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SEARCH STRATEGY

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S2	(blood bank technology) AND stype.exact("Scholarly Journals")	Ebook Central, Public Health Database, Publicly Available Content Database	24°
S1	blood bank technology	Ebook Central, Public Health Database, Publicly Available Content Database	32°

° Duplikat dihapus dari pencarian Anda dan dari jumlah hasil Anda.

Serum Ferritin Has Limited Prognostic Value on Mortality Risk in Patients with Decompensated Cirrhosis: A Propensity Score Matching Analysis

Guo, Gaoyue [1] ; Sun, Mingyu [1] ; Li, Yifan [1] ; Yang, Wanting [1] ; Wang, Xiaoyu [1] ; Yu, Zihan [1] ; Li, Chaoqun [1] ; Hui, Yangyang [1] ; Fan, Xiaofei [1] ; Jiang, Kui [1] ; Sun, Chao [1]

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ABSTRAK (ENGLISH)

Objective

The prognostic value of serum ferritin remains elusive in the literature. We aimed to examine the association between serum ferritin and mortality risk in cirrhosis.

Methods

A total of 257 cirrhotic patients were recruited. The cut-off of serum ferritin was determined by X-tile. The Cox regression and Kaplan-Meier method were used. A 1:1 propensity score matching (PSM) was performed to diminish the impacts of selection bias and possible confounders.

Results

The difference regarding mortality was mostly significant for serum ferritin >158 ng/mL. Before PSM, serum ferritin >158 ng/mL was an independent predictor of mortality. However, the clinical relevance of high ferritin level for prognostication was blunted after PSM (survival rate: 86.8% vs 96.3%, *P* = .078). Cox regression indicated that model for end-stage liver disease remains only independent risk factor of 180-day mortality after PSM.

Conclusion

Serum ferritin may not serve as an independent prognostic indicator of mortality risk in decompensated cirrhotic patients.

DETAIL

Subjek:	Hepatology; Patients; Biomarkers; Liver cirrhosis; Liver cancer; Liver diseases; Blood; Gastroenterology; Mortality; Leukocytes; Oxidative stress; Medical prognosis; Medical laboratories
Pengidentifikasi/kata kunci:	ferritin; propensity score matching analysis; liver cirrhosis; prognosis; MELD; mortality

Judul:	Serum Ferritin Has Limited Prognostic Value on Mortality Risk in Patients with Decompensated Cirrhosis: A Propensity Score Matching Analysis
Pengarang:	Guo, Gaoyue1; Sun, Mingyu1; Li, Yifan1; Yang, Wanting1; Wang, Xiaoyu1; Yu, Zihan1; Li, Chaoqun1; Hui, Yangyang1; Fan, Xiaofei1; Jiang, Kui1 ; Sun, Chao1 1 Department of Gastroenterology and Hepatology, Tianjin Medical University General Hospital , Tianjin , China
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A Meta-Analysis on the Association of Colibactin-Producing pks + Escherichia coli with the Development of Colorectal Cancer

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ABSTRAK (ENGLISH)

Objective

Previous studies on the association between *pks*$^{+}$*Escherichia coli* and colorectal cancer (CRC) demonstrated conflicting results. Hence, we performed a meta-analysis to obtain more precise estimates.

Methods

Related literature was obtained from PubMed, ScienceDirect, Google Scholar, and Cochrane Library. Data were then extracted, summarized, and subjected to analysis using Review Manager 5.4 by computing for the pooled odds ratios at the 95% confidence interval.

Results

Overall analysis showed that individuals carrying *pks*$^{+}$*E coli* had a greater risk of developing CRC. Subgroup analysis further showed that individuals from Western countries carrying *pks*$^{+}$*E coli* and individuals with *pks*$^{+}$*E coli* in their tissue samples had increased risk of developing CRC.

Conclusion

Results of this meta-analysis suggest that individuals with *pks*$^{+}$*E coli* have a greater risk of developing CRC. However, more studies are needed to confirm our claims.

DETAIL

Subjek:	Growth factors; E coli; Colorectal cancer; Peptides; Trends; Confidence intervals; Microorganisms; Mortality; Meta-analysis
Pengidentifikasi/kata kunci:	colorectal cancer; colon neoplasms; pathogenicity islands; polyketide synthase; Escherichia coli; meta-analysis
Judul:	A Meta-Analysis on the Association of Colibactin-Producing pks + Escherichia coli with the Development of Colorectal Cancer
Pengarang:	Gaab, Marcianne Elaine1 ; Prim Olivette Lozano1 ; Ibañez, Danica1 ; Korina Diane Manese1 ; Fatima May Riego1 ; Tiongco, Raphael Enrique2 ; Albano, Pia Marie1 1 Department of Biological Sciences, College of Science, University of Santo Tomas , Manila , Philippines2 Department of Medical Technology, College of Allied Medical Professions, Angeles University Foundation , Angeles City , Philippines
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Mycoplasma hominis Meningitis Diagnosed by Metagenomic Next-Generation Sequencing in a Preterm Newborn: a Case Report and Literature Review

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ABSTRAK (ENGLISH)

Mycoplasma hominis is mainly colonized in the genital tract and vertically transmitted to newborns; however, it rarely causes neonatal meningitis. We report a case of *M. hominis* meningitis in a premature infant. She was admitted to our hospital for treatment after 6 days of repeated fever. After admission, repeated cerebrospinal fluid (CSF) analysis showed that leukocytes and protein in CSF increased substantially and glucose decreased, but there was no growth in conventional CSF culture. The patient was diagnosed with *M. hominis* meningitis by metagenomic next-generation sequencing (mNGS). The antibiotic therapy used for the neonate was meropenem, vancomycin, and ampicillin against bacterial infection and azithromycin against mycoplasma infection. The child was subsequently considered cured and discharged from the hospital and followed up regularly in the neurology clinic. The mNGS may be a promising and effective diagnostic technique for identifying uncommon pathogens of meningitis in patients with meningitis symptoms and signs without microbial growth in routine CSF culture.

DETAIL

Subjek:	Infections; Adenosine; Birth defects; Pathogens; Pneumonia; Neutrophils; Premature birth; Antibiotics; Diagnostic tests; Premature babies; Lymphocytes; Glucose; Meningitis; Neurology; Fever; Polymerase chain reaction; Newborn babies; Microorganisms; Dehydrogenases; Proteins; Medical laboratories; Case reports
Pengidentifikasi/kata kunci:	mycoplasma hominis; meningitis; metagenomic next-generation sequencing; preterm; cerebrospinal fluid; case report

Judul:	Mycoplasma hominis Meningitis Diagnosed by Metagenomic Next-Generation Sequencing in a Preterm Newborn: a Case Report and Literature Review
Pengarang:	Che, Guanglu1; Liu, Fang1; Chang, Li1; Lai, Shuyu1; Teng, Jie1; Yang, Qiuxia11 Department of Laboratory Medicine, West China Second University Hospital, Key Laboratory of Birth Defects and Related Diseases of Women and Children, Ministry of Education, West China Second University Hospital, Sichuan University , Chengdu, Sichuan , People's Republic of China
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Increased Levels of ANGPTL3 and CTRP9 in Patients With Obstructive Sleep Apnea and Their Relation to Insulin Resistance and Lipid Metabolism and Markers of Endothelial Dysfunction

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ABSTRAK (ENGLISH)

Objective

Obstructive sleep apnea (OSA) has a close relation with obesity and perturbation in adipokines and hepatokines, which are linked to OSA consequences such as insulin resistance, dyslipidemia, and endothelial dysfunction. This study aimed to assess the relation of C1q/TNF-related protein 9 (CTRP9) and angiopoietin-like protein 3 (ANGPTL3) with OSA and biochemical measurements.

Methods

Serum levels of ANGPTL3, CTRP9, adiponectin, leptin, intercellular adhesion molecule 1 (ICAM-1), and vascular cell adhesion protein 1 (VCAM-1) were determined in 74 OSA patients and 27 controls using enzyme-linked immunosorbent assay kits.

Results

Levels of ANGPTL3, CTRP9, leptin, ICAM-1, and VCAM-1 were increased in the patients compared to the controls, whereas adiponectin levels decreased. ANGPTL3 had a positive correlation with total cholesterol, triglyceride, low-density lipoprotein cholesterol, ICAM-1, and VCAM-1 and was inversely correlated with leptin. CTRP9 showed a positive correlation with body mass index, insulin resistance, ICAM-1, and VCAM-1.

Conclusion

The results indicated the relation of ANGLTP3 and CTRP9 with OSA and its complications, which suggested a possible role for these factors in the consequences of OSA.

DETAIL

Subjek:	Cardiovascular disease; Insulin resistance; Body mass index; Kinases; Sleep apnea; High density lipoprotein; Metabolic disorders

Pengidentifikasi/kata kunci:	adipokine; hepatokine; endothelial dysfunction; dyslipidemia; lipoprotein lipase; adhesion molecule
Judul:	Increased Levels of ANGPTL3 and CTRP9 in Patients With Obstructive Sleep Apnea and Their Relation to Insulin Resistance and Lipid Metabolism and Markers of Endothelial Dysfunction
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Association of Catalase Gene Polymorphisms with Idiopathic Nephrotic Syndrome in a Chinese Pediatric Population

Shi, Jianrong [1] ; Li, Wei [1] ; Tao, Ran [1] ; Zhou, Dongming [1] ; Guo, Yajun [1] ; Fu, Haidong [2] ; Sun, Anna [1] ; Zhang, Junfeng [1] ; Mao, Jianhua [2 1] Department of Clinical Laboratory, The Children's Hospital, Zhejiang University School of Medicine, National Clinical Research Center For Child Health , Hangzhou , China [2] Department of Nephrology, The Children's Hospital, Zhejiang University School of Medicine, National Clinical Research Center For Child Health , Hangzhou , China

ABSTRAK (ENGLISH)

Objective

Our aim was to investigate the association between gene polymorphisms in *catalase* (*CAT*), a well-known oxidative stress regulator, and susceptibility to idiopathic nephrotic syndrome (INS) or responses to steroid therapy in a Chinese pediatric population.

Methods

We analyzed 3 *CAT* single-nucleotide polymorphisms (SNVs; rs7943316, rs769217, and rs12270780) using multi-polymerase chain reaction combined with next-generation sequencing in 183 INS patients and 100 healthy controls.

Results

For the allele and genotype frequencies of the *CAT* SNVs, no significant differences were observed between INS patients and controls. Patients with C allele of *CAT* rs769217 had a higher risk of developing steroid-dependent nephrotic syndrome than the steroid-sensitive nephrotic syndrome patients ($P = 0.018$; odds ratio = 1.76).

Conclusion

Our data suggests that genetic variations in *CAT* were unlikely to confer susceptibility to INS in Chinese children, whereas the C allele of the *CAT* rs769217 polymorphism showed a strong association with steroid-dependent responses in Chinese INS children.

DETAIL

Subjek:	Free radicals; Mutation; Steroids; Health risk assessment; Edema; Hospitals; Polymerase chain reaction; Ethnicity; Genotype &phenotype; Genes; Pathogenesis; Pediatrics; Polymorphism; Statistical analysis; Oxidative stress; Kidney diseases; Medical laboratories
Lokasi:	China
Pengidentifikasi/kata kunci:	catalase; idiopathic nephrotic syndrome; polymorphisms; susceptibility; single-nucleotide variants; children
Judul:	Association of Catalase Gene Polymorphisms with Idiopathic Nephrotic Syndrome in a Chinese Pediatric Population
Pengarang:	Shi, Jianrong1; Li, Wei1; Tao, Ran1; Zhou, Dongming1; Guo, Yajun1; Fu, Haidong2; Sun, Anna1; Zhang, Junfeng1; Mao, Jianhua21 Department of Clinical Laboratory, The Children's Hospital, Zhejiang University School of Medicine, National Clinical Research Center For Child Health , Hangzhou , China2 Department of Nephrology, The Children's Hospital, Zhejiang University School of Medicine, National Clinical Research Center For Child Health , Hangzhou , China
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Association between Methylene-Tetrahydrofolate Reductase C677T Polymorphism and Human Immunodeficiency Virus Type 1 Infection in Morocco

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; Saih, Asmae [1] ; Bensghir, Rajaa [2] ; Ouladlahsen, Ahd [2] ; Sodqi, Mustapha [2] ; Marih, Latifa [2] ; Zaidane, Imane [3] ; Kettani, Anass [4] ; Abidi, Omar [5] ; Wakrim, Lahcen [1] [1] Virology Unit, Immuno-virology Laboratory, Institut Pasteur du Maroc , Casablanca , Morocco [2] Service des Maladies Infectieuses, CHU Ibn Rochd , Casablanca , Morocco [3] Virology Unit, Viral Hepatitis Laboratory, Institut Pasteur du Maroc , Casablanca , Morocco [4] Laboratory of Biology and Health, URAC 34, Hassan II University-Casablanca, Faculty of Sciences Ben M'Sik , Casablanca , Morocco [5] Laboratory of Human Molecular Genetics and Medical Genomics, Institut Supérieur des Professions Infirmières et Techniques de Santé (ISPITS) de Casablanca , Casablanca , Morocco

ABSTRAK (ENGLISH)

Human immunodeficiency virus type 1 (HIV-1) infection varies substantially among individuals. One of the factors influencing viral infection is genetic variability. Methylenetetrahydrofolate reductase (*MTHFR*) C677T polymorphism is a genetic factor that has been correlated with different types of pathologies, including HIV-1. The *MTHFR* gene encodes the MTHFR enzyme, an essential factor in the folate metabolic pathway and in maintaining circulating folate and methionine at constant levels, thus preventing the homocysteine accumulation. Several studies have shown the role of folate on $CD4^+$ T lymphocyte count among HIV-1 subjects. In this case-control study we aimed to determine the association between the *MTHFR* C677T polymorphism and HIV-1 infection susceptibility, AIDS development, and therapeutic outcome among Moroccans. The C677T polymorphism was genotyped by

polymerase chain reaction followed by fragment length polymorphism digestion in 214 participants living with HIV-1 and 318 healthy controls. The results of the study revealed no statistically significant association between *MTHFR* C677T polymorphism and HIV-1 infection ($P > .05$). After dividing HIV-1 subjects according to their AIDS status, no significant difference was observed between C677T polymorphism and AIDS development ($P > .05$). Furthermore, regarding the treatment response outcome, as measured by HIV-1 RNA viral load and $CD4^+$ T cell counts, no statistically significant association was found with *MTHFR* C677T polymorphism. We conclude that, in the genetic context of the Moroccan population, *MTHFR* C677T polymorphism does not affect HIV-1 infection susceptibility, AIDS development, or response to treatment. However, more studies should be done to investigate both genetic and nutritional aspects for more conclusive results.

DETAIL

Subjek:	Infections; Human immunodeficiency virus--HIV; Acquired immune deficiency syndrome--AIDS; Viral infections; Immune system; Vitamin B; Polymorphism
Pengidentifikasi/kata kunci:	HIV-1; AIDS development; MTHFR C677T polymorphism; folate metabolism; Morocco; treatment response outcome
Judul:	Association between Methylene-Tetrahydrofolate Reductase C677T Polymorphism and Human Immunodeficiency Virus Type 1 Infection in Morocco
Pengarang:	Baba, Hanâ1 ; Bouqdayr, Meryem1 ; Saih, Asmae1; Bensghir, Rajaa2; Ouladlahsen, Ahd2; Sodqi, Mustapha2; Marih, Latifa2; Zaidane, Imane3; Kettani, Anass4; Abidi, Omar5; W akrim, Lahcen11 Virology Unit, Immuno-virology Laboratory, Institut Pasteur du Maroc , Casablanca , Morocco2 Service des Maladies Infectieuses, CHU Ibn Rochd , Casablanca , Morocco3 Virology Unit, Viral Hepatitis Laboratory, Institut Pasteur du Maroc , Casablanca , Morocco4 Laboratory of Biology and Health, URAC 34, Hassan II University-Casablanca, Faculty of Sciences Ben M'Sik , Casablanca , Morocco5 Laboratory of Human Molecular Genetics and Medical Genomics, Institut Supérieur des Professions Infirmières et Techniques de Santé (ISPITS) de Casablanca , Casablanca , Morocco
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Incidental Discovery of a Patient with the Bombay Phenotype

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Bombay phenotype, an exceptionally rare blood type in individuals outside of Southeast Asia, occurs in approximately 1 in 1,000,000 individuals in Europe. This blood phenotype is characterized by the absence of the H antigen on red blood cells (RBCs) and in secretions. As the H antigen is the structure on which the ABO system is built, individuals lacking this antigen are unable to produce A or B antigens and appear as type O on routine ABO phenotyping. H deficiency does not cause ill effect; however, these individuals produce an anti-H alloantibody capable of causing severe acute hemolytic transfusion reactions when exposed to RBCs that express the H antigen. In this case study, we highlight the incidental discovery of a patient with Bombay phenotype in a North American hospital system, expected test results, the immunologic and genetic basis underlying the Bombay and para-Bombay

phenotypes, and methods to ensure availability of compatible blood.

DETAIL

Subjek:	Plasma; Hemoglobin; Antigens; Blood &organ donations; Reagents; Blood groups; Genotype &phenotype; Genes; Mutation; Case reports; Medical laboratories
Pengidentifikasi/kata kunci:	ABO blood group system; Bombay phenotype; para-Bombay phenotype; H blood group system; ABO type; blood grouping and crossmatching
Judul:	Incidental Discovery of a Patient with the Bombay Phenotype
Pengarang:	Jacobs, Jeremy W1 ; Horstman, Erin1; Gisriel, Savanah D1 ; Tormey, Christopher A1; Sostin, Nataliya11 Department of Laboratory Medicine, Yale School of Medicine , New Haven, CT , USA
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Blood Donors with Thalassemic Trait, Glucose-6-Phosphate Dehydrogenase Deficiency Trait, and Sickle Cell Trait and Their Blood Products: Current Status and Future Perspective

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

The use of blood products for different medical purposes has increased in recent years. To meet increasing demand, some blood centers allow volunteer donors with thalassemic trait, glucose-6-phosphate dehydrogenase deficiency (G6PD) trait, and sickle cell trait (SCT) to donate blood if their hemoglobin values fall within acceptable ranges and show no signs of hemolysis. Currently, there are no standard guidelines or policies regarding the use or management of blood products obtained from these donors. However, in recent years, there has been advanced research on eligible donors who have these underlying conditions. In this review, we summarize the current knowledge from in vitro and in vivo studies regarding donor characteristics, changes in physical and biochemical parameters in blood products during processing and storage, and posttransfusion efficacy of blood products. In addition, we discuss some unresolved issues concerning blood products from thalassemic trait, G6PD-deficiency trait, and SCT donors.

DETAIL

Subjek:	Patient safety; Blood &organ donations; Blood diseases; Sickle cell disease

Pengidentifikasi/kata kunci:	donor; thalassemia; G6PD; sickle cell; microparticle; blood product
Judul:	Blood Donors with Thalassemic Trait, Glucose-6-Phosphate Dehydrogenase Deficiency Trait, and Sickle Cell Trait and Their Blood Products: Current Status and Future Perspective
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Pourbiax Diagrams as an Aid to Understanding the Impact of Acid/Base Disturbance on Blood Glucose Point-of-Care Testing

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ABSTRAK (ENGLISH)

Objective

Assays based on redox reactions that involve proton transfer are vulnerable to artifactual findings in metabolic acidosis/alkalosis. We evaluated the impact of pH on the measurement of blood glucose by the glucose dehydrogenase/pyrroloquinoline quinone system used in point-of-care-testing.

Methods

We applied a series of thermodynamic equations to adjust the Gibbs energy for the pyrroloquinoline quinone couple. This adjusts values taken under standard conditions to those more closely resembling the physiological state.

Results

Under standard conditions, the pyrroloquinoline quinone couple has E^{o} = −0.125 V whereas adjustment to the physiological state (pH 7.40, ionic strength 0.15 mol/L, and temperature 310.15°K) yields $E^{o\prime}$ = −0.166 V. This corresponds to an uncertainty in blood glucose determination of approximately 0.13 mmol/L.

Conclusion

We have demonstrated that the impact of pH on blood glucose determination by the glucose dehydrogenase/pyrroloquinoline quinone system (under physiologically relevant conditions of ionic strength and temperature) is not clinically significant.

DETAIL

Subjek: Body temperature; Aqueous solutions; Physiology; Glucose; Alkalosis; Metabolism; Acidosis; Ions; Point of care testing; Dehydrogenases; Medical laboratories

Pengidentifikasi/kata kunci:	diabetes mellitus; PQQ-dependent glucose dehydrogenase; capillary blood glucose; clinical chemistry; chemistry; basic science
Judul:	Pourbiax Diagrams as an Aid to Understanding the Impact of Acid/Base Disturbance on Blood Glucose Point-of-Care Testing
Pengarang:	McPherson, Peter A C1 ; McClements, Owen S2; Johnston, Ben M11 School of Science, Engineering &Construction, Belfast Metropolitan College, Titanic Quarter Campus , Belfast , UK2 Faculty of Medicine, Health &Life Sciences, Queen's University Belfast , UK
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Culturing Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) for Diagnosis and Genome Sequencing

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Objective

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) nucleic acid detection “re-positive” phenomenon is encountered clinically. The accuracy of a viral nucleic acid test is crucial to prevent reintroduction of the virus into the community. This study evaluated the effect of virus culturing on increasing the sensitivity and specificity of real-time polymerase chain reaction (RT-PCR) detection and viral genomic sequencing.

Methods

A series of tenfold dilutions of a SARS-CoV-2 viral stock were conducted and cultured for either 24 or 48 hours. The viral load of cultured samples was determined by RT-PCR. The cultured and non-cultured samples of 1x 50% tissue culture infectious dose (TCID50) were sequenced using metagenomic next-generation sequencing. The depth and coverage of SARS-CoV-2 genome were measured.

Results

The lowest viral load detectable in a sample with RT-PCR was 0.01 TCID50. After a 24-h culture, the viral ORF 1ab and *N*-gene cycle threshold (CT) values were reduced by 4.4 points and 1 point, respectively. One TCID50 viral load of post 24-h culture revealed the sequence depth reached an average of 752 reads, compared with 0.15 in the nonculture; furthermore, the coverage was 99.99% while 6.42% in the nonculture.

Conclusion

These results indicate that virus culturing can significantly increase the viral load, which can increase the certainty of true-positive detection of the viral nucleic acids, and improve the quality of virus genomic sequencing.

DETAIL

Subjek:	Infections; RNA polymerase; Severe acute respiratory syndrome coronavirus 2; Mutation; Microscopy; Public health; Viruses; Genomes; Polymerase chain reaction; Genes; Respiratory diseases; Cell culture; COVID-19; Medical diagnosis; COVID-19 diagnostic tests; Medical laboratories
Pengidentifikasi/kata kunci:	re-positive; SARS-CoV-2; virus culturing; viral load; diagnosis; sequencing
Judul:	Culturing Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) for Diagnosis and Genome Sequencing
Pengarang:	Zeng, Zhiqi1; Guo, Hua2; Chen, Liping1; Lin, Zhengshi1; Guan, Wenda1; Wang, Yutao1; Jiang, Haiming1; Wu, Xiao1; Yin, Yong2; Gao, Zelong2; Chen, Canxiong1; Yang, Zifeng11 State Key Laboratory of Respiratory Disease, National Clinical Research Center for Respiratory Disease, Guangzhou Institute of Respiratory Health, the First Affiliated Hospital of Guangzhou Medical University , Guangzhou , China2 Zhuhai Baso Diagnostics , Zhuhai , China
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Essential Thrombocythemia and Post-Essential Thrombocythemia Myelofibrosis: Updates on Diagnosis, Clinical Aspects, and Management

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Although several decades have passed since the description of myeloproliferative neoplasms (MPN), many aspects of their pathophysiology have not been elucidated. In this review, we discuss the mutational landscape of patients with essential thrombocythemia (ET), prognostic scores and salient pathology, and clinical points. We discuss also the diagnostic challenges of differentiating ET from prefibrotic MF.

We then focus on post-essential thrombocythemia myelofibrosis (post-ET MF), a rare subset of MPN that is usually studied in conjunction with post-polycythemia vera MF. The transition of ET to post-ET MF is not well studied on a molecular level, and we present available data. Patients with secondary MF could benefit from allogenic hematopoietic stem cell transplantation, and we present available data focusing on post-ET MF.

DETAIL

Subjek:	Medical prognosis; Leukemia; Clinical medicine; Mutation; Leukocytes; Stem cell transplantation; Blood platelets; Bone marrow; Pathology; Tumors; Blood; Morphology; Hematology; Medical diagnosis; Medical laboratories
Pengidentifikasi/kata kunci:	essential thrombocythemia; secondary myelofibrosis; post-essential thrombocythemia; hematopoietic stem cell transplantation; mutations; prognosis

Judul:	Essential Thrombocythemia and Post-Essential Thrombocythemia Myelofibrosis: Updates on Diagnosis, Clinical Aspects, and Management
Pengarang:	Omar Castaneda Puglianini1 ; Peker, Deniz2; Zhang, Linsheng2 ; Papadantonakis, Nikolaos31 H. Lee Moffitt Cancer Center &Research Institute, Department of Blood &Marrow Transplant &Cellular Immunotherapy , Tampa, FL , USA2 Department of Pathology and Laboratory Medicine, Emory University School of Medicine , Atlanta, GA , USA3 Winship Cancer Institute of Emory University, Department of Hematology and Medical Oncology , Atlanta, GA , USA
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MLL1:EZH2 Ratio in Uterine Secretions and Endometrial Receptivity in Patients with Endometriosis

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ABSTRAK (ENGLISH)

Objective

To establish a novel approach for diagnosing endometriosis (EM) in patients with impaired endometrial receptivity.

Method

Mixed lineage leukemia 1 (MLL1) and enhancer of zeste homolog 2 (EZH2) levels were analyzed. The MLL1:EZH2 ratio in identifying impaired endometrial receptivity has been established and validated.

Results

In normal endometrial tissue, the MLL1:EZH2 ratio increased significantly in the midsecretory phase, compared with that in the proliferative phase. In the midsecretory phase, the MLL1:EZH2 ratio in endometrial tissues and uterine secretions accurately identifies patients with EM who have impaired endometrial receptivity. In the validation group, the sensitivity and specificity of the MLL1:EZH2 ratio in the uterine secretions of the midsecretory phase, in diagnosing patients EM who have impaired endometrial receptivity, were 100% and 96.55%, respectively.

Conclusions

The MLL1:EZH2 ratio in uterine secretions of the midsecretory phase may serve as a marker to diagnose EM in patients with impaired endometrial receptivity.

DETAIL

Subjek: Embryos; Childrens health; Womens health; Maternal &child health; Gynecology; Immunology; Hospitals; Ovaries; Miscarriage; Biomarkers; Pregnancy; Endometriosis; Infertility; Polymerase chain reaction; Estrogens; Endometrium; Medical laboratories

Pengidentifikasi/kata kunci:	endometriosis; endometrial receptivity; mixed lineage leukemia 1; enhancer of zeste homolog 2; biomarker; diagnosis
Judul:	MLL1:EZH2 Ratio in Uterine Secretions and Endometrial Receptivity in Patients with Endometriosis
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Coping with the COVID-19 Pandemic: How a Master's in Clinical Laboratory Sciences Program Adapted Through the Modification of Existing Resources

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ABSTRAK (ENGLISH)

Objective

Our aim was to describe the rapid adaption of a Master of Clinical Laboratory Sciences (MCLS) program to the abrupt suspension of classroom instruction and laboratory training at affiliated hospitals in compliance with the New York governor's executive order in March 2020.

Methods

Teaching modifications included greater emphasis on Zoom video conferencing, Media Lab assignments, independent self-study, and online testing.

Results

Instruction of academic coursework continued uninterrupted using previously established teaching modalities. Clinical training presented 2-fold concerns, credit hours needed for the master's degree and clinical hours required for New York State licensing. The latter was delayed.

Conclusion

The real-time need to deliver laboratory science education during a time of statewide closure was fulfilled using available teaching modalities. The resulting uninterrupted academic and clinical training ensured the education of the incoming workforce of our clinical laboratories. This teaching strategy may be considered during new curricula development in preparation for times of future crises.

DETAIL

Subjek:	Teaching; Internships; Social distancing; Classrooms; Public speaking; Curricula; Severe acute respiratory syndrome coronavirus 2; Pandemics; Adaptation; Medical laboratories; Learning management systems; Medical students; Medical supplies; Masks; Onsite; COVID-19; Science education
Pengidentifikasi/kata kunci:	clinical laboratory; masters course teaching; COVID-19; Teaching modification; curriculum adaptation; regulatory compliance
Judul:	Coping with the COVID-19 Pandemic: How a Master's in Clinical Laboratory Sciences Program Adapted Through the Modification of Existing Resources
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A Literature Review on How We Can Address Medical Laboratory Scientist Staffing Shortages

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ABSTRAK (ENGLISH)

Objective

Laboratories are facing a critical shortage of medical laboratory scientists (MLS) and medical laboratory technicians (MLT) to address an increasing demand for laboratory testing. Training program closures, fewer student applicants, and financial decisions have contributed to staffing shortages. Lack of visibility, low wages, and perceived lack of opportunities for upward career mobility contribute to challenges in recruiting and retaining qualified individuals and students who are unaware of laboratory medicine careers. Our goal was to review the literature to determine the current state and consequences of staffing shortages, and potential solutions to address these shortages.

Methods

Medline/PubMed, PubMed Central, MeSH, Google Scholar, and Marshall Digital Scholar were used as resources.

Discussion/Conclusions

A collaboration of stakeholders is needed to identify staffing challenges, barriers, and solutions and to increase visibility of laboratory professionals. Early recruitment is best started in the middle and high school educational process.

DETAIL

Subjek:	Workforce planning; Retirement; Scientists; Collaboration; Careers; Accreditation; Employees; Employment; Labor shortages; Workforce; Tuition; Medical laboratories; Professionals; Literature reviews; Wages &salaries; COVID-19; Certification

Ketentuan indeks bisnis:	Subjek: Workforce planning Retirement Careers Employees Employment Labor shortages Workforce Professionals Wages &salaries
Pengidentifikasi/kata kunci:	report; address; clinical laboratory; scientist; staffing; shortages
Judul:	A Literature Review on How We Can Address Medical Laboratory Scientist Staffing Shortages
Pengarang:	Halstead, Diane C1; Sautter, Robert L21 Global Infectious Disease Consultants LLC , Jacksonville Beach, FL 32250 , USA2 RL Sautter Consulting LLC , Lancaster, SC 29720 , USA
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Dokumen 16 dari 48

Assessment of the Stability of Midregional Proadrenomedullin in Different Biological Matrices

Angeletti, Silvia [1] ; Legramante, Jacopo M [2] ; Lia, Maria Stella [3] ; Loreta D'Amico [3] ; Fogolari, Marta [1] ; Cella, Eleonora [1] ; De Cesaris, Marina [1] ; De Angelis, Fabio [2] ; Pieri, Massimo [4] ; Terrinoni, Alessandro [4] ; Bernardini, Sergio [4] ; Minieri, Marilena [4]

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ABSTRAK (ENGLISH)

Midregional proadrenomedullin (MR-proADM) has been shown to play a key role in endothelial dysfunction, with increased levels helping to prevent early stages of organ dysfunction. Recent clinical evidence has demonstrated MR-proADM to be a helpful biomarker to identify disease severity in patients with sepsis as well as pneumonia. This biomarker is helpful at triage in emergency departments to assess risk level of patients. The aim of this study is to evaluate the stability of MR-proADM in different biological matrices. The results, obtained by Bland-Altman and scatter plot analyses, demonstrate that deviation of MR-proADM concentration in serum compared to EDTA plasma unequivocally shows that serum should not be used as a sample matrix. Instead, the excellent correlation of heparin plasma vs EDTA plasma samples shows that heparin plasma can be used without reservation in clinical routine and emergency samples.

DETAIL

Subjek:	Emergency medical care; Biomarkers; Plasma; Blood &organ donations; Medical laboratories; Anticoagulants; Health risks
Pengidentifikasi/kata kunci:	midregional-proadrenomedullin; biological matrices; serum; EDTA plasma; heparin plasma; assay stability
Judul:	Assessment of the Stability of Midregional Proadrenomedullin in Different Biological Matrices

Pengarang:	Angeletti, Silvia1; Legramante, Jacopo M2; Lia, Maria Stella3; Loreta D'Amico3; Fogolari, Marta1; Cella, Eleonora1; De Cesaris, Marina1; De Angelis, Fabio2; Pieri, Massimo4 ; Terrinoni, Alessandro4; Bernardini, Sergio4; Minieri, Marilena4 1 Unit of Clinical Laboratory Science, University Campus Bio-Medico , Rome , Italy2 Emergency Department, Tor Vergata University Hospital , Rome , Italy3 Unit of Laboratory Medicine, Tor Vergata University Hospital , Rome , Italy4 Department of Experimental Medicine, University of Tor Vergata , Rome Italy
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Serum Leukocyte Cell-Derived Chemotaxin 2 (LECT2) Level Is Associated with Osteoporosis

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ABSTRAK (ENGLISH)

Objective

The aim of this study was to examine serum leukocyte cell-derived chemotaxin 2 (LECT2) levels in osteoporosis subjects to confirm its association with osteoporosis.

Methods

A total of 204 adult subjects were recruited. Bone mineral densities (BMD) were assessed and blood samples were collected for measurements of biomedical parameters and the bone turnover markers. Serum LECT2 levels were measured by enzyme-linked immunosorbent assay. The relationships between serum LECT2 levels and other parameters were analyzed using the Spearman correlation coefficient.

Results

Serum LECT2 levels were significantly increased in osteoporosis subjects over controls. We found a significantly negative correlation of serum LECT2 with BMD, 25-hydroxy-vitamin D, and creatinine and a significantly positive correlation with C-terminal telopeptide of type 1 collagen and total cholesterol.

Conclusion

Serum LECT2 levels were significantly upregulated in osteoporosis subjects and correlated with the severity of bone loss. Serum LECT2 could be a potential biomarker to assess the risk of bone loss.

DETAIL

Subjek:	Triglycerides; Collagen; Vitamin D; Leukocytes; Uric acid; Cytokines; Cholesterol; Obesity; Hospitals; Tumor necrosis factor-TNF; Metabolism; Liver diseases; Enzymes; Bone density; Osteoporosis; Creatinine; Proteins; Medical laboratories
Pengidentifikasi/kata kunci:	LECT2; osteoporosis; bone mineral density; C-terminal telopeptide of type 1 collagen; 25-hydroxy-vitamin D; enzyme-linked immunosorbent assay

Judul:	Serum Leukocyte Cell-Derived Chemotaxin 2 (LECT2) Level Is Associated with Osteoporosis
Pengarang:	Wang, Qiang1; Xu, Feng1; Chen, Jiong2; Yan-Qing Xie1; Su-Ling, Xu1; Wen-Ming, He11 Affiliated Hospital of Medical School of Ningbo University , Ningbo, Zhejiang , China2 Laboratory of Biochemistry and Molecular Biology, School of Marine Sciences, Meishan Campus, Ningbo University , Ningbo, Zhejiang , China
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COP27 Climate Change Conference: Urgent Action Needed for Africa and the World: Wealthy nations must step up support for Africa and vulnerable countries in addressing past, present and future impacts of climate change †

Atwoli, Lukoye [1] ; Erhabor, Gregory E [2] ; Gbakima, Aiah A [3] ; Haileamlak, Abraham [4] ; Jean-Marie Kayembe Ntumba [5] ; Kigera, James [6] ; Laybourn-Langton, Laurie [7] ; Mash, Bob [8] ; Muhia, Joy [9] ; Fhumulani Mavis Mulaudzi [10] ; Ofori-Adjei, David [11] ; Friday Okonofua [12] ; Rashidian, Arash [13] ; El-Adawy, Maha [14] ; Sidibé, Siaka [15] ; Snouber, Abdelmadjid [16] ; Tumwine, James [17] ; Yassien, Mohammad Sahar [18] ; Yonga, Paul [19] ; Zakhama, Lilia [20] ; Zielinski, Chris [21] [1] Editor-in-Chief, East African Medical Journal [2] Editor-in-Chief, West African Journal of Medicine [3] Editor-in-Chief, Sierra Leone Journal of Biomedical Research [4] Editor-in-Chief, Ethiopian Journal of Health Sciences [5] Chief Editor, Annales Africaines de Medecine [6] Editor-in-Chief, Annals of African Surgery [7] University of Exeter , UK [8] Editor-in-Chief, African Journal of Primary Health Care &Family Medicine [9] London School of Medicine and Tropical Hygiene [10] Editor-in-Chief, Curationis [11] Editor-in-Chief, Ghana Medical Journal [12] Editor-in-Chief, African Journal of Reproductive Health [13] Executive Editor, Eastern Mediterranean Health Journal [14] Director of Health Promotion, Eastern Mediterranean Health Journal [15] Director of Publication, Mali Médical [16] Managing Editor, Journal de la Faculté de Médecine d'Oran [17] Editor-in-Chief, African Health Sciences [18] Editor-in-Chief, Evidence-Based Nursing Research [19] Managing Editor, East African Medical Journal [20] Editor-in-Chief, La Tunisie Médicale [21] University of Winchester , UK

DETAIL

Judul:	COP27 Climate Change Conference: Urgent Action Needed for Africa and the World: Wealthy nations must step up support for Africa and vulnerable countries in addressing past, present and future impacts of climate change †

Pengarang:	Atwoli, Lukoye1; Erhabor, Gregory E2; Gbakima, Aiah A3; Haileamlak, Abraham4; Jean-Marie Kayembe Ntumba5; Kigera, James6; Laybourn-Langton, Laurie7; Mash, Bob8; Muhia, Joy9; Fhumulani Mavis Mulaudzi10; Ofori-Adjei, David11; Friday Okonofua12; Rashidian, Arash13; El-Adawy, Maha14; Sidibé, Siaka15; Snouber, Abdelmadjid16; Tumwine, James17; Yassien, Mohammad Sahar18; Yonga, Paul19; Zakhama, Lilia20; Zielinski, Chris211 Editor-in-Chief, East African Medical Journal2 Editor-in-Chief, West African Journal of Medicine3 Editor-in-Chief, Sierra Leone Journal of Biomedical Research4 Editor-in-Chief, Ethiopian Journal of Health Sciences5 Chief Editor, Annales Africaines de Medecine6 Editor-in-Chief, Annals of African Surgery7 University of Exeter , UK8 Editor-in-Chief, African Journal of Primary Health Care &Family Medicine9 London School of Medicine and Tropical Hygiene10 Editor-in-Chief, Curationis11 Editor-in-Chief, Ghana Medical Journal12 Editor-in-Chief, African Journal of Reproductive Health13 Executive Editor, Eastern Mediterranean Health Journal14 Director of Health Promotion, Eastern Mediterranean Health Journal15 Director of Publication, Mali Médical16 Managing Editor, Journal de la Faculté de Médecine d'Oran17 Editor-in-Chief, African Health Sciences18 Editor-in-Chief, Evidence-Based Nursing Research19 Managing Editor, East African Medical Journal20 Editor-in-Chief, La Tunisie Médicale21 University of Winchester , UK
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Compliance with the Current NCCN Guidelines and Its Critical Role in Pancreatic Adenocarcinoma

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ABSTRAK (ENGLISH)

Objectives

Since 2019, the National Comprehensive Cancer Network (NCCN) has recommended genetic testing for patients diagnosed with pancreatic adenocarcinoma that includes universal germline testing and tumor gene profiling for metastatic, locally advanced, or recurrent disease. However, testing compliance with this guideline has not yet been published in the English literature.

Methods

A quality assurance/quality improvement retrospective review was done to identify patients diagnosed with pancreatic adenocarcinoma from January 2019 to February 2021 to include the patient’s clinical status and genetic test results.

Results

There were 20 patient cases identified with pancreatic adenocarcinoma. A total of 11 cases had molecular tumor gene profiling and microsatellite instability/mismatch repair (MSI/MMR) testing performed and 1 case had only MSI/MMR testing by immunohistochemistry performed. Only 3 patients of the 20 in total received germline testing.

Conclusion

There was a significant number of patients for whom tumor gene profiling or germline testing had never been attempted as per recommended NCCN guidelines.

DETAIL

Subjek:	Genetic testing; Cellular biology; Metastasis; Cancer therapies; Mutation; Biopsy; Genetic counseling; Pathology; Genes; Precision medicine; Ultrasonic imaging; Chemotherapy; Endoscopy; Clinical outcomes; Adenosine diphosphate; Pancreatic cancer; Medical laboratories
Pengidentifikasi/kata kunci:	endoscopic ultrasound guided fine needle aspiration (EUS-FNA); pancreas; cancer; NCCN guidelines; molecular tumor profiling; germline profiling; quality assurance
Judul:	Compliance with the Current NCCN Guidelines and Its Critical Role in Pancreatic Adenocarcinoma
Pengarang:	Petersen, Jeffrey M1 ; Jhala, Darshana N11 Corporal Michael J Crescenz Veteran Affairs Medical Center , Philadelphia, Pennsylvania , USA
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Application of the Single-Molecule Real-Time Technology (SMRT) for Identification of HKαα Thalassemia Allele

Zhang, Min [1] ; Lin, Zhaodong [2] ; Chen, Meihuan [1] ; Pan, Yali [3] ; Zhang, Yanhong [4] ; Chen, Lingji [1] ; Lin, Na [1] ; Ren, Yuanyuan [5] ; Jia, Hongjin [5] ; Cai, Meiying [1] ; Xu, Liangpu [1] ; Huang, Hailong [1] [1] Medical Genetic Diagnosis and Therapy Center of Fujian Maternity and Child Health Hospital College of Clinical Medicine for Obstetrics &Gynecology and Pediatrics, Fujian Medical University, Fujian Provincial Key Laboratory of Prenatal Diagnosis and Birth Defect , Fuzhou , China [2] Department of Clinical Laboratorial Examination, The First Hospital Affiliated to Fujian Medical University , Fuzhou , China [3] Medical Technology and Engineering College of Fujian Medical University , Fuzhou , China [4] Fujian University of Traditional Chinese Medicine , Fuzhou , China [5] Berry Genomics Corporation , Beijing , China

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Objective

Single-molecule real-time technology (SMRT) is a sequencing technology using the DNA polymerases and fluorescently tagged nucleotides to accurately sequence DNA strands. The purpose of this study was to evaluate the detection accuracy of SMRT for identification of the Hong Kongαα (HKαα) thalassemia allele.

Methods

We conducted a blinded study of 33 samples of known HKαα alleles. These alleles were detected using SMRT to evaluate accuracy.

Results

We conducted a blinded study of 33 known HKαα samples and found all HKαα variants detected by SMRT to be concordant with those independently assigned by gap-polymerase chain reaction (gap-PCR), reverse dot blot hybridization, and 2-round nested PCR. In addition, SMRT detected 2 β-thalassemia variants that were missed by conventional techniques.

Conclusion

The results demonstrate that SMRT offers a higher detection accuracy of thalassemia rare and new loci. It is an efficient, reliable, and broad-spectrum test that can be widely used for thalassemia screening in the clinic.

DETAIL

Subjek:	Hybridization; Genetic counseling; Hemoglobin; Accuracy; Polymerase chain reaction; Blood diseases; Genotype &phenotype; Mutation; Medical laboratories
Pengidentifikasi/kata kunci:	single-molecule real-time technology (SMRT); Hong Kongαα; thalassemia; genetic diagnosis; α-globin; gap-PCR
Judul:	Application of the Single-Molecule Real-Time Technology (SMRT) for Identification of HKαα Thalassemia Allele
Pengarang:	Zhang, Min1; Lin, Zhaodong2; Chen, Meihuan1; Pan, Yali3; Zhang, Yanhong4; Chen, Lingji1; Lin, Na1; Ren, Yuanyuan5; Jia, Hongjin5; Cai, Meiying1; Xu, Liangpu1; Huang, Hailong11 Medical Genetic Diagnosis and Therapy Center of Fujian Maternity and Child Health Hospital College of Clinical Medicine for Obstetrics &Gynecology and Pediatrics, Fujian Medical University, Fujian Provincial Key Laboratory of Prenatal Diagnosis and Birth Defect , Fuzhou , China2 Department of Clinical Laboratorial Examination, The First Hospital Affiliated to Fujian Medical University , Fuzhou , China3 Medical Technology and Engineering College of Fujian Medical University , Fuzhou , China4 Fujian University of Traditional Chinese Medicine , Fuzhou , China5 Berry Genomics Corporation , Beijing , China
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Causes of Inappropriate Laboratory Test Ordering from the Perspective of Medical Laboratory Technical Professionals: Implications for Research and Education

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ABSTRAK (ENGLISH)

Objective

Inappropriate laboratory test ordering is a significant and persistent problem. Many causes have been identified and studied. Medical laboratory professionals (MLPs) are technical staff within clinical laboratories who are uniquely positioned to comment on why inappropriate ordering occurs. We aimed to characterize existing MLP perceptions in this domain to reveal new or underemphasized interventional targets.

Methods

We developed and disseminated a self-administered survey to MLPs in Canada, including open-ended responses to questions about the causes of inappropriate laboratory test ordering.

Results

Four primary themes were identified from qualitative analysis: ordering-provider factors, communication factors, existing test-ordering processes, and patient factors. Although these factors can largely be found in previous literature, some are under-studied.

Conclusion

MLP insights into nonphysician triage ordering and poor result communication provide targets for further investigation. A heavy focus on individual clinician factors suggests that current understandings and interprofessional skills in the MLP population can be improved.

DETAIL

Subjek:	Public health; Medical laboratories; Scope of practice; Professionals; Pathology; Communication; Professional ethics; Medical personnel; Clinical decision making; Medical education; Physicians; Medical tests
Ketentuan indeks bisnis:	Subjek: Professionals Professional ethics
Pengidentifikasi/kata kunci:	clinical laboratory services; medical laboratory personnel; medical laboratory science; allied health occupations; interprofessional skills; laboratory stewardship
Judul:	Causes of Inappropriate Laboratory Test Ordering from the Perspective of Medical Laboratory Technical Professionals: Implications for Research and Education
Pengarang:	VanSpronsen, Amanda D1; Zychla, Laura2; Turley, Elona3; Villatoro, Valentin1; Yuan, Yan4; Ohinmaa, Arto41 Department of Laboratory Medicine &Pathology, University of Alberta , Edmonton, Alberta , Canada2 Research, Canadian Association for Medical Radiation Technologists , Ottawa, Ontario , Canada3 Coagulation Medicine, Alberta Precision Laboratories , Edmonton, Alberta , Canada4 School of Public Health, University of Alberta , Edmonton, Alberta , Canada
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Evaluation of RT-LAMP Assay for Rapid Detection of SARS-CoV-2

Li, Ya-Ping [1] ; Xun-Jie Cao [1] ; Luo, Xin [1] ; Tian-Ao Xie [1] ; Wan-Jun, Liu [1] ; Shi-Ming, Xie [1] ; Lin, Min [1] ; Xu-Guang Guo [1] [1] Department of Clinical Laboratory Medicine, The Third Affiliated Hospital of Guangzhou Medical University , Guangzhou , China

ABSTRAK (ENGLISH)

Objective

To evaluate the accuracy of the reverse transcription loop-mediated isothermal amplification (RT-LAMP) assay for rapid detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in community or primary-care settings.

Method

We systematically searched the Web of Science, Embase, PubMed, and Cochrane Library databases. We

conducted quality evaluation using ReviewManager software (version 5.0). We then used MetaDisc software (version 1.4) and Stata software (version 12.0) to build forest plots, along with a Deeks funnel plot and a bivariate boxplot for analysis.

Result

Overall, the sensitivity, specificity, and diagnostic odds ratio were 0.79, 0.97, and 328.18, respectively. The sensitivity for the subgroup with RNA extraction appeared to be higher, at 0.88 (0.86–0.90), compared to the subgroup without RNA extraction, at 0.50 (0.45–0.55), with no significant difference in specificity.

Conclusion

RT-LAMP assay exhibited high specificity regarding current SARS-CoV-2 infection. However, its overall sensitivity was relatively moderate. Extracting RNA was found to be beneficial in improving sensitivity.

DETAIL

Subjek:	Infectious diseases; Software; Accuracy; Artificial intelligence; Clinical medicine; Severe acute respiratory syndrome coronavirus 2; Hospitals; Medical laboratories; Biosensors; Polymerase chain reaction; Point of care testing; Systematic review; Meta-analysis; Disease transmission; COVID-19; COVID-19 diagnostic tests
Ketentuan indeks bisnis:	Subjek: Artificial intelligence
Pengidentifikasi/kata kunci:	COVID-19; severe acute respiratory syndrome coronavirus 2; LAMP assay; COVID-19 diagnostic testing; meta-analysis; SARS-CoV-2
Judul:	Evaluation of RT-LAMP Assay for Rapid Detection of SARS-CoV-2
Pengarang:	Li, Ya-Ping1; Xun-Jie Cao1; Luo, Xin1; Tian-Ao Xie1; Wan-Jun, Liu1; Shi-Ming, Xie1; Lin, Min1; Xu-Guang Guo11 Department of Clinical Laboratory Medicine, The Third Affiliated Hospital of Guangzhou Medical University , Guangzhou , China
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Application of the Fluorescence Method on Sysmex XN9000 Hematology Analyzer for Correcting Platelet Count in Individuals with Microcytosis

Deng, Jiankai [1] ; Xie, Shuhua [1] ; Chen, Yaoming [1] ; Ma, Qinghua [1] ; He, Yuting [1] ; Liu, Min [1] ; Wang, Dong [1] ; Yu, Xuegao [1] [1] Department of Laboratory Medicine, The First Affiliated Hospital, Sun Yat-sen University , Guangzhou , China

ABSTRAK (ENGLISH)

Objective

Although small red blood cells are a well-known analytical pitfall that could cause artifactual increase of the platelet count, limited information is available on the accuracy of impedance platelet counting in cases with microcytosis. The aim of this study is to assess the accuracy of impedance platelet counting in the presence of small red blood cells, and to establish the optimal mean corpuscular volume (MCV) cutoff to endorse fluorescence platelet counting.

Methods

In this study, platelet counts estimated by the impedance method on the Sysmex XN9000 analyzer (Sysmex, Kobe, Japan) were compared with those provided by the fluorescence method. The accuracy of impedance platelet counting was assessed. Receiver operating characteristic curve was used to evaluate the performance of MCV in predicting falsely increased platelet counts.

Results

There was a tendency for the impedance method to overestimate the platelet count in samples with 70 fL <MCV ≤ 80 fL, 60 fL <MCV ≤ 70 fL, MCV ≤ 60 fL. Receiver operating characteristic curve analysis showed that a 73.5fL cutoff of MCV was highly sensitive in predicting falsely increased platelet counts.

Conclusion

In cases with MCV <73.5 fL, we strongly suggest that the platelet counts obtained by the impedance method on the Sysmex XN9000 analyzer should be checked and corrected by fluorescence counting.

DETAIL

Subjek:	Software; Accuracy; Blood platelets; Hematology; Medical laboratories; Blood tests; Erythrocytes
Pengidentifikasi/kata kunci:	platelet count; MCV cutoff; microcytosis; fluorescence method; impedance method; Sysmex XN9000 hematology analyzer
Judul:	Application of the Fluorescence Method on Sysmex XN9000 Hematology Analyzer for Correcting Platelet Count in Individuals with Microcytosis
Pengarang:	Deng, Jiankai1; Xie, Shuhua1; Chen, Yaoming1; Ma, Qinghua1; He, Yuting1 ; Liu, Min1; Wang, Dong1; Yu, Xuegao11 Department of Laboratory Medicine, The First Affiliated Hospital, Sun Yat-sen University , Guangzhou , China
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Diagnostic Efficiency of Serum-Based Infrared Spectroscopy in Detecting Breast Cancer: A Meta-Analysis

Pabico, Louise Julie [1] ; Jennica Naiomi Jaron [1] ; Marc Erickson Mosqueda [1] ; Wu, Jorge Jaesen [1] ; Tiongco, Raphael Enrique [2] ; Albano, Pia Marie [1] [1] Department of Biological Sciences, College of Science, University of Santo Tomas , Manila , Philippines [2] Department of Medical Technology, College of Allied Medical Professions, Angeles University Foundation , Angeles City , Philippines

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Background

The advancement of Fourier transform infrared (FTIR) spectroscopy as a potential diagnostic tool in the clinical setting has been studied over the years, particularly its application in cancer diagnostics.

Objective

To summarize previous research on FTIR spectroscopy in detecting breast cancer using serum specimens.

Methods

Related literature was searched and screened from various databases. Relevant data were then extracted, tabulated, and analyzed using Meta-DiSc 1.4 software.

Results

Sensitivity and specificity rates were 90% to 100% and 80% to 95%, respectively. The area under the receiver operating characteristic curve was at 0.9729, indicating that serum analysis via FTIR spectroscopy can accurately discriminate between healthy individuals and patients with breast cancer.

Conclusion

Overall, FTIR spectroscopy for breast cancer diagnosis using serum specimens shows promising results. However, further studies are still needed to validate these claims.

DETAIL

Subjek:	Spectrum analysis; Fourier transforms; Mortality; Breast cancer; Diagnostic tests
Pengidentifikasi/kata kunci:	breast cancer; FTIR; serum; diagnostic efficiency; liquid biopsy; meta-analysis
Judul:	Diagnostic Efficiency of Serum-Based Infrared Spectroscopy in Detecting Breast Cancer: A Meta-Analysis
Pengarang:	Pabico, Louise Julie1; Jennica Naiomi Jaron1; Marc Erickson Mosqueda1; Wu, Jorge Jaesen1; Tiongco, Raphael Enrique2 ; Albano, Pia Marie11 Department of Biological Sciences, College of Science, University of Santo Tomas , Manila , Philippines2 Department of Medical Technology, College of Allied Medical Professions, Angeles University Foundation , Angeles City , Philippines
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Chemerin Levels in Acute Coronary Syndrome: Systematic Review and Meta-Analysis

Ismaiel, Abdulrahman [1] ; Ashfaq, Mohammad Zeeshan [2] ; Daniel-Corneliu Leucuta [3] ; Ismaiel, Mohamed [4] ; Ismaiel, Dilara Ensar [5] ; Popa, Stefan-Lucian [1] ; Dumitrascu, Dan L [1] [1] 2nd Department of Internal Medicine, “Iuliu Hatieganu” University of Medicine and Pharmacy , Cluj-Napoca , Romania [2] Faculty of Medicine, “Iuliu Hatieganu” University of Medicine and Pharmacy , Cluj-Napoca , Romania [3] Department of Medical Informatics and Biostatistics, “Iuliu Hatieganu” University of Medicine and Pharmacy , Cluj-Napoca , Romania [4] Department of Surgery, St Michael’s Hospital , Dublin , Ireland [5] Department of Medicine, Tallaght University Hospital , Dublin , Ireland

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Objective

We evaluated the relevant published studies exploring the association between chemerin concentrations and acute coronary syndromes (ACSs).

Methods

A systematic search was performed in October 2021 using PubMed, Scopus, Embase, and Cochrane Library. We included full articles and assessed their quality using the Newcastle-Ottawa score.

Results

We found 6 studies in the systematic review and 5 of these were included in our meta-analysis. Mean difference (MD) of 41.69 ng/mL (95% CI, 10.07–73.30), 132.14 ng/mL (95% CI, −102.12–366.40), and 62.10 ng/mL (95% CI, 10.31–113.89) in chemerin levels was seen in ACS patients vs control subjects, ACS patients vs stable angina pectoris patients (SAP), and type 2 diabetes mellitus (T2DM) ACS patients vs nondiabetic ACS patients, respectively.

Conclusion

Chemerin levels were significantly elevated in patients with ACS compared to controls, as well as in T2DM–ACS patients compared to nondiabetic ACS patients. However, no significant MD in chemerin levels was observed between SAP and ACS patients.

DETAIL

Subjek:	Acute coronary syndromes; Diabetes; Vein &artery diseases; Pharmacy; Body mass index; Heart attacks; Coronary vessels; Cardiovascular disease; Body fat; Health informatics; Enzymes; Systematic review; Meta-analysis; Angina pectoris; Medical laboratories
Pengidentifikasi/kata kunci:	chemerin; acute coronary syndrome; stable angina pectoris; coronary artery disease; ischemic heart disease; diabetes mellitus
Judul:	Chemerin Levels in Acute Coronary Syndrome: Systematic Review and Meta-Analysis
Pengarang:	Ismaiel, Abdulrahman1 ; Ashfaq, Mohammad Zeeshan2; Daniel-Corneliu Leucuta3; Ismaiel, Mohamed4 ; Ismaiel, Dilara Ensar5; Popa, Stefan-Lucian1; Dumitrascu, Dan L11 2nd Department of Internal Medicine, “Iuliu Hatieganu” University of Medicine and Pharmacy , Cluj-Napoca , Romania2 Faculty of Medicine, “Iuliu Hatieganu” University of Medicine and Pharmacy , Cluj-Napoca , Romania3 Department of Medical Informatics and Biostatistics, “Iuliu Hatieganu” University of Medicine and Pharmacy , Cluj-Napoca , Romania4 Department of Surgery, St Michael’s Hospital , Dublin , Ireland5 Department of Medicine, Tallaght University Hospital , Dublin , Ireland
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Retrospective Assessment of a National Reflex Cryptococcal Antigen Screening Program in South Africa Through Interlaboratory Comparison of Lateral Flow Assay Results

Blasich, Nozuko P [1] ; Coetzee, Lindi M [2] ; Sriruttan, Charlotte [1] ; DeSanto, Daniel [1] ; Greene, Gregory S [1] ; Glencross, Deborah K [2] ; Govender, Nelesh P [1]

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ABSTRAK (ENGLISH)

Objective

Reflex cryptococcal antigen (CrAg) screening of blood specimens with a CD4 count of <100 cells/μL was performed at 45 South African CD4 laboratories using a lateral flow assay (LFA). Our objective was to evaluate the reliability of routine LFA results through comparative interlaboratory testing.

Methods

All CrAg-positive and a selected number of CrAg-negative samples from the CD4 laboratories were retested at paired microbiology laboratories using the same LFA. Samples with discordant results were tested at a reference laboratory, using the LFA (with CrAg titers).

Results

During interlaboratory testing, 12,502 samples were retested, with 93 (0.7%) discordant results and a between-laboratory agreement of 99.3% (Cohen's kappa, 0.98). The proportion of retested samples with discordant results ranged from 0.17% to 5.31% per laboratory pair (median 0.28%), with 3 reporting >3% of results as discordant.

Conclusion

Routine CrAg screening results were reliable, with <1% of samples having discordant results, mainly due to interpretation and transcription errors.

DETAIL

Subjek:	Human immunodeficiency virus--HIV; Cerebrospinal fluid; Asymptomatic; Mortality; Immune system; Diagnostic tests; Quality control; Public health; Meningitis; Antimicrobial agents; Information systems; Flow cytometry; Pathology; Antigens; Immunoassay; Enzymes; Drug resistance; Medical laboratories
Ketentuan indeks bisnis:	Subjek: Quality control Information systems
Lokasi:	South Africa
Pengidentifikasi/kata kunci:	cryptococcal antigen; interlaboratory comparison; discordant results; cryptococcal meningitis; lateral flow assay; advanced HIV disease
Judul:	Retrospective Assessment of a National Reflex Cryptococcal Antigen Screening Program in South Africa Through Interlaboratory Comparison of Lateral Flow Assay Results

Pengarang:	Blasich, Nozuko P1; Coetzee, Lindi M2; Sriruttan, Charlotte1; DeSanto, Daniel1; Greene, Gregory S1; Glencross, Deborah K2; Govender, Nelesh P1 1 Centre for Healthcare-Associated Infections, Antimicrobial Resistance and Mycoses, National Institute for Communicable Diseases, a Division of the National Health Laboratory Service , Johannesburg , South Africa2 School of Pathology, Faculty of Health Sciences, University of the Witwatersrand , Johannesburg , South Africa
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Validating the HPA-1 to -5 and -15 Detection by Homemade PCR-SSP, Real-Time PCR, and PCR-RFLP Methods

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ABSTRAK (ENGLISH)

Objective

Human platelet antigens (HPAs) are antigenic determinants on platelet membrane glycoproteins that stimulate the host's immune system and cause platelet destruction. In this study, we share our experience with implementing sequence-specific primer-polymerase chain reaction (PCR-SSP), real-time PCR, and PCR-RFLP (restriction fragment length polymorphism) and the validation process used to evaluate the results.

Methods

At the Ardabil Blood Transfusion Center, 10 samples were obtained from blood donors. Validation using PCR-SSP, real-time PCR, and PCR-RFLP methods for genotyping HPAs was done by sequencing. A commercial DNA sample and a commercial kit were also used for validation.

Results

The results of PCR-SSP, TaqMan Real-Time PCR, melting curve analysis (HPA-15), and PCR-RFLP (HPA-3) were 100% consistent with sequencing (gold standard) and commercial kit results.

Conclusions

There was a 100% correlation between repeating the methods and the expected results for repeatability, and no false positives and negatives were observed.

DETAIL

Subjek:	Genetic testing; Glycoproteins; Blood transfusions; Immune system; Sensors; Immunology; Blood platelets; Thrombocytopenia; Antigens; Polymerase chain reaction; Blood &organ donations; Enzymes; Polymorphism; Medical laboratories
Pengidentifikasi/kata kunci:	human platelet antigens; HPAs; TaqMan real-time PCR; PCRRFLP
Judul:	Validating the HPA-1 to -5 and -15 Detection by Homemade PCR-SSP, Real-Time PCR, and PCR-RFLP Methods
Pengarang:	Seyed Ghader Azizi1; Samiee, Shahram1; Zadsar, Maryam1; Shaiegan, Mojgan11 Iranian Blood Transfusion Research Center, High Institute for Research &Education in Transfusion Medicine , Tehran , Iran
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ASCP Board of Certification Survey of Medical Laboratory Science Education 2020: Faculty

Brown, Karen [1] ; Duzan, Dana [2] ; Fong, Karen [2] ; Freeman, Vicki S [3] ; Genzen, Jonathan [4] ; Goodyear, Nancy [5] ; Harrington, Susan M [6] ; Taff, Teresa [7] ; Tanabe, Patricia A [2 1] University of Utah Department of Pathology , Salt Lake City, Utah , USA [2] American Society for Clinical Pathology Board of Certification , Chicago, Illinois , USA [3] University of Texas Medical Branch Department of Clinical Laboratory Sciences , Galveston, Texas , USA [4] ARUP Laboratories University of Utah Department of Pathology , Salt Lake City, Utah , USA [5] University of Massachusetts Lowell Department of Biomedical and Nutritional Sciences , Lowell, Massachusetts , USA [6] Cleveland Clinic/ Lab Medicine , Cleveland, Ohio , USA [7] Mercy Hospital St. Louis School of Clinical Laboratory Science , Aurora, Missouri , USA

DETAIL

Judul:	ASCP Board of Certification Survey of Medical Laboratory Science Education 2020: Faculty
Pengarang:	Brown, Karen1; Duzan, Dana2; Fong, Karen2; Freeman, Vicki S3; Genzen, Jonathan4; Goodyear, Nancy5; Harrington, Susan M6; Taff, Teresa7; Tanabe, Patricia A21 University of Utah Department of Pathology , Salt Lake City, Utah , USA2 American Society for Clinical Pathology Board of Certification , Chicago, Illinois , USA3 University of Texas Medical Branch Department of Clinical Laboratory Sciences , Galveston, Texas , USA4 ARUP Laboratories University of Utah Department of Pathology , Salt Lake City, Utah , USA5 University of Massachusetts Lowell Department of Biomedical and Nutritional Sciences , Lowell, Massachusetts , USA6 Cleveland Clinic/ Lab Medicine , Cleveland, Ohio , USA7 Mercy Hospital St. Louis School of Clinical Laboratory Science , Aurora, Missouri , USA
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Metabolomics: A New Tool to Reveal the Nature of Diabetic Kidney Disease

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ABSTRAK (ENGLISH)

Metabolomics is a field of systems biology that draws on the scientific methods of other groups to qualitatively or quantitatively characterize small molecule metabolites in organisms, revealing their interconnections with the state of the organism at an overall relative macroscopic level. Diabetic kidney disease (DKD) is well known as a chronic metabolic disease, and metabolomics provides an excellent platform for its clinical study. A growing number of metabolomic analyses have revealed that individuals with DKD have metabolic disturbances of multiple substances in their bodies. With the continuous development and improvement of metabolomic analysis technology, the application of metabolomics in the clinical research of DKD is also expanding. This review discusses the recent progress of metabolomics in the early diagnosis, disease prognosis, and pathogenesis of DKD at the level of small molecule metabolites in vivo.

DETAIL

Subjek:	Cluster analysis; Genomics; Nuclear magnetic resonance--NMR; Metabolites; Diabetes; Kidney diseases
Ketentuan indeks bisnis:	Subjek: Cluster analysis
Pengidentifikasi/kata kunci:	metabolomics; diabetic kidney disease; biological markers; early diagnosis; disease prognosis; pathogenesis
Judul:	Metabolomics: A New Tool to Reveal the Nature of Diabetic Kidney Disease
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| **Basis data:** | Public Health Database |

Anti -Saccharomyces cerevisiae Antibodies in Rheumatoid Arthritis

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Objective

This study was conducted to evaluate the frequency of anti-*Saccharomyces cerevisiae* antibodies (ASCA) in patients with rheumatoid arthritis (RA).

Methods

Eighty-three RA patients with positive anti-cyclic citrullinated antibodies (anti-CCP) and 160 healthy blood donors were included in this study. ASCA IgG and IgA were assessed with enzyme-linked immunosorbent assay.

Results

The frequency of ASCA was significantly higher in RA patients than in healthy subjects (22.9% vs 3.7%, $P < 10^{-3}$). Both ASCA IgG and ASCA IgA were significantly more frequent in RA patients than in the control group (20.5% vs 3.1%, $P < 10^{-3}$and 9.6% vs 0.6%, $P = .002$, respectively). ASCA IgG and ASCA IgA levels were significantly higher in RA patients than in healthy subjects (7.8 ± 8.4 U/mL vs 2.3 ± 2.8 U/mL, $P < 10^{-6}$ and 6.2 ± 10.9 U/mL vs 3.4 ± 1.7 U/mL, $P = .002$, respectively).

Conclusion

A high frequency of ASCA IgG and ASCA IgA has been found in RA patients.

DETAIL

Subjek:	Glycoproteins; Antigens; Antibodies; Crohns disease; Peptides; Enzymes; Rheumatoid arthritis; Autoimmune diseases; Immunology; Medical laboratories; Blood tests
Pengidentifikasi/kata kunci:	anti- Saccharomyces cerevisiae antibodies; phosphopeptidomannan; rheumatoid arthritis; anti-CCP antibodies; rheumatoid factors; autoimmune disease
Judul:	Anti -Saccharomyces cerevisiae Antibodies in Rheumatoid Arthritis
Pengarang:	Melayah, Sarra1 ; Ghozzi, Mariem1; Malek Jemni1; Sakly, Nabil2; Ghedira, Ibtissem1; Mankaï, Amani11 Laboratory of Immunology, Farhat Hached Hospital , Sousse , Tunisia2 Department of Immunology, Faculty of Pharmacy, Monastir University , Monastir , Tunisia
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Pathogenic Homozygous Mutations in the DBT Gene (c.1174A>C) Result in Maple Syrup Urine Disease in a rs12021720 Carrier

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ABSTRAK (ENGLISH)

Objective

Maple syrup urine disease (MSUD; OMIM #248600) is an autosomal recessive metabolic disorder in the catabolism of branched-chain amino acids (leucine, isoleucine, and valine) and may be lethal if untreated in affected newborns.

Methods

Single-nucleotide polymorphism haplotyping and Sanger sequencing of *BCKDHA*, *BCKDHB*, and *DBT* genes were performed in a cohort of 10 MSUD patients.

Results

We identified a 16.6 Mb homozygous region harboring the *DBT* gene in an Iranian girl presenting with MSUD. Sanger sequencing revealed a pathogenic homozygous variant (NM_001918.3: c.1174A >C) in the *DBT* gene. We further found a controversial variant (rs12021720: c.1150 A >G) in the *DBT* gene. This substitution (p.Ser384Gly) is highly debated in literature. Bioinformatics and cosegregation analysis, along with identifying the real pathogenic variants (c.1174 A >C), lead to terminate these various interpretations of c.1150 A >G variant.

Conclusion

Our study introduced c.1150 A >G as a polymorphic variant, which is informative for variant databases and also helpful in molecular diagnosis.

DETAIL

Subjek:	Patients; Mass spectrometry; Bioinformatics; Mutation; Metabolic disorders; Vitamin B; Medical research; Urine; Amino acids; Scientific imaging; Chromatography; Polymerase chain reaction; Genes; Intellectual disabilities; Dehydrogenases; Pediatrics; Polymorphism; Medical laboratories
Pengidentifikasi/kata kunci:	DBT gene; MSUD; mutation; rs12021720; BCKDHA gene; BCKDHB gene
Judul:	Pathogenic Homozygous Mutations in the DBT Gene (c.1174A > C) Result in Maple Syrup Urine Disease in a rs12021720 Carrier
Pengarang:	Alijanpour, Morteza1 ; Jazayeri, Omid2 ; Shima Soleimani Amiri3; Brosens, Erwin4 1 Non-Communicable Pediatric Disease Research Center, Health Research Institute, Babol University of Medical Science , Babol , Iran2 Department of Molecular and Cell Biology, Faculty of Science, University of Mazandaran , Babolsar , Iran3 Razi Pathobiology and Genetic Diagnostic Laboratory, Babol , Iran4 Department of Clinical Genetics, Erasmus MC – Sophia Children's Hospital , Rotterdam , Netherlands
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Basis data:	Public Health Database

Call for Emergency Action to Limit Global Temperature Increases, Restore Biodiversity, and Protect Health: Wealthy nations must do much more, much faster †

Atwoli, Lukoye [1] ; Baqui, Abdullah H [2] ; Benfield, Thomas [3] ; Bosurgi, Raffaella [4] ; Godlee, Fiona [5] ; Hancocks, Stephen [6] ; Horton, Richard [7] ; Laybourn-Langton, Laurie [8] ; Monteiro, Carlos Augusto [9] ; Norman, Ian [10] ; Patrick, Kirsten [11] ; Praities, Nigel [12] ; Marcel G M Olde Rikkert [13] ; Rubin, Eric J [14] ; Sahni, Peush [15] ; Smith, Richard [16] ; Talley, Nick [17] ; Turale, Sue [18] ; Vázquez, Damián [19] 1 Editor in Chief, East African Medical Journal 2 Editor in Chief, Journal of Health, Population and Nutrition 3 Editor in Chief, Danish Medical Journal 4 Editor in Chief, PLOS Medicine 5 Editor in Chief, The BMJ 6 Editor in Chief, British Dental Journal 7 Editor in Chief, The Lancet 8 Senior Adviser, UK Health Alliance on Climate Change 9 Editor in Chief, Revista de Saúde Pública 10 Editor in Chief, International Journal of Nursing Studies 11 Interim Editor in Chief, CMAJ 12 Executive Editor, Pharmaceutical Journal 13 Editor in Chief, Dutch Journal of Medicine 14 Editor in Chief, NEJM 15 Editor in Chief, National Medical Journal of India 16 Chair, UK Health Alliance on Climate Change 17 Editor in Chief, Medical Journal of Australia 18

Editor in Chief, International Nursing Review [19] Editor in Chief, Pan American Journal of Public Health

Link dokumen ProQuest

DETAIL

Judul:	Call for Emergency Action to Limit Global Temperature Increases, Restore Biodiversity, and Protect Health: Wealthy nations must do much more, much faster †
Pengarang:	Atwoli, Lukoye1; Baqui, Abdullah H2; Benfield, Thomas3; Bosurgi, Raffaella4; Godlee, Fiona5; Hancocks, Stephen6; Horton, Richard7; Laybourn-Langton, Laurie8; Monteiro, Carlos Augusto9; Norman, Ian10; Patrick, Kirsten11; Praities, Nigel12; Marcel G M Olde Rikkert13; Rubin, Eric J14; Sahni, Peush15; Smith, Richard16; Talley, Nick17; Turale, Sue18; Vázquez, Damián191 Editor in Chief, East African Medical Journal2 Editor in Chief, Journal of Health, Population and Nutrition3 Editor in Chief, Danish Medical Journal4 Editor in Chief, PLOS Medicine5 Editor in Chief, The BMJ6 Editor in Chief, British Dental Journal7 Editor in Chief, The Lancet8 Senior Adviser, UK Health Alliance on Climate Change9 Editor in Chief, Revista de Saúde Pública10 Editor in Chief, International Journal of Nursing Studies11 Interim Editor in Chief, CMAJ12 Executive Editor, Pharmaceutical Journal13 Editor in Chief, Dutch Journal of Medicine14 Editor in Chief, NEJM15 Editor in Chief, National Medical Journal of India16 Chair, UK Health Alliance on Climate Change17 Editor in Chief, Medical Journal of Australia18 Editor in Chief, International Nursing Review19 Editor in Chief, Pan American Journal of Public Health
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Correction to: Treatment of COVID-19 Patients with Two Units of Convalescent Plasma in a Resource-Constrained State

DETAIL

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Prospective Validation of a Machine Learning Model for Low-Density Lipoprotein Cholesterol Estimation

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Objective

We aim to prospectively validate a previously developed machine learning algorithm for low-density lipoprotein cholesterol (LDL-C) estimation.

Methods

We retrospectively and prospectively evaluated a machine learning algorithm based on k-nearest neighbors (KNN) according to age, sex, health care setting, and triglyceridemia against a direct LDL-C assay. The agreement of low-density lipoprotein-k-nearest neighbors (LDL-KNN) with the direct measurement was assessed using intraclass correlation coefficient (ICC).

Results

The analysis comprised 31,853 retrospective and 6599 prospective observations, with a mean age of 54.2 ± 17.2 years. LDL-KNN exhibited an ICC greater than 0.9 independently of age, sex, and disease status. LDL-KNN was in satisfactory agreement with direct LDL-C in observations with normal triglyceridemia and mild hypertriglyceridemia but displayed an ICC slightly below 0.9 in severely hypertriglyceridemic patients and lower in very low LDL-C observations.

Conclusion

LDL-KNN performs robustly across ages, genders, health care settings, and triglyceridemia. Further algorithm development is needed for very low LDL-C observations.

DETAIL

Subjek:	Machine learning; Neural networks; High density lipoprotein; Cholesterol; Cardiovascular disease; Lipoproteins; Methods; Algorithms; Lipids; Cardiology; Diagnostic tests; Medical laboratories
Ketentuan indeks bisnis:	Subjek: Machine learning
Pengidentifikasi/kata kunci:	low-density lipoprotein cholesterol; machine learning; agreement study; method validation; triglycerides; clinical chemistry
Judul:	Prospective Validation of a Machine Learning Model for Low-Density Lipoprotein Cholesterol Estimation
Pengarang:	Ghayad, Jean Pierre1; Barakett-Hamadé, Vanda1; Sleilaty, Ghassan21 Department of Laboratory Medicine, Hôtel-Dieu de France University Hospital , Beirut , Lebanon2 Faculty of Medicine, Université Saint Joseph , Beirut , Lebanon
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IgG-RBD Response Due to Inactivated SARS-CoV-2 Vaccine: Alteration in D-Dimer and Fibrinogen Concentrations, Association with Comorbidities and Adverse Effects

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ABSTRAK (ENGLISH)

Objective

To examine the immunoglobulin G-receptor-binding domain (IgG-RBD) response and changes in fibrinogen and D-dimer concentrations in individuals with a past coronavirus infection and followed by CoronaVac.

Methods

The study consisted of a total of 116 participants. Blood samples were drawn from subjects 21–25 days after they received first and second doses of CoronaVac as well as from individuals with a past infection. Fibrinogen, D-dimer, and IgG-RBD concentrations were measured.

Results

The IgG concentrations of the vaccinated subjects were significantly higher (P <.001), fibrinogen levels were lower (P <.001), and D-dimer levels increased following the second vaccination compared with the first vaccination (P = .083). No difference was obtained in IgG-RBD between vaccinated and previously infected individuals (P = .063). The differences in fibrinogen and D-dimer were statistically nonsignificant between both groups.

Conclusion

The CoronaVac vaccine appears to be safe and effective. It is essential for individuals to take personal protective measures, such as using masks and distancing.

DETAIL

Subjek:	Infections; COVID-19 vaccines; mRNA vaccines; Antibodies; Severe acute respiratory syndrome coronavirus 2; Nanoparticles; Biochemistry; Mortality; Pandemics; Aluminum; Public health; Immunoglobulins; Polymerase chain reaction; Vectors (Biology); Enzymes; Chronic obstructive pulmonary disease; Drug dosages; Proteins; Medical laboratories
Pengidentifikasi/kata kunci:	COVID-19 infection; vaccination; D-dimer; fibrinogen; side effects
Judul:	IgG-RBD Response Due to Inactivated SARS-CoV-2 Vaccine: Alteration in D-Dimer and Fibrinogen Concentrations, Association with Comorbidities and Adverse Effects
Pengarang:	Kaytaz, Murat1 ; Akkaya, Emre1; Gumus, Sefika Nur1; Genc, Sema2; Issever, Halim3; Omer, Beyhan11 Department of Biochemistry Istanbul Faculty of Medicine Istanbul University , Capa, Istanbul , Turkey2 Department of Biochemistry, Acibadem Maslak Hospital , Istanbul , Turkey3 Department of Medical Sciences and Public Health, Istanbul Faculty of Medicine, Istanbul University , Capa, Istanbul , Turkey
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Basis data:	Public Health Database

Rare Case of Accelerated-Phase Chronic Myeloid Leukemia Diagnosed During Treatment for JAK2 V617F–Positive Primary Myelofibrosis

Ryu, Jeayeon [1] ; Chu, Daehyun [1] ; Park, Bosung [1] ; Kim, Miyoung [1] ; Young-Uk, Cho [1] ; Hwang, Sang-Hyun [1] ; Jang, Seongsoo [1] ; Eul-Ju Seo [1] ; Jung-Hee, Lee [2] ; Chan-Jeoung Park [1] [1] Department of Laboratory Medicine, Asan Medical Center, University of Ulsan College of Medicine , Seoul , Korea [2] Department of Hematology, Asan Medical Center, University of Ulsan College of Medicine , Seoul , Korea

ABSTRAK (ENGLISH)

Myeloproliferative neoplasms (MPNs) are clonal hematopoietic stem cell disorders characterized by the expansion of myeloid lineage cells. Chronic myeloid leukemia (CML) is characterized by a *BCR-ABL1* fusion gene that causes constitutive tyrosine kinase activity. Polycythemia vera, essential thrombocythemia, and primary myelofibrosis (PMF) are frequently associated with driver mutations in genes such as *JAK2, CALR,* and *MPL* and are mutually exclusive of *BCR-ABL1.* Herein, we report the first case study of a patient diagnosed with accelerated-phase CML while undergoing treatment for initial *JAK2* V617F–positive, *BCR-ABL1*-negative PMF. This finding emphasizes the importance of *BCR-ABL1* testing in patients with an atypical *BCR-ABL1*-negative MPN disease course.

DETAIL

Subjek:	Hemoglobin; Anemia; Blood tests; Collagen; Leukemia; Mutation; Cloning; Leukocytes; Biopsy; Blood platelets; Bone marrow; Polymerase chain reaction; Tumors; Kinases; Hematology; Stains &staining; Case reports; Medical laboratories; Inhibitor drugs
Pengidentifikasi/kata kunci:	BCR-ABL1; chronic myeloid leukemia; JAK2; primary myelofibrosis; myeloproliferative neoplasm; ruxolitinib
Judul:	Rare Case of Accelerated-Phase Chronic Myeloid Leukemia Diagnosed During Treatment for JAK2 V617F–Positive Primary Myelofibrosis
Pengarang:	Ryu, Jeayeon1; Chu, Daehyun1; Park, Bosung1; Kim, Miyoung1 ; Young-Uk, Cho1; Hwang, Sang-Hyun1; Jang, Seongsoo1; Eul-Ju Seo1; Jung-Hee, Lee2; Chan-Jeoung Park11 Department of Laboratory Medicine, Asan M edical Center, University of Ulsan College of Medicine , Seoul , Korea2 Department of Hematology, Asan Medical Center, University of Ulsan College of Medicine , Seoul , Korea
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Clinical Value of Early-Pregnancy Glycated Hemoglobin, Fasting Plasma Glucose, and Body Mass Index in Screening Gestational Diabetes Mellitus

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ABSTRAK (ENGLISH)

Objective

To investigate clinical values of early-pregnancy (8–13 weeks) glycated hemoglobin (HbA1c), fasting plasma glucose (FPG), and body mass index (BMI) in screening gestational diabetes mellitus (GDM).

Methods

A total of 1120 cases underwent a 75 g oral glucose tolerance test (OGTT), of which 216 cases with GDM were selected as the study group, and 278 cases without GDM were selected as the control group. FPG, HbA1c, and BMI in early pregnancy were measured. The correlation between FPG, HbA1c and BMI in early pregnancy and the incidence of GDM was analyzed by binary logistic regression, and the value of each index in predicting GDM alone or in combination was evaluated.

Results

FPG, HbA1c, and BMI in early pregnancy in the GDM group were higher than those in the control group, and the differences were statistically significant (*P* <.05). Binary logistic regression analysis showed that FPG, HbA1c, and BMI were risk factors for GDM in early pregnancy (odds ratio [OR] values were 3.374 [*P* <.05], 4.644 [*P* <.001], and 1.077 [*P* <.001], respectively). The area under the receiver operating characteristic (ROC) curve of FPG, glycated hemoglobin, and BMI in screening GDM for early pregnancy were 0.647, 0.661, and 0.608, respectively, while the area under the ROC curve of the combination of these 3 indicators was 0.736.

Conclusion

We found that FPG, HbA1c, and BMI in early pregnancy might be the potential risk factors for the occurrence of GDM, and the combination of them had certain clinical predictive value for GDM. However, it is still necessary for more studies, especially prospective studies, to validate our findings in the future.

DETAIL

Subjek:	Gestational diabetes; Glucose; Pregnancy; Hemoglobin; Regression analysis; Body mass index; Blood tests; Medical screening
Pengidentifikasi/kata kunci:	fasting plasma glucose; glycated hemoglobin; body mass index; gestational diabetes mellitus; pregnancy; receiver operator characteristic
Judul:	Clinical Value of Early-Pregnancy Glycated Hemoglobin, Fasting Plasma Glucose, and Body Mass Index in Screening Gestational Diabetes Mellitus
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Basis data:	Public Health Database

Evaluation of Intra- and Interlaboratory Variations in SARS-CoV-2 Real-Time RT-PCR Through Nationwide Proficiency Testing

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Objective

This study aimed to examine the intra- and interlaboratory variations of cycle threshold (Ct) values using the nationwide proficiency testing for SARS-CoV-2.

Methods

Triplicated strong-positive contrived samples duplicated weak-positive contrived samples, and 2 negative samples were transported to participating laboratories in October 2021.

Results

A total of 232 laboratories responded. All except 4 laboratories correctly answered. Six false-negative results, including 2 false-negatives with Ct values beyond the threshold and 1 clerical error, were noted from weak-positive samples. Intralaboratory variations of Ct values of weak-positive and strong-positive samples were not acceptable (Ct >1.66) in 17 and 7 laboratories, respectively. High interlaboratory variations of Ct values (up to 7 cycles) for the 2 commonly used polymerase chain reaction (PCR) reagents were observed.

Conclusion

The overall qualitative performance was acceptable; intralaboratory variation was acceptable. However, interlaboratory variations of Ct values were remarkable even when the same PCR reagents were used.

DETAIL

Subjek:	Software; Quality standards; RNA polymerase; Medicine; Reagents; Severe acute respiratory syndrome coronavirus 2; Quarantine; Public health; Data analysis; Biomedical materials; Polymerase chain reaction; Genes; COVID-19; COVID-19 diagnostic tests; Medical laboratories
Ketentuan indeks bisnis:	Subjek: Quality standards
Pengidentifikasi/kata kunci:	cycle threshold; external quality assessment; proficiency testing; SARS-CoV-2; COVID-19; interlaboratory variation
Judul:	Evaluation of Intra- and Interlaboratory Variations in SARS-CoV-2 Real-Time RT-PCR Through Nationwide Proficiency Testing
Pengarang:	Park, Kuenyoul1; Sung, Heungsup1; Chun, Sail1; Won-Ki, Min11 Department of Laboratory Medicine, Asan Medical Center, University of Ulsan College of Medicine , Seoul , Republic of Korea
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Use of Self-Collected Saliva Samples for the Detection of SARS-CoV-2

Kehinde Sogbesan [1] ; Taiwo Sogbesan [1] ; Hata, D Jane [1] ; White, Edward L [1] ; Wyeth, Daniel [1] ; Gasson, Samuel L [1] ; Jones, Dylan S [1] ; Vicari, Brittany R [1] ; Van Siclen, Carleen P [1] ; Palmucci, Carla [1] ; Marquez, Christopher P [1] ; Parkulo, Mark A [2] ; Thielen, Kent R [3] ; Nassar, Aziza [1]

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Objective

Using a US Food and Drug Administration (FDA) emergency use authorization (EUA) reverse transcription

polymerase chain reaction (RT-PCR) method, we examined the analytic performance accuracy of saliva specimens as compared to nasopharyngeal (NP) specimens in symptomatic patients. Correlation between test results and symptoms was also evaluated.

Methods

Over a 5-week period in 2020, 89 matched saliva and nasopharyngeal swabs were collected from individuals exhibiting symptoms consistent with SARS-CoV-2. Specimens were tested with an FDA EUA-approved RT-PCR method, and performance characteristics were compared.

Results

The concordance rate between saliva and nasopharyngeal testing was 93.26%. The mean cycle threshold value of saliva when compared to the NP specimen was 3.56 cycles higher. As compared to NP swab, saliva testing demonstrates acceptable agreement but lower sensitivity.

Conclusion

When compared to a reference method using NP swabs, the use of saliva testing proved to be a reliable method. Self-collected saliva testing for SARS-CoV-2 allows for a viable option when trained staff or collection materials are in short supply.

DETAIL

Subjek:	Severe acute respiratory syndrome coronavirus 2; Pandemics; Medical personnel; Testing laboratories; Pathology; Polymerase chain reaction; COVID-19 diagnostic tests; Disease control; Disease transmission; COVID-19; Body fluids
Pengidentifikasi/kata kunci:	saliva; SARS-CoV-2; self-collection; nasopharyngeal swab; sensitivity; cycle threshold
Judul:	Use of Self-Collected Saliva Samples for the Detection of SARS-CoV-2
Pengarang:	Kehinde Sogbesan1; Taiwo Sogbesan1; Hata, D Jane1 ; White, Edward L1; Wyeth, Daniel1; Gasson, Samuel L1; Jones, Dylan S1; Vicari, Brittany R1; Van Siclen, Carleen P1; Palmucci, Carla1; Marquez, Christopher P1 ; Parkulo, Mark A2; Thielen, Kent R3; Nassar, Aziza1 1 Department of Laboratory Medicine and Pathology, Mayo Clinic , Jacksonville, FL , USA2 Division of Community, Internal Medicine, Mayo Clinic , Jacksonville, FL , USA3 Department of Radiology, Mayo Clinic , Jacksonville, FL , USA
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Basis data:	Public Health Database

ASCP Board of Certification Survey of Medical Laboratory Science Education 2020: Programs

Brown, Karen [1] ; Duzan, Dana [1] ; Fong, Karen [2] ; Freeman, Vicki S [3] ; Genzen, Jonathan [4] ; Goodyear, Nancy [5] ; Harrington, Susan M [6] ; Taff, Teresa [7] ; Tanabe, Patricia A [2] [1] University of Utah Department of Pathology , Salt Lake City, Utah , USA [2] American Society for Clinical Pathology Board of Certification , Chicago, Illinois , USA [3] University of Texas Medical Branch Department of Clinical Laboratory Sciences , Galveston, Texas , USA [4] ARUP Labortories, University of Utah Department of Pathology , Salt Lake City, Utah , USA [5] University of Massachusetts Lowell Department of Biomedical and Nutritional Sciences , Lowell, Massachusetts , USA [6] Cleveland Clinic Laboratory Medicine , Cleveland, Ohio , USA [7] Mercy Hospital St. Louis School of Clinical Laboratory Science , Aurora, Missouri , USA

DETAIL

Judul:	ASCP Board of Certification Survey of Medical Laboratory Science Education 2020: Programs
Pengarang:	Brown, Karen1; Duzan, Dana1; Fong, Karen2; Freeman, Vicki S3; Genzen, Jonathan4; Goodyear, Nancy5; Harrington, Susan M6; Taff, Teresa7; Tanabe, Patricia A21 University of Utah Department of Pathology , Salt Lake City, Utah , USA2 American Society for Clinical Pathology Board of Certification , Chicago, Illinois , USA3 University of Texas Medical Branch Department of Clinical Laboratory Sciences , Galveston, Texas , USA4 ARUP Labortories, University of Utah Department of Pathology , Salt Lake City, Utah , USA5 University of Massachusetts Lowell Department of Biomedical and Nutritional Sciences , Lowell, Massachusetts , USA6 Cleveland Clinic Laboratory Medicine , Cleveland, Ohio , USA7 Mercy Hospital St. Louis School of Clinical Laboratory Science , Aurora, Missouri , USA
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High C-Reactive Protein-to-Lymphocyte Ratio Is Predictive of Unfavorable Prognosis in HBV-Associated Decompensated Cirrhosis

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ABSTRAK (ENGLISH)

Objective

Hepatitis B virus–associated decompensated cirrhosis (HBV-DeCi) is difficult to cure and has a very high risk of mortality. However, prediction of its prognosis is challenging. The C-reactive protein–to–lymphocyte ratio (CLR) is a newly discovered inflammatory indicator, but its role in HBV-DeCi remains unclear. In the present study, we sought to determine the prognostic role of the CLR in patients with HBV-DeCi.

Materials and Methods

This retrospective study enrolled 134 patients with HBV-DeCi. Independent prognostic markers were identified using multivariate regression analysis.

Results

The 30-day mortality rate was 12.7% (n = 17). The CLR was markedly higher in nonsurvivors compared with survivors. The multivariate analysis identified a high CLR as an independent risk factor for mortality.

Conclusion

We found that the CLR is an effective and simple prognostic marker in patients with HBV-DeCi.

DETAIL

Subjek:	Infections; Human immunodeficiency virus--HIV; Medical prognosis; Ascites; Mortality; Lymphocytes; Liver cirrhosis; Liver diseases; Clinical outcomes; Hepatitis B; Proteins; Medical laboratories
Pengidentifikasi/kata kunci:	hepatitis B virus; decompensated cirrhosis; CRP-to-lymphocyte ratio; prognostic factors; systemic inflammation; mortality
Judul:	High C-Reactive Protein-to-Lymphocyte Ratio Is Predictive of Unfavorable Prognosis in HBV-Associated Decompensated Cirrhosis
Pengarang:	Ye, Bin1; Ding, QiuMing2; He, Xia2; Liu, XiaoYun2; Shen, Jianjiang21 Department of Critical Care Medicine, Shengzhou People's Hospital, Shengzhou Branch of the First Affiliated Hospital of Zhejiang University , Shengzhou , China2 Department of Clinical Laboratory, Shengzhou People's Hospital, Shengzhou Branch of the First Affiliated Hospital of Zhejiang University , Shengzhou , China
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Acquired Thrombotic Thrombocytopenic Purpura After BNT162b2 COVID-19 Vaccine: Case Report and Literature Review

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ABSTRAK (ENGLISH)

Thrombotic thrombocytopenic purpura (TTP) is a thrombotic microangiopathy that is deadly if not treated promptly. The treatment of choice in patients presenting with TTP is plasma exchanges. However, immunosuppressive therapy and caplacizumab have significantly improved outcomes in TTP. This microangiopathy is classically divided into 2 entities: hereditary and acquired TTP (aTTP), caused by an autoantibody against *ADAMTS 13.* We present a case study of a patient wth TTP occurring after a second dose of the BNT162b2 (Pfizer-BioNTech) COVID-19 vaccine along with a review of the literature. A 55-year-old patient presented with gastrointestinal symptoms, anemia, and severe thrombocytopenia. The blood film revealed the presence of schistocytes. A diagnosis of aTTP was established because the patient had severe *ADAMTS 13* deficiency and autoantibodies against *ADAMTS 13* were positive. This episode occurred 10 days after the patient received the COVID-19 vaccine. The patient received plasma exchanges, prednisone, rituximab, and caplacizumab and achieved complete remission. Ten patients with aTTP induced by the COVID-19 vaccine have been reported in the literature. Most of these situations occurred after the second dose of COVID-19 vaccine, and 7 patients were noted to have received the BNT162b2 vaccine. Caplacizumab was used in 6 patients, and complete remission was achieved in 8 patients.

DETAIL

Subjek:	Plasma; Hemoglobin; Anemia; COVID-19 vaccines; Apheresis; Thrombosis; Neutrophils; Blood tests; Antibodies; Remission (Medicine); Purpura; Blood platelets; Anticoagulants; Thrombocytopenia; Case reports; Dehydrogenases; Drug dosages; Creatinine; Side effects; Literature reviews
Pengidentifikasi/kata kunci:	thrombotic thrombocytopenic purpura; COVID-19; vaccine; thrombosis; thrombocytopenia; microangiopathy
Judul:	Acquired Thrombotic Thrombocytopenic Purpura After BNT162b2 COVID-19 Vaccine: Case Report and Literature Review
Pengarang:	Hammami, Emna1 ; Lamarque, Mathilde2; Aujoulat, Olivier3; Debliquis, Agathe1; Drénou, Bernard2; Harzallah, Inès11 Laboratory of Hematology, Groupe Hospitalier de la région Mulhouse Sud Alsace , Mulhouse , France2 Service d'hématologie cliniqu e, Groupe Hospitalier de la région Mulhouse Sud Alsace , Mulhouse , France3 Pharmacie centrale, Groupe Hospitalier de la région Mulhouse Sud Alsace , Mulhouse , France
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Treatment of COVID-19 Patients with Two Units of Convalescent Plasma in a Resource-Constrained State

Ipe, Tina S [1] ; Blessing Ugwumba [1] ; Spencer, Horace J [2] ; Le, Tuan [3] ; Ridenour, Terry [3] ; Armitage, John [3] ; Ryan, Stefanie [4] ; Pearson, Shanna [4] ; Kothari, Atul [4] ; Patil, Naveen [4] ; Dare, Ryan [5] ; Crescencio, Juan C R [5] ; Anand, Venkata [6] ; Laudadio, Jennifer [1] ; Khalid, Mohammad [7] ; Jamal, Naznin [8] ; Thompson, John [9] ; Hailey McNew [10] ; Gibbs, McKenzie [11] ; Hennigan, Steve [12] ; Kellar, Stan [13] ; Reitzel, Keith [14] ; Walser, Brandon E [15] ; Novak, Amanda [16] ; Quinn, Brian [17] 1 Department of Pathology and Laboratory Medicine, University of Arkansas for Medical Sciences , Little Rock, AR , USA 2 Department of Biostatistics, University of Arkansas for Medical Sciences , Little Rock, AR , USA 3 Oklahoma/Texas/and Arkansas Blood Institute , Oklahoma City, OK , USA 4 Arkansas Department of Health , Little Rock, AR , USA 5 Department of Internal Medicine, Division of Infectious Diseases, University of Arkansas for Medical Sciences , Little Rock, AR , USA 6 Division of Pulmonary and Critical Care Medicine, Department of Internal Medicine, University of Arkansas for Medical Sciences , Little Rock, AR , USA 7 Division of Pulmonary and Critical Care Medicine, Department of Internal Medicine, Jefferson Regional Medical Center , Pine Bluff, AR , USA 8 Department of Internal Medicine, Jefferson Regional Medical Center , Pine Bluff, AR , USA 9 Division of Pulmonary and Critical Care Medicine, Department of Internal Medicine, St Bernards Healthcare , Jonesboro, AR , USA 10 Research Center, St Bernards Healthcare , Jonesboro, AR , USA 11 Department of Laboratory Medicine, Northwest Medical Center , Springdale, AR , USA 12 Department of Internal Medicine, Washington Regional Medical Center , Fayetteville, AR , USA 13 Department of Pulmonary Medicine, Baptist Health , Little Rock, AR , USA 14 Baptist Health , Fort Smith, AR , USA 15 Department of Infectious Diseases, Baptist Health , Little Rock, AR , USA 16 Department of Infectious Diseases, Baptist Health , North Little Rock, AR , USA 17 Department of Pathology, Baptist Health , Little Rock, AR , USA

ABSTRAK (ENGLISH)

Importance

Many therapies are used to treat COVID-19, the disease caused by the virus SARS-CoV-2, including convalescent plasma. The clinical utility of using 2 units of convalescent plasma for COVID-19 hospitalized patients is not fully understood.

Objective

Many therapies are used to treat COVID-19, the disease caused by the virus SARS-CoV-2, including convalescent plasma. The clinical utility of using 2 units of convalescent plasma for COVID-19 hospitalized patients is not fully understood. Our study aims to determine the safety and efficacy of treating hospitalized COVID-19 patients with 2 units of COVID-19 convalescent plasma (CCP).

Method

This was a retrospective study of Arkansas patients treated with CCP using the (US) Food and Drug Administration (FDA) emergency Investigational New Drug (eIND) mechanism from April 9, 2020, through August 9, 2020. It was a multicenter, statewide study in a low-resource setting, which are areas that lack funding for health care cost coverage on various levels including individual, family, or social. Adult patients (n = 165, volunteer sample) in Arkansas who were hospitalized with severe or life-threatening acute COVID-19 disease as defined by the FDA criteria were transfused with 2 units of CCP (250 mL/unit) using the FDA eIND mechanism. The primary outcome was 7- and 30-day mortality after the second unit of CCP.

Results

Unadjusted mortality was 12.1% at 7 days and 23.0% at 30 days. The unadjusted mortality was reduced to 7.7% if the first CCP unit was transfused on the date of diagnosis, 8.7% if transfused within 3 days of diagnosis, and 32.0% if transfused at or after 4 or more days of diagnosis. The risk of death was higher in patients that received low, negative, or missing titer CCP units in comparison to those that received higher titer units.

Conclusion

The provision of 2 units of CCP was associated with a reduction in mortality in patients treated with high titer units within 3 days of COVID-19 diagnosis. Given the results, CCP is a viable, low-cost therapy in resource-constrained states and countries.

DETAIL

Subjek:	Plasma; Severe acute respiratory syndrome coronavirus 2; Mortality; Hospitalization; COVID-19; Blood transfusions
Lokasi:	Arkansas; United States--US
Pengidentifikasi/kata kunci:	CCP; SARS-CoV-2; plasma; clinical study; outcome analysis; low-resource
Judul:	Treatment of COVID-19 Patients with Two Units of Convalescent Plasma in a Resource-Constrained State

Pengarang:	Ipe, Tina S1 ; Blessing Ugwumba1; Spencer, Horace J2; Le, Tuan3; Ridenour, Terry3; Armitage, John3; Ryan, Stefanie4; Pearson, Shanna4; Kothari, Atul4; Patil, Naveen4; Dare, Ryan5; Crescencio, Juan C R5; Anand, Venkata6; Laudadio, Jennifer1; Khalid, Mohammad7; Jamal, Naznin8; Thompson, John9; Hailey McNew10; Gibbs, McKenzie11; Hennigan, Steve12; Kellar, Stan13; Reitzel, Keith14; Walser, Brandon E15; Novak, Amanda16; Quinn, Brian171 Department of Pathology and Laboratory Medicine, University of Arkansas for Medical Sciences , Little Rock, AR , USA2 Department of Biostatistics, University of Arkansas for Medical Sciences , Little Rock, AR , USA3 Oklahoma/Texas/and Arkansas Blood Institute , Oklahoma City, OK , USA4 Arkansas Department of Health , Little Rock, AR , USA5 Department of Internal Medicine, Division of Infectious Diseases, University of Arkansas for Medical Sciences , Little Rock, AR , USA6 Division of Pulmonary and Critical Care Medicine, Department of Internal Medicine, University of Arkansas for Medical Sciences , Little Rock, AR , USA7 Division of Pulmonary and Critical Care Medicine, Department of Internal Medicine, Jefferson Regional Medical Center , Pine Bluff, AR , USA8 Department of Internal Medicine, Jefferson Regional Medical Center , Pine Bluff, AR , USA9 Division of Pulmonary and Critical Care Medicine, Department of Internal Medicine, St Bernards Healthcare , Jonesboro, AR , USA10 Research Center, St Bernards Healthcare , Jonesboro, AR , USA11 Department of Laboratory Medicine, Northwest Medical Center , Springdale, AR , USA12 Department of Internal Medicine, Washington Regional Medical Center , Fayetteville, AR , USA13 Department of Pulmonary Medicine, Baptist Health , Little Rock, AR , USA14 Baptist Health , Fort Smith, AR , USA15 Department of Infectious Diseases, Baptist Health , Little Rock, AR , USA16 Department of Infectious Diseases, Baptist Health , North Little Rock, AR , USA17 Department of Pathology, Baptist Health , Little Rock, AR , USA
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Influenza Vaccine Booster Stimulates Antibody Response in Beta Thalassemia Major Patients

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

The aim of this study was to evaluate antibody response against influenza vaccine in beta thalassemia major patients from Iran. Thirty beta thalassemia major patients were enrolled and divided into three groups: single dose (group 1), double dose (group 2), and control (group 3). Seroconversion, seroprotection, and geometric mean titer (GMT) assays were performed through hemagglutination inhibition (HI) on days 0, 14, and 60. Based on the results, the level of antibody titer was increased in group 2. Two weeks after vaccination, seroconversion rate was about 20% and 30% in groups 1 and 2. Sixty days after vaccination, the seroconversion rate was around 70% and GMT showed a more than 2-fold increase in group 2. Based on the results, the immunogenicity of double dose vaccination against influenza infection appears to be higher than the single dose vaccine in beta thalassemia major patients, and thus it is recommended to use two doses of vaccine, especially in splenectomized patients who are more sensitive than others.

DETAIL

Subjek:	Influenza; Vaccines; Antibodies; Blood diseases; Immunization
Pengidentifikasi/kata kunci:	influenza vaccine; trivalent; beta thalassemia major; immunogenicity; hemagglutination inhibition; seroconversion; seroprotection; geometric mean titers
Judul:	Influenza Vaccine Booster Stimulates Antibody Response in Beta Thalassemia Major Patients
Pengarang:	Sheikh, Maryam1; Ahmadi-Vasmehjani, Abbas2; Atashzar, Mohammad Reza3; Mohammad Hadi Karbalaie Niya4; Ebrahimian, Arefeh5; Baharlou, Rasoul1 1 Cancer Research Center, Semnan University of Medical Sciences , Semnan , Iran2 Department of Immunology and Microbiology, School of Medicine, Jahrom University of Medical Sciences , Jahrom , Iran3 Department of Immunology, School of Medicine, Fasa University of Medical Sciences , Fasa , Iran4 Gastrointestinal and Liver Disease Research Center, Iran University of Medical Sciences , Tehran , Iran5 Department of Microbiology, School of Medicine, Golestan University of Medical Sciences , Gorgan , Iran
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MicroRNA-149 rs2292832 C/T Polymorphism Predicts the Prognosis of Hepatocellular Carcinoma Patients With Bone Metastasis

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ABSTRAK (ENGLISH)

Objective

The prognostic markers of hepatocellular carcinoma (HCC) patients with bone metastasis are of great significance for the design of treatment strategy, the maintenance of life quality of the patients, and the improvement of cancer prognosis. MicroRNA-149 (miR-149) rs2292832 C/T polymorphism in HCC patients has been reported to be associated with the risk of HCC, but whether it can predict the prognosis of HCC patients with bone metastasis remains unclear. The goal of our study was to examine the prognostic impact of miR-149 rs2292832 C/T polymorphism on HCC patients with bone metastasis.

Methods

A total of 67 cases of HCC patients with bone metastasis (BC group) and 73 cases of HCC patients without bone metastasis (NC group) were included in this study. The miR-149 levels in blood leukocytes and tumor tissues were determined by qRT-PCR. Genotyping analysis of miR-149 rs2292832 was performed using polymerase chain reaction (PCR)-restriction fragment length polymorphism assay.

Results

The blood leukocyte miR-149 levels were significantly decreased in HCC patients, compared with the healthy controls, and they were significantly decreased in the BC patients, compared with the NC cases. BC patients carrying miR-149 rs2292832 CC+CT phenotype have a better overall survival (OS) rate, whereas no significant correlation was found between miR-149 rs2292832 CC+CT phenotype and the OS rate in NC group. The miR-149 rs2292832 CC+CT phenotype was correlated with certain bone turnover markers and bone metabolism markers but was not correlated with receptor activator of nuclear factor-kappaB ligand (RANKL) expression. Meanwhile, the combination of miR-149 rs2292832 CC+CT phenotype and RANKL expression could improve the prognosis assessment of HCC patients with bone metastasis.

Conclusion

miR-149 rs2292832 polymorphism might be a novel prognostic biomarker for HCC patients with bone metastasis. A follow-up study with a larger cohort from a multicenter should be performed to test our conclusions.

DETAIL

Subjek:	MicroRNAs; Medical prognosis; Metastasis; Liver cancer; Genotype &phenotype; Polymorphism
Pengidentifikasi/kata kunci:	HCC; microRNA; polymorphism; prognosis; bone metastasis; biomarker
Judul:	MicroRNA-149 rs2292832 C/T Polymorphism Predicts the Prognosis of Hepatocellular Carcinoma Patients With Bone Metastasis
Pengarang:	Feng, Jian1; Liu, Zhen2; Long, Yu3; Wu, Chaoyu4; Xiao-bo, Luo31 Department of Hepatopancreatobiliary Surgery, Peking University Shougang Hospital , Beijing , China2 Medical Supplies Center of PLA General Hospital , Beijing , China3 Senior Department of Orthopedics, The Fourth Medical Center of PLA General Hospital , Beijing , China4 Department of Infectious Diseases, Linyi Central Hospital , Linyi City , China
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T Cell Senescence by Extensive Phenotyping: An Emerging Feature of COVID-19 Severity

Zuin, Jenny [1] ; Fogar, Paola [1] ; Musso, Giulia [1] ; Padoan, Andrea [1] ; Piva, Elisa [1] ; Pelloso, Michela [1] ; Tosato, Francesca [1] ; Cattelan, Annamaria [2] ; Basso, Daniela [1] ; Plebani, Mario [1]

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Objective

To identify the potential prognostic value of lymphocyte subsets in COVID-19 patients, where lymphopenia is a common finding.

Methods

In 353 COVID-19 inpatients and 40 controls T cell subsets with markers of senescence and exhaustion were studied by flow cytometry.

Results

In severe illness, total lymphocytes B, NK, and all T subsets were dampened. Senescent CD4+, but mainly CD8+ T cells, increased in patients with respect to controls. The most significant index predicting fatal outcome was neutrophils/CD3+ T ratio.

Conclusion

In conclusion, an altered T cell pattern underlies COVID-19 severity and is involved in predicting the outcome.

DETAIL

Subjek:	Human immunodeficiency virus--HIV; Neutrophils; Trends; Age; Immune system; Respiratory distress syndrome; Lymphocytes; Blood &organ donations; Senescence; Viral infections; Hepatitis C; Coronaviruses; Hepatitis B; COVID-19; Medical prognosis; Biomarkers; Medical laboratories
Pengidentifikasi/kata kunci:	T cell subsets; COVID-19; extensive immunophenotyping; senescence; exhaustion; prognostic biomarker
Judul:	T Cell Senescence by Extensive Phenotyping: An Emerging Feature of COVID-19 Severity
Pengarang:	Zuin, Jenny1; Fogar, Paola1; Musso, Giulia1 ; Padoan, Andrea1; Piva, Elisa1; Pelloso, Michela1; Tosato, Francesca1; Cattelan, Annamaria2; Basso, Daniela1; Plebani, Mario1 1 Department of Laboratory Medicine, Padova University-Hospital , Padova , Italy2 Unit of Infectious and Tropical Diseases, Padova University-Hospital , Padova , Italy
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Whole-Exome Sequencing Revealed a Pathogenic Nonsense Variant in the SLC19A2 Gene in an Iranian Family with Thiamine-Responsive Megaloblastic Anemia

Mohsen-Pour, Neda [1] ; Naderi, Niloofar [2] ; Ghasemi, Serwa [3] ; Hesami, Mahshid [4] ; Maleki, Majid [2] ; Kalayinia, Samira [2]

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ABSTRAK (ENGLISH)

Objective

Solute carrier family 19 member 2 (*SLC19A2*, OMIM *603941) encodes thiamine human transporter 1 (THTR-1), which contributes to bringing thiamine (vitamin B1) into cells. Mutations in *SLC19A2* lead to a rare recessive genetic disorder termed thiamine-responsive megaloblastic anemia (TRMA) syndrome.

Methods

An Iranian family with TRMA was investigated by whole-exome sequencing (WES) to determine the genetic cause(s) of the disease. Accordingly, *SLC19A2* genetic variants were gathered through literature analysis.

Results

WES recognized a known pathogenic variant, c.697C >T (p. Q233X), within exon 2 of *SLC19A2* (NM_006996). Subsequently, the proband's parents and sister were confirmed as heterozygous carriers of the identified variant.

Conclusion

The diagnostic utility and affordability of WES were confirmed as the first approach for the genetic testing of TRMA to verify the diagnosis. This analysis can be used to guide future prenatal diagnoses and determine the consequences in the other family members.

DETAIL

Subjek:	Genetic testing; Parents &parenting; Diabetes; Hemoglobin; Anemia; Stroke; Genetic disorders; Mutation; Vitamin B; Cochlear implants; Hearing loss; Families &family life; Metabolism; Deafness; Polymerase chain reaction; Genes; Blood; Case reports; Medical laboratories
Lokasi:	Iran
Pengidentifikasi/kata kunci:	whole-exome sequencing; thiamine-responsive megaloblastic anemia; SLC19A2 mutation; diabetes mellitus; hearing loss; variant
Judul:	Whole-Exome Sequencing Revealed a Pathogenic Nonsense Variant in the SLC19A2 Gene in an Iranian Family with Thiamine-Responsive Megaloblastic Anemia
Pengarang:	Mohsen-Pour, Neda1; Naderi, Niloofar2; Ghasemi, Serwa3; Hesami, Mahshid4; Maleki, Majid2; Kalayinia, Samira2 1 Zanjan Pharmaceutical Biotechnology Research Center, Zanjan University of Medical Sciences , Zanjan , Iran2 Cardiogenetic Research Center, Rajaie Cardiovascular Medical and Research Center, Iran University of Medical Sciences , Tehran , Iran3 Department of Biology, Science and Research Branch, Islamic Azad University , Tehran , Iran4 Rajaie Cardiovascular Medical and Research Center, Iran University of Medical Sciences , Tehran , Iran
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Basis data:	Public Health Database

Guo, G., Sun, M., Li, Y., Yang, W., Wang, X., Yu, Z., . . . Sun, C. (2023). Serum ferritin has limited prognostic value on mortality risk in patients with decompensated cirrhosis: A propensity score matching analysis. Labmedicine, 54(1), 47-55. doi:https://doi.org/10.1093/labmed/lmac064

Objective The prognostic value of serum ferritin remains elusive in the literature. We aimed to examine the association between serum ferritin and mortality risk in cirrhosis. Methods A total of 257 cirrhotic patients were recruited. The cut-off of serum ferritin was determined by X-tile. The Cox regression and Kaplan-Meier method were used. A 1:1 propensity score matching (PSM) was performed to diminish the impacts of selection bias and possible confounders. Results The difference regarding mortality was mostly significant for serum ferritin >158 ng/mL. Before PSM, serum ferritin >158 ng/mL was an independent predictor of mortality. However, the clinical relevance of high ferritin level for prognostication was blunted after PSM (survival rate: 86.8% vs 96.3%, P = .078). Cox regression indicated that model for end-stage liver disease remains only independent risk factor of 180-day mortality after PSM. Conclusion Serum ferritin may not serve as an independent prognostic indicator of mortality risk in decompensated cirrhotic patients.

Gaab, M. E., Prim, O. L., Ibañez, D., Korina, D. M., Fatima, M. R., Tiongco, R. E., & Albano, P. M. (2023). A meta-analysis on the association of colibactin-producing pks+ escherichia coli with the development of colorectal cancer. Labmedicine, 54(1), 75-82. doi:https://doi.org/10.1093/labmed/lmac072

Objective Previous studies on the association between pks+Escherichia coli and colorectal cancer (CRC) demonstrated conflicting results. Hence, we performed a meta-analysis to obtain more precise estimates. Methods Related literature was obtained from PubMed, ScienceDirect, Google Scholar, and Cochrane Library. Data were then extracted, summarized, and subjected to analysis using Review Manager 5.4 by computing for the pooled odds ratios at the 95% confidence interval. Results Overall analysis showed that individuals carrying pks+E coli had a greater risk of developing CRC. Subgroup analysis further showed that individuals from Western countries carrying pks+E coli and individuals with pks+E coli in their tissue samples had increased risk of developing CRC. Conclusion Results of this meta-analysis suggest that individuals with pks+E coli have a greater risk of developing CRC. However, more studies are needed to confirm our claims.

Che, G., Liu, F., Chang, L., Lai, S., Teng, J., & Yang, Q. (2023). Mycoplasma hominis meningitis diagnosed by metagenomic next-generation sequencing in a preterm newborn: A case report and literature review. Labmedicine, 54(1), e24-e28. doi:https://doi.org/10.1093/labmed/lmac078

Mycoplasma hominis is mainly colonized in the genital tract and vertically transmitted to newborns; however, it rarely causes neonatal meningitis. We report a case of M. hominis meningitis in a premature infant. She was admitted to our hospital for treatment after 6 days of repeated fever. After admission, repeated cerebrospinal fluid (CSF) analysis showed that leukocytes and protein in CSF increased substantially and glucose decreased, but there was no growth in conventional CSF culture. The patient was diagnosed with M. hominis meningitis by metagenomic next-generation sequencing (mNGS). The antibiotic therapy used for the neonate was meropenem, vancomycin, and ampicillin against bacterial infection and azithromycin against mycoplasma infection. The child was subsequently considered cured and discharged from the hospital and followed up regularly in the neurology clinic. The mNGS may be a promising and effective diagnostic technique for identifying uncommon pathogens of meningitis in patients with meningitis symptoms and signs without microbial growth in routine CSF culture.

Fadaei, R., Samaneh, M. A., Laher, I., & Khazaie, H. (2023). Increased levels of ANGPTL3 and CTRP9 in patients with obstructive sleep apnea and their relation to insulin resistance and lipid metabolism and markers of endothelial dysfunction. Labmedicine, 54(1), 83-89. doi:https://doi.org/10.1093/labmed/lmac073

Objective Obstructive sleep apnea (OSA) has a close relation with obesity and perturbation in adipokines and hepatokines, which are linked to OSA consequences such as insulin resistance, dyslipidemia, and endothelial

dysfunction. This study aimed to assess the relation of C1q/TNF-related protein 9 (CTRP9) and angiopoietin-like protein 3 (ANGPTL3) with OSA and biochemical measurements. Methods Serum levels of ANGPTL3, CTRP9, adiponectin, leptin, intercellular adhesion molecule 1 (ICAM-1), and vascular cell adhesion protein 1 (VCAM-1) were determined in 74 OSA patients and 27 controls using enzyme-linked immunosorbent assay kits. Results Levels of ANGPTL3, CTRP9, leptin, ICAM-1, and VCAM-1 were increased in the patients compared to the controls, whereas adiponectin levels decreased. ANGPTL3 had a positive correlation with total cholesterol, triglyceride, low-density lipoprotein cholesterol, ICAM-1, and VCAM-1 and was inversely correlated with leptin. CTRP9 showed a positive correlation with body mass index, insulin resistance, ICAM-1, and VCAM-1. Conclusion The results indicated the relation of ANGLTP3 and CTRP9 with OSA and its complications, which suggested a possible role for these factors in the consequences of OSA.

Shi, J., Li, W., Tao, R., Zhou, D., Guo, Y., Fu, H., . . . Mao, J. (2023). Association of catalase gene polymorphisms with idiopathic nephrotic syndrome in a chinese pediatric population. Labmedicine, 54(1), 35-40. doi:https://doi.org/10.1093/labmed/lmac062

Objective Our aim was to investigate the association between gene polymorphisms in catalase (CAT), a well-known oxidative stress regulator, and susceptibility to idiopathic nephrotic syndrome (INS) or responses to steroid therapy in a Chinese pediatric population. Methods We analyzed 3 CAT single-nucleotide polymorphisms (SNVs; rs7943316, rs769217, and rs12270780) using multi-polymerase chain reaction combined with next-generation sequencing in 183 INS patients and 100 healthy controls. Results For the allele and genotype frequencies of the CAT SNVs, no significant differences were observed between INS patients and controls. Patients with C allele of CAT rs769217 had a higher risk of developing steroid-dependent nephrotic syndrome than the steroid-sensitive nephrotic syndrome patients (P = 0.018; odds ratio = 1.76). Conclusion Our data suggests that genetic variations in CAT were unlikely to confer susceptibility to INS in Chinese children, whereas the C allele of the CAT rs769217 polymorphism showed a strong association with steroid-dependent responses in Chinese INS children.

Baba, H., Bouqdayr, M., Saih, A., Bensghir, R., Ouladlahsen, A., Sodqi, M., . . . Wakrim, L. (2023). Association between methylene-tetrahydrofolate reductase C677T polymorphism and human immunodeficiency virus type 1 infection in morocco. Labmedicine, 54(1), 23-29. doi:https://doi.org/10.1093/labmed/lmac081

Human immunodeficiency virus type 1 (HIV-1) infection varies substantially among individuals. One of the factors influencing viral infection is genetic variability. Methylenetetrahydrofolate reductase (MTHFR) C677T polymorphism is a genetic factor that has been correlated with different types of pathologies, including HIV-1. The MTHFR gene encodes the MTHFR enzyme, an essential factor in the folate metabolic pathway and in maintaining circulating folate and methionine at constant levels, thus preventing the homocysteine accumulation. Several studies have shown the role of folate on CD4+ T lymphocyte count among HIV-1 subjects. In this case-control study we aimed to determine the association between the MTHFR C677T polymorphism and HIV-1 infection susceptibility, AIDS development, and therapeutic outcome among Moroccans. The C677T polymorphism was genotyped by polymerase chain reaction followed by fragment length polymorphism digestion in 214 participants living with HIV-1 and 318 healthy controls. The results of the study revealed no statistically significant association between MTHFR C677T polymorphism and HIV-1 infection (P > .05). After dividing HIV-1 subjects according to their AIDS status, no significant difference was observed between C677T polymorphism and AIDS development (P > .05). Furthermore, regarding the treatment response outcome, as measured by HIV-1 RNA viral load and CD4+ T cell counts, no statistically significant association was found with MTHFR C677T polymorphism. We conclude that, in the genetic context of the Moroccan population, MTHFR C677T polymorphism does not affect HIV-1 infection susceptibility, AIDS development, or response to treatment. However, more studies should be done to investigate both genetic and nutritional aspects for more conclusive results.

Jacobs, J. W., Horstman, E., Gisriel, S. D., Tormey, C. A., & Sostin, N. (2023). Incidental discovery of a patient with the bombay phenotype. Labmedicine, 54(1), e14-e17. doi:https://doi.org/10.1093/labmed/lmac075

Bombay phenotype, an exceptionally rare blood type in individuals outside of Southeast Asia, occurs in approximately 1 in 1,000,000 individuals in Europe. This blood phenotype is characterized by the absence of the H antigen on red blood cells (RBCs) and in secretions. As the H antigen is the structure on which the ABO system is built, individuals lacking this antigen are unable to produce A or B antigens and appear as type O on routine ABO phenotyping. H deficiency does not cause ill effect; however, these individuals produce an anti-H alloantibody capable of causing severe acute hemolytic transfusion reactions when exposed to RBCs that express the H antigen. In this case study, we highlight the incidental discovery of a patient with Bombay phenotype in a North American hospital system, expected test results, the immunologic and genetic basis underlying the Bombay and para-Bombay phenotypes, and methods to ensure availability of compatible blood.

About the journal. (2023). Labmedicine, 54(1), 1. doi:https://doi.org/10.1093/labmed/lmac144

Noulsri, E., & Lerdwana, S. (2023). Blood donors with thalassemic trait, glucose-6-phosphate dehydrogenase deficiency trait, and sickle cell trait and their blood products: Current status and future perspective. Labmedicine, 54(1), 6-12. doi:https://doi.org/10.1093/labmed/lmac061

The use of blood products for different medical purposes has increased in recent years. To meet increasing demand, some blood centers allow volunteer donors with thalassemic trait, glucose-6-phosphate dehydrogenase deficiency (G6PD) trait, and sickle cell trait (SCT) to donate blood if their hemoglobin values fall within acceptable ranges and show no signs of hemolysis. Currently, there are no standard guidelines or policies regarding the use or management of blood products obtained from these donors. However, in recent years, there has been advanced research on eligible donors who have these underlying conditions. In this review, we summarize the current knowledge from in vitro and in vivo studies regarding donor characteristics, changes in physical and biochemical parameters in blood products during processing and storage, and posttransfusion efficacy of blood products. In addition, we discuss some unresolved issues concerning blood products from thalassemic trait, G6PD-deficiency trait, and SCT donors.

McPherson, P. A. C., McClements, O. S., & Johnston, B. M. (2023). Pourbiax diagrams as an aid to understanding the impact of Acid/Base disturbance on blood glucose point-of-care testing. Labmedicine, 54(1), 72-74. doi:https://doi.org/10.1093/labmed/lmac069

Objective Assays based on redox reactions that involve proton transfer are vulnerable to artifactual findings in metabolic acidosis/alkalosis. We evaluated the impact of pH on the measurement of blood glucose by the glucose dehydrogenase/pyrroloquinoline quinone system used in point-of-care-testing. Methods We applied a series of thermodynamic equations to adjust the Gibbs energy for the pyrroloquinoline quinone couple. This adjusts values taken under standard conditions to those more closely resembling the physiological state. Results Under standard conditions, the pyrroloquinoline quinone couple has Eo = −0.125 V whereas adjustment to the physiological state (pH 7.40, ionic strength 0.15 mol/L, and temperature 310.15°K) yields Eo′ = −0.166 V. This corresponds to an uncertainty in blood glucose determination of approximately 0.13 mmol/L. Conclusion We have demonstrated that the impact of pH on blood glucose determination by the glucose dehydrogenase/pyrroloquinoline quinone system (under physiologically relevant conditions of ionic strength and temperature) is not clinically significant.

Zeng, Z., Guo, H., Chen, L., Lin, Z., Guan, W., Wang, Y., . . . Yang, Z. (2023). Culturing severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) for diagnosis and genome sequencing. Labmedicine, 54(1), 30-34. doi:https://doi.org/10.1093/labmed/lmac060

Objective The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) nucleic acid detection “re-positive” phenomenon is encountered clinically. The accuracy of a viral nucleic acid test is crucial to prevent reintroduction of the virus into the community. This study evaluated the effect of virus culturing on increasing the sensitivity and specificity of real-time polymerase chain reaction (RT-PCR) detection and viral genomic sequencing. Methods A series of tenfold dilutions of a SARS-CoV-2 viral stock were conducted and cultured for either 24 or 48 hours. The viral load of cultured samples was determined by RT-PCR. The cultured and non-cultured samples of 1x 50% tissue culture infectious dose (TCID50) were sequenced using metagenomic next-generation sequencing. The depth and

coverage of SARS-CoV-2 genome were measured. Results The lowest viral load detectable in a sample with RT-PCR was 0.01 TCID50. After a 24-h culture, the viral ORF 1ab and N-gene cycle threshold (CT) values were reduced by 4.4 points and 1 point, respectively. One TCID50 viral load of post 24-h culture revealed the sequence depth reached an average of 752 reads, compared with 0.15 in the nonculture; furthermore, the coverage was 99.99% while 6.42% in the nonculture. Conclusion These results indicate that virus culturing can significantly increase the viral load, which can increase the certainty of true-positive detection of the viral nucleic acids, and improve the quality of virus genomic sequencing.

Omar, C. P., Peker, D., Zhang, L., & Papadantonakis, N. (2023). Essential thrombocythemia and post-essential thrombocythemia myelofibrosis: Updates on diagnosis, clinical aspects, and management. Labmedicine, 54(1), 13-22. doi:https://doi.org/10.1093/labmed/lmac074

Although several decades have passed since the description of myeloproliferative neoplasms (MPN), many aspects of their pathophysiology have not been elucidated. In this review, we discuss the mutational landscape of patients with essential thrombocythemia (ET), prognostic scores and salient pathology, and clinical points. We discuss also the diagnostic challenges of differentiating ET from prefibrotic MF. We then focus on post-essential thrombocythemia myelofibrosis (post-ET MF), a rare subset of MPN that is usually studied in conjunction with post-polycythemia vera MF. The transition of ET to post-ET MF is not well studied on a molecular level, and we present available data. Patients with secondary MF could benefit from allogenic hematopoietic stem cell transplantation, and we present available data focusing on post-ET MF.

Zou, K., Du, Q., Chen, X., Tang, P., & Liang, H. (2023). MLL1:EZH2 ratio in uterine secretions and endometrial receptivity in patients with endometriosis. Labmedicine, 54(1), 90-97. doi:https://doi.org/10.1093/labmed/lmac067

Objective To establish a novel approach for diagnosing endometriosis (EM) in patients with impaired endometrial receptivity. Method Mixed lineage leukemia 1 (MLL1) and enhancer of zeste homolog 2 (EZH2) levels were analyzed. The MLL1:EZH2 ratio in identifying impaired endometrial receptivity has been established and validated. Results In normal endometrial tissue, the MLL1:EZH2 ratio increased significantly in the midsecretory phase, compared with that in the proliferative phase. In the midsecretory phase, the MLL1:EZH2 ratio in endometrial tissues and uterine secretions accurately identifies patients with EM who have impaired endometrial receptivity. In the validation group, the sensitivity and specificity of the MLL1:EZH2 ratio in the uterine secretions of the midsecretory phase, in diagnosing patients EM who have impaired endometrial receptivity, were 100% and 96.55%, respectively. Conclusions The MLL1:EZH2 ratio in uterine secretions of the midsecretory phase may serve as a marker to diagnose EM in patients with impaired endometrial receptivity.

Carbonaro, C. A., Isabella, D., & Faisal, H. R. (2023). Coping with the COVID-19 pandemic: How a Master's in clinical laboratory sciences program adapted through the modification of existing resources. Labmedicine, 54(1), e29-e30. doi:https://doi.org/10.1093/labmed/lmac086

Objective Our aim was to describe the rapid adaption of a Master of Clinical Laboratory Sciences (MCLS) program to the abrupt suspension of classroom instruction and laboratory training at affiliated hospitals in compliance with the New York governor's executive order in March 2020. Methods Teaching modifications included greater emphasis on Zoom video conferencing, Media Lab assignments, independent self-study, and online testing. Results Instruction of academic coursework continued uninterrupted using previously established teaching modalities. Clinical training presented 2-fold concerns, credit hours needed for the master's degree and clinical hours required for New York State licensing. The latter was delayed. Conclusion The real-time need to deliver laboratory science education during a time of statewide closure was fulfilled using available teaching modalities. The resulting uninterrupted academic and clinical training ensured the education of the incoming workforce of our clinical laboratories. This teaching strategy may be considered during new curricula development in preparation for times of future crises.

Halstead, D. C., & Sautter, R. L. (2023). A literature review on how we can address medical laboratory scientist staffing shortages. Labmedicine, 54(1), e31-e36. doi:https://doi.org/10.1093/labmed/lmac090

Objective Laboratories are facing a critical shortage of medical laboratory scientists (MLS) and medical laboratory technicians (MLT) to address an increasing demand for laboratory testing. Training program closures, fewer student applicants, and financial decisions have contributed to staffing shortages. Lack of visibility, low wages, and perceived lack of opportunities for upward career mobility contribute to challenges in recruiting and retaining qualified individuals and students who are unaware of laboratory medicine careers. Our goal was to review the literature to determine the current state and consequences of staffing shortages, and potential solutions to address these shortages. Methods Medline/PubMed, PubMed Central, MeSH, Google Scholar, and Marshall Digital Scholar were used as resources. Discussion/Conclusions A collaboration of stakeholders is needed to identify staffing challenges, barriers, and solutions and to increase visibility of laboratory professionals. Early recruitment is best started in the middle and high school educational process.

Angeletti, S., Legramante, J. M., Lia, M. S., Loreta D'Amico, Fogolari, M., Cella, E., . . . Minieri, M. (2023). Assessment of the stability of midregional proadrenomedullin in different biological matrices. Labmedicine, 54(1), 41-46. doi:https://doi.org/10.1093/labmed/lmac066

Midregional proadrenomedullin (MR-proADM) has been shown to play a key role in endothelial dysfunction, with increased levels helping to prevent early stages of organ dysfunction. Recent clinical evidence has demonstrated MR-proADM to be a helpful biomarker to identify disease severity in patients with sepsis as well as pneumonia. This biomarker is helpful at triage in emergency departments to assess risk level of patients. The aim of this study is to evaluate the stability of MR-proADM in different biological matrices. The results, obtained by Bland-Altman and scatter plot analyses, demonstrate that deviation of MR-proADM concentration in serum compared to EDTA plasma unequivocally shows that serum should not be used as a sample matrix. Instead, the excellent correlation of heparin plasma vs EDTA plasma samples shows that heparin plasma can be used without reservation in clinical routine and emergency samples.

Wang, Q., Xu, F., Chen, J., Yan-Qing Xie, Su-Ling, X., & Wen-Ming, H. (2023). Serum leukocyte cell-derived chemotaxin 2 (LECT2) level is associated with osteoporosis. Labmedicine, 54(1), 106-111. doi:https://doi.org/10.1093/labmed/lmac080

Objective The aim of this study was to examine serum leukocyte cell-derived chemotaxin 2 (LECT2) levels in osteoporosis subjects to confirm its association with osteoporosis. Methods A total of 204 adult subjects were recruited. Bone mineral densities (BMD) were assessed and blood samples were collected for measurements of biomedical parameters and the bone turnover markers. Serum LECT2 levels were measured by enzyme-linked immunosorbent assay. The relationships between serum LECT2 levels and other parameters were analyzed using the Spearman correlation coefficient. Results Serum LECT2 levels were significantly increased in osteoporosis subjects over controls. We found a significantly negative correlation of serum LECT2 with BMD, 25-hydroxy-vitamin D, and creatinine and a significantly positive correlation with C-terminal telopeptide of type 1 collagen and total cholesterol. Conclusion Serum LECT2 levels were significantly upregulated in osteoporosis subjects and correlated with the severity of bone loss. Serum LECT2 could be a potential biomarker to assess the risk of bone loss.

Atwoli, L., Erhabor, G. E., Gbakima, A. A., Haileamlak, A., Jean-Marie, K. N., Kigera, J., . . . Zielinski, C. (2023). COP27 climate change conference: Urgent action needed for africa and the world: Wealthy nations must step up support for africa and vulnerable countries in addressing past, present and future impacts of climate change †. Labmedicine, 54(1), 3-5. doi:https://doi.org/10.1093/labmed/lmac142

Petersen, J. M., & Jhala, D. N. (2023). Compliance with the current NCCN guidelines and its critical role in pancreatic adenocarcinoma. Labmedicine, 54(1), e1-e9. doi:https://doi.org/10.1093/labmed/lmac046

Objectives Since 2019, the National Comprehensive Cancer Network (NCCN) has recommended genetic testing for patients diagnosed with pancreatic adenocarcinoma that includes universal germline testing and tumor gene profiling for metastatic, locally advanced, or recurrent disease. However, testing compliance with this guideline has not yet been published in the English literature. Methods A quality assurance/quality improvement retrospective review was done to identify patients diagnosed with pancreatic adenocarcinoma from January 2019 to February

2021 to include the patient's clinical status and genetic test results. Results There were 20 patient cases identified with pancreatic adenocarcinoma. A total of 11 cases had molecular tumor gene profiling and microsatellite instability/mismatch repair (MSI/MMR) testing performed and 1 case had only MSI/MMR testing by immunohistochemistry performed. Only 3 patients of the 20 in total received germline testing. Conclusion There was a significant number of patients for whom tumor gene profiling or germline testing had never been attempted as per recommended NCCN guidelines.

Zhang, M., Lin, Z., Chen, M., Pan, Y., Zhang, Y., Chen, L., . . . Huang, H. (2023). Application of the single-molecule real-time technology (SMRT) for identification of HKαα thalassemia allele. Labmedicine, 54(1), 65-71. doi:https://doi.org/10.1093/labmed/lmac065

Objective Single-molecule real-time technology (SMRT) is a sequencing technology using the DNA polymerases and fluorescently tagged nucleotides to accurately sequence DNA strands. The purpose of this study was to evaluate the detection accuracy of SMRT for identification of the Hong Kongαα (HKαα) thalassemia allele. Methods We conducted a blinded study of 33 samples of known HKαα alleles. These alleles were detected using SMRT to evaluate accuracy. Results We conducted a blinded study of 33 known HKαα samples and found all HKαα variants detected by SMRT to be concordant with those independently assigned by gap-polymerase chain reaction (gap-PCR), reverse dot blot hybridization, and 2-round nested PCR. In addition, SMRT detected 2 β-thalassemia variants that were missed by conventional techniques. Conclusion The results demonstrate that SMRT offers a higher detection accuracy of thalassemia rare and new loci. It is an efficient, reliable, and broad-spectrum test that can be widely used for thalassemia screening in the clinic.

VanSpronsen, A. D., Zychla, L., Turley, E., Villatoro, V., Yuan, Y., & Ohinmaa, A. (2023). Causes of inappropriate laboratory test ordering from the perspective of medical laboratory technical professionals: Implications for research and education. Labmedicine, 54(1), e18-e23. doi:https://doi.org/10.1093/labmed/lmac076

Objective Inappropriate laboratory test ordering is a significant and persistent problem. Many causes have been identified and studied. Medical laboratory professionals (MLPs) are technical staff within clinical laboratories who are uniquely positioned to comment on why inappropriate ordering occurs. We aimed to characterize existing MLP perceptions in this domain to reveal new or underemphasized interventional targets. Methods We developed and disseminated a self-administered survey to MLPs in Canada, including open-ended responses to questions about the causes of inappropriate laboratory test ordering. Results Four primary themes were identified from qualitative analysis: ordering-provider factors, communication factors, existing test-ordering processes, and patient factors. Although these factors can largely be found in previous literature, some are under-studied. Conclusion MLP insights into nonphysician triage ordering and poor result communication provide targets for further investigation. A heavy focus on individual clinician factors suggests that current understandings and interprofessional skills in the MLP population can be improved.

Li, Y., Xun-Jie Cao, Luo, X., Tian-Ao Xie, Wan-Jun, L., Shi-Ming, X., . . . Xu-Guang Guo. (2023). Evaluation of RT-LAMP assay for rapid detection of SARS-CoV-2. Labmedicine, 54(1), 56-64. doi:https://doi.org/10.1093/labmed/lmac030

Objective To evaluate the accuracy of the reverse transcription loop-mediated isothermal amplification (RT-LAMP) assay for rapid detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in community or primary-care settings. Method We systematically searched the Web of Science, Embase, PubMed, and Cochrane Library databases. We conducted quality evaluation using ReviewManager software (version 5.0). We then used MetaDisc software (version 1.4) and Stata software (version 12.0) to build forest plots, along with a Deeks funnel plot and a bivariate boxplot for analysis. Result Overall, the sensitivity, specificity, and diagnostic odds ratio were 0.79, 0.97, and 328.18, respectively. The sensitivity for the subgroup with RNA extraction appeared to be higher, at 0.88 (0.86–0.90), compared to the subgroup without RNA extraction, at 0.50 (0.45–0.55), with no significant difference in specificity. Conclusion RT-LAMP assay exhibited high specificity regarding current SARS-CoV-2 infection. However, its overall sensitivity was relatively moderate. Extracting RNA was found to be beneficial in

improving sensitivity.

Deng, J., Xie, S., Chen, Y., Ma, Q., He, Y., Liu, M., . . . Yu, X. (2023). Application of the fluorescence method on sysmex XN9000 hematology analyzer for correcting platelet count in individuals with microcytosis. Labmedicine, 54(1), e10-e13. doi:https://doi.org/10.1093/labmed/lmac063

Objective Although small red blood cells are a well-known analytical pitfall that could cause artifactual increase of the platelet count, limited information is available on the accuracy of impedance platelet counting in cases with microcytosis. The aim of this study is to assess the accuracy of impedance platelet counting in the presence of small red blood cells, and to establish the optimal mean corpuscular volume (MCV) cutoff to endorse fluorescence platelet counting. Methods In this study, platelet counts estimated by the impedance method on the Sysmex XN9000 analyzer (Sysmex, Kobe, Japan) were compared with those provided by the fluorescence method. The accuracy of impedance platelet counting was assessed. Receiver operating characteristic curve was used to evaluate the performance of MCV in predicting falsely increased platelet counts. Results There was a tendency for the impedance method to overestimate the platelet count in samples with 70 fL < MCV ≤ 80 fL, 60 fL < MCV ≤ 70 fL, MCV ≤ 60 fL. Receiver operating characteristic curve analysis showed that a 73.5fL cutoff of MCV was highly sensitive in predicting falsely increased platelet counts. Conclusion In cases with MCV < 73.5 fL, we strongly suggest that the platelet counts obtained by the impedance method on the Sysmex XN9000 analyzer should be checked and corrected by fluorescence counting.

Pabico, L. J., Jennica, N. J., Marc, E. M., Wu, J. J., Tiongco, R. E., & Albano, P. M. (2023). Diagnostic efficiency of serum-based infrared spectroscopy in detecting breast cancer: A meta-analysis. Labmedicine, 54(1), 98-105. doi:https://doi.org/10.1093/labmed/lmac068

Background The advancement of Fourier transform infrared (FTIR) spectroscopy as a potential diagnostic tool in the clinical setting has been studied over the years, particularly its application in cancer diagnostics. Objective To summarize previous research on FTIR spectroscopy in detecting breast cancer using serum specimens. Methods Related literature was searched and screened from various databases. Relevant data were then extracted, tabulated, and analyzed using Meta-DiSc 1.4 software. Results Sensitivity and specificity rates were 90% to 100% and 80% to 95%, respectively. The area under the receiver operating characteristic curve was at 0.9729, indicating that serum analysis via FTIR spectroscopy can accurately discriminate between healthy individuals and patients with breast cancer. Conclusion Overall, FTIR spectroscopy for breast cancer diagnosis using serum specimens shows promising results. However, further studies are still needed to validate these claims.

Ismaiel, A., Ashfaq, M. Z., Daniel-Corneliu Leucuta, Ismaiel, M., Ismaiel, D. E., Popa, S., & Dumitrascu, D. L. (2022). Chemerin levels in acute coronary syndrome: Systematic review and meta-analysis. Labmedicine, 53(6), 552-560. doi:https://doi.org/10.1093/labmed/lmac059

Objective We evaluated the relevant published studies exploring the association between chemerin concentrations and acute coronary syndromes (ACSs). Methods A systematic search was performed in October 2021 using PubMed, Scopus, Embase, and Cochrane Library. We included full articles and assessed their quality using the Newcastle-Ottawa score. Results We found 6 studies in the systematic review and 5 of these were included in our meta-analysis. Mean difference (MD) of 41.69 ng/mL (95% CI, 10.07–73.30), 132.14 ng/mL (95% CI, −102.12–366.40), and 62.10 ng/mL (95% CI, 10.31–113.89) in chemerin levels was seen in ACS patients vs control subjects, ACS patients vs stable angina pectoris patients (SAP), and type 2 diabetes mellitus (T2DM) ACS patients vs nondiabetic ACS patients, respectively. Conclusion Chemerin levels were significantly elevated in patients with ACS compared to controls, as well as in T2DM–ACS patients compared to nondiabetic ACS patients. However, no significant MD in chemerin levels was observed between SAP and ACS patients.