BALTIC CONGRESS IN
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16th Baltic Congress in Laboratory Medicine

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Society affiliated to IFCC

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EESTI LABORIMEDITSIINI ÜHING
ELMÜ

Latvijas Laboratorās medicīnas biedrība

LIETUVOS LABORATORINĖS MEDICINOS DRAUGIJA

16th Baltic Congress in Laboratory Medicine

September 22-24, 2022

Abstracts

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TRIOLAB

Welcome to the 16th Baltic Congress in Laboratory Medicine!

Dear Colleagues,

On behalf of the Organizing Committee, I am delighted to invite you to the XVI Baltic Congress in Laboratory Medicine, which will take place on September 22-24th, 2022 in Tallinn, Estonia.

We would like to bring together the laboratory professionals, students and health care personnel with an interest in laboratory medicine from our three Baltic states as well as from other countries. We expect to share the latest scientific achievements and experience in the wide field of laboratory medicine.

The congress will be held in Tallinn Song Festival Grounds, one of the most important places in our late history, the cradle of the singing revolution. The venue has perfect possibilities for scientific lectures and lively discussions as well as for the exhibition by the diagnostic companies. Additionally, a quick and interactive overview of our latest 30 years is presented in the Visitor Centre of the Song Festival Grounds.

We hope we can gather and enjoy social relationships together after long years of isolation. Looking forward to meet you in Tallinn.

Anu Tamm,
President of the Congress

Committees

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Baltic Congresses in Laboratory Medicine

1st	1992 Tartu, Estonia
2nd	1994 Vilnius, Lithuania
3rd	1996 Jurmala, Latvia
4th	1998 Tartu, Estonia
5th	2000 Vilnius, Lithuania
6th	2002 Riga, Latvia
7th	2004 Pärnu, Estonia
8th	2006 Vilnius, Lithuania
9th	2008 Jurmala, Latvia
10th	2010 Tallinn, Estonia
11th	2012 Vilnius, Lithuania
12th	2014 Riga, Latvia
13th	2016 Tartu, Estonia
14th	2018 Vilnius, Lithuania
15th	2020 Riga, Latvia
16th	2022 Tallinn, Estonia

Congress Programme

THURSDAY, SEPTEMBER 22		
18.00–19.30	**Opening**	**Tallinn Song Festival Grounds, Hall 1**
18.00-18.15	Welcome	Anu Tamm, Estonia
18.15–18.45	New possibilities in EFLM	Dalius Vitkus, Lithuania
18.45–19.15	DigiLaboratory and harmonization in Estonia	Anu Tamm, Estonia
19.30	**Welcome Reception**	**Tallinn Song Festival Grounds, Hall 1**

FRIDAY, SEPTEMBER 23		
8.30–9.00	**Coffee, posters**	
9.00–9.45	**Plenary session**	**Hall 1**
	Biological and analytical variation of biomarkers	Sverre Sandberg, Norway
9.50–11.30	**MORNING SESSIONS**	
SESSION 1	**Hematology and coagulation** Moderators: Karel Tomberg, Estonia; Ludmila Volozonoka, Latvia; Valdas Banys, Lithuania	**Hall 1**
9.50-10.10	Hemogram reference values in Estonia	Karel Tomberg, Estonia; Marika Pikta, Estonia
10.10-10.30	Comparison of automated red cell parameters with bone marrow iron staining	Triin Paabo, Estonia
10.30-10.50	Multiple myeloma immunophenotype related to genetic aberrancies used in risk stratification	Mantas Radzevičius, Lithuania
10.50-11.10	Clinical implications of genetic testing for thrombophilia	Ludmila Volozonoka, Latvia
11.10-11.30	Added-value of viscoelastic assays in haemostasis evaluation in patients undergoing invasive procedures	Daiva Urbonienė, Lithuania
SESSION 2	**Clinical genetics and rare diseases** Moderators: Neeme Tõnisson, Estonia; Inga Nartisa, Latvia	**Hall 2+3**
9.50-10.10	Advances in rare disease diagnostics and research	Sander Pajusalu, Estonia
10.10-10.30	Hyperphenylalaninemias and neurophysiological disorders	Hardo Lilleväli, Estonia
10.30-10.50	Novel genetic methods for improved diagnostics of inborn errors of immunity	Inga Nartisa, Latvia
10.50-11.10	Delineation of the genetic causes of rare diseases by the use of NGS and functional studies	Gunda Petraitytė, Lithuania
11.10-11.30	nDNA and mtDNA analysis of patients with suspected mitochondrial disease: a wide diagnostic spectrum	Kristina Grigalionienė, Lithuania
11.30–12.00	**Coffee break, posters**	
Commercial presentation		**Hall 1**
12.00–12.30	Roche Cardiovascular disease solutions: helping to solve challenges and unmet needs with high medical value tests	Aleksandra Lezaja (Roche Diagnostics International)
Commercial presentation		**Hall 2+3**
12.00–12.30	The Roche portfolio of digital solutions connects the healthcare community	Jaroslav Vohánka (Roche Information Solutions)

PROGRAMME

12.35–14.10	**MID-DAY SESSIONS**	
SESSION 3	**Quality management** Moderators: Agnes Ivanov, Estonia; Dalius Vitkus, Lithuania	**Hall 1**
12.35-13.05	The new IVD Regulation 2017/746: Where we are?	Elisabeth M.C. Dequeker, Belgium
13.05-13.35	EQA of 2020's: needs and trends	Dalius Vitkus, Lithuania
13.35-13.50	Compliance of blood sampling practice in Lithuania with the EFLM-COLABIOCLI recommendations	Ričardas Stonys, Lithuania
13.50-14.10	Quality of laboratory results. Definition and estimation	Anders Kallner, Sweden
SESSION 4	**Microbiology and infectious diseases. Zoonoses.** Moderators: Irja Lutsar, Estonia; Aleksandra Rudzāte, Latvia; ; Asta Dambrauskiene, Lithuania	**Hall 2+3**
12.35-13.05	Emerging and re-emerging infectious diseases in 2022	Irja Lutsar, Estonia
13.05-13.20	Tick-borne pathogens	Julia Geller, Estonia
13.20-13.35	Zoophilic dermatophytes	Piia Hurt, Estonia
13.35-13.50	HORIZON 2020 PERFORM and DIAMONDS projects: new genomic and proteomic approaches to provide rapid and accurate diagnosis of febrile illnesses - turning fiction into a reality	Aleksandra Rudzāte, Latvia
13.50-14.05	Etiologic agents of community acquired and nosocomial bacteremias, differences in antimicrobial susceptibility	Asta Dambrauskiene, Lithuania
14:15–15.15	**Lunch, posters**	
Commercial presentation		**Hall 1**
15.15–15.45	Expediting the diagnosis of Myocardial Infarction: which role can hs-cTn at the Point-of-Care play?	Niels Kramer (Siemens Healthineers)
Commercial presentation		**Hall 2+3**
15.15–15.45	mTBI – game changing assay	Ksenia Musaelyan (Abbot Ireland)

16.00–17.30	**AFTERNOON SESSIONS**	
SESSION 5	**New Biomarkers in Laboratory Medicine** Moderators: Kalle Kisand, Estonia; Baiba Šlisere, Latvia; Dovilė Karčiauskaitė, Lithuania	**Hall 1**
16.00-16.30	Enhanced Liver Fibrosis (ELF) score in the general population	Fredrik Åberg, Finland
16.30-16.50	Uncovering the impact of weight loss on biomarkers of obesity	Baiba Šlisere, Latvia
16.50-17.10	Therapeutic Drug Monitoring in the Era of LC-MS/MS in the Laboratory Without LC-MS/MS	Jānis Meisters, Latvia
17.10-17.30	CEACAM6 as a diagnostic and prognostic biomarker of pancreatic adenocarcinoma	Benediktas Kurlinkus, Lithuania
SESSION 6	**Cancer Screening today and tomorrow** Moderators: Katrin Reimand, Estonia; Neeme Tõnisson, Estonia	**Hall 2+3**
16.00-16.20	Colorectal cancer screening – Latvian experience	Tatjana Zablocka, Latvia
16.20-16.40	Estonian experience in colorectal cancer screening	Katrin Reimand, Estonia
16.40-17.00	Colorectal cancer screening in Lithuania	Vytenis Petkevicius, Lithuania
17.00-17.20	Perspectives of personalized breast cancer screening	Neeme Tõnisson, Estonia
19.30–23.00	**Congress dinner**	**Seaplane Harbour**

SATURDAY, SEPTEMBER 24		
8.30–9.00	**Coffee break, posters**	
9.00–9.40	**Plenary session**	**Hall 1**
	Smart Lab medicine in the digital era	Bernard Gouget, France

9.50–11.30	MORNING SESSIONS	
SESSION 7	**Patient focused laboratory medicine** Moderators: Janis Stasulans, Latvia; Marge Kütt, Estonia	**Hall 1**
9.50-10.20	Quality and POCT	Sverre Sandberg, Norway
10.20-10.35	POCT in Tartu Ambulance Service	Agnes Ivanov, Estonia
10.35-10.50	Experience of using automation for management of self-sampling kits in E.Gulbja laboratory	Didzis Gavars, Latvia
10.50-11.05	Direct self-sampled gargle water LAMP as a screening method for the detection of SARS-CoV-2 infections	Skaistė Arbačiauskaitė, Lithuania
11.05-11.25	What people ask from laboratory doctors?	Marge Kütt, Estonia
SESSION 8	**Sexually transmitted diseases** Moderators: Kai Jõers, Estonia; Vesta Kućinskiene, Lithuania; Marta Priedīte, Latvia	**Hall 2+3**
9.50-10.10	Hypothesis and the need for confirmation of the diagnosis by the laboratory. Clinician's view.	Margus Punab, Estonia
10.10-10.40	Detection of M.genitalium and antibiotic resistance in Europe	Magnus Unemo, Sweden
10.40-11.00	HPV self-sampling in cervical cancer screening: a pilot study in Estonia	Piret Veerus, Estonia
11.00-11.15	HPV screening programme in Latvia – laboratory experience	Marta Priedīte, Latvia
11.15-11.30	STI diagnostiscs in Lithuania	Vesta Kućinskiene, Lithuania
11.30–12.00	**Coffee break, posters**	

12.00–13.40	MID-DAY SESSIONS	
SESSION 9	**SARS-CoV2 epidemic (epidemiology, diagnostic etc)** Moderators: Siiri Kõljalg, Estonia; Laura Ansone, Latvia	**Hall 1**
12.00-12.20	SARS-CoV2 in Estonia. Immune response.	Paul Naaber, Estonia
12.20-12.40	Multi-omics approach in the identification of molecular footprints of SARS-CoV-2 infection	Laura Ansone, Latvia
12.40-13.00	Innate immune response to COVID-19	Laura Pereckaitė, Lithuania
13.00-13.20	SARS-CoV2 and fungal infections	Helle Järv, Estonia
13.20-13.40	SARS-CoV2 testing in wastewater	Tanel Tenson, Estonia
SESSION 10	**Harmonization in laboratory medicine** Moderators: Liisa Kuhi, Estonia; Dalius Vitkus, Lithuania	**Hall 2+3**
12.00-12.30	The revised European Urinalysis Guideline	Timo Kouri, Finland
12.30-12.50	Harmonization of electrophoretic investigations in evaluation of monoclonal gammopathies in Estonia	Kaja Vaagen, Estonia; Galina Zemtsovskaja, Estonia
12.50-13.10	Harmonization of verification	Agnes Ivanov, Estonia
13.10-13.30	Harmonization in satellite labs	Marge Kütt, Estonia
13.45–14.15	**Presentations of Selected Abstracts (3 oral presentations)**	**Hall 1**
	COVID-19: Prolonged viral shedding in an HIV patient	Oksana Savicka, Latvia
	Non-polio enteroviruses - are we looking in the right place and quickly enough?	Baiba Niedre-Otomere, Latvia
	Landscape of genetic alterations of Estonian patients with MDS and AML diagnosis	Maria Keernik, Estonia
14.15-14.30	**BALM 2022 Best Poster Recognition Ceremony**	**Roche representative and Kalle Kisand, Estonia**
14.30–14.45	**Closing Ceremony**	**Hall 1**

Venue

CONGRESS

The main event takes place in Tallinn Song Festival Grounds (Narva mnt 95, Tallinn).

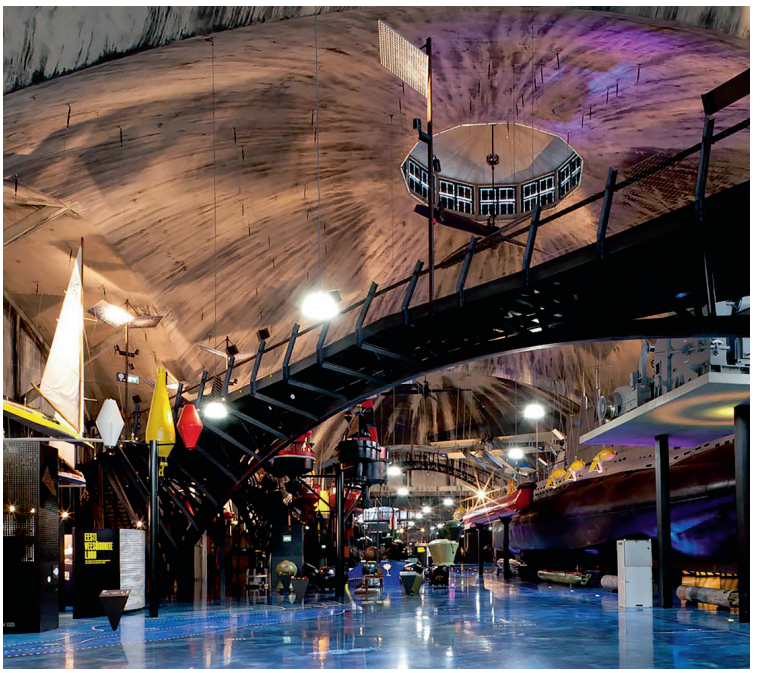
Transportation: Closest bus station to the venue is „Lauluväljak“. You can travel there from downtown by taxi or by bus from Viru Keskus bus terminal: buses nr 8, 38, 34, 1.

DINNER

The dinner on September 23rd takes place at Seaplane Harbour (Vesilennuki 6, Tallinn).

The Seaplane Harbour is a maritime museum in Tallinn, opened in spring 2012. The museum is part of the Estonian Maritime Museum.

Transportation: Closest bus station to the venue is „Lennusadam“. You can travel there from Tallinn Song Festival Grounds by taxi or by bus: go to „Oruvärava“ stop (40 m from Tallinn Song Festival Grounds), board the bus nr 51, exit bus at „Hobujaama“ bus stop , walk to „Mere puiestee“ stop (distance is 250 m) and board the bus nr 73, exit bus at „Lennusadam“ stop, distance to The Seaplane Harbour is 150 m.



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COMMERCIAL PRESENTATIONS

POSTER PRESENTATIONS

PLENARY LECTURES

PL-1. Biological and analytical variation of biomarkers

Sverre Sandberg[1] – [1] Norwegian Quality Improvement of Laboratory Examinations (Noklus), Bergen, Norway

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Data from biological variation are used for many purposes; the most common is to set performance specifications, to generate personal reference intervals, and calculate reference change values and index of individualities

A WG and TG in EFLM developed a critical appraisal check list to evaluate the literature on biological variation and extract essential information from the papers as well as summarise the information. The WG has also collected data from about 100 healthy persons in 6 different European countries and is now generating new data for a lot of measurands. One of the results of these initiatives was to deliver a database on biological variation on the EFLM website.

The biological variation database on the EFLM website (https://biologicalvariation.eu) consists of essential information about the biological variation and derived performance specifications and reference change values for different measurands as well as the evidence behind it. The TG is a cooperation between the TFG, the Analytical Quality Commission of the Spanish Society of Clinical Chemistry, the WG of biological variation in EFLM and interested individuals —altogether more than 30 persons. Different groups are established for different measurands. The groups have categorised papers as A, B, C and D depending on their methodological quality, with category A papers indicating high quality and D poor quality using a checklist that contains 14 items. From each paper, 22 items are extracted and presented in the database. The lecture will give a status of the present work.

In addition, the WG on biological variation has collected data from about 100 healthy persons in 6 different European countries and is now generating new data for a lot of measurands. The results from this study will be compared with data after the literature search.

In the lecture, the development of the biological variation database will be described as well as how these data can be used in practical laboratory life.

PL-2. Smart lab medicine in the digital era

Bernard Gouget[1] – [1] Chair IFCC Committee on Mobile Health and bioengineering in Lab Medicine (IFCC-C-MHBLM)

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The world of Biomedical innovation is complex and diverse, full of promising technologies that will improve care, the patient-physician relationship and take laboratory medicine and healthcare to the next level. The COVID-19 pandemic has significantly favored digital transitions and emerging technologies to deal with emergency health situations, the shift towards remote working and mobility restrictions. The use of cutting-edge technologies, including artificial intelligence (AI), big data, telemedicine, blockchain, 5G technology, smart applications, Internet of Medical Things (IoMT), robotics, geospatial technology, and drones are substantially important for COVID-19 detecting, monitoring, diagnosing, screening, surveillance, mapping, tracking, and creating awareness.

Smart technologies are transforming healthcare and smartphone applications that connect large populations can be configured to tackle emergency situations. Patients have moved dramatically toward online channels. Technology and social media companies are already on their own mission to achieve global spread, reaching a point where everyone on this planet who wants one can have a digital and online presence. Smart healthcare not only means adopting new products and technologies for diagnosis and treatment, but it includes a greater exchange of information among the parties. With smart medical devices paving the way for physicians and specialists of lab medicine to monitor patients outside of the hospital and sensor and imaging technology evolving at a rapid rate, the amount of valuable patient data the healthcare world collects will continue to increase.

The crisis has demonstrated that it is impossible to ignore technological advancements and the digital opportunities that can support the long-term sustainable development of each country. Digital transformation is changing the face of healthcare; however, to effectively use these technologies, we first need to fully understand the challenges that the healthcare sector experiences from multiple perspectives, including patients, healthcare professionals, management and public health.

ORAL PRESENTATIONS: SESSION 1

OP-1. DigiLaboratory and harmonization in Estonia

Anu Tamm[1] – [1] Tartu University Hospital, United Laboratories, Tartu, Estonia

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Clinical laboratories all over the world produce huge amounts of data which has to be organized in order to get the best use of it. The process of laboratory data harmonization in Estonia started with the unification of terminology and units, ledby the Estonian Society for Laboratory Medicine (ESLM). The laboratory community agreed on the principles of the generation of names of tests in use, and a list of official names was generated. In order to afford electronic data exchange and the collection of data to the personal electronic records (EHR), LOINC was chosen to code the tests. SNOMED CT is used for coding test results as well as the substances the tests are performed with.

The state institution, Health and Welfare Information Systems Centre (TEHIK) generated an HL7-based standard for lab data flow with the aim to collect data centrally. A local public database of lab tests, ELHR, was created, which includes information on the name, unit, LOINC code and the way the result should be reported in case of non-quantitative tests. ESLM is responsible for the validity of data in the database. Laboratories should register all the tests they run in ELHR, and thus, information about their test menus is also available.

By now, the majority of clinical laboratories report their data to the EHR, which is accessible to all relevant medical personnel andeach person individually. In order to optimize the use of medical data, TEHIK is developing a platform named Data Viewer, providing a condensed overview of all health information delivered by different health institutions. Part of that, the crosstable of laboratory results which enables viewing data in continuous timelines, was the first function available for users.

Data quality issues should still be solved in EHR in cooperation with TEHIK and the laboratories. The achievement of comparable analytical quality results provided by different laboratories and visualized in the same table rows remains a never-ending challenge for ESLM.

OP-2. Hemogram reference values in Estonia

Karel Tomberg[1,2], **Marika Pikta**[1,2] – [1] on behalf of the Working Group of Laboratory Hematology, Estonian Society for Laboratory Medicine; [2] North Estonia Medical Centre, Laboratory, Tallinn, Estonia

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OBJECTIVES. Complete blood count (CBC) is one of the most commonly requested laboratory tests in clinical practice. In Estonia, despite the relative uniformity of analysers, each laboratory used different reference values for CBC. The aim of the study was to develop and implement common reference values for CBC in adults.

METHODS. The collaborating 4 laboratories recruited first-time blood donors and appropriate healthy volunteers by invitation, drew blood, and measured CBC-6 diff parameters. The participants had to feel subjectively well and did not have a history of chronic disease, or using prescribed medications. They were assessed by completed questionnaires according to defined exclusion criteria. EDTA blood samples were tested within 3 hours after collection. CBC-6 diff parameters were measured by analysers XE-2100, XE-5000, XN-2000, and XN-1000 (Sysmex, Kobe, Japan). Each participating laboratory is accredited according to ISO 15189:2012. The nonparametric method was used to calculate reference intervals with 90% confidence intervals.

RESULTS. Blood samples from a total of 314 clinically asymptomatic and apparently healthy adults were evaluated. After applying exclusion criteria, 259 subjects were included in the study: 132 men and 127 women aged 18 to 87. Reference intervals were calculated for the following parameters: RBC, Hb, Hct, MCV, MCH, MCHC, RDW, PLT, MPV, Pct, P-LCR, PDW, IPF, WBC, and absolute counts of immature granulocytes, neutrophils, lymphocytes, monocytes, basophils and eosinophils. All hospital and private laboratories using Sysmex analysers for CBC, implemented harmonised reference intervals into practice. Three laboratories using other manufacturers' analysers verified and implemented the same reference intervals.

CONCLUSIONS. Population-based CBC reference ranges were established. The results provided the basis for harmonisation of automated CBC–6 diff reference intervals across laboratories. It assists laboratorians and clinicians in the uniform interpretation of test results for the clinical management of patients.

ORAL PRESENTATIONS: SESSION 1

OP-3. Comparison of automated red cell parameters with bone marrow iron staining

Triin Paabo[1, 2], Piret Mihkelson[1], Jelena Beljantseva[1], Ain Rähni[1], Signe Täkker[1], Kalle Kilk[2], Katrin Reimand[1] – [1] Tartu University Hospital; [2] University of Tartu, Institute of Biomedicine and Translational Medicine

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OBJECTIVE. The aim of the study is to evaluate the role of novel automated red cell parameters in the estimation of bone marrow iron stores and diagnosis of iron deficiency.

METHODS. The study is a retrospective single-center study based on data from an automated hematology analyzer and results of bone marrow iron staining, conducted in Tartu University Hospital, Estonia. The red cell parameter measurements were performed on a Sysmex XN-series hematology analyzer (Sysmex Corp., Kobe, Japan). Bone marrow iron stores were assessed semiquantitatively by cytochemical reaction according to Perls.

RESULTS. The analysis included 429 bone marrow aspirate smears from 393 patients (all from the years 2020 and 2021), where results of bone marrow iron staining, automated red cell parameters and ferritin were available. Children under 18 years of age were excluded. The median age of patients was 67 years, and 51.8% of patients were female. The most common indication for bone marrow examination was a lymphoproliferative disorder (n= 127, 29.6%).

Median values of red blood cells with a low (hypochromic) hemoglobin equivalent (Hypo-He) and reticulocyte hemoglobin equivalent (Ret-He) were statistically significantly different between patients with decreased and sufficient bone marrow iron stores. In logistic regression models, the combination of ferritin, soluble transferrin receptors and Hypo-He was the best predictor of bone marrow iron stores (AUC=0.92). Among the 429 cases, 26 (6%) cases had a decreased Ret-He value (<29 pg), 11 of them with normal bone marrow iron stores. Traditional iron biomarkers suggested iron deficiency in 5out of these 11 cases, inconsistent with the normal bone marrow iron stores. Ret-He was decreased in 2cases of myelodysplastic syndrome, indicating inefficient iron incorporation to erythropoiesis rather than true iron deficiency.

CONCLUSIONS. Novel automated red cell parameters can be helpful in combination with other iron biomarkers to predict bone marrow iron stores.

OP-4. Multiple myeloma immunophenotype related to genetic aberrancies used in risk stratification

Mantas Radzevičius[1] – [1] Vilnius University, Department of Physiology, Biochemistry, Microbiology and Laboratory Medicine

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In multiple myeloma (MM) risk estimation, increasing emphasis is placed on genetics, with methods like R-ISS and m-SMART involving high-risk genetic aberrancies. Molecular karyotyping allows for more detailed and precise chromosomal analysis than traditional methods, allowing precise detection.

Multiparameter flow cytometry (MFC) is used in MM diagnostics by detecting MM immunophenotype. MFC is not always considered in risk estimation, however, MM plasma cell (MMPC) immunophenotype has shown a relationship to prognostics. Next-generation flow (NGF) methods, like MM minimal residual disease (MRD) guidelines provided by the Euroflow consortium, allow for easier comparison of antigen expression due to standardization. There is a lack of data on the association between MMPC immunophenotype and genetic factors.

We gathered data from newly diagnosed MM patients, analyzed it using standardized NGF MM-MRD panels and received detailed chromosomal analysis by molecular karyotyping and FISH after CD138 positive cell selection. Antigen expression percentage and mean fluorescence intensity (MFI) were recorded on MMPCs. Patients were analyzed according to chromosomal aberrancies and translocations.

Patients with hyperdiploid karyotype had a distinct immunophenotype, with higher expression of CD45, CD56, CD117, and CD138. Dup(1q) showed higher CD27 and CD117 expression. Monosomy 14 showed lower CD117 expression. Del(1p) showed lower CD27 expression. Higher ISS stages (which don't consider genetics) had lower CD27 and CD38 expression, higher R-ISS showed lower CD27, CD38, and CD138 expression. Higher m-SMART categories had lower MMPC CD27 expression.

There were specific trends observed — a lower expression of CD27, CD38, CD56, CD117 and CD138 was related to unfavorable genetic factors, and higher MM percentages were related to unfavorable genetic factors. A larger long-term study that measures survival would be necessary to determine the impact of these on patient outcomes.

ORAL PRESENTATIONS: SESSION 1

OP-5. Changes in genes involved in coagulation: myths and truth

Ludmila Volozonoka[1] – [1] E. Gulbja Laboratory, Riga, Latvia

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An array of genes are coding proteins playing their role in maintaining normal blood coagulation. Genetic changes can lead to various conditions affecting hemostasis, including severe ones like hemophilia A, or those only acting as a genetic risk factor, e.g., the FV Leiden variant increasing the likelihood of thrombophilia. In recent times, the testing of genetic variants of thrombophilia (particularly the ones in FII, F5, and MTHFR) became increasingly demanded in clinics in association with a variety of disorders — deep vein thrombosis, miscarriage, infertility, and even autism as well as other directly unrelated conditions.

In this presentation, I will provide evidence-based information on what different variants in hemostasis genes do and don't do, mainly focusing on understanding the role of genetic risk factors, as well as providing clear indications for the genetic testing of these variants.

ORAL PRESENTATIONS: SESSION 2

OP-6. Advances in rare disease diagnostics and research

Sander Pajusalu[1, 2] – [1] Genetics and Personalized Medicine Clinic, Tartu University Hospital, Estonia; [2] Department of Clinical Genetics, Institute of Clinical Medicine, Tartu University, Estonia

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Next-generation sequencing of panels and exomes and copy-number variant detection using microarrays have facilitated diagnostics of rare genetic disorders for the past decade. By standard clinically available methods, around one-third of patients receive an exact molecular diagnosis that can guide the treatment, surveillance, and/or family counseling.

More advanced analysis methods are needed to increase the diagnostic yield and maximize the benefit of genetic diagnostics in the era of personalized medicine. I will present the possible benefits of genome sequencing and RNA sequencing and discuss their role in diagnosing genetic disorders. I will focus on the non-coding genome and the approaches to decipher the functional impact of intronic and untranslated region variants. In addition, I will present possibilities for structural variant detection from genome sequencing and highlight different approaches to maximizing the use of RNA sequencing.

ORAL PRESENTATIONS: SESSION 2

OP-7. Delineation of the genetic causes of rare diseases by the use of NGS and functional studies

Gunda Petraitytė[1] – [1] Department of Human and Medical Genetics, Institute of Biomedical Sciences, Vilnius University, Vilnius, Lithuania

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Next-generation sequencing (NGS) transformed the diagnostics of rare diseases by significantly accelerating the identification process of the hereditary cause. However, with these advanced technologies came the burden of analyzing large amounts of data to determine the single variant responsible for the disease. Furthermore, nearly half of identified unique DNA variants' pathogenicity could be stated as uncertain significance, as their functional impact is poorly understood or has not yet been investigated.

During our research project, computational and bioinformatical, different experimental techniques and methods wereapplied to get a broader understanding of the disturbances of molecular and cellular processes caused by NGS-identified genetic variants in patients with diagnosed rare hereditary disorders. *In silico* methods were applied to analyze the effect on protein structures of missense variants identified in genes *PIGN*, *RLIM*, and *DNMT3A*. To investigate the *DYNC1H1* and *FAS* genes' splice site variants' impact on mRNA structure, Sanger sequencing of the affected individuals' cDNA, synthesized using RNA, extracted from whole blood samples or fibroblasts, was performed. Western blotting was applied to determine protein levels in samples of affected individuals with truncating DNA variants in *MED13L*, *NAA15*, and *DYNC1H1*. Also, a DNA variant identified in *DYNC1H1* is being investigated by immunofluorescence microscopy to assess the variant's impact on the cell's inner structures and protein localization.

The implementation of techniques such as whole exome sequencing allows the discovery of novel genome variants that are potentially the cause of hereditary disorders. Different molecular and cellular approaches, as well as immunocytochemistry, provide possibilities to uncover the influence of DNA variants on mRNA, protein structure, function, and cellular changes.

OP-8. nDNA and mtDNA analysis of patients with suspected mitochondrial disease: a wide diagnostic spectrum

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Mitochondrial diseases (MDs) are clinically and genetically heterogeneous groups of inherited metabolic disorders characterized by mitochondrial dysfunction. Pathogenic variants have been identified in more than 350 genes. The implementation of next-generation sequencing (NGS) methods allowed a significant improvement inthe diagnosis of MDs, however, a substantial fraction of patients remain undiagnosed.

83 unrelated individuals with suspected mitochondrial disease were included in the study. A whole mtDNA sequence was analyzed using mtDNA Sanger sequencing and deletion/duplication analysis methods. NGS methods were applied to30 patients. Targeted gene sequencing for mitochondrial and other neuromuscular disorders was performed for 9 patients, and whole exome sequencing was performed for 21 patients.

Mitochondrial disease was confirmed in 13 patients (15.3%) in the study group. Pathogenic mtDNA variants were detected in nine patients, confirming the diagnosis of MELAS, MERRF, Leigh, and Kearns-Sayre syndromes. Pathogenic nDNA variants in *TRMU*, *SURF1*, *PNPLA8*, *RRM2B*, and *BTD* genes causing mitochondrial diseases were identified in four patients (13.3%). Other neuromuscular diseases caused by pathogenic variants in *CACNA1A, DDX3X, TPP1, KIF1A, YARS1* and *ANO5* genes were confirmed in seven patients (23.3%). Two patients were found to have two diseases caused by pathogenic variants in nuclear (*RRM2B* and *BTD*) or in both mitochondrial (*MT-ND4*) and nuclear (*ANO5*) genes.

In the study, 10.8% of patients with suspected mitochondrial disease were identified to have pathogenic mtDNA variants. The application of NGS allowed for confirmation of other rare mitochondrial or neuromuscular disorders, emphasizing the importance of clinical genetic-based research in improving the care of these patients.

ORAL PRESENTATIONS: SESSION 3

OP-9. Compliance of blood sampling practice in Lithuania with the EFLM-COLABIOCLI recommendations

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Venipuncture is a common task in health care, and training for this procedure is included in nursing and biomedical technicians' programs but not always taught in the same way, which is the cause of the same procedure being commonly performed in different ways. In 2018, joint recommendations from the European Federation of Clinical Chemistry and Laboratory Medicine and Latin America Confederation of Clinical Biochemistry (EFLM-COLABIOCLI) were published to maintain consistency and minimize the risk to patient safety. Our hypothesis was that specialists who draw venous blood may have their routine practice to perform this procedure, which is not always compliant with recommendations, especially factors influencing the quality of blood samples. This study's aims were to assess the general practice of phlebotomy in Lithuania and its compliance with EFLM-COLABIOCLI recommendations, and to determine the steps which are most error-prone and have to be improved. An anonymous phlebotomy practice questionnaire was designed based on the EFLM-COLABIOCLI recommendations and conducted involving more than 250 nurses and biomedical technicians from various regions and hospitals in Lithuania. The compliance with the EFLM-COLABIOCLI recommendations level on phlebotomy among Lithuanian nurses and biomedical technicians was found unsatisfactory in some areas and needed some improvement in order to maintain good quality blood samples.

OP-10. The importance of comparability, compatibility and transferability of results

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Results of measurements are used to diagnose disease in individuals and populations and to monitor treatment, recovery, and progress of disease. To be meaningful, results must be referable to a fixed point that was recognized by Archimedes. The obvious is the unit, and a practical unit was introduced by the first European who was acknowledged as the first Holy Roman Emperor in the year 800, Charles I, also known as Charlemagne. The unit states the size of a quantity in relation to an agreed amount, but it should also refer to the question posed. Simply put, ten meters is interpreted as a length ten times longer than one meter. A meter is a meter wherever it is measured, even in space. Biomarkers present irregularities that must be overcome differently to ascertain that the results are clinically useful. We will discuss international principles and efforts to find solutions and express the clinical usefulness of results in Bayesian terms.

ORAL PRESENTATIONS: SESSION 4

OP-11. Emerging and re-emerging infectious diseases in 2022

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Emerging infectious diseases are commonly defined as outbreaks of previously unknown diseases or known diseases that are rapidly increasing in incidence or geographic range in the last decades or the persistence of infectious diseases that cannot be controlled. The reappearance of a previously known infection after a period of disappearance or decline in incidence is known as re-emergence. Many factors contribute to the emergence or re-emergence of a disease. Research indicates that newly emergent infections may result from changes in or the evolution of existing organisms, the spread of known diseases to new geographic areas or new hosts (e.g. humans), or the appearance of previously unrecognized infections in persons living or working in areas undergoing ecologic changes. This increases individual exposure to insects, animals, and environmental sources which may harbor new or unusual infectious agents. Recent decades have seen several emerging and re-emerging infections like HIV, SARS-1, MERS, Zika virus and most recently SARS-CoV-2 and monkeypox. Some of them, like the Zika virus or Ebola virus diseases, have had a limited global impact. Others, however, have affected the entire world. The SARS-CoV-2 pandemic is present on all continents and has caused approximately 18 million deaths worldwide thus far. The full economic and social impact of the SARS-CoV-2 pandemic is still under investigation, but is likely to be massive. In my presentation, I will analyze how we managed the SARS-CoV-2 pandemic in Estonia, what measures were correct and which mistakes have been made. We still are learning how to live with the virus so that our lives are minimally disturbed. Another global threat is constantly increasing antibiotic resistance that could be controlled by improving antibiotic stewardship and hospital hygiene. Improved control over the spread of antibiotic-resistant encoding genes would enable stopping antibiotic resistance as well. In my presentation, I will also look at the future — it is unlikely that emerging/re-emerging infections are completely avoided, but their societal damage could be minimized by better preparedness for emerging situations. The latter requires cooperation between neighboring countries and outside, especially strengthening research on host-pathogen interactions.

OP-12. Tick-borne pathogens on the rise

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In 2020, the National Institute for Health Development (NIHD) launched a nationwide citizen science campaign on human tick risk areas and tick-borne pathogen distribution mapping. Over 21,000 tick findings were mapped and over 6400 ticks were received for analysis. Over 35% of all tick finding recordings originated from home gardens. Over 3,500 ticks were analyzed for the presence of pathogens causing tick-borne encephalitis, Lyme disease, human anaplasmosis, neoehrlichiosis, relapsing fever spirochete *Borrelia miyamotoi*, and tick-borne rickettsiosis. The most common were tick-borne rickettsioses (up to 53% of all ticks) and Lyme disease (up to 41% of all ticks) agents of *Rickettsia* and *Borrelia burgdorferi* s.l. species, respectively. *Neoehrlichia mikurensis*, which is the pathogen causing neoehrlichiosis in humans, was detected in up to 28%; *Anaplasma phagocytophilum* causing human anaplasmosis, in up to 18%, *Borrelia miyamotoi* disease pathogen in up to 8% and the presence of the tick-borne encephalitis virus was detected in up to 1% of ticks. TBE, LB, and since 2013, ehrlichiosis, are the only notifiable TBDs in Estonia; thus no information on any human cases for other TBDs is widely available. Up to 29% of ticks were found to have multiple pathogens. The highest share of infected ticks was observed in Tartu (77%) and the lowest in Ida-Viru county (39%).

The results of the study indicate a significant, 2–10-fold increase in the spread, prevalence level and diversity of tick-borne pathogens with identified potential for infection over the last decade in Estonia. It is also noteworthy that a large proportion of ticks have been reported in people's home gardens, which significantly changes the hitherto widespread belief that the risk of ticks is only related to forests, shrubs, or other unmaintained areas. Moreover, this study provides insight into the pathogens of various diseases found in human-biting ticks in Estonia.

ORAL PRESENTATIONS: SESSION 4

OP-13. Analysis of point mutations in dermatophyte squalene. Epoxidase (SQLE) gene using the Luminex xMAP® platform

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About 20–25% of the world's population is affected by dermatophytosis — one of the most common infectious diseases in the world. In recent years, antifungal resistance in India has taken epidemic dimensions. A study published in 2021 showed that in Europe, 85% of countries that participated in that study reported antifungal resistance.

For dermatophytosis, the most used antifungal drug is Terbinafine. In India, there is a high prevalence of Terbinafine-resistant dermatophytes. The cause of Terbinafine resistance is believed to be different point mutations in the squalene epoxidase (SQLE) gene that causes different amino acid replacements. The most common amino acid replacement that causes very high Terbinafine MIC values is Phe397Leu.

Antifungal susceptibility testing for dermatophytes is not routinely done in microbiology laboratories because it is a complicated and slow process. Also, there hasn´t been a previous need for it. Because of the spreading antifungal resistance, it is important to have alternative methods to determine resistance strains. One of the alternative methods is molecular testing of point mutations that lead to antifungal resistance.

Therefore one aim of this study was to add specific SQLE point mutations that lead to amino acid replacement Phe397Leu and wild-type region to a molecular panel that is routinely used for dermatophyte detection from skin and nail materials. By adding SQLE wild-type and SQLE mutations that cause amino acid replacement Phe397Leu to the molecular panel, we designed new SQLE=specific primers and hybridization oligonucleotides and used them in the Luminex xMAP® multiplex diagnostics platform.

The second aim of this study was to experimentally prove that the newly updated test panel works. That was achieved with clinical samples that sequenced and carried point mutations or were SQLE wild-type strains.

We used this newly updated test panel to screen clinical samples for SQLE point mutations. We screened 278 samples and found two samples that were *Trichophyton rubrum* positive and carried point mutations in the SQLE gene.

OP-14. HORIZON 2020 PERFORM and DIAMONDS projects: new genomic and proteomic approaches to provide rapid and accurate diagnosis of febrile illnesses – turning fiction into reality

Aleksandra Rudzāte, prof. Dace Zavadska, Dagne Grāvele on behalf of the PERFORM and DIAMONDS consortia (grant agreement No 668303)

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OBJECTIVES. The PERFORM project aimed to develop a comprehensive management plan for febrile patients, capable of being rolled out in different healthcare systems across Europe by linking sophisticated new genomic and proteomic approaches to careful clinical phenotyping, and building on pilot data from previous studies. A set of promising proteomic and genomic biomarkers were identified and validated during the study. DIAMONDS is a follow-up EU Horizon 2020 project to develop a molecular test for rapid diagnosis of serious infectious and inflammatory diseases using personalised gene signatures.

The PERFORM team consisted of 18 partner institutions across 10 countries, while DIAMONDS had28 institutions across 13 countries. Latvia is the only Baltic country represented in both projects by Riga Stradins University (RSU).

METHODS. In total, 6320 Emergency department (ED) patients with fever/suspicion of infection were included in the PERFORM database: 738 patients with Paediatric ICU form, 646 patients with High-Risk form, and 280 patients with Inflammatory form. Latvia recruited 462 ED patients in Riga Children's Clinical University Hospital: 62 PIC patients, 25 INF and 27 HR patients. Descriptive statistics were used for the Latvian cohort.

RESULTS. 99 of the ED patients in Latvia had laboratory evidence of viral infection and 123 of bacterial infection. The main viral pathogens were Rotavirus (n = 16), Influenza A and B (n = 18), EBV(n = 13), Adenovirus (n = 11), Rhinovirus(n = 10) and Enterovirus (n = 9). Main bacterial pathogens were Group A Streptococci (n = 21), S.aureus (n = 20), E.coli (n = 19), Mycoplasma spp.(n = 15), Salmonella spp.(n = 7), Staphylococcus coagulase negative (n = 6), S.pneumoniae (n = 4), Borrelia burgorferi(n= 4). The main clinical phenotypes were: Definite Bacterial (n = 64), Probable Bacterial (n = 110), Bacterial Syndrome (low/unavailable inflam.markers, n = 60), Unknown Bacterial or Viral (n = 38), Probable Viral (n = 98), Definite Viral (n = 47).

The enrolment of patients to DIAMONDS is ongoing.

ORAL PRESENTATIONS: SESSION 4

OP-15. Etiologic agents of community-acquired and nosocomial bacteremias, differences in antimicrobial susceptibility

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Antibiotic resistance is one of the most serious public health concerns worldwide and is increasing, making antimicrobial prescription more complicated. This study is aimed at identifying local bacterial isolates and their antimicrobial susceptibility patterns to reduce excessive antibiotic usage.

A hospital-based retrospective study was conducted from January 2016 to December 2020. All positive blood cultures of this period were included in this study. Typical skin contaminants (e.g. coagulase-negative staphylococci (CoNS)) were excluded. We included 3815 bacteremia isolates. The most common etiology was *E. coli* 987 (25.9%), followed by *S. aureus* 668(17.5%), *Klebsiella* spp. 445 (11.7%), *Enterococcus* spp. 328(8.6%), *P. aeruginosa* 174(4.6%), Streptococcus viridians group 211 (5.5%). *Enterobacter* spp, other Enterobacteriales, *Acinetobacter* spp., *Streptococcus pneumoniae,* Beta haemolytic streptococci, *Candida* spp., grampositive rods and anaerobes were isolated less frequently (1-5% of cases).

Hospital-acquired *E. coli* strains were more resistant to ampicillin/sulbactam (68.4% and 31.6%), piperacillin/tazobactam (15% and 4.6%) (p < 0,000), cefuroxime (73.7% and 13.1%), cefotaxime (22.6% and 10.9%, p < 0,001) compared to community–acquired strains. Hospital-acquired *Staphylococcus aureus* strains were more resistant to oxacillin (11.8% and 1.9%, p = 0.000) and gentamicin (5.4% and 0.6%, p = 0.001) compared tocommunity-acquired strains. Hospital-acquired *K. pneumoniae* strains were more resistant to ampicillin/sulbactam (81.8% and 43.3%), piperacillin/tazobactam (69.2% and 31.2%), cefotaxime (81.3% and 37.6%), ciprofloxacin (75.8% and 40.4%), gentamicin (59.1% and 31.2%), (p = 0.005), meropenem (4% and 0%, p = 0.016), amikacin (9.1% and 2.8%, p = 0.021).

Conclusions. It is important to evaluate the risk factors for patients before prescribing empirical antimicrobial treatment of bacteremias — whether the infection has been acquired in a community or hospital setting.

ORAL PRESENTATIONS: SESSION 5

OP-16. Enhanced Liver Fibrosis (ELF) score in the general population

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Non-alcoholic fatty liver disease (NAFLD) and alcohol-related liver disease (ArLD) are the leading causes ofchronic liver disease in the population. The stage of liver fibrosis is the best predictor of liver-related outcomes in both NAFLD and ArLD. Therefore, there is an urgent need for accessible non-invasive instruments for early detection of advanced liver fibrosis in primary care.

The Enhanced Liver Fibrosis (ELF™) test is a blood-based direct liver fibrosis marker based on three serum markers of matrix turnover: TIMP-1, HA, and PIIINP. In samples of patients with NAFLD, ArLD, chronic viral hepatitis or cholestatic liver disease, ELF shows high diagnostic accuracy for detecting advanced liver fibrosis. However, large cohort studies assessing the predictive performance of ELF in the unselected general population have been lacking.

Based on the Finnish Health 2000 health-examination survey, representative of the general population, with linked electronic healthcare registry data for hospitalizations, death and cancer related to liver disease, we recently analyzed the performance of the ELF test for predicting liver-related outcomes.

The cohort comprised 6040 adults with a median follow-up of 13.1 years. The mean ELF score at baseline was 8.85 (median 8.74, IQR 8.22–9.36). Accounting for the competing risk of death without liver disease, the time-dependent AUC value was 0.8 at 5 years and 0.7 at 10 years. Cumulative incidences of liver-related outcomes among individuals with ELF <9.8 was 0.5% at 10 years, with ELF 9.8–11.3, 2.2%, and with ELF ≥11.3, 7.1%, respectively. The risk for liver-related outcomes at any given ELF test value was higher among men than women. 5-year AUC were excellent among individuals with ALT > 40 U/L, diabetes or obesity (AUC ~0.9).

These findings suggest that the ELF test could be useful for making predictions of liver-related outcomes in the general adult population, especially in those with risk factors for liver disease.

ORAL PRESENTATIONS: SESSION 5

OP-17. Uncovering the impact of weight loss on the B cell profile and biomarkers of obesity

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OBJECTIVES. Globally, obesity has tripled in less than 50 years, and is a major risk factor for many disorders, including type 2 diabetes mellitus, cardiovascular disease, and cancer. B cells are implicated in obesity-associated meta-inflammation and skewed immunity. We characterized the B cell compartment and biomarkers of obesity prior to and following bariatric surgery–induced weight loss in individuals living with obesity.

METHODS. We prospectively followed up a group of patients (n = 22) undergoing bariatric surgery as part of treatment for obesity; matched lean controls were also recruited (n = 16). Blood samples from individuals with obesity were collected immediately before surgery and 6 months after. We assessed changes in the B cell compartment, specific factors involved in regulating B cell survival and function (serum levels of BAFF (B-cell-activating factor of the TNF family), APRIL (a proliferation-inducing ligand)), and total IgG, IgM, IgA. We additionally analyzed the full blood count, lipid profile (total cholesterol, triglyceride, high-density and low-density lipoprotein cholesterol levels), glucose metabolism (glucose, insulin, HOMA-IR, HbA1c), inflammatory markers (high sensitivity CRP, lipopolysaccharide-binding protein, erythrocyte sedimentation rate), leptin, and adiponectin.

RESULTS. We observed significantly improved glucose and lipid metabolism in obese individuals following bariatric surgery, as well as a reduction in inflammatory markers. We observed a slight but significant reduction in circulating IgG levels following surgery. When characterizing the B cell profile, we observed that the changes to the memory B cell compartment associated with obesity were no longer present at the 6-month time point.

CONCLUSIONS. Our study has uncovered the impact of weight loss on known biomarkers and the B cell compartment in obesity.

OP-18. Therapeutic drug monitoring in the era of LC-MS/MS in the laboratory without LC-MS/MS

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Once only seen in scientific laboratories, liquid chromatography, especially in combination with tandem mass spectrometry (LC-MS/MS), has gradually made its way into clinical laboratories' routine practice. Therapeutic drug monitoring (TDM) is one of the most common applications of LC-MS/MS. Because of its superior analytical performance, some consider it the "gold standard" for TDM. The manual labor required to set up and run the assays has reducedsignificantly and the cost for a single run can be less than alternative immunoassays. A wide number of assays are commercially available — the range extends from immunosuppressants to antibiotics, and from anti-depressants to anti-epileptics. It all sounds great, so why don't we see LC-MS/MS in every other clinical laboratory? For many, its biggest drawback is its starting cost.It could reach levels where lab directors start asking questions — do we need that level of quality, and what are the alternatives? Luckily there is more than one.

ORAL PRESENTATIONS: SESSION 5

OP-19. CEACAM6 as a diagnostic and prognostic biomarker of pancreatic adenocarcinoma

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Survival rates from pancreatic cancer have remained stagnant for decades due to the heterogenic nature of the disease. This study aimed to find a new advanced biomarker and evaluate its clinical capabilities, thus enabling more individualised pancreatic cancer management. Between 2013 and 2020, 267 patients were included in the study. Surgically collected pancreatic tissue samples were analysed via high-definition mass spectrometry. Carcinoembryonic antigen-related cell adhesion molecule 6 (CEACAM6) was discovered as a possible promising pancreatic cancer biomarker. The predominance of CEACAM6 to pancreatic cancer was validated using antibodies in tissue samples. CEACAM6, carbohydrate antigen 19-9 (CA19-9), and carcinoembryonic antigen (CEA) blood serum concentrations were evaluated for clinical evaluation and comparison. Kaplan–Meier survival analyses were used to evaluate disease-free survival and overall survival. Poorer overall survival was significantly dependent on increased CEACAM6 blood serum concentrations (17.0 vs. 12.6 months, $p = 0.017$) in pancreatic cancer patients after radical treatment and adjuvant chemotherapy. Increased CEA and CA19-9 concentrations showed no significant dependencies with survival. Thus, CEACAM6 is a promising new biomarker with significant prognostic value and prediction of chemoresistance properties, enabling the improvement of individualised approaches to patients with pancreatic cancer.

ORAL PRESENTATIONS: SESSION 6

OP-20. Colorectal cancer screening — the Latvian experience

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The presentation included four major topics in the colorectal cancer field.

1. The incidence of colorectal carcinoma in Latvia.
   Colorectal cancer (CRC) screening in Latvia. From 2009 to 2021, almost 910,000 Latvian inhabitants were invited to participate in the CRC screening programme. The participation rate in 2009, 2015, 2021 and 2022 was 6.95%, 10.9%, 14.6% and 18.8% respectively. In 2021, the participation rate was highest in Riga, representing 44% of the total targeted population, but it was quite low in other Latvian districts. The trend of incidence and mortality from colorectal carcinoma will now be discussed.
2. The organization of colorectal carcinoma screening in Latvia.
   The CRC screening in Latvia was introduced in 2009. The organized CRC screening programme was stepwise implemented since 2019 with the fecal immunological test. Since 2019, fecal immunochemical tests (FITs) for hemoglobin (Hb) have been a common screening method in Latvia.
3. Colorectal premalignant lesions. Colorectal serrated lesions and polyps. Conventional colorectal adenoma.
   Neoplastic precursor lesions are broadly divided into two distinct histological types: conventional adenomas and serrated polyps. These lesions could progress to carcinoma through a dysplasia-carcinoma pathogenetic sequence.
4. Colorectal carcinoma histopathology.
   The histopathological CRC tumor subtypes TNM classification. Molecular pathology. The role of BRAFand KRAS pathways in pathogenesis, prognosis and personalized diagnostics and treatment.

ORAL PRESENTATIONS: SESSION 6

OP-21. The Estonian experience in colorectal cancer screening

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The Council of the European Union has recommended the implementation of national population-based screening programmes for breast, cervical and colorectal cancer. In Estonia, corresponding programmes have been in place since 2004 (breast), 2006 (cervical), and 2016 for colorectal cancer.

Men and women aged 60–69, regardless of health insurance status, undergo colorectal cancer (CRC) screening biennially. When the programme launched in 2016, one cohort with a single common birth year took part. From 2017 to 2020, an additional birth year cohort was added every year. Since then, men and women of five different years of birth have been invited to take part every year.

The Estonian Cancer Screening Registry forms the target group by collecting data from the Estonian Population Register, the Estonian Cancer Registry and the Health Information System. Individuals with a previous CRC diagnosis and/or previously performed screening colonoscopy are excluded. Invitations are sent via email to the addresses shown in the population register and are also visible in personal electronic health records. The invitees are instructed to book an appointment with their general practice nurse in order to receive a stool sampling kit. The kit comprises a specimen collection device, an information leaflet, a form, and a reply-paid envelope. Samples are taken at home and sent by post to the laboratory. The tests for occult blood are performed in two labs: at the North Estonia Medical Centre and at Tartu University Hospital, using a highly sensitive quantitative fecal immunochemical test for hemoglobin (FIT) from Aidian Oy. Samples with a hemoglobin amount of <20 µgHb/gfeces are considered negative. If the test result exceeds the threshold of 20µg/g, the individual is referred for a screening colonoscopy. From the beginning of the programme until the end of 2020 (a 4.5 year period), 110,865 tests for occult blood were performed, from which 6388 (5.8%) were positive. The positivity rate is comparable with other European CRC screening programmes. The overall participation rate (2016-2020) remained under 60% for females and 50% for males. In 2020, participation dropped 3–4 percentage points due to epidemiologic reasons. Despite the relatively low participation, screening programmes have helped prevent new cancer cases and reduce cancer deaths in Estonia. Therefore, it is crucial to increasingly focus on improving the coverage and quality of cancer screening programmes.

OP-22. Colorectal cancer screening in Lithuania

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In Lithuania, colorectal cancer (CRC) is the third leading cause of cancer death in men and the second in women. The screening programme was initiated as a pilot project in 2009 in the two largest cities. Since 2014, the programme has run nationwide among men and women aged 50–74. It is divided into four services: (1) Information about the program and faecal immunochemical test (FIT), (2) Referral for colonoscopy, (3) Colonoscopy with or without biopsy, and (4) Pathological examination and diagnosis. The programme is financed by the National Health Insurance Fund and is free of charge for participants. The primary healthcare centres are responsible for informing the registered residents about the programme and offering a faecal immunochemical test (FIT) every other year. The FIT kit is given to the participant with detailed instructions on specimen collection and kit processing. Test-positive subjects are referred for colonoscopy with or without general anaesthesia. If no changes are found during colonoscopy, the FIT is repeated after 10 years. If polyps are identified, they should be removed and examined histologically.

The participation rate varied from 16% to 26.8% per year, being higher among women than men. The proportion of positive FIT results was 8% approximately during the whole study period. More than half of test-positive participants (55.5% in 2019) were referred for colonoscopy. The proportion of colonoscopy under general anaesthesia has increased over time and reached 76.7% in 2019. A biopsy was taken in every third patient (36.5% in 2019) who underwent colonoscopy or in every fifth test-positive patient (21.1% in 2019). The results of all biopsies performed from 2009 to 2019 showed that the adenoma was assessed in 57.9%, high-grade dysplasia in 11.6% and CRC in 6.2%. CRC detection rate among test-positive individuals varied between 0.93% and 1.28%. To increase the coverage and effectiveness of CRC screening, a central screening registry and active invitation system are required in Lithuania.

ORAL PRESENTATIONS: SESSION 7

OP-23. Quality and POCT

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POCT is the most rapidly growing field in laboratory medicine. With increasing technological and analytical possibilities, an increasing number of analyses can now be carried out on POC instruments. Although the costs of POC instruments are less than hospital instruments, the number of users of POC instruments is much larger, ranging from wards in hospitals, GP offices, nursing homes, pharmacies, and last but not least, tests for self-measurements. With the increasing emphasis on patient empowerment, this is a wanted development.

The ultimate goal of using POC testing is that patient outcomes should be improved and/or that it should be more cost-effective than the use of conventional laboratory testing. To achieve this, the role of POCT in the different clinical settings as well as the responsibility for introducing and managing the instruments and use of the instruments should be clearly defined. The main reason for using a POC instrument is that a rapid result is more useful than waiting for a result from a central laboratory. An essential question is, therefore: Should performance specifications for POC instruments be different from that of instruments in a central laboratory? Many will say "yes", but taking into account the different use of such instruments, performance specifications could probably be modified. Many POC instruments are used for specific clinical settings and one should therefore try to develop performance specifications for that setting, i.e. based on clinical outcomes. It is also probable that time and location is an important quality factor and that performance specifications can be less strict if a result is provided rapidly — especially in cases where you would like to know if the result is "very high" or "very low"; e.g. hypo- and hyperglycemia. However, if performance specifications for some POC measurement procedures should be less stringent compared to the central laboratory, it is important that this is communicated to the users of tests.

Quality control is a well-established routine in laboratory medicine. Since POCT is carried out in a different environment with different users and often with different performance specifications and different types of inbuilt controls, we have to re-evaluate how and which types of quality control we should use. Little evidence is available, for example, for how often to use internal and external quality control for POC instruments. (1,2) Noklus has established a system for both internal and external quality control of POC instruments and serves about 3300 POC units in Norway. The way this is done will be described in the lecture.

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OP-24. POCT in Tartu's Ambulance Service

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Ambulance services are often focused on rapid diagnostic and treatment of patients with acute and urgent illnesses and injuries. The Tartu Ambulance Services provides a medical emergency service in Estonia — the number of patients in 2021 was 61613, and 35% of patients were hospitalized in Tartu University Hospital. According to a 2015 clinical audit, "Management of severe sepsis and septic shock in Estonia", only 33% of cases were assessed as critical conditions at admission to an emergency department (red or yellow triage category).

The objective of this clinical study was to verify professional StatStripXpress2 meters for future use in the Tartu Ambulance Service. The laboratory assessed the performance of lactate, hemoglobin and glucose by using the spreadsheet program for estimating the bias between two methods. The verification of the precision lactate, hemoglobin, glucose and ketones were performed using control samples. A blood gas analyzer as a comparative method was used for the study. According to EP09, 40 whole blood heparinized samples were analyzed in duplicate. The precision of meters was estimated by measuring 2 levels of quality control samples measured in 5 replicates during 5 days (EP15).

Verified by the laboratory, 10 glucose/ketone and 10 lactate/hemoglobin meters have been used in the Tartu Ambulance Service. Pre-hospital verification of lactate and hemoglobin was performed by comparison results of Tartu Ambulance Service and after patient hospitalization in Tartu University Hospital. Overall, 37 (10%) patients with prehospital lactate measured were hospitalized. 27 (73%) of them had a pre-hospital lactate above 4,0 mmol/L and 10 (27%) below 4,0 mmol/L. The mean bias of results was 0,67 mmol/L (8,8%) and the pre-hospital lactate method has no significant difference from the hospital lactate ($p = 0{,}060$).

We conclude that the StatStrip Xpress2 lactate/hemoglobin and glucose/ketone meters are suitable for use in the Tartu Ambulance Service. Pre-hospital lactate measurement improves outcomes via the early identification of sepsis.

ORAL PRESENTATIONS: SESSION 7

OP-25. Direct self-sampled gargle water LAMP as a screening method for the detection of SARS-CoV-2 infections

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The COVID-19 pandemic accelerated the development of diagnostic alternatives. One of the alternatives to RT-PCR (the gold standard for SARS-CoV-2 diagnostics) is direct reverse transcription loop-mediated isothermal amplification (direct RT-LAMP or just LAMP). A LAMP reaction can be completed in about 30 min. and requires no temperature cycling. Furthermore, LAMP allows for various read-out options, such as fluorescence, electrochemical, or probe-based methods combined with real-time or endpoint detection.

In this study, we assessed the viability of self-sampled gargle water direct RT-LAMP (LAMP) for detecting SARS-CoV-2 infections by estimating its sensitivity with respect to the gold standard indirect RT-PCR of paired oro-nasopharyngeal swab samples. We also assessed the impact of symptom onset to test time (STT) — i.e., symptom days at sampling, on LAMP. In addition, we appraised the viability of gargle water self-sampling versus oro-nasopharyngeal swab sampling, by comparing paired indirect RT-PCR results. 202 oro-nasopharyngeal swab and paired self-sampled gargle water samples were collected from hospital patients with COVID-19-associated symptoms. LAMP, indirect and direct RT-PCR were performed on all gargle water samples, and indirect RT-PCR was performed on all oro-nasopharyngeal samples. LAMP presented a sensitivity of 80.8% (95% CI: 70.8–90.8%) for sample pairs with sub-25 Ct oro-nasopharyngeal indirect RT-PCR results, and 77.6% (66.2–89.1%) sensitivity for sub-30 Ct samples with STT ≤ 7 days. STT, independently of Ct value, correlated negatively with LAMP performance. 80.7% agreement was observed between gargle water and oro-nasopharyngeal indirect RT-PCR results. In conclusion, LAMP presents an acceptable sensitivity for low Ct and low STT samples. Gargle water may be considered as a viable sampling method, and LAMP as a screening method, especially for symptomatic persons with low STT values.

OP-26. What do people ask from laboratory doctors?

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There is an increasing interest among patients to receive their laboratory medicine results. Every patient in Estonia can view their own laboratory result through the patient portal of the Health and Welfare Information Systems Centre (TEHIK).

Every patient can also order additional laboratory tests for themselves and pay for them. This creates a situation for the need of additional support for patients in understanding their own laboratory results. There is the possibility to send questions to different doctors via the website www.kliinik.ee. This includes the possibility to ask a question from a laboratory doctor, as well.

It is difficult, however, to answer a question without seeing a patient and without the possibility to ask additional questions. Many questions are about different parameters of a hematology test, and sometimes patient picks up a single parameter. Diagnosis of borreliosis is also a popular theme — patients often ask questions about the numbers attached to the results of *B burgdorferi* IgG and IgM. And sometimes the questions are diffficult to answer.

The possibility to order laboratory tests for yourself and to ask a question has its advantages, but also disadvantages. It can avoid unnecessary appointments at the general practitioner's office. And sometimes, we can find occasional pathologies, such as anaemia, inflammation, and hyperglycaemia.

But there is also a danger that apatient who is not feeling well avoids a visit to a doctor because they find out their occasionally selected laboratory tests are within reference ranges.

That is why a laboratory doctor can never tell the patient they are healthy. One can only say that the lab tests are within reference intervals. We must remember that we do not have a marker for full health yet.

ORAL PRESENTATIONS: SESSION 8

OP-27. HPV self-sampling in cervical cancer screening: a randomised feasibility study in Estonia in 2020

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INTRODUCTION. A randomised intervention study was conducted in Estonia in 2020 in order to assess the feasibility of HPV self-sampling and the acceptance of this method among long-term non-attenders in the national organised cervical cancer screening programme.

METHODS. Altogether 65,218 women born between 1958–1983 without a Pap smear in the previous eight years were identified in the Estonian Health Insurance Fund database. From them, 12,000 women were randomly allocated to three equal-sized study groups. The opt-out group received a questionnaire and a Qvintip® sampling device by regular mail. Two opt-in groups received a questionnaire and an e-mail invitation to order a self-sampler online; one received the Qvintip and the other an Evalyn® Brush. Participants' background characteristics were obtained from the Estonian Population Registry. The effect of background characteristics on participation rate was estimated with multivariate Poisson regression. Acceptance of self-sampling was analysed according to agreement with statements in the questionnaire.

RESULTS. The overall participation rate was 16%, with significant differences between the opt-out (26%) and opt-in (11%) groups. Compared to the opt-out Qvintip group, adjusted relative risks for participation in the Qvintip and Evalyn Brush opt-in groups were 0.41(95% confidence interval (CI) 0.37–0.45) and 0.44 (95% CI 0.40–0.49), respectively. The mean participant age was 51 years.Participation was associated with place of residence, citizenship, and education. The overall hrHPV positivity rate in the study was 10%. Self-sampling was well accepted: 98% agreed that it was easy to use, and 88% preferred it as a screening method in the future.

CONCLUSION. The results showed the feasibility and good acceptance of HPV self-sampling in Estonia. In 2021, a randomised pilot study was carried out within the cervical cancer screening programme, and in 2022, self-sampling will be further implemented as part of the screening programme in Estonia.

OP-28. HPV screening programme in Latvia – the laboratory experience

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OBJECTIVES. According to statistics, cervical cancer is one of the most commonly diagnosed types of cancer in the world and in Latvia as well. Human papilloma virus (HPV), which is the causative agent of cervical cancer, is one of the most common viral infections of the reproductive system and can be easily diagnosed. To reduce the incidence of cervical cancer, a nationwide screening program is of great importance.

In order to evaluate changes in Latvia's national cervical cancer screening program, laboratory data from the year 2022 was gathered. The screening is performed via liquid-based cytology, and high-risk HPV DNA testing.

METHODS. Data on the overall participation in a cervical cancer screening program in recent years was evaluated. Statistical data gathering in SIA "Centrālā laboratorija" from 2022 (1st January to 28th June) of two major types of screening program tests in Latvia — liquid-based cytology and high-risk HPV DNA testing by Cobas 6800, Roche — were performed. The amount of high-risk HPV DNA positive samples was estimated.

RESULTS. Cervical cancer screening has been organized in Latvia since 2009. Since the beginning of the screening program, the overall responsiveness rate each year has varied between 14.9 – 43.8%.

Overall, in 2022 from 1st January to 28th June in SIA "Centrālā laboratorija", 31,900 liquid-based cytology tests were performed. If the abnormal smear results were obtained, high risk HPV DNA tests were performed. In the given period of time, 1,490 such tests were performed or 4.7% of all liquid-based cytology samples. Out of these abnormal smear results 42.27% were positive to at least one HPV type. 9.3 % were HPV 16 positive, 1.6% HPV 18 positive, 25.8% had another high-risk HPV type (31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66 or 68) positive. Number of samples were positive to multiple types of HPV: 0.07% were HPV 16 and 18 positive, 3.8% were HPV 16 and other high-risk HPV type positive, 1,4% were HPV 18 and other high-risk HPV type positive and 0.3% were HPV 16, HPV 18, and other high-risk HPV type positive.

CONCLUSIONS. Participation rate in Latvia's cervical cancer screening program is low but has slowly increased over the years. Testing data indicate that only a small portion of liquid-based cytology samples had abnormal smear results, from whom less than half are positive to at least one high risk HPV type.

ORAL PRESENTATIONS: SESSION 8

OP-29. Sexually transmitted infections (STIs) diagnostics in Lithuania

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In Lithuania, various clinicians (general practitioners, urologists, gynaecologists, dermatovenereologists, infectionists, etc.) diagnose and treat STIs. Therefore it's important to make updated STI management guidelines available for all health care specialists to designate adequate laboratory diagnosis and timely initiate appropriate treatment. From 2010-2020, the reported cases of syphilis ranged from 10.3 to 2, chlamydial infection 11.0 to 6, and gonococcal infection 9.4 to 1 per 100,000 inhabitants. After the coronavirus pandemic, syphilis cases increased, but the numbers of chlamydial, gonococcal, and mycoplasmal infections remained similar. A data review of the Hospital of LUHS Kauno Klinikos shows that in 2021, there were twice as many registered syphilis cases compared to 2020 or 2019.

IUSTI guidelines on bacterial STI management are being adopted at a national level and distributed among clinicians through publications in the journal *Lithuanian General Practitioner*. Though theoretically, there are no major discrepancies concerning diagnostics and treatment schemes, in practice there are some inequalities in the country of the performing laboratory diagnostics for different STI microorganisms. The international guidelines on the organization of consultation for STIs indicate the necessity to offer all patients testing for syphilis, *Chlamydia trachomatis, Neisseria gonorrhoeae* (NAAT), and HIV. But in rural districts, the main test for STIs is genital smear microscopy in a laboratory as the primary level where most patients with STIs are processed have no laboratory facilities to determine the etiological agents by performing NAATS. First choice antibiotics for the treatment of *Syphilis*, *Chlamydia trachomatis*, and *Mycoplasma genitalium* are acceptable and being prescribed for patients. Uncomplicated gonorrhoeae treatment goes with chinolones more often than ceftriaxone because of the inconvenient organization of the administration of the latter.

CONCLUSIONS. In Lithuania, the international guidelines on STIs diagnostics and treatment are followed in University hospitals considering all its aspects but at the district level, discrepancies in the adherence to it are common.

ORAL PRESENTATIONS: SESSION 9

OP-30. Immune response after COVID-19 vaccination

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We report a longitudinal analysis of 111 vaccinated individuals for their antibody levels, memory CD4+ and CD8+ T, and spike protein's receptor binding domain (RBD) interaction with the ACE2 receptor up to six months after the third dose of the BNT162b2 vaccine.

We found a robust antibody response to spike protein after the second dose. However, the antibody levels declined at 3, 6 and 9 months post-vaccination, indicating a waning of the immune response over time. At 6 months after the second dose, the spike antibody levels were similar to the levels in persons vaccinated with one dose or in COVID-19 convalescent individuals. The third dose, given 9 months after the second one, restored antibodies to the same level as found after the second dose. After the third dose, the antibody levels declined but less than after the second dose. The booster dose remarkably increased the serum ability to block wild-type or Omicron variant spike protein's receptor binding domain (RBD) interaction with the ACE2 receptor, and these protective antibodies persisted three months later. Three months after the booster dose, memory CD4+ and CD8+ T cells to the wild-type and Omicron variant were detectable in the majority of vaccinated individuals. Our data shows that the third dose restores the high levels of blocking antibodies and enhancing T cell responses to Omicron.

ORAL PRESENTATIONS: SESSION 9

OP-31. Inflammatory response to COVID-19

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Innate immune and inflammatory responses play a major role in the pathogenesis of the COVID-19 disease. In normal conditions, they are necessary for the effective clearance of SARS-CoV-2. However, an uncontrolled pro-inflammatory response results in severe COVID-19 disease, acute respiratory distress syndrome, and cytokine storm.

Quantitative analysis of the cytokines is useful for COVID-19 disease severity and mortality risk evaluation. According to literature data, SARS-CoV-2 infected patients have significantly higher concentrations of interleukin (IL)-6, IL-10, IL-8, interferon (IFN)-γ, tumor necrosis factor (TNF)-α, and monocyte chemoattractant protein (MCP)-1 compared to healthy controls. Severe-critical COVID-19 is discriminated from mild-moderate disease by significantly higher concentrations of IL-6, IL-8, IFN-γ-inducible protein (IP)-10, TNF-a, IL-10, and MCP-1, while COVID-19 patient mortality is associated with significantly higher concentrations of IL-6, IFN-γ, IP-10, and IL-10.

Patients treated in the specialized COVID-19 department of the Hospital of Lithuanian University of Health Sciences Kauno klinikos had significantly higher concentrations of IL-6, IL-10, IFN-γ, and neutrophil-gelatinase-associated lipocalin than healthy individuals. Deceased patients had a significantly higher concentration of IL-6 compared to those who recovered. Regarding routinely performed inflammatory marker assays, severe, critical and deceased COVID-19 patients had significantly higher neutrophil-lymphocyte ratio and ferritin concentration compared to mild-moderate and recovered patients, respectively. Deceased patients additionally had a significantly higher white blood cell count and C reactive protein concentration compared to those who recovered.

To conclude, hyper-inflammation is the main factor influencing COVID-19 disease severity and mortality. IL-6, IL-10, and routinely tested inflammatory markers could be used to predict unfavorable outcomes of COVID-19.

OP-32. Waste water surveillance of infectious diseases

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Traditionally, infectious diseases are monitored based on patient data. This is an expensive approach and might not detect the beginning of epidemics. Infectious agents are released into waste water via feces, urine and saliva. Measuring the signal in waste water can give an estimate of the epidemiological situation in the population. The approach has been used for poliovirus, SARS-CoV2, antibiotic- resistant bacteria, etc. The Estonian experience will be reviewed.

ORAL PRESENTATIONS: SESSION 9

OP-33. Harmonization of electrophoretic investigations in the evaluation of monoclonal gammopathies in Estonia

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Electrophoretic investigation of serum and urine proteins is an important step in the evaluation of monoclonal gammopathies (MGs).

MGs are a group of disorders marked by the proliferation of a single plasma cell clone resulting in an abnormal increase of monoclonal immunoglobulin in the serum and/or urine. The main conditions of MGs are monoclonal gammopathy of undetermined significance (MGUS), multiple myeloma, AL amyloidosis, etc.

The laboratory investigation of MGs consists of serum protein electrophoresis, immunofixation and determination of free light chain ratio in serum. Urine protein electrophoresis and immunofixation may also be needed.

These tests are available only in three laboratories in Estonia. However, the ordering and choice of tests were different between laboratories. Thus, harmonization was needed to ensure the performance of all necessary tests and to avoid the measurement of inappropriate analysis.

We formed a special working group on electrophoretic investigations. In cooperation with hematologists, we developed an algorithm of electrophoretic protein workup. The algorithm was confirmed by the Estonian Society for Laboratory Medicine and the Estonian Society of Hematology in the summer of 2021. According to the algorithm, while ordering an electrophoretic test, a physician must choose from 1 of 4 prearranged standardized clinical indications for the protein electrophoresis: the suspicion or exclusion of MG, treatment response assessment, follow-up and suspicion of the relapse. Based on this information, the laboratory staff add other relevant tests. Common interpretation is made by considering the results of the performed tests. Interpretive comments are also harmonized between laboratories, and relevant retest intervals are recommended.

Implementation of the algorithm has shifted the work in this field to a more systematic and evidence-based approach. Both algorithm and interpretive comments are reviewed and updated periodically.

ORAL PRESENTATIONS: SESSION 10

OP-34. Harmonization of verification in Estonia

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Verification of laboratory methods is a requirement of accreditation. The verification procedure of methods is an important aspect of the quality of tests and patient safety. The aim of this work is to create a guideline to provide support on the use verification to laboratory personnel and accreditation assessors. A working group of quality under the Estonian Society for Laboratory Medicine (ESLM) performed a pilot survey on the present situation of the verification of methods for creating a united guideline for different laboratories. Our recommendation is based on the field of tests and on the hierarchy of models of quality specifications and gives instructions for the estimation of precision and bias separately (table 1 and table 2). Optimum quality specification is based on the Clinical and Laboratory Standards Institute (CLSI) evaluation protocols.

Table 1. Precision estimation.

Number of levels (number of rows); Number of replicate in run (n); Number of runs (n+n+n+n+n)

Field of the test	Optimum	Desirable	Minimum
Clinical chemistry and antigen-antibody methods, quantitative	5+5+5+5+5 5+5+5+5+5	3+3+3+3+3 3+3+3+3+3	2+2+2 2+2+2
Clinical chemistry and antigen-antibody methods, qualitative	3+3+3+3+3 3+3+3+3+3 (3+3+3+3+3, cut-off)	2+2+2 2+2+2 (2+2+2, cut-off)	2+2 2+2
NAT, quantitative	3+3+3 3+3+3 3+3+3, cut-off	2+2+2 2+2+2 2+2+2, cut-off	1+1+1 1+1+1 1+1+1, cut-off
NAT, qualitative and Immunohematology	3+3+3 3+3+3	2+2+2 2+2+2	1+1+1 1+1+1
Flow cytometry	3+3+3 3+3+3	3+3 3+3	3 3 3
Microbiology	3+3+3 3+3+3 3+3+3 3+3+3 3+3+3	3+3 3+3	3 3 3

Table 2. Bias estimation (number of samples)

Field of the test	Optimum	Desirable	Minimum
Clinical chemistry and antigen-antibody methods, quantitative	40	20	6
Clinical chemistry and antigen-antibody methods (qualitative) NAT (quantitative), microbiology	20	10	6
NAT, qualitative	20	6	3
Flow cytometry and immunohematology	10	6	3

According to the ESLM guideline, the laboratories from regional and central hospitals have used optimum or desirable quality specifications, and laboratories from general and local hospitals have used desirable or minimum quality specifications of verification.

ORAL PRESENTATIONS: SESSION 10

OP-35. Harmonisation in satellite labs

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Clinical laboratory testing is changing, as laboratories are no longer working in isolation. We are building regional healthcare networks, which involve different hospitals and local laboratories.

For example, the North Estonia Medical Centre (NEMC) is one of the owners of the Lääne County, Rapla County and Hiiu County hospitals, and the only owner of these three laboratories.

Our vision is to use evidence-based methods in clinical medicine. The level of medical work expresses quality indicators that are comparable with other recognised medical centres in Europe. It also demands laboratory results of equal quality not only in the main lab but also in satellite labs.

Effective patient care and patient safety call for comparability of laboratory results independent of time, place and measurement method. Harmonisation of laboratory medicine refers to our ability to achieve the same result within clinically acceptable limits. It is a great challenge to harmonise the test results between 4 different hospital laboratories. To achieve this goal, we have changed the preanalytical phase, quality control procedures, test menu and reflex testing procedures, but there is still a lot to do.

As harmonisation always changes old habits in small hospitals, one must have good communication with the hospital boards and also with doctors and nurses of the county hospitals.

Our aim is to achieve comparable test results in all our laboratories, as our doctors and patients move between different hospitals and we have to avoid misinterpretation of test results due to different measuring methods and reference intervals.

POSTER ABSTRACTS ORAL PRESENTATIONS

POP-1. Landscape of genetic alterations of Estonian patients with MDS and AML diagnosis

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Myelodysplastic syndromes (MDS) are a heterogeneous group of clonal hematopoietic disorders characterized by cytopenias, bone marrow dysplasia, ineffective haematopoiesis and a high risk of transformation into acute myeloid leukemia (AML). Primary AML (pAML) develops without prior haematological neoplasia; secondary AML (sAML) may develop upon transformation of a previous disease or treatment-emergent AML.

AIM. To find genetic similarities and differences in three groups of disorders (MDS, pAML and sAML)

METHOD. The cohort consisted of patients with diagnosed MDS and AML and treated in the Tartu University Hospital or The North Estonia Medical Centre during 01.01.19-18.05.21. Bone marrow or whole blood was tested using TruSight Myeloid Panel (TSM, Illumina), karyotyping and FISH.

RESULTS. The cohort consisted of 133 patients with findings on TSM analysis, who were diagnosed with MDS, pAML or sAML at the time of analysis. 348 molecular changes and 120 cytogenetical aberrations were identified in the cohort of patients. Alterations in *DNMT3A*, *TET2* and *ASXL1* genes were most common in MDS patients. The most frequently altered genes in pAML patients were *NPM1*, *DNMT3A* and *FLT3*, and in the case of sAML were *TET2*, *RUNX1*, *DNMT3A*. The most common cytogenetic findings in all three groups were 5q and 7q deletions. Both the pAML and sAML groups were defined by the presence of a complex karyotype and by the deletion of the tumor suppressor gene *TP53*.

CONCLUSIONS. The most common molecular pathogenic variants for these three disease groups were alterations in the *DNMT3A* and *TET2* genes and 5q and 7q deletions in cytogenetics. In the MDS group there were more pathogenic variants in the *SF3B1*, *SRSF2* and *U2AF1* genes compared to the pAML and sAML-group. *NPM1*, *FLT3* and *IDH2* genes were most often mutated in the pAML-group, while the sAML-group had the most *KRAS* gene variants. Comprehensive cytogenetic and molecular characteristics are important prognostic indicators in the diagnostics and treatment of MDS and AML.

POSTER ABSTRACTS ORAL PRESENTATIONS

POP-2. Non-polio enteroviruses — are we looking in the right place and quickly enough?

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BACKGROUND. Non-polio enteroviruses (NPEV) mainly cause self-resolving disease, but several are occasionally associated with severe neurological conditions, such as meningitis/meningoencephalitis (M/ME) and acute flaccid paralysis (AFP)/myelitis. NPEVs are transmitted by the fecal-oral and respiratory routes. According to recommendations for NPEV diagnostics published in 2018, these clinical presentations require the collection of not only cerebrospinal fluid (CSF) and blood, but also stool and respiratory specimens.

OBJECTIVES. Analyse specimen types collected by clinicians from cases with clinical presentation of M/ME and AFP/myelitis, submitted for enterovirus detection to the Riga East Clinical University Hospital laboratory from 2019 to 2021 to determine compliance to recommendations and identification of isolated NPEV types.

METHODS. CSF, nasopharyngeal (NP) swabs, stool and blood specimens were subjected to RT-PCR targeting the 5'UTR of the enterovirus genome. For type identification, virus isolation from stool samples was performed in RD cells, followed by a neutralization assay with enterovirus type-specific antisera.

RESULTS. Specimens from 511 cases with M/ME were submitted from 2019 to 2021. 465 CSF specimens were submitted and 6% were positive by RT-PCR. Of 56 NP swabs, 18% were positive, while from 150 stool specimens, 17% were positive. None of the 10 blood specimens were positive. 114 cases of AFP/myelitis were represented by 110 CSF, three NP swabs, 13 stool, and one blood specimen. NPEVs were isolated from 7 cases of M/ME: EV-A71 from 3 cases, Coxsackie B5 from 2 cases, Coxsackie B2 from one case and Echo 14 from one case. The mean duration from specimen collection to NPEV type determination was 23 days. NPEVs were not detected from AFP/myelitis cases.

CONCLUSIONS. The specimen collection pattern is characterized by poor submission of stool and respiratory specimens. The collection of these is crucial for epidemiologically important EV-D68 and EV-A71 detection. NPEVs were isolated from M/ME but not AFP/myelitis cases. More rapid type determination demands the introduction of virus capsid protein gene VP1 sequencing. Awareness of the necessity for respiratory and stool specimen collection from patients with neurological infections needs to be raised.

POP-3. COVID-19: Prolonged viral shedding in an HIV patient

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OBJECTIVES. COVID-19 is a novel infectious disease with an evolving understanding of its epidemiology and clinical manifestations. Immunocompromised patients often present atypical presentations of viral infected diseases. The aim of the study was to show laboratory results for a case simultaneously infected by HIV and the SARS-CoV-2 virus with prolonged viral shedding.

MATERIALS AND METHODS. Nasopharyngeal swabs to detect SARS-CoV-2 RNA by real-time polymerase chain reaction (RT PCR) and Next Generation Sequencing (NGS) to detect variant, serum to detect IgA, IgM, IgG antibodies by ELISA, and nasopharyngeal swab to detect SARS-CoV-2 virus by VeroSlam cell culture.

RESULTS. A 27-year-old woman was hospitalized in the Infectology Centre of Latvia in July with a COVID-19 infection. During the hospitalization, HIV was confirmed with 8 CD4 cells/µl. The first positive RT PCR SARS-CoV-2 RNA test was made on 1st June. Also in July and August (three times), results were positive by RT PCR. The last positive RT PCR test was on 30th September. All nasopharyngeal swabs results were "Detected SARS-CoV-2 RNA (E, RdRP/S, N genes)", and Ct values were between 15 and 26. Five positive nasopharyngeal swabs by RT PCR were sequenced by NGS with the detected B1.17 (alfa) variant. IgA, IgM and IgG antibodies weren't developed. NRL firstly performed cell culture for the SARS-CoV-2 virus and checked it by RT PCR.

CONCLUSIONS. We present a unique case of significantly prolonged viral shedding (122 days) in an HIV-positive patient with acquired immunodeficiency syndrome (AIDS) without antibodies development against the SARS-CoV-2 virus. Cell culture allowed one to understand that it was prolonged viral shedding, and by NGS that it wasn't reinfection by another SARS-CoV-2 virus variant.

COMMERCIAL PRESENTATIONS

CP-1. mTBI – a game-changing assay

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Approximately 2.5 million patients are diagnosed with traumatic brain injury (TBI) in Europe every year (1). The majority (80–90%) of these cases are classified as mild, and only around 10% are likely to have any intracranial lesions visible on a computed tomography (CT) scan (2). However, a CT scan is routinely used in the evaluation of these patients, leading to many unnecessary scans being conducted. Novel blood biomarkers have been developed which can aid in the evaluation of adult mild TBI patients and assist in determining the need for a CT scan. Glial fibrillary acidic protein (GFAP) and ubiquitin C-terminal hydrolase L1 (UCH-L1) comprise a novel Alinity i TBI test panel. Simultaneous below cutoff levels for both biomarkers are associated with the absence of intracranial lesions, and in conjunction with other clinical information, can be used to aid in ruling out the need for a CT scan. Clinical performance of the TBI test was demonstrated in a pivotal study (3). This study analysed 1899 archived (frozen) plasma specimens from mild TBI (GCS 13-15) patients 18 years of age or older who presented at 22 clinical sites across the United States, Germany and Hungary. Subjects had blood drawn within 12 hours of a head injury. Cases were identified as CT positive or negative, as defined by the presence or absence of acute traumatic intracranial lesions visible on a CT scan. 717 out of 1066 CT negative cases turned out to be negative on the TBI test. Hence 40% of CT scans could have been ruled out with the use of the test. The TBI test identified CT-positive patients with a sensitivity of 96.7% (116 out of 120 cases). None of the 4 CT-positive patients with a negative TBI test had lesions requiring neurosurgical intervention. The negative predictive value (NPV) of the test was 99.4% (713 out of 717 test-negative patients were CT negative). High sensitivity and NPV support the clinical utility of the test to assist in determining the need for a CT scan in adult mild TBI patients.

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CP-2. Expediting the diagnosis of myocardial infarction: what role can hs-cTn play at the point-of-care?

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Globally, the demand for quality healthcare services is rising, and as a consequence, so are the costs. Emergency departments (EDs), as the gateway to hospital care, are one of the first to notice this increase in demand and also substantially contribute to the overall costs incurred within the broader healthcare system. Internationally, EDs are overcrowded and are looking for ways to improve their workflow. The efficient management of chest pain patients, who are often times suspected of having acute coronary syndrome (ACS), could play a role in reducing crowding. They form the 2nd largest group of presenters to the ED and, based on the risk for ACS, require a rapid diagnosis.

Hs-cTnI plays a vital role in the diagnosis of MI, as directed by the 4th Universal Definition of Myocardial Infarction (MI), and also can risk stratifying patients. Moreover, the European Society of Cardiology (ESC) promotes the use of rapid algorithms in order to rapidly rule and rule out patients suspected of having an MI. Given that the majority of patients presenting with chest pain do not suffer an MI, nor do they have any underlying cardiac disease, rapid rule out of low-risk patients can have a significant impact. Facilitated by a point-of-care (POC) platform that provides an hs-cTnI result in minutes, rather than hours, fast rule-out and disposition of low-risk patients can potentially play a significant role in the management of chest pain patients. This in itself can contribute to the reduction of ED crowding and thereby help maintain access to healthcare and reduce costs. We examine the analytical and clinical performance data generated for Siemens' hs-cTnI assay on the Atellica VTLi (POC) platform and demonstrate the potential of Atellica VTLi to support in the rapid rule in and rule out of suspected MI patients.

COMMERCIAL PRESENTATIONS

CP-3. Roche cardiovascular disease solutions: helping to solve challenges and unmet needs with high medical value tests

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In 2019, cardiovascular diseases (CVD) accounted for roughly 17.9 million deaths globally. And of 17 million premature deaths (under the age of 70) in 2019, 38% were caused by CVDs. (1) Disease prevalence and treatment costs are escalating, driven largely by population growth and ageing (2). The use of diagnostic tests to assess risk, screen, diagnose and monitor cardiac disease are vital tools in protecting patients and helping save lives. Roche has led the way in cardiac care by developing multiple unique In Vitro Diagnostic Solutions solutions for heart failure (HF), acute coronary syndrome (ACS), and atrial fibrillation (AF) to support diagnosis and clinical decision-making, and improve patient management. In this presentation, we will discuss three key cardiac indications in which the use of blood-based biomarkers plays a pivotal role in the diagnostic and prognostic setting. You will learn what impact Elecsys® immunoassays using the blood-based biomarkers high-sensitive cardiac troponin T (*c*TnT-hs), N-terminal pro-brain natriuretic peptide (NT-proBNP) and growth differentiation factor 15 (GDF-15) have in regards to their utility in clinical practice.

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CP-4. The Roche portfolio of digital solutions connects the healthcare community

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Roche's portfolio of digital solutions combines innovative technologies, with deep analytics and health science expertise. We're empowering lab professionals, clinicians and even patients to make insights-based decisions across their care.

For 120 years, Roche has been rooted in medicine and biology. At our core, we are a healthcare company. In 2018 alone, we performed over 19 billion tests worldwide, and our Pharma group has 3 of the top 5 cancer drugs on the market.

We are moving into this new era of digital, technology, and data. We are bringing to the market our expertise in the clinical decision support space. Digital disruption is transforming every industry, including healthcare. Everyone moved from paper medical records to EMRs and soon, everyone will also be moving from the current time-consuming process of data management to incorporating technology and automation with clinical decision support. At Roche, ewe are bringing healthcare to IT.

At Roche, we see care as a patient-centric discipline, where data connected across systems, providers, and even institutions, can enable insights that improve care for each patient. Historically, healthcare information and delivery have been organized around a disease-centered approach that services individual medical specialties and healthcare professionals. These data sets were traditionally stored in individual silos that were not connected and the individual patient was rather on the outside of the — or at the end of this — process.

We bring together different players to create new digital ecosystems in healthcare — systems that put improved and sustainable patient outcomes at the center. We aim to generate information that impacts patient lives at the point of care, and that improves the delivery of healthcare in sustainable, efficient ways.

Transforming healthcare goes beyond providing digital solutions to changing workflows, roles and responsibilities, laws & regulations, and mindsets.

POSTER PRESENTATIONS

PP-1. Development and analytical validation of LCMSMS method for quantitative determination of five antipsychotic drugs and their metabolites in human plasma samples

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OBJECTIVES. The aim of our work was to develop and analytically validate a liquid chromatography-mass spectrometry-based method for the simultaneous quantification of five antipsychotic drugs (aripiprazole, risperidone, olanzapine, quetiapine and haloperidol) along with their active metabolites (dehydroaripiprazole and 9-OH-risperidone) in human plasma samples.

METHOD. Simple protein precipitation with methanol and consequent sample dilution was chosen as the most convenient sample preparation method. Chromatographic separation was carried out in reverse phase mode on Kinetex® Biphenyl (100 x 2.1; 2.6 µm) column. Samples were eluted by water-methanol gradient, containing 2 mM ammonium formate and 0.002% of formic acid. The overall chromatographic run-time was 8,5 minutes. Positive ion fragments formed with electrospray ionization (ESI) were detected by triple quadrupole mass spectrometer in multiple reaction monitoring (MRM) mode.

RESULTS. The standard calibration curves for each drug consisted of six concentrations, covering the expected sub-therapeutic and therapeutic concentration values. Linearity of calibration curves was acceptable with determination coefficients (r2) greater than 0,999 for all drugs. Intra- and inter-day precision was less than 13.5%, and accuracy ranged between 95.7 – 104.8%. Although a strong matrix effect was observed in the case of some drugs (e.g average of 192,9% in the case of olanzapine), the variance of the matrix effect remained acceptable (CV did not exceed 10%). Mean extraction recoveries ranged from 82/8 – 95.6%.

CONCLUSION. The method is proven to be simple, accurate and precise and is successfully applied in therapeutic drug monitoring of psychiatric patients at Tartu University Hospital.

PP-2. Comparison of fatty acid composition in platelet and erythrocyte phospholipid membranes of healthy individuals

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OBJECTIVES. To analyze and compare the differences of fatty acid (FA) composition in platelet and erythrocyte phospholipid membranes of apparently healthy individuals.

METHODS. FA methyl esters from platelet and erythrocyte phospholipid membranes of 41 apparently healthy individuals (15 men and 26 women, aged 35.5 ± 6.1 years) were identified using gas chromatography/mass spectrometry. Then the composition of platelet and erythrocyte phospholipid membrane FAs was compared.

RESULTS. The total sum of saturated FAs was higher in the platelet phospholipid membrane compared to the erythrocyte phospholipid membrane (med. 91.99 vs med. 85.5, p = 0.00001936) due to C16:0 FA. The level of monounsaturated FAs was higher in the erythrocyte membrane (med. 4.13 vs med. 10.08, p = 0.000002299) with statistically significantly increased percentage of C16:1ω7 (med. 1.05 vs med. 0.495, p = 0.002624), C18:1ω7 (med. 1.2 vs med. 0.58, p = 0.000005827) and C18:1ω9 (med. 6.45 vs med. 2.31, p = 0.000005929) FAs. The total sum of ω3 FAs was also greater in the erythrocyte membrane (med. 0.885 vs med. 0.6, p = 0.002511) due to elevated levels of C20:5ω3 (med. 0.29 vs med. 0.12, p = 0.0001523), C22:5ω3 (med. 0.07 vs med. 0.04, p = 0.001896) and C22:6ω3 (med. 0.11 vs med. 0.05, p = 0.00002438) FAs. But, the ratios of C18:2ω6/C20:4ω6 FAs and C18:3ω3/C20:5ω3 FAs were statistically significantly higher in the platelet phospholipid membrane (med. 4.08 vs med. 2.57, p = 0.002537; med 2.47 vs med. 1.45, p = 0.01209) of healthy individuals.

CONCLUSIONS. Due to significantly higher levels of monounsaturated and polyunsaturated FAs, the erythrocyte phospholipid membrane could be used for an easier evaluation of unsaturated FAs in observed subjects.

POSTER PRESENTATIONS

PP-3. Antibacterial effect of copper oxide containing sol-gel surface coatings against Staphylococcus aureus

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Nanoparticles, ranging in dimensions from 1 to 100 nm, possess unique physico-chemical, optical and biological properties that can be manipulated suitably for desired applications. Currently, the antimicrobial properties of metallic nanoparticles are being explored and investigated. The antimicrobial activity of nanomaterials is known to be due to contact with microorganisms which carries a broad range of probable antimicrobial activity. Surfaces coated with antimicrobial metallic nanoparticles can be used in a wide range of applications, such as water treatment, biomedical and surgical devices, and food processing.

Currently, copper and copper oxide have received growing attention due to their low toxicity, broad spectrum, and reasonable price features. CuO nanoparticles exert antibacterial activity on bacteria – *E. coli* and *S. aureus*.

METHOD. A total of 120 different sol-gel surface coatings deposited onto polished and phosphated AISI 304 steel (10x3 mm) were examined.

Coatings contained 0.5, 1, 2, 3 weight % CuO. The number of deposited layers was 1, 3, and 5. Differentially aged sol-gel coating solutions were used to obtain dip-coating compositions – 1, 8, 15, 22, or 28 days. The antibacterial effect was determined in all samples with the novel dried droplet method using *S.aureus* 6538 strain.

RESULTS. The highest antibacterial effects were against coatings with phosphated steel — on average, 65.2% against 27.1% for polished steel. Phosphated steel coatings with 28 days of aging exerted the highest antibacterial effect on average 95%, with some samples being close to 100%.

CONCLUSION. CuO surface coatings made using the sol-gel method in many cases show high antibacterial effects and could be used in different medical applications.

This study was financed by a local grant of P.Stradiņš Clinical University Hospital – Evaluation of nanostructured stainless steel coating antibacterial effect.

PP-4. Evaluation of NG-test CTX-M and NG-test CARBA5 immunochromatographic assays for rapid detection of CTX-M extended-spectrum beta lactamases and carbapenemases

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OBJECTIVES. Extended-spectrum beta lactamases producing (ESBL) and Carbapenem-resistant *Enterobacterales* (CRE) and other organisms (CRO) are considered a serious threat to healthcare facilities and patients. Fast, rapid detection of ESBL and CRO allows for appropriate antimicrobial therapy, and it allows for better control and a reduction in outbreaks.

METHODS. Since the beginning of the year 2020, 82 samples from all around Latvia were sent to a reference laboratory for ESBL and CRE confirmatory testing. We compared lateral flow immunoassays (NG-test CTX-M and CARBA5) with phenotypic (ROSCO test kits 98008 and 98015) or molecular tests (XPERT CARBA-R) for extended-spectrum beta lactamases producing *Enterobacteracea* (ESBL) and carbapenem resistant *Enterobacteracea* (CRE) detection. Testing was performed in the Riga East University Hospital National Microbiology Reference laboratory of Latvia.

RESULTS. From all samples, 31 were ESBL positive (*K.pneumoniae* – 14, *P.mirabilis* – 6, *E.aerogenes* – 3, *E.cloacae* – 3, *E.coli* -4, *C.freundii* – 1), and 29 samples were CRE (*K.pneumoniae* – 24, *E.coli* -3, *C.freundii* – 1, *S.marcescens* – 1). In 25 ESBL samples, NG-test CTX-M results matched with phenotypic ROSCO 98008 ESBL + AmpC Screen Kit, except in 3 AmpC beta lactamases producing samples where NG-Test CTX-M showed negative results.

All CRE samples were tested with Xpert Carba-R, and 22 of 29 CRE samples were additionally tested with NG-CARBA5 lateral flow assay and the results matched. Both tests detected the five most common carbapenemase families (OXA-48-like, KPC, NDM, VIM and IMP). With both tests OXA-48-like were detected in 13 samples, KPC – 3, VIM – 1 and 2 samples were found with OXA-48-like and NDM carbapenemases. In 17 out of 22 CRE results matched in between NG-Test CARBA5 and phenotypic ROSCO carbapenemases Confirm Kit.

CONCLUSIONS. NG-test CTX-M and NG-test CARBA 5 lateral flow assays are fast and cost-effective assays for ESBL and CRE detection with high-performance compared with more cost and time-consuming molecular tests. Our laboratory will continue to use this test for rapid CRE detection from bacterial colonies.

POSTER PRESENTATIONS

PP-5. Reference intervals for serum trace elements in the Angolan male adult population

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OBJECTIVES. Well-established reference intervals (RIs) are essential for the correct interpretation of individual patient laboratory results. Under ideal conditions, laboratory-specific RIs should be established, which take into account the analytical methodology used and the characteristics of the population covered. The objective of the present work was to establish RIs for serum trace elements in the Angolan male adult population.

METHODS. Serum samples were collected from blood donors who attended the Hospital Militar Principal/IS, Luanda, Angola, from 02.2020 to 07.2020. A total of 139 apparently healthy subjects were included in the study. The mean age was 30.7±8.0 years. Samples were collected into BD Vacutainer® Trace Element Serum tubes. After coagulation, serum was separated into decontaminated Eppendorf tubes. Trace element analysis was performed by inductively coupled plasma mass spectrometry (ICP-MS; Thermo iCAP™ Q instrument) using a validated analytical procedure under strict analytical quality control (Seronorm™ Trace Elements Serum, L-1 and L-2). RIs were calculated according to the Clinical Laboratory Standards Institute (CLSI) EP28-A3c guideline. The Kolmogorov-Smirnov test was used to verify the normality of the data distribution. Tukey's method was used to detect outliers.

RESULTS. The 95% RI (µg/L) obtained were as follows: a) essential trace elements – **Mn**: 0.34-1.41; **Co**: 0.21-0.63; **Cu**: 658-1410; **Zn**: 498-921; **Se**: 85-141; **Mo**: 0.39-2.28; b) non-essential/toxic trace elements – **Li**: 0.57-1.93; **Be**: < 0.03; **B**: 6.4-36.4; **Ni**: 0.57-1.82; **As**: <11.5; **Rb**: 144-338; **Sr**: 26-73; **Cd**: < 0,05; **Sn**: 0.07-0.38; **Sb**: 1.37-2.76; **Cs**: 0.29-1.04; **Ba**: 0.38-2.27; **Tl**: < 0.04; **Pb**: 0.07-0.43; **Bi**: < 0.02. For **Mg**: 14.7-22.7 mg/L.

CONCLUSIONS. RIs have been established for a wide panel of trace elements in the Angolan male adult population, thus providing an important tool for future research studies and the clinical and toxicological laboratory evaluation of individual patients.

PP-6. Case report of macro-AST in an asymptomatic 71-year-old Lithuanian female

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OBJECTIVES. In the absence of signs or symptoms of chronic liver disease, and cardiac or skeletal abnormalities, isolated aspartate aminotransferase (AST) elevation is indicative of macro aspartate aminotransferase (macro-AST). Misdiagnosis of this benign condition could lead to highly unnecessary and invasive procedures, such as liver biopsy, which may cause complications in patients and additional costs for the hospital.

METHODS. We report the first described case in Lithuania of macro-AST in an asymptomatic 71- year-old female, referred to a gastroenterologist because of isolated elevation of AST, resulting in a diagnostic dilemma. AST activity in serum was evaluated spectrophotometrically using an enzymatic IFCC (NADH, pyridoxal-5'-phosphate) method. The sample was also assessed for the presence of macro-AST using a polyethylene glycol precipitation (PEG) assay. In short, 25% PEG solution was mixed with the patient's serum in equal parts and vortex mixed for 1 minute. After mixing, centrifugation was performed at 3000 rpm for 10 minutes. Finally, the supernatant was carefully removed from the precipitate and used for post-PEG AST activity assay.

RESULTS. The patient's AST activity was 653 U/l. Post-PEG precipitation AST activity was 10 U/l. AST PEG recovery was 1.78% and PEG precipitation activity (PPA) was 98.22%. Post-PEG precipitation AST activity, PEG recovery and PPA results indicated the presence of macro-AST.

CONCLUSIONS. This case report highlights the presence of macro-AST in an asymptomatic 71- year-old Lithuanian female and demonstrates the importance of clinical laboratory in diagnosing this rare and usually benign condition. PEG assay is a simple, rapid and low-cost method that could be extremely useful for macro-AST screening. Timely detection of macro-AST allows for a reduction in the number of unnecessary procedures, testing and costs in a hospital setting.

POSTER PRESENTATIONS

PP-7. The effect of repeated blood donation on serum trace element status — a cross-sectional study in Angolan donors

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OBJECTIVES. Except for iron, there is a great paucity of data on the effect of repeated blood donation on trace elements status. The aim of this study was to assess the effect of repeated blood donation on serum trace element levels.

METHODS. The study was carried out with samples collected from apparently healthy adult blood donors at Hospital Militar Principal/IS, Luanda, Angola, from 02.2020 to 07.2020 (n = 164; 30.8±7.7 years old). Samples were collected into BD Vacutainer® Trace Element Serum tubes. After coagulation, serum was separated into decontaminated Eppendorf tubes. Trace element determination (Li, Be, B, Mg, Mn, Co, Ni, Cu, Zn, Se, As, Rb, Sr, Mo, Cd, Sn, Sb, Cs, Ba, Tl, Pb, Bi) was performed by inductively coupled plasma mass spectrometry (ICP-MS; Thermo iCAP™ Q instrument) using a validated analytical procedure, under strict analytical quality control (Seronorm™ Trace Elements Serum, L-1 and L-2). Tukey's method was used to detect outliers. The Shapiro-Wilk test was used to verify the normality of the data distribution. ANOVA and Kruskal Wallis tests (for normal or non-normal distributions, respectively) with Bonferroni correction were used to determine if there were significant differences between groups.

RESULTS. According to the answers to a written questionnaire, patients were divided into 4 groups: First-time donors (group I) and one (group II), two (group III) or ≥3 (group IV) blood donations in the last 3 years. No statistically significant differences were observed between the four groups.

CONCLUSIONS. Repeated blood donation does not appear to significantly affect the serum status of trace elements, in particular with regard to the most important essential trace elements.

PP-8. Comparison of Abbott CMIA and EUROIMMUN ELISA Anti-SARS-CoV-2 IgG Results

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OBJECTIVES. A variety of different anti-SARS-CoV-2 IgG antibody tests are already available in medical laboratories worldwide, and it is quite difficult to compare obtained results due to the diversity and lack of standardization.

METHODS. The study included 16 serum samples of patients vaccinated against COVID-19 with different kinds of vaccines and their combinations. Two commonly used anti-SARS-CoV-2 IgG spike protein antibody quantitative assays (Abbott Chemiluminescent Microparticle Immunoassay (CMIA) and EUROIMMUN ELISA) were evaluated for correlation.

RESULTS. SARS-CoV-2 IgG antibody results of Abbott CMIA and EUROIMMUN ELISA assays demonstrated a good correlation (r = 0.7902) between obtained results among patients. Only one sample showed discordant results, respectively; CMIA displayed positive (68 AU/mL; cut-off value is 50 AU/mL), but ELISA – a negative (0.7 ratio; cut-off value is 0.8 ratio) result.

CONCLUSIONS. Anti-SARS-Cov-2 IgG spike protein antibody results correlate between Abbott CMIA and EUROIMMUN ELISA assay, despite the lack of standardization of these assays. However, more studies with a wider range of participants need to be carried out to fully demonstrate and prove this correlation, also considering each patient's history of vaccination against COVID-19 and possible COVID-19 infection in their medical history.

POSTER PRESENTATIONS

PP-9. Experience of using automation for management of self-sampling kits in E.Gulbja laboratory

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OBJECTIVES. The goal was to introduce an automated and effective solution for the management of self-collected samples. E. Gulbja Laboratory collected the data of using automated self-sampling kit collection from 1st January 2021 until 31st December 2021. We have formulated conclusions about the data and the use of automation in self-sample kit collection.

MATERIALS AND METHODS. E. Gulbja Laboratory collected data about SARS-CoV-2 saliva sample kit collection in automated devices, average processing time between sample collection and result reception by the patient, proportion of positive tests, the age distribution of patients who used automated collection devices, and the ratio of sample kits that were collected outside of regular working hours (20:00 – 08:00).

RESULT. Results were collected from 18 automated (contactless) sample collection devices used by E. Gulbja Laboratory. 64,257 saliva kits for SARS-CoV-2 PCR testing were conducted, and 3.92% of them were positive (SARS-CoV-2 virus RNA found in saliva sample). The average processing time in automated devices located in the capital city was 11.13 hours, in the suburbs — 15.52 hours, and the rest of the country —17.60 hours. The average age of patients that chose an automatic device to hand in their saliva sample kits was 33.94 years.

CONCLUSIONS. By using automated devices, patient contacts were decreased, and direct communication with medical staff was excluded, which reduced the risk of infection during processing.

Automated devices make sample kit distribution available 24 hours. It saves workforce resources in the laboratory that are already very limited, especially during a pandemic.

PP-10. The prevalence and age distribution of high-risk human papillomavirus (HPV) among cervical cancer screening patients in East-Tallinn Central Hospital

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OBJECTIVES. Cervical cancer is one of the most common female cancers in Estonia. In order to improve the detection of cervical cancer and precancerous conditions, Estonia switched from cytology-based screening to HPV-based screening of cervical cancer in January 2021. Women aged 30-65 years are invited for screening at five-year intervals. In this study, we evaluate the prevalence of high-risk HPV and its distribution in different age groups among women who have been screened in our hospital.

METHODS. The study included all women whose cervical specimens had been tested for high-risk HPV under cervical cancer screening from January 2021 to April 2022 in the laboratory of East-Tallinn Central Hospital. Cervical samples were collected into vials with ThinPrep Preservcyt solution (Hologic, Inc USA). HPV was tested by real-time PCR using the cobas 4800 system (Roche Diagnostics GmbH, Germany). The method genotypes HPV16 and HPV18, and detects other 12 high-risk HPV genotypes (31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, 68) as a pool. Results were calculated for the entire study group and separately for 8 different age groups with 5-year intervals according to screening coverage.

RESULTS. A total of 7769 women were included. The overall prevalence of high-risk HPV in the study group was 8.3%. The frequency of HPV16 and HPV18 was 1.5% and 0.6%, respectively. The age-specific prevalence was significantly higher in the age groups 30 and 35 years, 14.2% and 10.3%, respectively, and it decreased to 5.7-8.0% in women aged 40-65 years. The prevalence of HPV16 was highest in 30-year-olds, at 3.8%, accounting for 27.2% of all HPV-positive cases in this age group.

CONCLUSIONS. The overall prevalence of high-risk HPV among screening patients was approximately as expected from the data of other European countries. The detection rate was highest among the youngest age group, and it decreased with age. Hopefully, future studies will evaluate the benefit of HPV-based screening in our country.

POSTER PRESENTATIONS

PP-11. Validating the Roche Cobas serum haemolysis index for the assessment of plasma cell-free haemoglobin concentration

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OBJECTIVES. Plasma cell-free haemoglobin (P-Hb) can be used in the early detection of haemolysis in patients on extracorporeal membrane oxygenation as well as in some haematological diseases. However, an automatic method for P-Hb measurement that is suitable for routine use was missing in our laboratory until now. Roche Cobas 6000 c501 Serum Indices Gen.2 H-index (H-index) is intended to check the haemolysis in patient samples as part of a preanalytical assessment of sample quality. It is easily performed around the clock. The purpose of this study was to validate the H-index for the measurement of P-Hb concentration.

METHODS. Random blood samples were collected and haemolysed. Haemoglobin concentration was measured with Sysmex XN, and hemolysate was diluted to target concentrations of 50, 100, 200, 500, and 10000 mg/L. The linearity was checked at this concentration range. For precision, samples were measured twice a day for 10 days at each level. The accuracy was evaluated by comparison with the conventional spectrophotometric method on Genesys 150 (Gen), and additionally by using the external quality assessment (EQA) scheme.

RESULTS. The H-index was linear over a range of 50-10000 mg/L (y=1.0628x-10.989; r=0.9999). The within-run and total coefficients of variation were 0.5-15.9% and 0.8-18.4%, respectively, with the lower CV at the highest concentration. The differences between the means of H-index and Gen were lower than 1SD of the Gen method at each level indicating that there was no systematic bias between the methods. The difference with the EQA group mean was 1.2%. The CV at the Roche H-index lower limit of detection of 50 mg/L was 18.4%. The lower limit of quantitation was 100 mg/L with a CV of 7.7%, and this was set as a clinically relevant decision limit.

CONCLUSIONS. Roche Cobas haemolysis index check function meets the analytical requirements to measure P-Hb in clinically relevant concentrations in our laboratory.

PP-12. Increasing incidence and antimicrobial resistance amongst nosocomial isolates in Latvia poses a significant public health challenge

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OBJECTIVES. Nosocomial infections or healthcare-associated infections (HAIs) are defined as hospital-acquired infections in patients who were previously free from infection at the time of admission to a hospital. They are associated with increased complications, costs, and prolonged hospitalization durations. Hence, it is essential to observe and manage the situation as it evolves. To achieve this, constant surveillance and monitoring of the trends of isolation, antimicrobial properties, etc., and of nosocomial infections should be done. Therefore, in the present study, we investigated the incidence of antimicrobial resistant strains of the most important nosocomial pathogens in a hospital in Latvia from 2020–2021.

METHODS. The data regarding antimicrobial resistance, patient sample of isolation, and department of isolation were obtained from the Joint Laboratory digital records (anonymized before processing). Antimicrobial resistance was checked using disk diffusion, and broth dilution based on the latest EUCAST guidelines. The data was compiled and analyzed using SPSS version 27.0.

RESULTS. There was a significant increase in the isolation of Carbapenem-resistant Enterobacteria species between 2020 and 2021 ($p < 0.05$), especially *K. pneumoniae*, *E. coli*, and *C. freundii*. Most samples were isolated from urine and faecal matter samples amongst patients admitted to an intensive care unit. Similar observations were made for Vancomycin-resistant Enterococcus, with *E. faecium* being the most commonly isolated species from urine and faecal matter samples. Most of the Vancomycin-resistant Enterococcus infections were reported in nephrology, gastroenterology, and intensive care units. There was a decrease noted in the incidence of MRSA (Methicillin-resistant Staphylococcus aureus) isolates between 2020 and 2021. The majority of the samples were isolated from bronchial wash and nasal swab. Vascular surgery and intensive care units were the two departments with the highest caseload of MRSA infections in the hospital. Finally, amongst the extended-spectrum beta-lactamase (ESBL) Enterobacterales, *E. coli*, *P. mirabilis*, and *K. pneumoniae* were the most isolated pathogens. They were commonly isolated from urine samples from patients admitted to the intensive care unit and gastroenterology departments.

CONCLUSIONS. Vigilant monitoring and implementation of proper precautions and biosafety protocols are essential in reducing the incidence of antimicrobial-resistant nosocomial strains.

POSTER PRESENTATIONS

PP-13. Proteomic and biochemical analysis of extracellular vesicles isolated from the blood serum of patients with melanoma

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OBJECTIVES. Extracellular vesicles (EVs) have the potential as new tumor markers that could be used as diagnostic and prognostic markers for the early detection of melanoma.

METHODS. In this study, EVs were purified from the blood serum of melanoma patients using two methods – ultracentrifugation (UC) and PEG precipitation – and analyzed by mass spectrometry and immunoblot.

RESULTS. We identified a total of 585 unique proteins; 334 proteins were detected in PEG-precipitated samples and 515 in UC-purified EVs. EVs purified from patients varied in size and concentration in different individuals. EVs obtained from stage II and III patients were, on average, smaller and more abundant than others. A detailed analysis of three potential biomarkers — SERPINA3, LGALS3BP, and gelsolin was conducted. SERPINA3 has been shown to correlate with worse patient outcomes, as it has pro-migration and pro-invasion functions in melanoma cells. LGALS3BP promotes integrin-mediated cell adhesion and may stimulate host defense against viruses and cancer cells. Gelsolin has been shown to occur in acidic exosomes, and its expression is highest in metastatic melanoma patients. The analysis revealed that the expression of SERPINA3 and LGALS3BP was higher in melanoma patients than healthy controls, while gelsolin exhibited higher expression in healthy controls.

CONCLUSION. We suggest that all three proteins might have the potential to be used as biomarkers, but a number of issues, such as purification of EVs, standardization, and validation of methods suitable for everyday clinical settings, still need to be addressed.

PP-14. Trends in the prevalence and antibiotic susceptibility of anaerobic gram-negative bacteria causing clinical infections in Estonia

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OBJECTIVE. The aim of our study was to describe the species distribution and changes in the resistance profile of anaerobic bacteria isolated at Tartu University Hospital.

METHODS. We retrospectively analysed the data for 2010 and 2020. The strains were identified by Vitek2 (2010) and MALDI-TOF MS (2020), and the MIC values for the antibiotics were determined using gradient tests. Resistance was interpreted using EUCAST breakpoints.

RESULTS. The number of anaerobic cultures increased from 1,551 to 5,983, an additional 4,432 cultures per 10 years. The percentage of positive cultures did not differ significantly, being 12.5% and 10.4%, respectively.

In 2010, we detected 139, and in 2020, 490 different gram-negative anaerobe isolates. The most common pathogens were gram-negative anaerobic rod-shaped bacteria (*Bacteroides fragilis, Bacteroides spp., Fusobacterium spp.* and *Prevotella spp.*). The percentage of susceptible strains in the two years studied was similar, but there were significant differences in the MIC values ($p < 0.05$) for metronidazole, penicillin and cefoxitin in *Prevotella spp.*, which were higher in 2020 than in 2010. In contrast, the MIC values were lower in 2020 than in 2010 for *Fusobacterium spp.* (ampicillin-sulbactam, imipenem, penicillin, cefoxitin, clindamycin) and for *Bacteroides spp.* (imipenem).

CONCLUSIONS. There was no shift in the spectrum of microbial groups as causative agents of clinical infections during the 2010–2020 period, but due to the improvement of identification methods, the number of identified species increased. The resistance pattern of anaerobes was stable, but the changes in MIC values may indicate a further steady increase in resistance as well as sensitivity. The link between the use of antibiotics and the development of resistance is difficult to prove due to the short period of time and relatively limited data. The surveillance of antibiotic resistance of anaerobes is important to predict the efficiency of empirical treatment.

POSTER PRESENTATIONS

PP-15. A comparison of two methods — MYCOPLASMA IST3 and multiplex PCR — for the detection of urogenital mycoplasma

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BACKGROUND. Genital mycoplasmas, including *Mycoplasma genitalium, M. hominis* and *Ureaplasma spp.* are potentially pathogenic bacteria that frequently colonize the genitourinary system of sexually active individuals. Infections by these bacteria can lead to genital infections as well as undesirable sequelae during pregnancy, genitourinary tract, reproductive failure, and neonatal morbidity and mortality. Infection with genital mycoplasmas has been linked with infertility.

OBJECTIVES. To compare parallel testing results for the detection of urogenital mycoplasma by two different methods – MYCOPLASMA IST3 and multiplex PCR.

MATERIAL AND METHODS. Clinical samples were obtained from patients visiting the Latvian Centre of Infection diseases outpatient department at the Riga East University Hospital. Samples were collected through regular screening or for confirmation of urogenital mycoplasma diagnosis in 2021. MYCOPLASMA IST 3 is a manual qualitative and semi-quantitative in vitro diagnostic test for the culture, identification, indicative enumeration and antibiotic susceptibility testing of genital mycoplasmas. Standard multiplex PCR (Allplex STI7, Seegene) following DNA extraction from the modified amies transport medium, specimens were subjected to a multiplex PCR assay for the detection of genital mycoplasmas.

RESULTS. A total of 1,073 samples were analyzed. 676 (63%) of tested samples were negative, and 397 (37%) of tested samples were positive for urogenital mycoplasma infection. 300 (76%) were *Ureaplasma spp.* positive, 60 (15%) were *Mycoplasma hominis* positive and 37 (9%) were *Ureaplasma spp.+Mycoplasma spp.* positive. Results demonstrated 100% conformity of two methods – MYCOPLASMA IST3 and multiplex PCR – used for the detection of urogenital mycoplasma.

CONCLUSIONS. MYCOPLASMA IST3 and multiplex PCR methods are recommended for detecting a urogenital mycoplasma infection separately or together.

PP-16. Comparison of new sepsis marker "monocyte distribution width" (MDW) against routinely used inflammation markers

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When a septic patient arrives at the emergency room (ER), time is of the essence. Evaluation based on vital signs, SOFA scores, SIRS criteria, and different laboratory analytes allows for the identification of the majority of cases. That leaves a handful of patients that go misdiagnosed or who need a more thorough investigation. Monocyte distribution width (MDW) is a new sepsis marker that could increase the likelihood of recognizing septic patients. It's included in every complete blood count with differential (CBC-DIFF) report and therefore is readily available and doesn't add extra costs.

OBJECTIVES. To verify the validity of MDW as an early sepsis biomarker in Pauls Stradinš Clinical University Hospital (PSKUS).

METHODS. We performed retrospective comparative result analysis for patients that were hospitalized in PSKUS from 15.03 until 21.04.2022 and for whom in the ER phase, the following tests were performed – CBC-DIFF with MDW, C reactive protein (CRP), procalcitonin (PCT) and subsequent blood culture (BC). Based on BC results, they were sorted into groups of positive or negative results. Mean results for white blood cell count (WBC), CRP, PCT and MDW were determined and comparisons were made.

RESULTS. In the BC positive group (n = 13) the mean results were as follows —WBC 13.6 x109, CRP 155.7 g/L, PCT 10.41 ng/mL and MDW 28.15 units. Results in a BC negative group (n = 27) – WBC 11.35 x109, CRP 129.36 g/L. PCT 5.29 ng/mL and MDW 26.21 units. Values in the BC positive group compared with the culture-negative group were larger by — WBC 16.5%, CRP 16.9%, PCT 49.2% and MDW 6.9%.

CONCLUSIONS. In the BC positive group, all selected analytes were greater than in the BC negative group. MDW shows some positive correlation if used on its own, but its predictive value increases if used in combination with other routinely used inflammation markers. As sepsis can occur without positive BC and SIRS criteria includes not only elevated but also decreased WBC count, a comparison could be misleading and MDW offers more value than meets the eye.

POSTER PRESENTATIONS

PP-17. EQA for FIT point-of-care tests (POCT) – should preanalytics be included?

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OBJECTIVES. Colorectal cancer is a common cancer and cause of death worldwide. Screening is done with fecal immunochemical tests (FIT) detecting human hemoglobin, and there are several tests on the market. The results are used for diagnosing patients, and they should be correct and monitored with quality assessment procedures. Labquality has organized a quantitative fecal blood program since 2020. We present results from 8 EQA rounds, including either liquid samples monitoring the analytical phase or lyophilized fecal samples monitoring both the preanalytical and analytical phase.

METHODS. Participant results with method information were gathered. For this study, only POCT with a total of >30 results with at least 2 results per round were included. Samples were pretested using QuikReadGo iFOB (Aidian). Results were compared within method groups using the method mean as the target value. Lyophilized fecal samples were used on 2 rounds and liquid samples on 6 rounds.

RESULTS. There were 152 to 313 participants in each round, distributed in 5 different method groups, with QuikReadGo iFOB representing the largest group. All methods performed better with liquid than lyophilized samples. The results outside the method groups' own target area were smaller for liquid than lyophilized samples. There were 3 to 6-fold differences in the lyophilized sample results, ranging from 10 to 179 µg/g in the different samples. For low concentration lyophilized samples, interpretations varied a lot between and within the method groups. For the higher concentration lyophilized samples, 67 to 100 % interpreted them as positive within the method groups.

CONCLUSION. Based on our results, differences between method groups and interpretations exist. Our results show that there is more variation when EQA samples, including preanalytical steps, are used. When patient samples are analyzed, the preanalytical phase is often performed by the patient, however, the EQA process should also include the extra analytical phases.

PP-18. Laboratory experience in massive SARS-CoV-2 mutation screening using laboratory-developed tests

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OBJECTIVES. The main goal of the study was to develop laboratory-developed tests (LDT) for monitoring SARS-CoV-2 variants of concern (VOC) currently present in Latvia.

METHODS. We have studied the latest scientific articles to prognose specific mutations that could be indicators of VOC. Mutations responsible for immune escape were chosen as targets for our LDTs. Multiple TaqMan RT-PCR LDTs detecting alfa, beta, gamma, delta and omicron strains in nasopharyngeal swab and saliva samples were developed and validated in our laboratory.

RESULTS. More than 15,000 SARS-CoV-2 positive samples were tested. In total, 10,874 different VOCs of SARS-CoV-2 were found by our LDTs. Beta, delta and omicron strains were first detected in Latvia by E. Gulbis Laboratory. Sanger sequencing methods for RT-PCR result confirmation were also developed. The first cases of VOCs detected by the RT-PCR method were also confirmed in our laboratory by Sanger sequencing. Our results were later confirmed by the National Reference Laboratory.

CONCLUSIONS. Using our laboratory capacity and intellectual potential, we have developed skills for an urgent response to future VOCs of SARS-CoV-2 or other potentially harmful infectious diseases.

POSTER PRESENTATIONS

PP-19. The spread of SARS-CoV-2 Omicron (B.1.1.529) variant and its subtypes in Latvia in 2021/2022

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OBJECTIVES. Due to the rapid spread of the SARS-CoV-2 Omicron variant (B.1.1.529) in Latvia at the end of 2021 and the beginning of 2022, it has become essential to determine the rate of its epidemiological spread and the rate of its dominance over the SARS-CoV-2 Delta variant (B.1.617.2).

The aim of the study was to determine the rate of Omicron variant prevalence in Latvia and, at the same time, differentiate Omicron subtypes BA.1 (variant B.1.1.529.1) and BA.2 (variant B.1.1.529.2).

METHODS. The presence of the SARS-CoV-2 virus in nasopharyngeal and oropharyngeal swab samples was determined by RNA extraction and reverse transcription polymerase chain reaction. Altogether 36,719 samples were tested for mutations E484A, N501Y and deletion 69/70del. The RNA was extracted by fully automated nucleic acid extraction device Seegene NIMBUS and using STARMag 96 X 4 Universal Cartridge Kit (Seegene Inc.) reagents. For the RT-PCR reaction, the *Novaplex™* SARS-CoV-2 *Variants VII Assay* (Seegene Inc.) reagent kit was used. The RT-PCR test kit can determine SARS-CoV-2 Omicron variant specific mutations (E484A and N501Y) as well as deletion 69/70del, with which it is possible to determine the sample affiliation to the Omicron subtypes BA.1 (with the deletion) or BA.2 (without the deletion).

RESULTS. SARS-CoV-2 Omicron variant (B.1.1.529) became a dominant SARS-CoV-2 virus variant within 10 weeks in the territory of Latvia. Its presence in the population in the 48th week of 2021 was determined as 2% and in the 5th week of 2022 hit the rate of 98%. The highest increase took place in the first and second week of 2022 with an overall increase rate of 17%. The change of SARS-CoV-2 Omicron (B.1.1.529) subvariant BA.1 to BA.2 was found to happen within 6 weeks. The spread of the BA.2 subtype in the population in the 52nd week of 2021 was at the rate of 12%, however, in the 5th week of 2022, it hit almost 100%. The BA.2 subtype became a dominant subvariant in the 2nd week of 2022.

CONCLUSIONS. The SARS-CoV-2 Omicron variant (B.1.1.529) became a dominant variant of the virus in the population of Latvia at the end of 2021 and the beginning of 2022. The rapid spread of the Omicron variant can be associated with its high infectivity.

PP-20. Towards precision medicine in the health of women – BRCA related ovarian pathology

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OBJECTIVES. The application of personalized medicine in oncology has expanded the use of novel technologies for obtaining genomic data with the aim of providing predictive information and tailoring individualized therapies. Genetic screening for BRCA gene status in patients with primary ovarian cancer has the potential to significantly impact cancer risk management and subsequent treatment options. The Estonian example of freely available genetic screening for ovarian cancer has already become a routine practice, which has enabled patients to receive targeted cancer treatment. In Latvia, next-generation sequencing is a relatively new approach in clinical genetics, and due to the lack of information on the BRCA gene status in the Latvian population, more attention should be paid to the obtained results.

METHODS. From 117 ovarian cancer patient FFPE samples (biopsies or operation material), DNA libraries were constructed using QIAseq Breast Cancer Panel followed by sequencing on the Illumina NextSeq 550 platform. Allelic variants were obtained with QIAGEN CLC Genomics Workbench and interpreted with QIAGEN Clinical Insight.

RESULTS. Pathogenic BRCA1/2 mutations were identified in 44% of tested ovarian cancer patient samples. The most frequent allelic variants were: c.4035del, c.5117G>A, c. 5266dupC, c.1961delA for BRCA1 gene and c.1813delA, c.9097delA for BRCA2 gene.

CONCLUSIONS. We observed a relatively high incidence of pathogenic BRCA1/2 mutations in tested samples compared to other European countries, which could be partially explained by not differentiating between somatic and germline allelic variants, and primary and recurrent cases. As some of the BRCA1/2 gene allelic variations are classified as germline, genetic counseling would be preferable, followed by confirmatory germline BRCA testing for the patient and their family members. Consideration should be given to following Estonia's example by including BRCA germline screening for ovarian cancer patients or women in high-risk groups as a basic diagnostic step, given the high incidence of pathogenic BRCA1/2 mutations in the primary data set. Further studies of BRCA prevalence in the Latvian population are warranted.

POSTER PRESENTATIONS

PP-21. *Aspergillus* antigen detection two years before (2018–2019) and during the COVID-19 pandemics (2020–2022) in Latvia

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OBJECTIVES. Aspergillus infection usually starts in the lungs as the port of entry following inhalation of Aspergillus spores which are present in the environment. Invasive forms, which have been on the increase for the past 10 years, constitute the most serious infections. They mainly occur in neutropenic patients, patients with a severe lung condition, and patients treated with immunosuppressants and corticosteroids. The diagnosis is often based on nonspecific diagnostic or radiological evidence (clinical symptoms, computed tomography scan, chest x-ray, etc.). The test for soluble galactomannan antigen in serum and bronchoalveolar lavage (BAL) appears to be a serological method able to aid in the diagnosis of Invasive Aspergillosis.

The aim of the study was to analyse *Aspergillus* Ag detection in NRL of Latvia during 2018-2019 and in 2020–2022 (until May).

METHODS. In 2018-2019, 680 samples, and in 2020–2022 (until May), 2285 samples were tested in the NRL of Latvia to detect *Aspergillus* Ag by ELISA FungiXpert Aspergillus Galactomannan testsystem (Genobio, Germany). The sample's materials were blood serum and BAL.

RESULTS. We obtained 80/680 (11.8%) positive *Aspergillus* Ag results in 2018-2019 and 376/2285 (16.5%) in 2020–2022 (until May). The male/female ratio was 48/32 (2018-2019) and 225/151 (2020-2020(until May)). The age ranged from 1 month to 80 years, with a median age of 54 years (2018-2019) and 1 month to 91 years, with a median age of 57 years (2020-2022(until May)). Of the total, 16.2% (13/80) were children (aged 1 month -17 years) and 83.8% (67/80) were adults (aged 18-80) in 2018-2019 and 19.9% (75/376) were children (aged 1 month - 17 years) and 80.1% (301/376) were adults (aged 18-91) in 2020-05.2022. The analysis of data showed that 35% (28/80) positive *Aspergillus* Ag was detected in BAL and 65% (52/80) in blood serum (2018-2019) and 28.2% (106/376) in BAL and 71.8% (270/376) in blood serum (2020-2022(until May)).

CONCLUSIONS. During the COVID-19 pandemics, *Aspergillus* Ag testing increased by 236% and positive cases by 370%. *Aspergillus* Ag testing and positivity increased due to patients with a COVID-19 infection, especially those in intensive care departments, who were on steroid therapy and lung ventilation. The age range was similar in the two periods, but the male/female ratio was 3:2. *Aspergillus* Ag test has the potential to overcome invasive aspergillosis detection on time, and the results allow clinicians to start appropriate therapy.

POSTER PRESENTATIONS

PP-22. Identification and comparative testing of pneumonia agents using molecular and microbiological identification methods

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OBJECTIVES. The aim of the study was to identify and compare bacterial and viral pneumonia agents in the study material using molecular and microbiological methods.

MATERIALS AND METHODS. In the study, patients' lower respiratory tract materials were tested on various pneumonia agents using molecular and microbiological examination methods. Molecular sample testing was performed using multiplex PCR - BioFire "FilmArray Pneumoniae Panel plus".

For microbiological examination, the test material was inoculated onto various selective media. The identification of grown microorganisms was made using their biochemical properties and automated identification systems.

RESULTS. In the examination of 9 patients' lower respiratory tract specimens, one was tracheal aspirate, and eight were bronchoalveolar lavage.

A complete match of results with molecular and microbiological methods was observed in three samples (33.33%), a partial match of results was observed in two samples (22.22%), while in four samples, the results were an absolute mismatch (44.44%).

Bacteria with a DNA concentration of 10^4 copies/ml were identified in four samples by molecular analysis but were not identified by microbiological methods.

DNA from more than one bacterium was identified in two samples by molecular analysis. In these samples, bacteria with a concentration of more than 10^7 copies/ml were also identified by microbiological methods, while bacteria with a concentration of 10^4 copies/ml could not be identified by microbiological methods.

CONCLUSIONS. A complete match between the results of the BioFire "FilmArray Pneumoniae Panel plus" and the microbiological identification method was observed in 33.33%.

The discrepancy between the results of microbiological and molecular tests can be explained by the higher sensitivity of molecular methods and the possible influence of various preanalytical factors on the bacterial growth process.

PP-23. CD8+ B cells in marginal zone lymphoma: a rare case report

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OBJECTIVES. Here we present a rare case of marginal zone lymphoma with aberrant CD8 expression on B cells.

METHODS. A peripheral blood sample from an 81-year-old patient with a history of lymphadenopathy was received for a differential diagnosis of lymphocytosis. Flow cytometry was used to evaluate B cell, T cell, T helper (Th), T cytotoxic (Tc) cell and natural killer (NK) cell counts. Afterwards, an expression of commonly used markers for lymphoid malignancies was determined: surface kappa, lambda, CD19, CD20, CD22, CD5, CD23, CD10, CD103, CD11c and CD200.

RESULTS. Full blood count revealed absolute lymphocytosis 4.1 x109/L, normochromic normocytic anemia and trombocytopenia. Lactate dehydrogenase was within the reference range (220 U/L), but beta-2 microglobulin — significantly elevated (11.0 mg/L, reference range 1.09 – 2.53 mg/L). Lymphocyte subpopulations showed elevated B cells (967 cells/mkl), T cells (2944 cells/mkl), Th (1538 cells/mkl), Tc cells (1650 cells/mkl) and within reference range NK cells (194 cells/mkl). Unexpectedly, the B cell population showed co-expression of CD8 antigen. Analysis of the B cells' clonality established monoclonal B-cell lymphocytosis with 97% of B cells with lambda light chain restriction. Further phenotyping eventually showed clone $CD19^{hi}CD20^{hi}CD22^{+}CD5^{dim}CD23^{+}CD200^{+}CD11c^{+}CD38^{+}s\lambda^{hi}$ without expression of CD103 or CD10. A review of lymph node biopsy confirmed the diagnosis of marginal zone lymphoma.

CONCLUSIONS. In this case report, we show CD5, CD23, and CD200 expression in marginal zone lymphoma, demonstrating the need for careful phenotype evaluation not to confuse it with chronic lymphocytic leukaemia. Moreover, aberrant expression of T cell marker CD5 is quite common on mature B cell lymphomas, but phenotype with CD8 positivity is strikingly rare.

POSTER PRESENTATIONS

PP-24. The characterisation of residual non-malignant B cell populations in chronic lymphocytic leukaemia

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OBJECTIVES. The aim of this study was to characterise the residual non-malignant peripheral blood (PB) B cell compartment in chronic lymphocytic leukaemia (CLL) patients compared to B cell populations in healthy controls (HC).

METHODS. PB mononuclear cells were isolated from untreated (newly diagnosed and watch-and-wait, n = 6) or chemotherapy-receiving (n = 5) CLL patients and HCs (n = 7). B cell immunophenotyping with flow cytometry was done using monoclonal antibodies against cell surface markers CD19, CD5, CD27, IgD, CD38, and CD24. Non-malignant B cells were defined as $CD5^{-}CD19^{+}$ among viable lymphocytes. From these, we established the frequencies of antigen-inexperienced B cells ($CD27^{-}IgD^{+}$), including transitional ($CD24^{hi}CD38^{hi}$) and mature naïve ($CD24^{int}CD38^{int}$) B cells. We also determined the composition of the 'memory' B cell compartment – unswitched ($IgD^{+}CD27^{+}$), switched ($IgD^{-}CD27^{+}$) and double negative ($IgD^{-}CD27^{-}$) B cell subpopulations. Data analysis was done with FlowJo and GraphPad Prism software version 9.2.0.

RESULTS. The frequency of non-malignant B cells was significantly reduced in CLL patients, yet absolute numbers were similar to those in HCs. Among $CD5^{-}CD19^{+}$ B cells, naïve B cells ($IgD^{+}CD27^{-}$) were significantly reduced in both untreated and chemotherapy-receiving CLL patients. While the frequency of unswitched and switched memory B cells was comparable to HCs, we observed an expansion of double negative ($IgD^{-}CD27^{-}$) B cells in untreated CLL patients.

CONCLUSIONS. CLL patients present with an altered composition of the residual non-malignant B cell compartment. A reduction in naïve and expansion of double negative B cells in untreated CLL patients suggests atypical activation of B cells in this group, and may have implications for mounting immune responses in infection and vaccination.

PP-25. Colorectal cancer screening – the Latvian experience

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OBJECTIVE. The incidence of colorectal cancer (CRC) is increasing worldwide. Screening is the most powerful public health tool to reduce mortality. Screening methods are effective, but have limitations. The aim of our study was to provide the current status of colorectal cancer screening in Latvia.

METHODS. Patients from 50 to 74 years old were invited to participate in a CRC screening programme in Latvia since 2009. For CRC screening from 2009, the fecal occult blood test (FOBT) was used. Furthermore, the organised CRC screening programme was stepwise implemented since 2019 with the fecal immunological test, which is widely provided in Latvia by Centrala Laboratorija, Ltd.

RESULTS. From 2009 to 2021, almost 910,000 Latvian inhabitants were invited to participate in the CRC screening programme. The participation rate in 2009, 2015, 2021 and 2022 year was 6.95%, 10.9%, 14.6% and 18.8% respectively. In 2021, the participation rate was highest in Riga, representing 44.0% of all the targeted population, but was quite low in other Latvian districts. The participation rate in Kurzeme, Vidzeme, Zemgale and Latgale was 15.0%, 12.0%, 15.0% and 14.0% respectively. The overall positive test was found in 8.6% of subjects in 2021. The high positive test rate was in Latgale (9.2%), with the lower rate in Vidzeme (8.1%).

CONCLUSION. In Latvia, the CRC screening programme has continuously achieved an increased participation rate from 6.95% to18.8%. However, unfortunately, the participation rate is still low. The positive test has been found in 8.6% of enrolled patients. The promotion of the CRC screening programme among the Latvian population is of utmost significance in decreasing the burden of CRC.

POSTER PRESENTATIONS

PP-26. Prevalence of molecular allergens in selected Latvian population

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OBJECTIVES. Although allergies are recognized as a growing public health problem worldwide, data on the prevalence of various allergen groups is still limited. The aim is to analyze the frequency of sensitization to molecular allergens by serum-specific IgE and total IgE in a randomized allergic patient group in Latvia. The term "molecular allergology" refers to the use of allergen molecules for the diagnosis and allergen-specific immunotherapy of allergic diseases.

METHODS. Statistical data were gathered from May 2021 to May 2022. Serum samples from 189 children and adults with suspected allergies were tested by *ALEX2® Allergy Explorer.* The *Allergy Explorer ALEX2®* test includes a larger number of allergens, allowing a broader molecular detection. 8 groups of allergens were analyzed, and special attention was paid to molecular allergens and their protein families.

RESULTS. Of189 patients, 77 were multi-sensitized. Results were divided into the following allergen groups: Pollen group (Lol p1: 10; Phl p1: 11; Bet v1: 15; Aln g 1: 8; Cor a 1.0103: 9; Fag s 1: 9;); Mites group (Der f 1: 10; Der f 2: 9; Der p 1: 8; Der p 2: 9; Der p 23: 8;); Plant-based food group (Mal d 1: 7; cor a 1.0401: 8; Fra a 1+3: 7;); Epithelial tissues of animal group (Can f_male urine "extract": 6; Fel d 1: 8;); Animal-derived food group (Xip g1: 3; Thu a 1: 2; Sco s 1: 2;); Insects and venoms group (Ves v 1: 3; Ves v 5: 3;) other group (Hev b8: 3;). In total, 261 allergens were detected in 77 patients. The highest sensitization levels were registered for the following allergen groups: pollen (37.5%), mites (26.8%), plant-based food group (13.8%), epithelial tissues of animal group (11.5%), animal-derived food group (6.9%), insects and venoms (3.1%), microorganisms and others (0.38%).

CONCLUSIONS. Almost all patients were only sensitized to molecular allergens. This serves as crucial information for further treatment decisions. sIgE in blood sera shows patient sensitization to the allergen, not allergy. Important to note is not the amount of total IgE or sIgE in blood sera, but the ratio between sIgE/bIgE. The sensitization status of the patient cannot be evaluated according to the classes.

PP-27. Workflow analysis in the United Laboratories of Tartu University Hospital based on clinical chemistry and immunochemistry analyzer Cobas 6000

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Turnaround times (TAT) of all released tests are keenly monitored in the United Laboratories. During the past years, the percentage of results that have exceeded the agreed TAT has gradually increased from 3% in 2020 to 5.3% in 2022. However, the amount of ordered tests has also risen remarkably: 17.8% since 2020. The aim of this study was to visualize the workflow of Cobas 6000 analyzers during the day in order to find problematic time periods when obtaining results lasts longer than usual, and analyze the reasons behind the increase in TAT.

Real-world one-month data for May 2022 was used to investigate the problem. Data was exported from the laboratory information system and processed in R program using mainly *tidyverse* and *lubridate* packages. All graphs were generated using the *ggplot2* package.

The study showed that the average time from sample registration until result release was 1 hour and 42 minutes on workdays. Time differences between *cito* and non-*cito* orders were identified, and the average time to result release was 77 minutes and 106 minutes, respectively. There were also time diversities between autovalidated versus manually validated results, with the peak at around 3 p.m., when manually validated results were lagging 59 minutes behind the autovalidated results.

We speculate that manually validated results at 3 p.m. are lagging due to the shift exchange at the end of the working day, but further investigation is needed to find the exact reasons behind that lag. This study helps laboratory personnel to uncover critical aspects of the lab workflow and find solutions for problematic issues.

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