, S.	SE2.4
Szilasi, J.T.	PS4.10
Szirmay, B.	SE5.4, PS1.3, PS1.5, PS1.6
Szoboszlay, I.	PS3.15
Szűcs, J.	SE2.1, PS1.11
Szűcs, M.	PS4.10
Szurovecz, M.	SE1.2, SE2.1, PS1.11

(continued)

Tajti, B.T.	SE6.2, PS3.1
Takács, B.	PS3.6
Tankó, L.	SE5.1, SE5.6, PS1.4, PS3.9
Tardy, E.P.	SE2.5
Telkes, M.	PS2.6, PS2.9
Tisza, K.	SE5.6
Tóbiás, Á.	PS2.7
Tomán, A.	SE1.6, SE3.5, SE3.6
Tóth, A.	PS4.4
Tóth, Á.	PS4.8
Tóth, E.L.	PS3.16
Tóth, G.	SE1.1
Tóth, P.	PS1.6
Tóth, Z.B.	PS1.9
Török Sőrés, É.	PS4.6, PS4.7
Trifán, V.	SE3.6
Uj, E.A.	PS3.13, PS3.14
Valkusz, Z.	PS2.9
Vályi-Nagy, I.	SE5.6
Varga, C.	PS2.7
Varga, L.	PS3.2, PS3.9
Varga, R. (Miskolc)	PS2.5
Varga, R. (Székesfehérvár)	PS3.4
Varjú, O.	PS4.2
Várkonyi, A.	PS3.9
Vasas, N.	SE3.2
Vásárhelyi, B.	SE2.2
Vass, L.	PS2.1
Vén, B.	SE4.3
Vereb, G.	SE6.1, PS4.9
Virág, L.	PS2.12
Wittmann, I.	SE3.3
Zemplenyi, M.	SE1.2
Zombori, M.	SE4.1
Zsjak, K.	PS2.11
Zsolnay, H.	SE2.2