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Plasma Sarcosine Measured by Gas Chromatography-Mass Spectrometry Distinguishes Prostatic Intraepithelial Neoplasia and Prostate Cancer from Benign Prostate Hyperplasia

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ABSTRAK (ENGLISH)

Objective

Sarcosine was postulated in 2009 as a biomarker for prostate cancer (PCa). Here, we assess plasma sarcosine as a biomarker that is complementary to prostate-specific antigen (PSA).

Methods

Plasma sarcosine was measured using gas chromatography-mass spectrometry (GC-MS) in adults classified as noncancerous controls (with benign prostate hyperplasia [BPH], n = 36), with prostatic intraepithelial neoplasia (PIN, n = 16), or with PCa (n = 27). Diagnostic accuracy was assessed using receiver operating characteristic curve analysis.

Results

Plasma sarcosine levels were higher in the PCa (2.0 μM [1.3–3.3 μM], *P* <.01) and the PIN (1.9 μM [1.2–6.5 μM], *P* <.001) groups than in the BPH (0.9 μM [0.6–1.4 μM]) group. Plasma sarcosine had “good” and “very good” discriminative capability to detect PIN (area under the curve [AUC], 0.734) and PCa (AUC, 0.833) versus BPH, respectively. The use of PSA and sarcosine together improved the overall diagnostic accuracy to detect PIN and PCa versus BPH.

Conclusion

Plasma sarcosine measured by GC-MS had “good” and “very good” classification performance for distinguishing PIN and PCa, respectively, relative to noncancerous patients diagnosed with BPH.

DETAIL

Subjek:	Mass spectrometry; Biomarkers; Plasma; Scientific imaging; Chromatography; Hyperplasia; Prostate cancer
Pengidentifikasi/kata kunci:	prostate cancer; sarcosine; prostate-specific antigen; prostatic intraepithelial neoplasia; mass spectrometry; biomarkers
Judul:	Plasma Sarcosine Measured by Gas Chromatography-Mass Spectrometry Distinguishes Prostatic Intraepithelial Neoplasia and Prostate Cancer from Benign Prostate Hyperplasia
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A Rapid and Accurate Detection Approach for Multidrug-Resistant Tuberculosis Based on PCR-ELISA Microplate Hybridization Assay

Ye-Cheng, Zhou [1] ; Shu-Mei, He [2] ; Zi-Lu, Wen [3] ; Jun-Wei, Zhao [4] ; Yan-Zheng, Song [3] ; Zhang, Ying [5] ; Shu-Lin, Zhang [6] [1] Shanghai Public Health Clinical Center, Shanghai, China; Key Laboratory of Biological Resource and Ecological Environment of the Ministry of Education, College of Life Sciences, Sichuan University, Chengdu, China; Department of Immunology and Microbiology, Shanghai Jiao Tong University School of Medicine, Shanghai, China [2] Key Laboratory for Basic Life Science Research of Tibet Autonomous Region, Xianyang, China; Key Laboratory of High Altitude Environment and Gene-Related Disease of Tibet Ministry of Education, School of Medicine, Xizang Minzu University, Xianyang, China [3] Shanghai Public Health Clinical Center, Shanghai, China [4] Clinical Laboratory, First Affiliated Hospital of Zhengzhou Universityy, Zhengzhou, China [5] Department of Molecular Microbiology and Immunology, Bloomberg School of Public Health, Johns Hopkins University, Baltimore, Maryland [6] Shanghai Public Health Clinical Center, Shanghai, China; Department of Immunology and Microbiology, Shanghai Jiao Tong University School of Medicine, Shanghai, China

ABSTRAK (ENGLISH)

Rapid and accurate diagnosis of multidrug-resistant tuberculosis (MDR-TB) is important for timely and appropriate therapy. In this study, a rapid and easy-to-perform molecular test that integrated polymerase chain reaction (PCR) amplification and a specific 96-well microplate hybridization assay, called PCR-ELISA (enzyme-linked immunosorbent assay), were developed for detection of mutations in *rpoB*, *katG*, and *inhA* genes responsible for rifampin (RIF) and isoniazid (INH) resistance and prediction of drug susceptibility in *Mycobacterium tuberculosis* clinical isolates. We evaluated the utility of this method by using 32 multidrug-resistent (MDR) isolates and 22 susceptible isolates; subsequently, we compared the results with data obtained by conventional drug susceptibility testing and DNA sequencing. The sensitivity and specificity of the PCR-ELISA test were 93.7% and 100% for detecting RIF resistance, and 87.5% and 100% for detecting INH resistance, respectively. These results were comparable to those yielded by commercially available molecular tests such as the GenoType MTBDRplus assay. Based on the aforementioned results, we conclude that the PCR-ELISA microplate hybridization assay is a rapid, inexpensive, convenient, and reliable test that will be useful for rapid diagnosis of MDR-TB, for improved clinical care.

DETAIL

Subjek:	Hybridization; Multidrug resistant organisms; Tuberculosis
Pengidentifikasi/kata kunci:	Mycobacterium tuberculosis; drug resistance; isoniazid; rifampicin; PCR; hybridization assay
Judul:	A Rapid and Accurate Detection Approach for Multidrug-Resistant Tuberculosis Based on PCR-ELISA Microplate Hybridization Assay
Pengarang:	Ye-Cheng, Zhou1; Shu-Mei, He2; Zi-Lu, Wen3; Jun-Wei, Zhao4; Yan-Zheng, Song3; Zhang, Ying5; Shu-Lin, Zhang61 Shanghai Public Health Clinical Center, Shanghai, China; Key Laboratory of Biological Resource and Ecological Environment of the Ministry of Education, College of Life Sciences, Sichuan University, Chengdu, China; Department of Immunology and Microbiology, Shanghai Jiao Tong University School of Medicine, Shanghai, China2 Key Laboratory for Basic Life Science Research of Tibet Autonomous Region, Xianyang, China; Key Laboratory of High Altitude Environment and Gene-Related Disease of Tibet Ministry of Education, School of Medicine, Xizang Minzu University, Xianyang, China3 Shanghai Public Health Clinical Center, Shanghai, China4 Clinical Laboratory, First Affiliated Hospital of Zhengzhou Universityy, Zhengzhou, China5 Department of Molecular Microbiology and Immunology, Bloomberg School of Public Health, Johns Hopkins University, Baltimore, Maryland6 Sh anghai Public Health Clinical Center, Shanghai, China; Department of Immunology and Microbiology, Shanghai Jiao Tong University School of Medicine, Shanghai, China
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COVID-19 Pandemic Once Again Exposes the Weakest Link in Laboratory Services: Specimen Delivery

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ABSTRAK (ENGLISH)

Objective

Reorganization of the emergency department (ED) during the COVID-19 pandemic implied closure of the ED-dedicated laboratory and manual transport of all specimens to the dislocated central laboratory. The impact of such reorganization on laboratory turnaround time (TAT) was examined.

Methods

The TAT from blood sampling to specimen reception (TAT1), from specimen reception to test reporting (TAT2), and from sampling to test reporting (TAT3) were compared between the pandemic peak month in 2020 and the same month in 2019. We evaluated whether TAT2 fulfills the recommended 60-minute criteria.

Results

A statistically significant difference was observed for all comparisons (*P* <.001), with TAT1 prominently contributing to TAT3 prolongation (from 48 minutes to 108 minutes) and exceeding the recommended 60-minute criteria. The TAT2 was extended from 33 minutes to 49 minutes.

Conclusion

An ED reorganization compromised the usual laboratory services for patients in the ED, with manual specimen delivery being the main cause for TAT prolongation.

DETAIL

Subjek:	Laboratories; Coronaviruses; Pandemics; COVID-19
Pengidentifikasi/kata kunci:	preanalytical phase; emergency department; COVID-19; specimen delivery; turnaround time; emergency laboratory
Judul:	COVID-19 Pandemic Once Again Exposes the Weakest Link in Laboratory Services: Specimen Delivery
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Comparison of Turbidimetric Inhibition Immunoassay, High-Performance Liquid Chromatography, and Capillary Electrophoresis Methods for Glycated Hemoglobin Determination

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Objective

The purpose of this study was to compare the performances of and evaluate the agreement among glycated hemoglobin values analyzed by using National Glycohemoglobin Standardization Program-certified and International Federation of Clinical Chemistry-standardized analyzers.

This cross-sectional study was conducted at the

Armed Forces Institute of Pathology, Department of Chemical Pathology from March 2019 to May 2019.

Methods

Glycated hemoglobin (HbA_{1c}) was measured in the blood specimens from 100 patients on an ADVIA 1800 by a turbidimetric inhibitory immunoassay (TINIA), Sebia instrument by electrophoresis, and Bio-Rad Variant II Turbo system by high-performance liquid chromatography (HPLC). Quantitative variables were calculated as the mean ± standard deviation (SD). Precision and method comparisons were carried out according to Clinical and Laboratory Standards Institute recommendations. The results obtained from each analyzer were compared by correlation analysis. Method comparison was done by linear regression and Bland-Altman plots using the SPSS software version 24.

Results

The mean ± SD HbA_{1c} values from TINIA, electrophoresis, and HPLC were 7.188% ± 1.89%, 7.164% ± 1.866%, and 7.160% ± 1.85%, respectively. The between-run coefficients of variation for TINIA, electrophoresis, and HPLC were 0.64%, 0.61%, and 0.60%, respectively. All 3 showed good correlation (TINIA, R^2 = .994, P = .00; electrophoresis, R^2 = .992, P = 0.00; and HPLC, R^2 = .994, P = 0.00).

Conclusion

The good clinical agreements of HbA_{1c} and strong correlations between analyzers indicate that these analyzers can be used interchangeably.

DETAIL

Subjek:	Hemoglobin; Chromatography; Immunoassay; Diabetes
Pengidentifikasi/kata kunci:	comparison, chromatography; diabetes; glycated hemoglobin; electrophoresis; immunoassay
Judul:	Comparison of Turbidimetric Inhibition Immunoassay, High-Performance Liquid Chromatography, and Capillary Electrophoresis Methods for Glycated Hemoglobin Determination
Pengarang:	Gilani, Mehwish1; Mohammad Aamir1; Ammad Akram2; Zujaja Hina Haroon1; Ijaz, Aamir3; Muhammad Tahir Khadim11 Armed Forces Institute of Pathology, Rawalpindi, Pakistan2 Pak Emirates Military Hospital, Rawalpindi, Pakistan3 Rehman Medical Institute, Peshawar, Pakistan
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Unexpected Cholera Bacteremia in a 91 Year Old Caucasian Male Patient

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ABSTRAK (ENGLISH)

Cholera is an illness caused by *Vibrio cholerae*; its main symptom is acute watery diarrhea. Some infections are asymptomatic or result in patients presenting with mild diarrhea, but complications, such as bacteremia, can be fatal. Being endemic in Africa, Southeast Asia, and Haiti, *V. cholerae* infection cases in the United States are primarily considered travel-related. Herein, we report a case of a 91 year old Caucasian man, a Texas Gulf Coast resident, who developed bacteremia due to *V. cholerae* despite having no international travel history. Culture workup by mass spectrometry, automated biochemical system, and 16S ribosomal RNA (rRNA) gene sequencing confirmed *V. cholerae.* This case conveys an important reminder to clinicians and laboratory professionals regarding potentially serious cholera illnesses due to the domestic prevalence of *V. cholerae* in the coastal regions of the United States.

DETAIL

Subjek:	Cholera
Lokasi:	United States--US
Pengidentifikasi/kata kunci:	cholera; Vibrio cholerae; bacteremia; Gulf Coast; domestic; non-toxigenic
Judul:	Unexpected Cholera Bacteremia in a 91 Year Old Caucasian Male Patient
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Unexpected Short-Tandem-Repeat Patterns in Posttransplant Chimerism Testing: Investigation of 3 Cases with Help from Forensic Science

Gvozdjan, Kristina [1] ; Casey, Heather [1] ; Mowery, Carrie [1] ; Kumer, Lorie [1] ; Fisher, Carolyn [1] ; Tyler, Jennifer [1] ; Bayerl, Mike G [1] ; Malysz, Jozef [1] ; Naik, Seema [2] ; Rybka, Witold [2] ; Ehmann, Christopher [2] ; Claxton, David [2] ; Shin Mineishi [2] ; Baker, Maria [2] ; Zheng, Hong [2] ; Shike, Hiroko [1]

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ABSTRAK (ENGLISH)

Chimerism testing by short tandem repeats (STRs) is used to monitor engraftment after allogeneic hematopoietic stem cell transplantation (HSCT). Generally, STR alleles are stable and transferred from parent to child or from donor to recipient. However, 3 cases did not follow this norm. Additional work-up with help from forensic literature solved these mysteries.

In case 1, the patient received HSCT from his son. The son shared STR alleles in 22/23 loci except Penta E, which was explained by repeat expansion in the son.

In case 2, the patient had been in remission for 14 years after HSCT for lymphoma and developed repeat expansion in CSF1PO in granulocytes.

In case 3, a pre-HSCT patient demonstrated 3 alleles, with 2 peaks taller than the third, in the FGA locus (chromosome 4). A combination of a triallelic variant and leukemia-associated trisomy 4 explained the finding. STR number variants are rare and clinically inconsequential but can overlap malignancy-associated, clinically significant changes.

DETAIL

Subjek:	Laboratories; Chromosomes; Remission (Medicine); Bone marrow; Forensic sciences; Antigens; Leukemia; Lymphoma; Blood; Mutation; Stem cell transplantation
Pengidentifikasi/kata kunci:	STR; atypical STR; unexpected STR; triallelic STR; STR mutation; repeat gain
Judul:	Unexpected Short-Tandem-Repeat Patterns in Posttransplant Chimerism Testing: Investigation of 3 Cases with Help from Forensic Science
Pengarang:	Gvozdjan, Kristina1; Casey, Heather1; Mowery, Carrie1; Kumer, Lorie1; Fisher, Carolyn1; Tyler, Jennifer1; Bayerl, Mike G1; Malysz, Jozef1; Naik, Seema2; Rybka, Witold2; Ehmann, Christopher2; Claxton, David2; Shin Mineishi2; Baker, Maria2; Zheng, Hong2; Shike, Hiroko1 1 Department of Pathology, Penn State Milton S. Hershey Medical Center, Hershey, PA2 Department of Hematology Oncology, Penn State Milton S. Hershey Medical Center, Hershey, PA
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T-Cell Molecular Modulation Responses in Atherosclerosis Anergy

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ABSTRAK (ENGLISH)

Atherosclerosis continues to be a major cause of death in patients with cardiovascular diseases. The cooperative role of immunity has been recently considered in atherosclerotic plaque inflammation, especially adaptive immune response by T cells. In this review, we examine the possible role of T cells in atherosclerosis-mediated inflammation and conceivable therapeutic strategies that can ameliorate complications of atherosclerosis. The cytokines secreted by T-lymphocyte subsets, different pathophysiological profiles of microRNAs (miRs), and the growth factor/receptor axis have diverse effects on the inflammatory cycle of atherosclerosis. Manipulation of miRNA expression and prominent growth factor receptors involved in inflammatory cytokine secretion in atherosclerosis can be considered diagnostic biomarkers in the induction of anergy and blockade of atherosclerotic development. This manuscript reviews immunomodulation of T cells responses in atherosclerosis anergy.

DETAIL

Subjek:	Growth factors; Lymphocytes; MicroRNAs; Atherosclerosis
Pengidentifikasi/kata kunci:	t-lymphocyte; atherosclerosis; therapeutic; microrna; cholesterol; anergy
Judul:	T-Cell Molecular Modulation Responses in Atherosclerosis Anergy
Pengarang:	Pakzad, Bahram1; Rajae, Elham2; Shahrabi, Saeid3; Mansournezhad, Somayeh4; Davari, Nader4; Azizidoost, Shirin4; Najmaldin Saki4 1 Internal Medicine Department, Isfahan University of Medical Sciences, Isfahan, Iran2 Department of Rheumatology, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran3 - Department of Biochemistry and Hematology, Faculty of Medicine, Semnan University of Medical Sciences, Semnan, Iran4 Thalassemia and Hemoglobinopathy Research Center, Research Institute of Health, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
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Soluble CD14 Subtype in Peripheral Blood is a Biomarker for Early Diagnosis of Sepsis

Zhou, Wuqiong [1] ; Rao, Heping [2] ; Ding, Qiuming [1] ; Xiang, Lou [1] ; Shen, Jianjiang [1] ; Ye, Bin [3] ; Xiang, Caixia [4] [1] Department of Diagnosis, Shengzhou People's Hospital (the First Affiliated Hospital of Zhejiang University Shengzhou Branch), Shaoxing, Zhejiang, China [2] Department of Nursing, School of Medicine, Quzhou College of Technology, Quzhou, Zhejiang, China [3] Intensive Care Unit, Shaoxing, Zhejiang, China [4] Department of Pediatrics, Shengzhou People's Hospital (the First Affiliated Hospital of Zhejiang University Shengzhou Branch), Shaoxing, Zhejiang, China

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Objective

To study the value of serum soluble CD14 subtype (sCD14-ST) in early diagnosis of sepsis.

Methods

Seventy-two patients were diagnosed with systemic inflammatory response syndrome, sepsis, or septic shock. Peripheral blood was collected at 0, 12, 24, and 48 hours after admission to the hospital. Levels of sCD14-ST, procalcitonin (PCT), hypersensitive C-reactive protein (CRP), and white blood cells (WBC) were determined.

Results

Levels of sCD14-ST in the patients with septic shock were higher than those in the other patients (P <.01) and peaked at 48 h. PCT and CRP levels were similar in the patients at admission but increased by 5 times to 10 times in the next 48 h, especially in the patients with septic shock. WBC levels remained high and did not change dramatically. Receiver operating characteristic analysis revealed that the area under the curve, sensitivity, and specificity values of sCD14-ST to diagnose sepsis were much higher than those of the other markers.

Conclusion

Compared with PCT, CRP, and WBC, sCD14-ST is a better biomarker for the early diagnosis of sepsis.

DETAIL

Subjek:	Biomarkers; Sepsis; Medical diagnosis
Pengidentifikasi/kata kunci:	soluble CD14 subtype; sepsis; procalcitonin; C-reactive protein; white blood cell; diagnosis; biomarker
Judul:	Soluble CD14 Subtype in Peripheral Blood is a Biomarker for Early Diagnosis of Sepsis
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Detection of Circulating Antibodies to p16 Protein-Derived Peptides in Hepatocellular Carcinoma

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ABSTRAK (ENGLISH)

Objective

This study aimed at confirming the alteration of circulating anti-p16 immunoglobulin G (IgG) levels in hepatocellular carcinoma (HCC).

Methods

An in-house-developed enzyme-linked immunosorbent assay was used for determining plasma IgG antibodies against p16-derived antigens in 122 HCC patients and 134 healthy controls.

Results

Plasma anti-p16 IgG levels were significantly higher in HCC patients than in the controls ($Z = 3.51$, $P = 0.0004$), with no difference between males and females. A trend of increasing plasma anti-p16 IgG levels was associated with increasing HCC stage, with group 3 patients having the highest anti-p16 IgG levels ($Z = 3.38$, $P = 0.0008$). Group 3 exhibited the best sensitivity (19.6%) and specificity (95%) for plasma anti-p16 IgG detection, with an area under the receiver operating characteristic curve of 0.659 (95% confidence interval, 0.564–0.754).

Conclusion

Circulating IgG antibody to p16 protein might be a useful biomarker for HCC prognosis assessment rather than for early malignancy diagnosis.

DETAIL

Subjek:	Plasma; Liver cancer
Pengidentifikasi/kata kunci:	autoantibody; biomarker; hepatocellular carcinoma; p16 protein; tumor-associated antigens; receiver operating characteristic
Judul:	Detection of Circulating Antibodies to p16 Protein-Derived Peptides in Hepatocellular Carcinoma
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Clinical Laboratory Employees' Attitudes Toward Artificial Intelligence

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ABSTRAK (ENGLISH)

Objective

The objective of this study was to determine the attitudes of laboratory personnel toward the application of artificial intelligence (AI) in the laboratory.

Methods

We surveyed laboratory employees who covered a range of work roles, work environments, and educational levels.

Results

The survey response rate was 42%. Most respondents (79%) indicated that they were at least somewhat familiar with AI. Very few (4%) classified themselves as experts. Contact with AI varied by educational level (P = .005). Respondents believed that AI could help them perform their work by reducing errors (24%) and saving time (16%). The most common concern (27%) was job security (being replaced by AI). The majority (64%) of the respondents expressed support for the development of AI projects in the organization.

Conclusions

Laboratory employees see the potential for AI and generally support the adoption of AI tools but have concerns regarding job security and quality of AI performance.

DETAIL

Ketentuan indeks bisnis:	Subjek: Employees Employment security
Pengidentifikasi/kata kunci:	artificial intelligence; machine learning; employee attitudes; survey; clinical laboratory; laboratory personnel
Judul:	Clinical Laboratory Employees' Attitudes Toward Artificial Intelligence
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Terakhir diperbarui:	2021-01-08
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Scientific Evidence, Medical Practice, and the Insidious Danger of Anecdotal Reports

Bertholf, Roger L

DETAIL

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Phenotypes Associated with 16p11.2 Copy Number Gains and Losses at a Single Institution

Chu, Caleb [1] ; Wu, Haotian [2] ; Xu, Fangling [2] ; Ray, Joseph W [3] ; Britt, Allison [3] ; Robinson, Sally S [3] ; Lupo, Pamela J [3] ; Murphy, Christine R C [3] ; Dreyer, Charles F [3] ; Lee, Phillip D K [3] ; Hu, Peter C [1] ; Dong, Jianli [2] [1] School of Health Professions, University of Texas MD Anderson Cancer Center, Houston, Texas [2] Department of Pathology, University of Texas Medical Branch, Galveston, Texas [3] Department of Pediatrics, University of Texas Medical Branch, Galveston, Texas

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Chromosome 16p11.2 is one of the susceptible sites for recurrent copy number variations (CNVs) due to flanking near-identical segmental duplications. Five segmental duplications, named breakpoints 1 to 5 (BP1–BP5), have been defined as recombination hotspots within 16p11.2. Common CNVs on 16p11.2 include a proximal ~593 kb between BP4 and BP5, and a distal ~220 kb between BP2 and BP3. We performed a search for patients carrying 16p11.2 CNVs, as detected using chromosome microarray (CMA), in the Molecular Diagnostic Laboratory at the University of Texas Medical Branch (UTMB), in Galveston. From March 2013 through April 2018, a total of 1200 CMA results were generated for germline testing, and 14 patients tested positive for 16p11.2 CNVs, of whom 7 had proximal deletion, 2 had distal deletion, 4 had proximal duplication, and 1 had distal duplication. Herein, we provide detailed phenotype data for these patients. Our study results show that developmental delay, abnormal body weight, behavioral problems, and hypotonia are common phenotypes associated with 16p11.2 CNVs.

DETAIL

Subjek:	Laboratories; Autism; Chromosomes; Medical records; Patients; Scoliosis; Microcephaly; Body mass index; Obesity
Pengidentifikasi/kata kunci:	chromosome 16p11.2; copy number variation; chromosome microarray; genotype-phenotype correlation; developmental delay; phenotypic heterogeneity
Judul:	Phenotypes Associated with 16p11.2 Copy Number Gains and Losses at a Single Institution

Pengarang:	Chu, Caleb1; Wu, Haotian2; Xu, Fangling2; Ray, Joseph W3; Britt, Allison3; Robinson, Sally S3; Lupo, Pamela J3; Murphy, Christine R C3; Dreyer, Charles F3; Lee, Phillip D K3; Hu, Peter C1; Dong, Jianli21 School of Health Professions, University of Texas MD Anderson Cancer Center, Houston, Texas2 Department of Pathology, University of Texas Medical Branch, Galveston, Texas3 Department of Pediatrics, University of Texas Medical Branch, Galveston, Texas
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Hak cipta:	
Terakhir diperbarui:	2021-09-21
Basis data:	Public Health Database

Presepsin and Midregional Proadrenomedullin in Pediatric Oncologic Patients with Febrile Neutropenia

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ABSTRAK (ENGLISH)

Objective

In this study, we investigated the roles of presepsin (PSP) and midregional proadrenomedullin (mr-proADM) in children with febrile neutropenia (FN) due to chemotherapy.

Methods

We assessed 36 FN episodes in 26 children. Patients were classified into bacteremia (B) and fever of unknown origin (FUO) groups. We evaluated PSP and mr-proADM at admission (T0), after 24/48 h (T1), and after 5 days (T2).

Results

PSP and mr-proADM levels were elevated at T0 and significantly decreased at T2. mr-proADM levels did not significantly differ between the B and FUO groups. PSP levels significantly differed between the B and FUO groups only at T1. Both PSP and mr-proADM levels at T0 were a predictor of length of hospital stay but not of the duration of fever. Finally, receiver operating characteristic curve analysis showed that PSP and mr-proADM had low diagnostic accuracy for blood culture positivity.

Conclusion

PSP and mr-proADM display poor clinical usefulness for FN in oncologic children.

DETAIL

Subjek:	Neutropenia; Pediatrics

Pengidentifikasi/kata kunci:	Presepsin; mr-proADM; Adrenomedullin; neutropenia; fever; pediatric; oncologic; malignancies
Judul:	Presepsin and Midregional Proadrenomedullin in Pediatric Oncologic Patients with Febrile Neutropenia
Pengarang:	Agnello, Luisa1; Bivona, Giulia1; Parisi, Elisa2; Giuseppe Dejan Lucido3; Iacona, Alessandro4; Ciaccio, Anna Maria5; Giglio, Rosaria Vincenza4; Ziino, Ottavio2; Ciaccio, Marcello6 1 Department of Biomedicine, Neurosciences and Advanced Diagnostics, Institute of Clinical Biochemistry, Clinical Molecular Medicine and Laboratory Medicine, University of Palermo, Palermo, Italy2 Pediatric Hematology and Oncology, ARNAS Civico Hospital, Palermo, Italy3 Department of Earth and Sea Sciences, Palermo, Italy4 Department of Laboratory Medicine, Palermo, Italy5 University of Palerm o, Palermo, Italy6 Department of Biomedicine, Neurosciences and Advanced Diagnostics, Institute of Clinical Biochemistry, Clinical Molecular Medicine and Laboratory Medicine, University of Palermo, Palermo, Italy; Department of Laboratory Medicine, Palermo, Italy
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Molecular Epidemiology of Carbapenem-Resistant Enterobacterales Strains Isolated from Blood Cultures in Antalya, Turkey

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ABSTRAK (ENGLISH)

Objective

The aim of this study was to investigate the prevalence of carbapenemase and CTX-M genes among 330 blood culture isolates of Enterobacterales with reduced susceptibility to at least 1 carbapenem, between 2010 and 2015.

Methods

BD Max CRE assay and in-house PCR were used to detect carbapenemase and CTX-M genes.

Results

At least 1 carbapenemase gene was detected among 113 (74.3%) of the 152 carbapenem resistant isolates. The OXA-48 (69.7%) was the most common carbapenemase followed by VIM, NDM and IMP, whereas no tested isolates were KPC-positive. Eighty-six isolates (56.6%) had CTX-M and 65 had both OXA-48 and CTX-M. Carbapenemase production in Enterobacterales was significantly increased in years (P <.05).

Conclusion

Our study indicates that there is ongoing endemic circulation of the OXA-48 producing organism in our facility. It is noteworthy that more than half of the OXA-48 producing strains also produced CTX-M enzyme.

DETAIL

Subjek:	Antibiotics
Pengidentifikasi/kata kunci:	carbapenem resistant enterobacteriaceae; carbapenemase-producing carbapenem-resistant Enterobacteriaceae; CTX –M; bloodstream isolates; Enterobactericeae isolates; OXA-48
Judul:	Molecular Epidemiology of Carbapenem-Resistant Enterobacterales Strains Isolated from Blood Cultures in Antalya, Turkey
Pengarang:	Su, Harun Reşid1; Turhan, Özge2 ; Cemile Aylin Erman Daloğlu3; Öğünç, Meral Dilara3 ; Özhak, Betil3; Öngüt, Gözde3; Mert Ahmet Kuşkucu4; Midilli, Kenan4; Mamıkoğlu, Latife21 Tokat Hospital, Tokat, Turkey2 Department of Infectious Disease and Clinical Microbiology, University School of Medicine, Akdeniz University, Anta lya, Turkey3 Department of Medical Microbiology, University School of Medicine, Akdeniz University, Antalya, Turkey4 Department of Medical Microbiology, University Cerrahpaşa School of Medicine, Istanbul University, Istanbul, Turkey
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Quantification by Ultrafiltration and Immunofixation Electrophoresis Testing for Monoclonal Serum Free Light Chains

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ABSTRAK (ENGLISH)

Objective

Measurement of monoclonal immunoglobulins is a reliable estimate of the plasma cell tumor mass. About 15% of plasma cell myelomas secrete light chains only. The concentration of serum free light chains is insufficient evidence of the monoclonal light chain burden. A sensitive quantitative estimate of serum free monoclonal light chains could be useful for monitoring patients with light chain myeloma. We describe such an assay that does not require mass-spectrometry equipment or expertise.

Methods

Serum specimens from patients with known light chain myelomas and controls were subjected to ultrafiltration through a membrane with pore size of 50 kDa. The filtrate was concentrated and tested by immunofixation electrophoresis. The relative area under the monoclonal peak, compared to that of the total involved light chain composition, was estimated by densitometric scanning of immunofixation gels. The proportion of the area occupied by the monoclonal peak in representative densitometric scans was used to arrive at the total serum concentration of the monoclonal serum free light chains.

Results

Using an ultracentrifugation and concentration process, monoclonal serum free light chains were detectable, along with polyclonal light chains, in all 10 patients with active light chain myelomas. Monoclonal light chains were identified in serum specimens that did not reveal monoclonal light chains by conventional immunofixation electrophoresis. The limit of detection by this method was 1.0 mg/L of monoclonal serum free light chains.

Conclusion

The method described here is simple enough to be implemented in academic medical center clinical laboratories and does not require special reagents, equipment, or expertise. Even though urine examination is the preferred method for the diagnosis of light chain plasma cell myelomas, measurement of the concentration of serum free light chains provides a convenient, albeit inadequate, way to monitor the course of disease. The method described here allows effective electrophoretic differentiation of monoclonal serum free light chain from polyclonal serum free light chains and provides a quantitation of the monoclonal serum free light chains in monitoring light chain monoclonal gammopathies.

DETAIL

Subjek:	Light
Pengidentifikasi/kata kunci:	plasma cell myeloma; light chain myeloma; ultrafiltration; immunofixation electrophoresis; monoclonal serum free light chains; multiple myeloma
Judul:	Quantification by Ultrafiltration and Immunofixation Electrophoresis Testing for Monoclonal Serum Free Light Chains
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Verification of 20 Mathematical Formulas for Discriminating Between Iron Deficiency Anemia and Thalassemia Trait in Microcytic Anemia

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ABSTRAK (ENGLISH)

Background

Currently, more than 45 mathematical formulas based on simple red blood cell (RBC) parameters have been proposed for differentiating between iron deficiency and thalassemia in microcytic anemia, of which 20 are relatively new and have not been thoroughly independently verified. The study goal was to verify these 20 new formulas and to identify which RBC parameters have a decisive impact on the performance of those formulas.

Methods

A database containing laboratory and diagnostic data from 2788 subject individuals with microcytic anemia was used for assessing performance by receiver operating characteristic (ROC) analysis.

Results

The new Index26 had excellent performance, equivalent to the Green and King, Jayabose, and Janel formulas previously identified in the literature. The discriminant power of nearly all newer formulas was lower in our study than that claimed by the original authors. We discovered that a well-performing formula requires mean cell volume (MCV), RBC distribution width (RDW), and RBC measurements, whereas hemoglobin measurements appeared not to be essential.

Conclusions

Only the new Index26 performed at a level comparable to the very strongest established formulas. All other new formulas had lower performance than was claimed in the original publications, underscoring that independent verification of new formulas is indispensable.

DETAIL

Subjek:	Anemia; Medical diagnosis
Pengidentifikasi/kata kunci:	hematology; clinical pathology; thalassemia; microcytic anemia; iron deficiency anemia; discriminant formula; diagnostic performance
Judul:	Verification of 20 Mathematical Formulas for Discriminating Between Iron Deficiency Anemia and Thalassemia Trait in Microcytic Anemia
Pengarang:	Johannes J M L Hoffmann1 ; Urrechaga, Eloísa21 H3L Consult, Nuenen, The Netherlands2 CORE Laboratory, Hospital Galdakao—Usansolo, Galdakao, Spain
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Basis data:	Public Health Database

Incident Command in the Time of COVID-19

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ABSTRAK (ENGLISH)

The SARS-CoV-2 virus was initially contained in China but rapidly spread across the globe. The grave threat was not apparent until it was already in our midst. Our organization implemented an Incident Command System (ICS), based on previous experience, to respond to the COVID-19 pandemic in a comprehensive and effective manner. This well-known management and response framework is used by many specialties and organizations in disasters of different complexity and size. Our ICS was able to assemble the appropriate people, assess the situation, and develop and implement plans to deal with the COVID-19 crisis. The effectiveness of the ICS structure and its execution was instrumental in getting in front of the virus and managing regional activities. The ICS is an effective tool to improve safety and mitigate risk when dealing with large-scale disasters and should be implemented and practiced before the need arises.

Our organization implemented a formal Incident Command System (ICS) very early as a response to the COVID-19 pandemic. Although it recently disbanded, we are maintaining its core functionality and communication as we continue to deal with COVID-19 into the future. The author has observed the ICS being used at hospitals through hurricanes, blizzards, and riots but never saw it work as well as it did during the initial weeks of the pandemic. This group deftly navigated through uncharted waters by leveraging the spirit and structure of Incident Command.

DETAIL

Subjek:	Severe acute respiratory syndrome coronavirus 2; Coronaviruses; Pandemics; COVID-19
Pengidentifikasi/kata kunci:	management; operations; incident command; COVID; supply chain; pandemic
Judul:	Incident Command in the Time of COVID-19
Pengarang:	Cook, Jim1 1 Laboratory Services, Houston Methodist, Houston, Texas, USA
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Basis data:	Public Health Database

Serum and Saliva Levels of Cancer Antigen 15-3, Carcinoembryonic Antigen, Estradiol, Vaspin, and Obestatin as Biomarkers for the Diagnosis of Breast Cancer in Postmenopausal Women

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ABSTRAK (ENGLISH)

Objective

To find suitable biomarkers for diagnosis of Breast cancer in serum and saliva; also, to examine the correlation between salivary and serum concentrations of suitable biomarkers.

Methods

This case-control study included 30 women with breast cancer as a case group and 30 healthy women as a matched control group. Blood and saliva specimens were collected from all participants. We evaluated serum and salivary cancer antigen 15-3 (CA15-3), carcinoembryonic antigen (CEA), estradiol, vaspin, and obestatin concentrations. Mann-Whitney *U* testing and Spearman correlation coefficients were used for statistical analysis.

Results

Serum and salivary concentrations of estradiol were significantly higher in patients with breast cancer (BC) than in healthy women (P <.05). Also, serum CEA and salivary obestatin concentrations were significantly higher in BC patients than in the control group (P <.05). However, there was no significant difference between other parameters in patients with BC and controls. We observed a positive correlation between serum and salivary concentrations of CA15-3, as well as a negative correlation between serum and salivary concentrations of vaspin and obestatin.

Conclusion

The results of this study demonstrated that concentrations of CEA and estradiol in serum, obestatin in serum and saliva, and estradiol in saliva were significantly different between the 2 groups.

DETAIL

Subjek:	Biomarkers; Antigens; Breast cancer; Medical diagnosis
Pengidentifikasi/kata kunci:	breast cancer; saliva; serum; vaspin; obestatin; estradiol; CA15-3; CEA
Judul:	Serum and Saliva Levels of Cancer Antigen 15-3, Carcinoembryonic Antigen, Estradiol, Vaspin, and Obestatin as Biomarkers for the Diagnosis of Breast Cancer in Postmenopausal Women
Pengarang:	Farahani, Hyder1; Amri, Jamal2; Alaee, Mona2; Mohaghegh, Fathollah3; Rafiee, Mohammad41 Department of Clinical Biochemistry and Genetic, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran2 Department of Clinical Biochemistry and Genetic, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran; Traditional and Complementary Medicine Research Center, Arak University of Medical Sciences, Arak, Iran3 Department of Radiotherapy Oncology, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran4 Department of Biostatistics and Epidemiology, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran
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URL Dokumen:	https://www.proquest.com/scholarly-journals/serum-saliva-levels-cancer-antigen-15-3/docview/2476165788/se-2?accountid=211160

Intraosseous Specimens Submitted to the Laboratory: A Case Report and Review

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ABSTRAK (ENGLISH)

Intraosseous (IO) devices are used for vascular access in settings where venous access is initially unobtainable, such as prehospital trauma care or cardiac arrest. While IO devices are effective for infusion of blood, fluids, and medications, there is limited data on the analytical equivalence of specimens taken out of IO devices and peripheral venous blood. Despite this, IO device manufacturers and clinical resources state that IO specimens can be submitted for laboratory analysis. As reported in this case, IO specimens may be drawn and labeled as ‘peripheral blood’. IO specimens are not always caught by automated sample quality testing and may proceed through analysis without any warning signal to the laboratory. There are potential regulatory risks in accepting IO samples for analysis without validation. IO infusion is a valuable technique for vascular access in critically ill patients, but clinical laboratories will need to determine their own policies for identifying and handling IO specimens.

DETAIL

Subjek:	Laboratories; Case reports
Judul:	Intraosseous Specimens Submitted to the Laboratory: A Case Report and Review
Pengarang:	Song, Linda1; Koka, Rima1; Reese, Erika2; Mullins, Kristin1; Murphy, Colin1 1 Department of Pathology, University of Maryland School of Medicine, Baltimore, MD2 Division of Transfusion Medicine, University of Maryland Medical Center, Baltimore, MD
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Basis data:	Public Health Database

Intravenous Immunoglobulin-Associated Hemolytic Anemia

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Intravenous immunoglobulin (IVIG) is an important therapeutic tool for the treatment of a variety of conditions, including immune thrombocytopenic purpura (ITP). Although IVIG has many approved indications and is typically well tolerated, a number of adverse effects have been reported. Hemolysis is a documented but under-recognized adverse effect associated with large individual or cumulative doses of IVIG. Hemolytic complications are typically mild and detected incidentally when screening tests, such as a complete blood count (CBC) showing decreased hemoglobin or a complete metabolic panel (CMP) resulting in elevated bilirubin, are performed for another reason. Herein, we report a case of significant hemolytic anemia in a 59 year old Caucasian woman, who required packed red blood cell transfusion after administration of IVIG for the treatment of ITP. Increased awareness of the potential for clinically significant hemolysis after the use of moderate cumulative doses of IVIG is needed, particularly in patients with risk factors for hemolysis.

DETAIL

Subjek:	Anemia; Immunoglobulins
Judul:	Intravenous Immunoglobulin-Associated Hemolytic Anemia
Pengarang:	Jacobs, Jeremy1 ; Kneib, Jessica1; Gabbard, Amy11 Department of Pathology, Microbiology and Immunology, Vanderbilt University Medical Center, Nashville, Tennessee
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Bahasa publikasi:	English

Interference of M-protein on Thrombin Time Test: A Case Report

Njegovan, Milena [1] ; Margetić, Sandra [1] ; Kuna, Andrea Tešija [1] ; Đerek, Lovorka [1] ; Ćelap, Ivana [1] ; Pavičić, Tomislav [1] ; Čaržavec, Dubravka [2] ; Gaćina, Petar [2] [1] Departments of Clinical Chemistry, Zagreb, Croatia [2] Departments of Internal Medicine, Sestre Milosrdnice University Hospital Center, Zagreb, Croatia

ABSTRAK (ENGLISH)

Objective

A case of interference of monoclonal protein (M-protein) on thrombin time (TT) test in a 39-year-old Caucasian male patient is presented.

Methods

Coagulation screening tests were performed where altered results only for TT result (>150 seconds) and activated

partial thromboplastin time (aPTT) result (36 seconds) were measured. Further specific coagulation testing included measurement of individual coagulation factors FII, FV, FVII, FVIII, FIX, FX, FXI, and FXII. Diagnostic steps in detection and identification of monoclonal protein included serum protein electrophoresis and immunofixation (both serum and urine specimen).

Results

Monoclonal protein immunoglobulin G kappa detection and identification in serum and urine clarified the situation.

Conclusion

Unexpectedly altered results of screening coagulation tests without any appropriate clinical signs and symptoms in a patient without any anticoagulant therapy needs to be critically considered in the context of extended next diagnostic steps in order to clarify the cause of pathological test results.

DETAIL

Subjek:	Proteins; Case reports
Pengidentifikasi/kata kunci:	M-protein; thrombin time test; interference; coagulation; immunology; hematology
Judul:	Interference of M-protein on Thrombin Time Test: A Case Report
Pengarang:	Njegovan, Milena1 ; Margetić, Sandra1; Kuna, Andrea Tešija1 ; Đerek, Lovorka1; Ćelap, Ivana1 ; Pavičić, Tomislav1; Čaržavec, Dubravka2; Gaćina, Petar21 Departments of Clinical Chemistry, Zagreb, Croatia2 Departments of Internal Medicine, Sestre Milosrdnice University Hospital Center, Zagreb, Croatia
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Basis data:	Public Health Database

Roger L. Bertholf, PhD, Editor in Chief, 2012-Present

DETAIL

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Development and Clinical Validation of a Multiplex Gene Fusion Assay

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Southwestern Medical Center; Department of Pathology, Children’s Medical Center; Eugene McDermott Center for Human Growth and Development, UT Southwestern Medical Center, Dallas, TX

ABSTRAK (ENGLISH)

Objective

The detection of gene fusion events is important for the diagnosis and management of malignancies. In this study, we describe the validation of a next-generation sequencing assay for multiplex detection of gene fusions.

Methods

Based on previously described gene fusion events that occur in pediatric oncology, a custom anchored multiplex next-generation sequencing assay was designed to target 93 genes.

Results

A total of 24 previously characterized specimens were examined. Twenty specimens had 1 or more previously described fusion events, and 4 specimens were negative for fusion events. The accuracy across specimens was 100% (20 of 20 specimens). The analytical sensitivity and specificity were both 100%. Interday reproducibility for fusion events was 94%; in comparison, intraday reproducibility was 90%.

Conclusion

This multiple-gene fusion assay demonstrated appropriate sensitivity, specificity, and accuracy for clinical use. We anticipate that this assay will improve the diagnosis and management of patients with pediatric solid tumors.

DETAIL

Subjek:	Pediatrics
Pengidentifikasi/kata kunci:	anchored multiplex PCR sequencing; gene fusion events; pediatric tumors; RNAseq; gene fusion; anchored multiplex; genomic; pediatric oncology
Judul:	Development and Clinical Validation of a Multiplex Gene Fusion Assay
Pengarang:	García, Rolando1; Patel, Nirav2; Uddin, Naseem1; Park, Jason Y3 1 Department of Pathology, UT Southwestern Medical Center; Department of Pathology, Children’s Medical Center2 Department of Pathology, Children’s Medical Center3 Department of Pathology, UT Southwestern Medical Center; Department of Pathology, Children’s Medical Center; Eugene McDermott Center for Human Growth and Development, UT Southwestern Medical Center, Dallas, TX
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Basis data:	Public Health Database

Serum Folate of Less than 7.0 ng/mL is a Marker of Malnutrition

Kozman, Diana [1] ; Mattox, Samantha [1] ; Singh, Gurmukh [1]
[1] Department of Pathology, Medical College of Georgia at Augusta University, Augusta, GA

ABSTRAK (ENGLISH)

Objective

To identify clinical/laboratory factors associated with folate deficiency in tertiary care patients.

Methods

We reviewed the medical records of 1019 patients with serum folate <7.0 ng/mL, 301 patients with serum folate of 15 ng/mL, and 300 patients with serum folate >23 ng/mL.

Results

Serum prealbumin levels were subnormal in 54.8% of patients with serum folate <7.0 ng/mL. Vitamin B12, hemoglobin, and serum albumin levels were significantly lower in the <7.0 ng/mL folate group. In 62.4% of patients with serum folate <7.0 ng/mL, 1 or more markers of malnutrition were present. The low-folate group had a significantly higher prevalence of gastrointestinal (GI) disorders, sepsis, and abnormal serum creatinine level. There were no significant differences in the 2 groups regarding diabetes; behavioral/neurological disorders, including drug and alcohol abuse; bariatric surgery; or a diagnosis of malnutrition. The average body mass index (BMI) for the <7.0 ng/mL and 15 ng/mL folate groups was significantly different (28.89 and 28.31, respectively), although the difference does not appear to be clinically meaningful.

Conclusions

The prevalence of folate deficiency depends on what is considered a normal serum folate level. Approximately 10% of tertiary-care patients have levels <7.0 ng/mL and exhibit other markers of malnutrition. It is recommended that patients with GI disorders, chronic kidney disease, and sepsis be routinely tested for serum folate levels, before administration of vitamin supplements. Patients with serum folate levels <7.0 ng/mL should be evaluated for malnutrition, despite BMI >25. Folate supplementation should be administered only after excluding coexisting vitamin B12 deficiency.

DETAIL

Subjek:	Vitamin deficiency; Gastrointestinal surgery; Malnutrition; Sepsis; Vitamin B; Preservatives
Pengidentifikasi/kata kunci:	serum folate; malnutrition; vitamin B12; tertiary care; prealbumin; BMI
Judul:	Serum Folate of Less than 7.0 ng/mL is a Marker of Malnutrition
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Hak cipta:	
Terakhir diperbarui:	2020-12-30
Basis data:	Public Health Database

The History of Laboratory Medicine Part 5: 2012 – Present; A New Distinction

Strzelecki, Molly [1] ; Swails, Kelly [1 1] ASCP, Chicago, IL

DETAIL

Judul:	The History of Laboratory Medicine Part 5: 2012 – Present; A New Distinction
Pengarang:	Strzelecki, Molly1; Swails, Kelly11 ASCP, Chicago, IL
Judul publikasi:	Labmedicine; Chicago
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The Association between Serum Retinol-Binding Protein 4 Levels and Cardiovascular Events in Patients with Chronic Kidney Disease

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ABSTRAK (ENGLISH)

Objective

The study aimed to assess whether serum retinol-binding protein 4 (RBP4) is associated with a risk of cardiovascular (CV) events in chronic kidney disease (CKD) patients.

Methods

One hundred sixty-nine patients with CKD were followed for a mean of 36 months (range, 5–39 months). Serum RBP4 and other laboratory indicators were measured at baseline. The relationship between RBP4 and the risk of CV events was evaluated by using Cox regression analysis.

Results

Patients with higher serum RBP4 levels had a higher rate of CV events and a higher mortality in a univariate analysis (P <0.001). The multivariate Cox proportional hazard analysis revealed that RBP4 (hazard ratio, 2.259;

95% confidence interval, 2.067–5.489; *P* = 0.002) is an independent prognostic factor for CV events in patients with CKD. Kaplan-Meier analysis demonstrated that patients with RBP4 above the median value (>33.86 mg/L) had a higher rate of CV events than did patients with RBP4 at or below the median value (≤33.86 mg/L; *P* <0.001).

Conclusion

RBP4 levels are associated with CV events in patients with CKD. Elevated serum RBP4 levels may indicate an increased risk of CV complications in CKD patients.

DETAIL

Subjek:	Kidney diseases; Medical prognosis
Pengidentifikasi/kata kunci:	retinol-binding protein 4; chronic kidney disease; cardiovascular event; Cox regression; prognostic value; survival analysis
Judul:	The Association between Serum Retinol-Binding Protein 4 Levels and Cardiovascular Events in Patients with Chronic Kidney Disease
Pengarang:	Su, Yuhao1; Huang, Ying1 ; Jiang, Ying2; Zhu, Meilan21 Department of Cardiovascular Medicine, The Second Affiliated Hospital of Nanchang University, Nanchang, Jiangxi, China2 Department of Rehabilitation, The Second Affiliated Hospital of Nanchang University, Nanchang, Jiangxi, China
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Laboratory Assay Evaluation Demystified: A Review of Key Factors Influencing Interpretation of Test Results Using Different Assays for SARS-CoV-2 Infection Diagnosis

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ABSTRAK (ENGLISH)

Laboratory tests are an integral part of the diagnosis and management of patients; however, these tests are far from perfect. Their imperfections can be due to patient health condition, specimen collection, and/or technological difficulty with performing the assay and/or interpretation. To be useful clinically, testing requires calculation of positive predictive values (PPVs) and negative predictive values (NPVs). During the current global pandemic of COVID-19 (coronavirus disease 2019), multiple assays with unknown clinical sensitivity and specificity have been rapidly developed to aid in the diagnosis of the disease. Due to a lack of surveillance testing, the prevalence of COVID-19 remains unknown. Hence, using this situation as an clinical example, the goal of this article is to clarify

the key factors that influence the PPV and NPV yielded by diagnostic testing, By doing so, we hope to offer health-care providers information that will help them better understand the potential implications of utilizing these test results in clinical patient management.

DETAIL

Subjek:	Laboratories; Severe acute respiratory syndrome coronavirus 2; Coronaviruses; COVID-19; Medical diagnosis
Pengidentifikasi/kata kunci:	clinical interpretation; negative predictive value; positive predictive value; sensitivity; specificity; test parameters
Judul:	Laboratory Assay Evaluation Demystified: A Review of Key Factors Influencing Interpretation of Test Results Using Different Assays for SARS-CoV-2 Infection Diagnosis
Pengarang:	Pham, Huy P1 ; Staley, Elizabeth M2; Raju, Dheeraj3; Marin, Maximo J1; Kim, Chong H41 Department of Pathology, University of Southern California, Los Angeles2 Department of Laboratory Medicine, University of Washington, Seattle3 Cancer Treatment Centers of America, Boca Raton, Florida4 Department of Clinical Pharmacy, University of Colorado Anschutz Medical Campus, Aurora
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About the Journal

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DETAIL

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Basis data:	Public Health Database

Monocytic Maturation Induced by FLT3 Inhibitor Therapy of Acute Myeloid Leukemia: Morphologic and Immunophenotypic Characteristics

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Background

FMS-like tyrosine kinase-3 (FLT3-ITD) mutations are some of the most common mutations in acute myeloid leukemia (AML), and patient outcomes have improved since the advent of tyrosine kinase inhibitors. First, granulocytic differentiation was described in FLT3-positive AML treated with FLT3 inhibitors, and more recently, monocytic differentiation was reported.

Methods

Two patients with myelomonocytic cells in their bone marrow were identified during routine follow-up after AML treatment that included FLT3 inhibitors. The bone marrow study was done as standard of care.

Results

Both patients had FLT3-ITD^{+} AML and showed an atypical maturing monocytic cell population and a decrease in the leukemic blast cell population after FLT3 inhibitor therapy. Concurrent genetic testing revealed persistent genetic abnormalities.

Conclusions

These cases illustrate monocytic maturation in FLT3^{+} AML after FLT3 inhibitor treatment. It is critical for pathologists and clinicians to be aware of the differentiation phenomenon, as these patients have persistent molecular abnormalities despite response to treatment and normalization of blast counts.

DETAIL

Subjek:	Bone marrow; Leukemia; Mutation
Pengidentifikasi/kata kunci:	hematopathology; hematology; FLT3-ITD; FLT3 inhibitor; maturation; terminal differentiation; acute myeloid leukemia
Judul:	Monocytic Maturation Induced by FLT3 Inhibitor Therapy of Acute Myeloid Leukemia: Morphologic and Immunophenotypic Characteristics
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Clinical Usefulness of Hematologic Indices as Predictive Parameters for Systemic Lupus Erythematosus

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ABSTRAK (ENGLISH)

Objective

This study assessed the neutrophil-to-lymphocyte ratio (NLR), platelet-to-lymphocyte ratio (PLR), mean platelet volume, platelet distribution width, and red cell distribution width (RDW) in systemic lupus erythematosus (SLE) patients and their correlation with disease activity.

Methods

Two hundred eight SLE patients and 205 age- and sex-matched healthy controls were included. Disease activity was assessed using the systemic lupus erythematosus disease activity index 2000, and hematological indices were determined.

Results

Lymphocyte and platelet counts were significantly lower in SLE patients than in the controls, while the NLR, PLR, and RDW were significantly higher (P <.05). In patients with active disease, the neutrophil counts, NLR, and PLR were significantly higher than in those with inactive disease (P <.05), while the lymphocyte count was significantly lower (P <.05). Based on receiver operating characteristic curve analyses, only for lymphocyte count and PLR. The area under curve was significantly higher (P = .001 and P = .053, respectively).

Conclusion

PLR can serve as a biomarker for indicating SLE disease activity.

DETAIL

Subjek:	Lymphocytes; Lupus; Neutrophils
Pengidentifikasi/kata kunci:	neutrophil-to-lymphocyte ratio; platelet-to-lymphocyte ratio; mean platelet volume; lymphocyte; neutrophil; platelet; systemic lupus erythematosus
Judul:	Clinical Usefulness of Hematologic Indices as Predictive Parameters for Systemic Lupus Erythematosus
Pengarang:	Peirovy, Amirhossein1; Aida Malek Mahdavi1; Khabbazi, Alireza1 ; Hajialilo, Mehrzad1; Sakhinia, Ebrahim2; Rashtchizadeh, Nadereh11 Connective Tissue Diseases Research Center, Tabriz University of Medical Sciences, Tabriz, Iran2 Connective Tissue Diseases Research Center, Tabriz University of Medical Sciences, Tabriz, Iran; Division of Regenerative Medicine, School of Medicine, Faculty of Medical and Human Sciences, University of Manchester, Manchester, UK
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Basis data:	Public Health Database

Types of Assays for SARS-CoV-2 Testing: A Review

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ABSTRAK (ENGLISH)

Clinical laboratory testing routinely provides actionable results, which help direct patient care in the inpatient and outpatient settings. Since December 2019, a novel coronavirus (SARS-CoV-2) has been causing disease (COVID-19 [coronavirus disease 2019]) in patients, beginning in China and now extending worldwide. In this context of a novel viral pandemic, clinical laboratories have developed multiple novel assays for SARS-CoV-2 diagnosis and for managing patients afflicted with this illness. These include molecular and serologic-based tests, some with point-of-care testing capabilities. Herein, we present an overview of the types of testing available for managing patients with COVID-19, as well as for screening of potential plasma donors who have recovered from COVID-19.

DETAIL

Subjek:	Laboratories; Severe acute respiratory syndrome coronavirus 2; Coronaviruses; COVID-19
Judul:	Types of Assays for SARS-CoV-2 Testing: A Review
Pengarang:	Smithgall, Marie C1; Dowlatshahi, Mitra1; Spitalnik, Steven L1; Hod, Eldad A1; Rai, Alex J1 Department of Pathology and Cell Biology, Columbia University Irving Medical Center, New York City, NY
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Severe Platelet Transfusion Refractoriness in Association with Antibodies Against CD36

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Platelet-transfusion refractoriness (PTR) is common in patients with hematological malignancies. The etiology of immune PTR is typically human leukocyte antigen (HLA) antibodies (Abs) from pregnancy or previous transfusion. Herein, we report PTR in the setting of induction chemotherapy for acute myelogenous leukemia (AML) from Abs against CD36/glycoprotein (GP)IV. A 66-year-old African American woman presented with anemia and thrombocytopenia. She was found to have transfusion-dependent AML, and a 7 + 3 regimen (7 days of standard-dose cytarabine and 3 days of an anthracycline antibiotic or an anthracenedione, most often daunorubicin) was

initiated. The patient developed profound thrombocytopenia, with platelet nadir of 0 by day 13. The results of HLA antibody screening were negative. However, the results of a screening test for platelet-specific antibodies screen showed Abs against cluster of differentiation (CD)36. The platelets of the patient lacked expression of CD36, and DNA analysis showed mutations in the *CD36* gene. HLA Ab–mediated PTR is common in patients with hematological malignancies. However, once HLA Abs are excluded, other less-frequent Abs should be considered, particularly in patient populations of Asian, African, or Middle Eastern descent.

DETAIL

Subjek:	Blood platelets; Thrombocytopenia; Antibodies; Hematology
Pengidentifikasi/kata kunci:	platelet; CD36; transfusion refractoriness; isoimmunization; platelet antibody; human platelet antigen
Judul:	Severe Platelet Transfusion Refractoriness in Association with Antibodies Against CD36
Pengarang:	Schmidt, Amy E1 ; Sahai, Tanmay2; Refaai, Majed A1; Sullivan, Mia3; Curtis, Brian R31 Department of Pathology and Laboratory Medicine, University of Rochester Medical Center, Rochester, New York2 Department of Pathology and Laboratory Medicine, University of Rochester Medical Center, Rochester, New York; Department of Hematology and Oncology, Lenox Hill Hospital, New York, New York3 The Platelet &Neutrophil Immunology Laboratory, Blood Center of Wisconsin (part of Versiti), Milwaukee, WI
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A New Indicator Derived From Reticulocyte Hemoglobin Content for Screening Iron Deficiency in an Area Prevalent for Thalassemia

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ABSTRAK (ENGLISH)

Objective

To establish a new indicator derived from reticulocyte hemoglobin (Ret-He) content and red blood cell (RBC) indices for screening for iron deficiency anemia (IDA) in an area in whch thalassemia is prevalent.

Methods

Blood specimens from 304 women aged between 18 and 30 years residing in northeast Thailand were collected and measured for RBC and reticulocyte parameters. Iron deficiency was diagnosed when a participant had a serum

ferritin level of less than 15 ng per mL. Thalassemia genotypes were defined by hemoglobin (Hb) and DNA analyses.

Results

Of the total participants, 25% had iron deficiency (ID) and 50% carried the thalassemia gene. Various mathematical formulas were established and analyzed using the receiver operating characteristic (ROC) curve. The formula derived from Ret-He: (Ret-He/RDW-SD) × 10, was the best predictor for identifying ID among participants (area under the curve [AUC] = 0.812). Further testing of this indicator among individuals with positive thalassemia-screening results revealed stronger performance with an AUC of 0.874.

Conclusions

The findings indicate that the formula derived from Ret-He might be applicable for screening ID in areas in which thalassemia is prevalent.

DETAIL

Subjek:	Hemoglobin; Iron
Pengidentifikasi/kata kunci:	iron deficiency; anemia; thalassemia; reticulocyte hemoglobin content; Ret-He
Judul:	A New Indicator Derived From Reticulocyte Hemoglobin Content for Screening Iron Deficiency in an Area Prevalent for Thalassemia
Pengarang:	Jamnok, Jutatip1; Sanchaisuriya, Kanokwan2; Chaitriphop, Chaninthorn2; Sanchaisuriya, Pattara3; Fucharoen, Goonnapa2; Supan Fucharoen21 Graduate School, Medical Science Program, Thailand2 Centre for Research and Development of Medical Diagnostic Laboratories (CMDL), Faculty of Associated Medical Sciences, Thailand3 Faculty of Public Health, Khon Kaen University, Thailand
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Basis data:	Public Health Database

Red Blood Cells and Platelets Conventional and Research Parameters: Stability Remarks Before Their Interpretation: A Method to Quantify and Correct Time-Dependent Changes

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ABSTRAK (ENGLISH)

Objectives

To analyze the stability of red blood cells, platelets, and reticulocytes of the research parameters, in combination

with the respective conventional parameters, for each analyte; and to quantify the morphological changes in these analytes, to propose a correction factor for each.

Methods

Ethylenediaminetetraacetic acid (EDTA) blood specimens from patients were reanalyzed in 2-hour intervals and then, the mean percentage ($\bar{X}t\%$) changes were calculated. To evaluate the stability of the analyzed material, we used different criteria according to within-run and between-batch analytical variation, as well as intraindividual biological variation. Next, the mean deviation percentage of the parameters that undergo time-dependent significant changes was calculated, to obtain a correction factor.

Results

Several conventional and research parameters showed significant alterations in the stability at an early time after arrival at the laboratory.

Conclusion

Cell variations over time can be quantified and corrected by applying a multiplying factor to the signal obtained in the analyzer.

DETAIL

Subjek:	Blood platelets; Erythrocytes; Pediatrics; Morphology; Medical research; Data analysis
Pengidentifikasi/kata kunci:	stability; research parameters; preanalytical error; Sysmex XN; cell population data; cell population data parameters
Judul:	Red Blood Cells and Platelets Conventional and Research Parameters: Stability Remarks Before Their Interpretation: A Method to Quantify and Correct Time-Dependent Changes
Pengarang:	Pérez, Irene; Redín, Maria Elena11 Department of Laboratory Medicine, Core Laboratory, University Hospital Donostia, Guipuzcoa, Spain
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Quantitation of Cell-Derived Microparticles in Blood Products and Its Potential Applications in Transfusion Laboratories

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Cell-derived microparticles (MPs) are small fragments released from various cells when they are activated or undergo apoptosis. In the field of transfusion medicine, a number of studies have documented increased levels of MPs in blood products, which have been associated with multiple factors, including donor variability, blood component processing, and storage. In addition, transfusions that contain high levels of MPs are linked to posttransfusion complications. Considering the clinical importance of MP levels, transfusion laboratories should routinely screen blood products for them. However, this practice is not yet applied routinely, perhaps in part because of a lack of understanding of how to apply MP data to transfusion medicine. We describe the methods used to quantitate MPs in blood components and discuss the application of these quantitative data in routine transfusion laboratories in order to manage quality, improve the outcomes of transfusions, and minimize their complications.

DETAIL

Subjek:	Laboratories; Blood products
Pengidentifikasi/kata kunci:	microparticle; quantitation; flow cytometry; transfusion; blood component; laboratory
Judul:	Quantitation of Cell-Derived Microparticles in Blood Products and Its Potential Applications in Transfusion Laboratories
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14-3-3η Protein in Rheumatoid Arthritis: Promising Diagnostic Marker and Independent Risk Factor for Osteoporosis

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Background

Early identification and disease monitoring are challenges facing rheumatologists in the management of rheumatoid arthritis (RA).

Methods

We utilized enzyme-linked immunosorbent assay (ELISA) to determine 14-3-3η and anticyclic citrullinated peptide antibody (anti-CCP) levels, with rheumatoid factor (RF) level detected by rate nephelometry. The diagnostic value of each index was determined via receiver operating characteristic (ROC) curve, and the association between 14-3-3η and osteoporosis was assessed using multiple logistic regression analysis.

Results

Serum levels of 14-3-3η were 3.26 ng per mL in patients with RA. These levels were helpful in identifying patients with the disease, with the area under the curve (AUC) being 0.879 and 0.853, respectively, from all healthy control individuals and patients with RA. Combining 14-3-3η with RF or anti-CCP increased the diagnostic rate. Logistic regression analysis identified 14-3-3η as an independent risk factor for RA-related osteoporosis (odds ratio [OR], 1.503; 95% confidence interval [CI], 1.116–2.025; *P* <.01).

Conclusions

Serum 14-3-3η detection by itself or combined with other serum indices was helpful in differentiating patients with RA. Also, it was a promising biomarker for disease monitoring in RA.

DETAIL

Subjek:	Regression analysis; Rheumatoid arthritis; Osteoporosis; Medical diagnosis
Pengidentifikasi/kata kunci:	rheumatoid arthritis; 14-3-3η protein; rheumatoid factor; anticyclic citrullinated peptide antibody; osteoporosis; diagnostic
Judul:	14-3-3η Protein in Rheumatoid Arthritis: Promising Diagnostic Marker and Independent Risk Factor for Osteoporosis
Pengarang:	Zeng, Tingting1; Tan, Liming2; Wu, Yang2; Yu, Jianlin21 The First Affiliated Hospital of Nanchang University2 Key Laboratory of Laboratory Medicine in Jiangxi Province, Department of Clinical Laboratory, the Second Affiliated Hospital of Nanchang University, Nanchang, China
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Highly Effective Model for Implementation of In-House Platelets in a Tertiary Veteran Hospital Setting Without a Trauma Center

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Link dokumen ProQuest

ABSTRAK (ENGLISH)

Background

Platelet products have a limited shelf life and are costly. Therefore, to balance clinical usage/availability and wastage in a tertiary hospital setting without a trauma center, an innovative system model was established. This system

reduced wastage by transferring platelet unit approaching their expiration date to a nearby facility (with the same blood supplier and a trauma center) before expiration, when there is no anticipated need for the product at the original location.

Methods

A review of data to determine the degree of platelet wastage and wastage costs one year before implementation of this measure in October 2017 and one year after implementation of this measure.

Results

Since the implementation of this measure, no platelet units have expired on the shelf. In contrast, from October 2016 to October 2017, before implementation of platelet transfer, platelet products expired regularly.

Conclusion

This new system model is highly effective in maintaining platelet inventory without wastage.

DETAIL

Subjek:	Trauma centers; Quality control
Ketentuan indeks bisnis:	Subjek: Quality control
Pengidentifikasi/kata kunci:	blood product management; blood inventory management; wastage; platelet; quality improvement; quality assurance; blood supply chain; interhospital collaboration; laboratory medicine; utilization management
Judul:	Highly Effective Model for Implementation of In-House Platelets in a Tertiary Veteran Hospital Setting Without a Trauma Center
Pengarang:	Petersen, Jeffrey M1 ; Patel, Vijal2; Jhala, Darshana11 Department of Pathology and Laboratory Medicine, Michael J. Crescenz Veterans Affairs Medical Center, Philadelphia, PA; University of Pennsylvania Perelman School of Medicine, Philadelphia, PA2 Department of Pathology and Laboratory Medicine, Michael J. Crescenz Veterans Affairs Medical Center, Philadelphia, PA
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Establishment of Reference Intervals for Alkaline Phosphatase in Pakistani Children Using a Data Mining Approach

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ABSTRAK (ENGLISH)

Objective

To establish reference intervals (RIs) for alkaline phosphatase (ALP) levels in Pakistani children using an indirect data mining approach.

Methods

ALP levels analyzed on a Siemens Advia 1800 analyzer using the International Federation of Clinical Chemistry's photometric method for both inpatients and outpatients aged 1 to 17 years between January 2013 and December 2017, including patients from intensive care units and specialty units, were retrieved. RIs were calculated using a previously validated indirect algorithm developed by the German Society of Clinical Chemistry and Laboratory Medicine's Working Group on Guide Limits.

Results

From a total of 108,845 results, after the exclusion of patients with multiple specimens, RIs were calculated for 24,628 males and 18,083 females with stratification into fine-grained age groups. These RIs demonstrate the complex age- and sex-related ALP dynamics occurring during physiological development.

Conclusion

The population-specific RIs serve to allow an accurate understanding of the fluctuations in analyte activity with increasing age and to support clinical decision making.

DETAIL

Subjek:	Phosphatase; Data mining; Pediatrics
Ketentuan indeks bisnis:	Subjek: Data mining
Pengidentifikasi/kata kunci:	alkaline phosphatase; reference intervals; pediatrics; laboratory; data; Pakistan
Judul:	Establishment of Reference Intervals for Alkaline Phosphatase in Pakistani Children Using a Data Mining Approach
Pengarang:	Sibtain Ahmed1 ; Zierk, Jakob2; Aysha Habib Khan11 Section of Clinical Chemistry, Department of Pathology &Laboratory Medicine, Aga Khan University, Karachi, Pakistan2 Department of Pediatr ics and Adolescent Medicine, University Hospital Erlangen, Erlangen, Germany
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Measurements of Endpoint Titers Based on the Fluorescence Intensity Trend in Anti-Nuclear Antibody Testing

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ABSTRAK (ENGLISH)

Background

Automated systems for antinuclear antibody (ANA) testing provide endpoint titers that are predicted based on the fluorescence intensity (FI) value at a screening dilution (single-well titration [SWT]) showing frequent titration errors (more than plus or minus 1 dilution).

Methods

Line slope titration (LST) was based on the trend of FI values on dilutions. Three dilutions per specimen were prepared considering a patient's previous titer or FI at the screening dilution. On the XY plot, with the reciprocal of dilution as the X-axis and FI value as the Y-axis, a fitted line was drawn to obtain the endpoint titers.

Results

The titration error rate (no. of errors/total no.) of LST using a regression line was lower than that of SWT (31/710 [4.4%] and 152/674 [22.6%], respectively; $P < .000000001$), with serial dilution as a reference. When comparing a regression line using 3 dilution points with a line using 2 dilution points, the error rate of the former was not significantly different from that of the latter (31/710 [4.4%] and 31/746 [4.2%], respectively; $P = .842$).

Conclusions

This LST method is useful as an accurate, cost-effective, and rapid approach to measure endpoint titers in routine ANA testing.

DETAIL

Subjek:	Lupus; Rheumatic diseases; Automation; Antibodies; Transfer RNA; Variance analysis; Fluorescence; Diagnostic tests
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Markin, P. A., Brito, A., Moskaleva, N., Fodor, M., Lartsova, E. V., Shpot, Y. V., . . . Appolonova, S. A. (2020). Plasma sarcosine measured by gas chromatography-mass spectrometry distinguishes prostatic intraepithelial neoplasia and prostate cancer from benign prostate hyperplasia. Labmedicine, 51(6), 566-573. doi:https://doi.org/10.1093/labmed/lmaa008

Objective Sarcosine was postulated in 2009 as a biomarker for prostate cancer (PCa). Here, we assess plasma sarcosine as a biomarker that is complementary to prostate-specific antigen (PSA). Methods Plasma sarcosine was measured using gas chromatography-mass spectrometry (GC-MS) in adults classified as noncancerous controls (with benign prostate hyperplasia BPH], n = 36), with prostatic intraepithelial neoplasia (PIN, n = 16), or with PCa (n = 27). Diagnostic accuracy was assessed using receiver operating characteristic curve analysis. Results Plasma sarcosine levels were higher in the PCa (2.0 μM 1.3–3.3 μM], P <.01) and the PIN (1.9 μM 1.2–6.5 μM], P <.001) groups than in the BPH (0.9 μM 0.6–1.4 μM]) group. Plasma sarcosine had “good” and “very good” discriminative capability to detect PIN (area under the curve AUC], 0.734) and PCa (AUC, 0.833) versus BPH, respectively. The use of PSA and sarcosine together improved the overall diagnostic accuracy to detect PIN and PCa versus BPH. Conclusion Plasma sarcosine measured by GC-MS had “good” and “very good” classification performance for distinguishing PIN and PCa, respectively, relative to noncancerous patients diagnosed with BPH.

Ye-Cheng, Z., Shu-Mei, H., Zi-Lu, W., Jun-Wei, Z., Yan-Zheng, S., Zhang, Y., & Shu-Lin, Z. (2020). A rapid and accurate detection approach for multidrug-resistant tuberculosis based on PCR-ELISA microplate hybridization assay. Labmedicine, 51(6), 606-613. doi:https://doi.org/10.1093/labmed/lmaa016

Rapid and accurate diagnosis of multidrug-resistant tuberculosis (MDR-TB) is important for timely and appropriate therapy. In this study, a rapid and easy-to-perform molecular test that integrated polymerase chain reaction (PCR) amplification and a specific 96-well microplate hybridization assay, called PCR-ELISA (enzyme-linked immunosorbent assay), were developed for detection of mutations in rpoB, katG, and inhA genes responsible for rifampin (RIF) and isoniazid (INH) resistance and prediction of drug susceptibility in Mycobacterium tuberculosis clinical isolates. We evaluated the utility of this method by using 32 multidrug-resistent (MDR) isolates and 22 susceptible isolates; subsequently, we compared the results with data obtained by conventional drug susceptibility testing and DNA sequencing. The sensitivity and specificity of the PCR-ELISA test were 93.7% and 100% for detecting RIF resistance, and 87.5% and 100% for detecting INH resistance, respectively. These results were comparable to those yielded by commercially available molecular tests such as the GenoType MTBDRplus assay. Based on the aforementioned results, we conclude that the PCR-ELISA microplate hybridization assay is a rapid, inexpensive, convenient, and reliable test that will be useful for rapid diagnosis of MDR-TB, for improved clinical care.

Lapić, I., Komljenović, S., Knežević, J., & Rogić, D. (2020). COVID-19 pandemic once again exposes the weakest link in laboratory services: Specimen delivery. Labmedicine, 51(6), e83-e86. doi:https://doi.org/10.1093/labmed/lmaa081

Objective Reorganization of the emergency department (ED) during the COVID-19 pandemic implied closure of the ED-dedicated laboratory and manual transport of all specimens to the dislocated central laboratory. The impact of such reorganization on laboratory turnaround time (TAT) was examined. Methods The TAT from blood sampling to specimen reception (TAT1), from specimen reception to test reporting (TAT2), and from sampling to test reporting (TAT3) were compared between the pandemic peak month in 2020 and the same month in 2019. We evaluated whether TAT2 fulfills the recommended 60-minute criteria. Results A statistically significant difference was observed for all comparisons (P <.001), with TAT1 prominently contributing to TAT3 prolongation (from 48 minutes to 108 minutes) and exceeding the recommended 60-minute criteria. The TAT2 was extended from 33 minutes to 49 minutes. Conclusion An ED reorganization compromised the usual laboratory services for patients in the ED, with manual specimen delivery being the main cause for TAT prolongation.

Gilani, M., Aamir, M., Akram, A., Zujaja, H. H., Ijaz, A., & Muhammad, T. K. (2020). Comparison of turbidimetric inhibition immunoassay, high-performance liquid chromatography, and capillary electrophoresis methods for glycated hemoglobin determination. Labmedicine, 51(6), 579-584. doi:https://doi.org/10.1093/labmed/lmaa010

Objective The purpose of this study was to compare the performances of and evaluate the agreement among glycated hemoglobin values analyzed by using National Glycohemoglobin Standardization Program-certified and International Federation of Clinical Chemistry-standardized analyzers. This cross-sectional study was conducted at the Armed Forces Institute of Pathology, Department of Chemical Pathology from March 2019 to May 2019. Methods Glycated hemoglobin (HbA1c) was measured in the blood specimens from 100 patients on an ADVIA 1800 by a turbidimetric inhibitory immunoassay (TINIA), Sebia instrument by electrophoresis, and Bio-Rad Variant II Turbo system by high-performance liquid chromatography (HPLC). Quantitative variables were calculated as the mean ± standard deviation (SD). Precision and method comparisons were carried out according to Clinical and Laboratory Standards Institute recommendations. The results obtained from each analyzer were compared by correlation analysis. Method comparison was done by linear regression and Bland-Altman plots using the SPSS software version 24. Results The mean ± SD HbA1c values from TINIA, electrophoresis, and HPLC were 7.188% ± 1.89%, 7.164% ± 1.866%, and 7.160% ± 1.85%, respectively. The between-run coefficients of variation for TINIA, electrophoresis, and HPLC were 0.64%, 0.61%, and 0.60%, respectively. All 3 showed good correlation (TINIA, R2 = .994, P = .00; electrophoresis, R2 = .992, P = 0.00; and HPLC, R2 = .994, P = 0.00). Conclusion The good clinical agreements of HbA1c and strong correlations between analyzers indicate that these analyzers can be used interchangeably.

Thwe, P. M., Schilling, M., Reynoso, D., & Ren, P. (2020). Unexpected cholera bacteremia in a 91 year old caucasian male patient. Labmedicine, 51(6), e71-e74. doi:https://doi.org/10.1093/labmed/lmaa028

Cholera is an illness caused by Vibrio cholerae; its main symptom is acute watery diarrhea. Some infections are asymptomatic or result in patients presenting with mild diarrhea, but complications, such as bacteremia, can be fatal. Being endemic in Africa, Southeast Asia, and Haiti, V. cholerae infection cases in the United States are primarily considered travel-related. Herein, we report a case of a 91 year old Caucasian man, a Texas Gulf Coast resident, who developed bacteremia due to V. cholerae despite having no international travel history. Culture workup by mass spectrometry, automated biochemical system, and 16S ribosomal RNA (rRNA) gene sequencing confirmed V. cholerae. This case conveys an important reminder to clinicians and laboratory professionals regarding potentially serious cholera illnesses due to the domestic prevalence of V. cholerae in the coastal regions of the United States.

Gvozdjan, K., Casey, H., Mowery, C., Kumer, L., Fisher, C., Tyler, J., . . . Shike, H. (2020). Unexpected short-tandem-repeat patterns in posttransplant chimerism testing: Investigation of 3 cases with help from forensic science. Labmedicine, 51(6), 635-641. doi:https://doi.org/10.1093/labmed/lmaa022

Chimerism testing by short tandem repeats (STRs) is used to monitor engraftment after allogeneic hematopoietic stem cell transplantation (HSCT). Generally, STR alleles are stable and transferred from parent to child or from donor to recipient. However, 3 cases did not follow this norm. Additional work-up with help from forensic literature solved these mysteries. In case 1, the patient received HSCT from his son. The son shared STR alleles in 22/23 loci except Penta E, which was explained by repeat expansion in the son. In case 2, the patient had been in remission for 14 years after HSCT for lymphoma and developed repeat expansion in CSF1PO in granulocytes. In case 3, a pre-HSCT patient demonstrated 3 alleles, with 2 peaks taller than the third, in the FGA locus (chromosome 4). A combination of a triallelic variant and leukemia-associated trisomy 4 explained the finding. STR number variants are rare and clinically inconsequential but can overlap malignancy-associated, clinically significant changes.

About the journal. (2020). Labmedicine, 51(6), 553. doi:https://doi.org/10.1093/labmed/lmaa090

Pakzad, B., Rajae, E., Shahrabi, S., Mansournezhad, S., Davari, N., Azizidoost, S., & Saki, N. (2020). T-cell molecular modulation responses in atherosclerosis anergy. Labmedicine, 51(6), 557-565. doi:https://doi.org/10.1093/labmed/lmaa003

Atherosclerosis continues to be a major cause of death in patients with cardiovascular diseases. The cooperative role of immunity has been recently considered in atherosclerotic plaque inflammation, especially adaptive immune response by T cells. In this review, we examine the possible role of T cells in atherosclerosis-mediated inflammation and conceivable therapeutic strategies that can ameliorate complications of atherosclerosis. The cytokines secreted by T-lymphocyte subsets, different pathophysiological profiles of microRNAs (miRs), and the growth factor/receptor axis have diverse effects on the inflammatory cycle of atherosclerosis. Manipulation of miRNA expression and prominent growth factor receptors involved in inflammatory cytokine secretion in atherosclerosis can be considered diagnostic biomarkers in the induction of anergy and blockade of atherosclerotic development. This manuscript reviews immunomodulation of T cells responses in atherosclerosis anergy.

Zhou, W., Rao, H., Ding, Q., Xiang, L., Shen, J., Ye, B., & Xiang, C. (2020). Soluble CD14 subtype in peripheral blood is a biomarker for early diagnosis of sepsis. Labmedicine, 51(6), 614-619. doi:https://doi.org/10.1093/labmed/lmaa015

Objective To study the value of serum soluble CD14 subtype (sCD14-ST) in early diagnosis of sepsis. Methods Seventy-two patients were diagnosed with systemic inflammatory response syndrome, sepsis, or septic shock. Peripheral blood was collected at 0, 12, 24, and 48 hours after admission to the hospital. Levels of sCD14-ST, procalcitonin (PCT), hypersensitive C-reactive protein (CRP), and white blood cells (WBC) were determined. Results Levels of sCD14-ST in the patients with septic shock were higher than those in the other patients ($P < .01$) and peaked at 48 h. PCT and CRP levels were similar in the patients at admission but increased by 5 times to 10 times in the next 48 h, especially in the patients with septic shock. WBC levels remained high and did not change dramatically. Receiver operating characteristic analysis revealed that the area under the curve, sensitivity, and specificity values of sCD14-ST to diagnose sepsis were much higher than those of the other markers. Conclusion Compared with PCT, CRP, and WBC, sCD14-ST is a better biomarker for the early diagnosis of sepsis.

Xu, Y., Gu, L., Wang, J., Wang, Z., Zhang, P., & Zhang, X. (2020). Detection of circulating antibodies to p16 protein-derived peptides in hepatocellular carcinoma. Labmedicine, 51(6), 574-578. doi:https://doi.org/10.1093/labmed/lmaa006

Objective This study aimed at confirming the alteration of circulating anti-p16 immunoglobulin G (IgG) levels in hepatocellular carcinoma (HCC). Methods An in-house-developed enzyme-linked immunosorbent assay was used for determining plasma IgG antibodies against p16-derived antigens in 122 HCC patients and 134 healthy controls. Results Plasma anti-p16 IgG levels were significantly higher in HCC patients than in the controls ($Z = 3.51$, $P = 0.0004$), with no difference between males and females. A trend of increasing plasma anti-p16 IgG levels was associated with increasing HCC stage, with group 3 patients having the highest anti-p16 IgG levels ($Z = 3.38$, $P = 0.0008$). Group 3 exhibited the best sensitivity (19.6%) and specificity (95%) for plasma anti-p16 IgG detection, with an area under the receiver operating characteristic curve of 0.659 (95% confidence interval, 0.564–0.754). Conclusion Circulating IgG antibody to p16 protein might be a useful biomarker for HCC prognosis assessment rather than for early malignancy diagnosis.

Ardon, O., & Schmidt, R. L. (2020). Clinical laboratory employees' attitudes toward artificial intelligence. Labmedicine, 51(6), 649-654. doi:https://doi.org/10.1093/labmed/lmaa023

Objective The objective of this study was to determine the attitudes of laboratory personnel toward the application of artificial intelligence (AI) in the laboratory. Methods We surveyed laboratory employees who covered a range of work roles, work environments, and educational levels. Results The survey response rate was 42%. Most respondents (79%) indicated that they were at least somewhat familiar with AI. Very few (4%) classified themselves as experts. Contact with AI varied by educational level ($P = .005$). Respondents believed that AI could help them perform their work by reducing errors (24%) and saving time (16%). The most common concern (27%) was job security (being replaced by AI). The majority (64%) of the respondents expressed support for the development of AI projects in the organization. Conclusions Laboratory employees see the potential for AI and generally support the adoption of AI tools but have concerns regarding job security and quality of AI performance.

Bertholf, R. L. (2020). Scientific evidence, medical practice, and the insidious danger of anecdotal reports. Labmedicine, 51(6), 555-556. doi:https://doi.org/10.1093/labmed/lmaa093

Chu, C., Wu, H., Xu, F., Ray, J. W., Britt, A., Robinson, S. S., . . . Dong, J. (2020). Phenotypes associated with 16p11.2 copy number gains and losses at a single institution. Labmedicine, 51(6), 642-648. doi:https://doi.org/10.1093/labmed/lmaa026

Chromosome 16p11.2 is one of the susceptible sites for recurrent copy number variations (CNVs) due to flanking near-identical segmental duplications. Five segmental duplications, named breakpoints 1 to 5 (BP1–BP5), have been defined as recombination hotspots within 16p11.2. Common CNVs on 16p11.2 include a proximal ~593 kb between BP4 and BP5, and a distal ~220 kb between BP2 and BP3. We performed a search for patients carrying 16p11.2 CNVs, as detected using chromosome microarray (CMA), in the Molecular Diagnostic Laboratory at the University of Texas Medical Branch (UTMB), in Galveston. From March 2013 through April 2018, a total of 1200 CMA results were generated for germline testing, and 14 patients tested positive for 16p11.2 CNVs, of whom 7 had proximal deletion, 2 had distal deletion, 4 had proximal duplication, and 1 had distal duplication. Herein, we provide detailed phenotype data for these patients. Our study results show that developmental delay, abnormal body weight, behavioral problems, and hypotonia are common phenotypes associated with 16p11.2 CNVs.

Agnello, L., Bivona, G., Parisi, E., Giuseppe, D. L., Iacona, A., Ciaccio, A. M., . . . Ciaccio, M. (2020). Presepsin and midregional proadrenomedullin in pediatric oncologic patients with febrile neutropenia. Labmedicine, 51(6), 585-591. doi:https://doi.org/10.1093/labmed/lmaa011

Objective In this study, we investigated the roles of presepsin (PSP) and midregional proadrenomedullin (mr-proADM) in children with febrile neutropenia (FN) due to chemotherapy. Methods We assessed 36 FN episodes in 26 children. Patients were classified into bacteremia (B) and fever of unknown origin (FUO) groups. We evaluated PSP and mr-proADM at admission (T0), after 24/48 h (T1), and after 5 days (T2). Results PSP and mr-proADM levels were elevated at T0 and significantly decreased at T2. mr-proADM levels did not significantly differ between the B and FUO groups. PSP levels significantly differed between the B and FUO groups only at T1. Both PSP and mr-proADM levels at T0 were a predictor of length of hospital stay but not of the duration of fever. Finally, receiver operating characteristic curve analysis showed that PSP and mr-proADM had low diagnostic accuracy for blood culture positivity. Conclusion PSP and mr-proADM display poor clinical usefulness for FN in oncologic children.

Su, H. R., Turhan, Ö., Cemile Aylin Erman Daloğlu, Öğünç, M. D., Özhak, B., Öngüt, G., . . . Mamıkoğlu, L. (2020). Molecular epidemiology of carbapenem-resistant enterobacterales strains isolated from blood cultures in antalya, turkey. Labmedicine, 51(6), 601-605. doi:https://doi.org/10.1093/labmed/lmaa017

Objective The aim of this study was to investigate the prevalence of carbapenemase and CTX-M genes among 330 blood culture isolates of Enterobacterales with reduced susceptibility to at least 1 carbapenem, between 2010 and 2015. Methods BD Max CRE assay and in-house PCR were used to detect carbapenemase and CTX-M genes. Results At least 1 carbapenemase gene was detected among 113 (74.3%) of the 152 carbapenem resistant isolates. The OXA-48 (69.7%) was the most common carbapenemase followed by VIM, NDM and IMP, whereas no tested isolates were KPC-positive. Eighty-six isolates (56.6%) had CTX-M and 65 had both OXA-48 and CTX-M. Carbapenemase production in Enterobacterales was significantly increased in years ($P < .05$). Conclusion Our study indicates that there is ongoing endemic circulation of the OXA-48 producing organism in our facility. It is noteworthy that more than half of the OXA-48 producing strains also produced CTX-M enzyme.

Singh, G., & Bollag, R. (2020). Quantification by ultrafiltration and immunofixation electrophoresis testing for monoclonal serum free light chains. Labmedicine, 51(6), 592-600. doi:https://doi.org/10.1093/labmed/lmaa012

Objective Measurement of monoclonal immunoglobulins is a reliable estimate of the plasma cell tumor mass. About 15% of plasma cell myelomas secrete light chains only. The concentration of serum free light chains is insufficient evidence of the monoclonal light chain burden. A sensitive quantitative estimate of serum free monoclonal light chains could be useful for monitoring patients with light chain myeloma. We describe such an assay that does not

require mass-spectrometry equipment or expertise. Methods Serum specimens from patients with known light chain myelomas and controls were subjected to ultrafiltration through a membrane with pore size of 50 kDa. The filtrate was concentrated and tested by immunofixation electrophoresis. The relative area under the monoclonal peak, compared to that of the total involved light chain composition, was estimated by densitometric scanning of immunofixation gels. The proportion of the area occupied by the monoclonal peak in representative densitometric scans was used to arrive at the total serum concentration of the monoclonal serum free light chains. Results Using an ultracentrifugation and concentration process, monoclonal serum free light chains were detectable, along with polyclonal light chains, in all 10 patients with active light chain myelomas. Monoclonal light chains were identified in serum specimens that did not reveal monoclonal light chains by conventional immunofixation electrophoresis. The limit of detection by this method was 1.0 mg/L of monoclonal serum free light chains. Conclusion The method described here is simple enough to be implemented in academic medical center clinical laboratories and does not require special reagents, equipment, or expertise. Even though urine examination is the preferred method for the diagnosis of light chain plasma cell myelomas, measurement of the concentration of serum free light chains provides a convenient, albeit inadequate, way to monitor the course of disease. The method described here allows effective electrophoretic differentiation of monoclonal serum free light chain from polyclonal serum free light chains and provides a quantitation of the monoclonal serum free light chains in monitoring light chain monoclonal gammopathies.

Johannes, J. M. L. H., & Urrechaga, E. (2020). Verification of 20 mathematical formulas for discriminating between iron deficiency anemia and thalassemia trait in microcytic anemia. Labmedicine, 51(6), 628-634. doi:https://doi.org/10.1093/labmed/lmaa030

Background Currently, more than 45 mathematical formulas based on simple red blood cell (RBC) parameters have been proposed for differentiating between iron deficiency and thalassemia in microcytic anemia, of which 20 are relatively new and have not been thoroughly independently verified. The study goal was to verify these 20 new formulas and to identify which RBC parameters have a decisive impact on the performance of those formulas. Methods A database containing laboratory and diagnostic data from 2788 subject individuals with microcytic anemia was used for assessing performance by receiver operating characteristic (ROC) analysis. Results The new Index26 had excellent performance, equivalent to the Green and King, Jayabose, and Janel formulas previously identified in the literature. The discriminant power of nearly all newer formulas was lower in our study than that claimed by the original authors. We discovered that a well-performing formula requires mean cell volume (MCV), RBC distribution width (RDW), and RBC measurements, whereas hemoglobin measurements appeared not to be essential. Conclusions Only the new Index26 performed at a level comparable to the very strongest established formulas. All other new formulas had lower performance than was claimed in the original publications, underscoring that independent verification of new formulas is indispensable.

Cook, J. (2020). Incident command in the time of COVID-19. Labmedicine, 51(6), e78-e82. doi:https://doi.org/10.1093/labmed/lmaa073

The SARS-CoV-2 virus was initially contained in China but rapidly spread across the globe. The grave threat was not apparent until it was already in our midst. Our organization implemented an Incident Command System (ICS), based on previous experience, to respond to the COVID-19 pandemic in a comprehensive and effective manner. This well-known management and response framework is used by many specialties and organizations in disasters of different complexity and size. Our ICS was able to assemble the appropriate people, assess the situation, and develop and implement plans to deal with the COVID-19 crisis. The effectiveness of the ICS structure and its execution was instrumental in getting in front of the virus and managing regional activities. The ICS is an effective tool to improve safety and mitigate risk when dealing with large-scale disasters and should be implemented and practiced before the need arises. Our organization implemented a formal Incident Command System (ICS) very early as a response to the COVID-19 pandemic. Although it recently disbanded, we are maintaining its core functionality and communication as we continue to deal with COVID-19 into the future. The author has observed the ICS being used at hospitals through hurricanes, blizzards, and riots but never saw it work as well as it did during the initial weeks of the pandemic. This group deftly navigated through uncharted waters by leveraging the spirit and

structure of Incident Command.

Farahani, H., Amri, J., Alaee, M., Mohaghegh, F., & Rafiee, M. (2020). Serum and saliva levels of cancer antigen 15-3, carcinoembryonic antigen, estradiol, vaspin, and obestatin as biomarkers for the diagnosis of breast cancer in postmenopausal women. Labmedicine, 51(6), 620-627. doi:https://doi.org/10.1093/labmed/lmaa013

Objective To find suitable biomarkers for diagnosis of Breast cancer in serum and saliva; also, to examine the correlation between salivary and serum concentrations of suitable biomarkers. Methods This case-control study included 30 women with breast cancer as a case group and 30 healthy women as a matched control group. Blood and saliva specimens were collected from all participants. We evaluated serum and salivary cancer antigen 15-3 (CA15-3), carcinoembryonic antigen (CEA), estradiol, vaspin, and obestatin concentrations. Mann-Whitney U testing and Spearman correlation coefficients were used for statistical analysis. Results Serum and salivary concentrations of estradiol were significantly higher in patients with breast cancer (BC) than in healthy women ($P < .05$). Also, serum CEA and salivary obestatin concentrations were significantly higher in BC patients than in the control group ($P < .05$). However, there was no significant difference between other parameters in patients with BC and controls. We observed a positive correlation between serum and salivary concentrations of CA15-3, as well as a negative correlation between serum and salivary concentrations of vaspin and obestatin. Conclusion The results of this study demonstrated that concentrations of CEA and estradiol in serum, obestatin in serum and saliva, and estradiol in saliva were significantly different between the 2 groups.

Song, L., Koka, R., Reese, E., Mullins, K., & Murphy, C. (2020). Intraosseous specimens submitted to the laboratory: A case report and review. Labmedicine, 51(6), e75-e77. doi:https://doi.org/10.1093/labmed/lmaa029

Intraosseous (IO) devices are used for vascular access in settings where venous access is initially unobtainable, such as prehospital trauma care or cardiac arrest. While IO devices are effective for infusion of blood, fluids, and medications, there is limited data on the analytical equivalence of specimens taken out of IO devices and peripheral venous blood. Despite this, IO device manufacturers and clinical resources state that IO specimens can be submitted for laboratory analysis. As reported in this case, IO specimens may be drawn and labeled as ‘peripheral blood’. IO specimens are not always caught by automated sample quality testing and may proceed through analysis without any warning signal to the laboratory. There are potential regulatory risks in accepting IO samples for analysis without validation. IO infusion is a valuable technique for vascular access in critically ill patients, but clinical laboratories will need to determine their own policies for identifying and handling IO specimens.

Jacobs, J., Kneib, J., & Gabbard, A. (2020). Intravenous immunoglobulin-associated hemolytic anemia. Labmedicine, 51(5), e47-e50. doi:https://doi.org/10.1093/labmed/lmaa019

Intravenous immunoglobulin (IVIG) is an important therapeutic tool for the treatment of a variety of conditions, including immune thrombocytopenic purpura (ITP). Although IVIG has many approved indications and is typically well tolerated, a number of adverse effects have been reported. Hemolysis is a documented but under-recognized adverse effect associated with large individual or cumulative doses of IVIG. Hemolytic complications are typically mild and detected incidentally when screening tests, such as a complete blood count (CBC) showing decreased hemoglobin or a complete metabolic panel (CMP) resulting in elevated bilirubin, are performed for another reason. Herein, we report a case of significant hemolytic anemia in a 59 year old Caucasian woman, who required packed red blood cell transfusion after administration of IVIG for the treatment of ITP. Increased awareness of the potential for clinically significant hemolysis after the use of moderate cumulative doses of IVIG is needed, particularly in patients with risk factors for hemolysis.