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DAFTAR ISI

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Serum and Saliva Concentrations of Biochemical Parameters in Men with Prostate Cancer and Benign Prostate Hyperplasia

Farahani, Hyder [1] ; Alaee, Mona [2] ; Amri, Jamal [2] ; Mahmoud-Reza Baghinia [3] ; Rafiee, Mohammad [4] [1] Department of Clinical Biochemistry and Genetic, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran [2] 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, Iran [3] Department of Urology, Arak, Iran Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran [4] Department of Biostatistics and Epidemiology, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran

ABSTRAK (ENGLISH)

Objectives

To find suitable biomarkers for diagnosis of prostate cancer (PC) in serum and saliva; also, to evaluate the diagnostic efficacy of saliva in patients with PC.

Methods

This case-control study included 20 patients with PC and 20 patients with benign prostatic hyperplasia (BPH). Blood and saliva were collected from the participants and centrifuged. Serum and supernatant saliva were used for biochemical analysis. We evaluated serum and salivary levels of urea, creatinine, prostate-specific antigen (PSA), creatine kinase BB (CK-BB), zinc, β-2 microglobulin (B2M), and melatonin. Also, we used Mann-Whitney U testing, Spearman correlation coefficients, and receiver operating characteristic (ROC) analysis to evaluate the data.

Results

Serum and salivary concentrations of urea, creatinine, PSA, CK-BB, zinc, and B2M were significantly higher in patients with PC, compared with the BPH group (P <.05). However, serum and salivary concentrations of melatonin were significantly lower in patients with PC, compared with BPH group (P <.05). In both groups, salivary concentrations of all markers were lower (P <.05), compared with those values in serum. We observed positive correlation between serum and salivary concentrations of all markers studied (P <.05).

Conclusion

From the data, we conclude that investigation using saliva specimens is a noninvasive, simple, and effective tool for screening of biochemical parameters.

DETAIL

Subjek:	Hyperplasia; Prostate cancer; Creatinine; Melatonin
Pengidentifikasi/kata kunci:	prostate cancer; biochemical parameters; saliva; serum; correlation, benign prostatic hyperplasia
Judul:	Serum and Saliva Concentrations of Biochemical Parameters in Men with Prostate Cancer and Benign Prostate Hyperplasia
Pengarang:	Farahani, Hyder1; Alaee, Mona2; Amri, Jamal2; Mahmoud-Reza Baghinia3; 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 Urology, Arak, Iran 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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Unexpectedly Weak Anti-B in 2 Group O Pediatric Patients on Parenteral Nutrition and Disease Specific Supplemental Enteral Feeds

Kaplan, Alesia [1] ; Gabert, Kimberly A [2] ; Yazer, Mark H [3 1] Department of Pathology, University of Pittsburgh, Pittsburgh, PA [2] Immunohematology Reference Laboratories (IRL), Vitalant, Pittsburgh, PA [3] Department of Pathology, University of Pittsburgh, Pittsburgh, PA; Immunohematology Reference Laboratories (IRL), Vitalant, Pittsburgh, PA

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ABSTRAK (ENGLISH)

Anti-A and anti-B antibodies are naturally occurring and develop from exposure to intestinal bacteria after age 4 to 6 months. In the laboratory, strong agglutination with A1 and B cells, or B cells only and A1 cells only, on reverse typing in a healthy person with immunocompetence is expected for patients with ABO types O, A, and B, respectively. However, absent or weak anti-A and anti-B antibodies can be observed in some clinical scenarios, such as patients with immunodeficiencies, newborns, elderly patients, and patients who have recently received bone marrow transplants. In this article, we report the cases of 2 pediatric patients with group O blood type who were receiving total parenteral nutrition (TPN) and disease-specific enteral feeds and who have strong anti-A and absent/weak anti-B.

DETAIL

Subjek:	Parenteral nutrition; Pediatrics
Pengidentifikasi/kata kunci:	absent/weak anti-B; ABO discrepancy; total parenteral nutrition (TPN); gut microbiota
Judul:	Unexpectedly Weak Anti-B in 2 Group O Pediatric Patients on Parenteral Nutrition and Disease Specific Supplemental Enteral Feeds
Pengarang:	Kaplan, Alesia1; Gabert, Kimberly A2; Yazer, Mark H31 Department of Pathology, University of Pittsburgh, Pittsburgh, PA2 Immunohematology Reference Laboratories (IRL), Vitalant, Pittsburgh, PA3 Department of Pathology, University of Pittsburgh, Pittsburgh, PA; Immunohematology Reference Laboratories (IRL), Vitalant, Pittsburgh, PA

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Q&A with Dr Paul Phillip Sher, Editor in Chief 1986-2004

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Myelodysplastic Syndrome/Myeloproliferative Neoplasm with Ring Sideroblasts and Thrombocytosis with Cooccurrent SF3B1 and MPL Gene Mutations: A Case Report and Brief Review of the Literature

Chang-Hun, Park [1] ; Yun, Jae Won [2] ; Hyun-Young, Kim [3] ; Ki-O, Lee [4] ; Sun-Hee, Kim [2] ; Hee-Jin, Kim [2] [1] Department of Laboratory Medicine &Genetics, Samsung Changwon Hospital, Sungkyunkwan University School of Medicine, Changwon, Korea [2] Department of Laboratory Medicine &Genetics, Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, Korea [3] Department of Laboratory Medicine &Genetics, Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, Korea; Department of Laboratory Medicine, Gyeongsang National University Hospital, Jinju, Korea [4] Samsung Biomedical Research Institute, Samsung Medical Center, Seoul, Korea

ABSTRAK (ENGLISH)

Background

Myelodysplastic syndrome/myeloproliferative neoplasm with ring sideroblasts and thrombocytosis (MDS/MPN-RS-T) is a new disease entity in the current WHO classification. Genetically, 60%–90% of cases have mutations in *SF3B1*, strongly associated with RS, and more than half of them cooccur with *JAK2* V617F. This report describes the rare case of MDS/MPN-RS-T with *SF3B1* mutation cooccurring with an *MPL* mutation.

Methods

We report a 79-year-old man who was referred because of generalized edema. Peripheral blood testing showed macrocytic anemia and thrombocytosis, and bone marrow analysis demonstrated dyserythropoiesis with RS and increased megakaryocytes. A molecular study was performed to detect *SF3B1* mutations and recurrent mutations in MPN disease (*JAK2* V617F/exon 12, *CALR* gene exon 9, and *MPL* gene exon 10 mutations).

Results

The molecular study revealed *SF3B1* K666T and *MPL* W515R mutations, while *BCR-ABL1* or *JAK2* V617F/exon 12 and *CALR* mutations were all negative.

Conclusion

This is a rare case of concomitant *SF3B1* and *MPL* mutations in MDS/MPN-RS-T.

DETAIL

Subjek:	Tumors; Mutation; Case reports
Pengidentifikasi/kata kunci:	myelodysplastic syndrome; myeloproliferative neoplasm; ring sideroblasts; SF3B1; MPL
Judul:	Myelodysplastic Syndrome/Myeloproliferative Neoplasm with Ring Sideroblasts and Thrombocytosis with Cooccurrent SF3B1 and MPL Gene Mutations: A Case Report and Brief Review of the Literature
Pengarang:	Chang-Hun, Park1; Yun, Jae Won2; Hyun-Young, Kim3; Ki-O, Lee4; Sun-Hee, Kim2; Hee-Jin, Kim21 Department of Laboratory Medicine &Genetics, Samsung Changwon Hospital, Sungkyunkwan University School of Medicine, Changwon, Korea2 Department of Laboratory Medicine &Genetics, Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, Korea3 Department of Laboratory Medicine &Genetics, Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, Korea; Department of Laboratory Medicine, Gyeongsang National University Hospital, Jinju, Korea4 Samsung Biomedical Research Institute, Samsung Medical Center, Seoul, Korea
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The Cost of Pre-Analytical Errors in INR Testing at a Tertiary-Care Hospital Laboratory: Potential for Significant Cost Savings

Kulkarni, Sumedha [1] ; Piraino, Dina [2] ; Strauss, Rachel [1] ; Proctor, Eva [1] ; Waldman, Suzanne [1] ; King, Jacqueline [1] ; Selby, Rita [3 1] Department of Laboratory Medicine and Molecular Diagnostics, Sunnybrook Health Sciences Centre, and Ontario, Canada [2] Department of Laboratory Medicine and Molecular Diagnostics, Sunnybrook Health Sciences Centre, and Ontario, Canada; Department of Laboratory Medicine and Molecular Diagnostics, Sunnybrook Health Sciences Centre, and Ontario, Canada [3] Department of Laboratory Medicine and Molecular Diagnostics, Sunnybrook Health Sciences Centre, and Ontario, Canada; Department of Laboratory Medicine and Pathobiology and Department of Medicine, University of Toronto, Ontario, Canada

ABSTRAK (ENGLISH)

Background

Preanalytical errors account for most laboratory errors. Although the frequencies of preanalytical errors are well characterized in the literature, little is known regarding the costs of these errors to the laboratory.

Objective

To analyze costs associated with preanalytical errors associated with the international normalized ratio (INR) test.

Methods

We performed a retrospective analysis of INR requests associated with preanalytical error codes from January 2009 through September 2013. Preanalytical error types were those related to order entry (no specimen collected) and those unrelated to order entry (insufficient specimen quantity or specimen-integrity concerns). We calculated the cost of analysis of a specimen and the cost of investigating errors.

Results

During the study period, there were 557,411 INR requests, 13.1% of which were associated with a preanalytical error code. The total annual cost of INR testing was USD $379,222.50. Investigation and reporting of preanalytical errors not related to order entry represented 10.5% of our annual INR testing budget (USD $39,939.00).

Conclusions

Minimizing preanalytical errors has the potential to result in significant cost savings.

DETAIL

Subjek:	Laboratories; Cost control; Order entry; Quality control
Ketentuan indeks bisnis:	Subjek: Cost control Quality control
Pengidentifikasi/kata kunci:	blood coagulation; cost analysis; INR; preanalytical phase; clinical laboratory services; quality improvement
Judul:	The Cost of Pre-Analytical Errors in INR Testing at a Tertiary-Care Hospital Laboratory: Potential for Significant Cost Savings
Pengarang:	Kulkarni, Sumedha1; Piraino, Dina2; Strauss, Rachel1; Proctor, Eva1; Waldman, Suzanne1; King, Jacqueline1; Selby, Rita31 Department of Laboratory Medicine and Molecular Diagnostics, Sunnybrook Health S ciences Centre, and Ontario, Canada2 Department of Laboratory Medicine and Molecular Diagnostics, Sunnybrook Health Sciences Centre, and Ontario, Canada; Department of Laboratory Medicine and Molecular Diagnostics, Sunnybrook Health Sciences Centre, and Ontario, Canada3 Department of Laboratory Medicine and Molecular Diagnostics, Sunnybrook Health Sciences Centre, and Ontario, Canada; Department of Laboratory Medicine and Pathobiology and Department of Medicine, University of Toronto, Ontario, Canada
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Mixed Phenotype Acute Leukemia that Evolved from Myelodysplastic Syndrome with Excess Blasts

Kim, Miyoung [1] ; Dae Young Zang [2] ; Lee, Jiwon [1] ; Ji-Young, Park [3] ; Chung, Yousun [3] ; Young Kyung Lee [1] [1] Department of Laboratory Medicine, Hallym University Sacred Heart Hospital, Anyang, South Korea [2] Department of Internal Medicine, Hallym University Sacred Heart Hospital, Anyang, South Korea [3] Department of Laboratory Medicine, Kangdong Sacred Heart Hospital, Seoul, South Korea

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Myelodysplastic syndrome (MDS) that evolves into acute leukemia with blasts of mixed phenotypes has rarely been reported and has no distinct diagnostic category. Herein, we describe a 79-year-old Korean female patient with MDS–excess blasts (MDS-EB) that evolved into acute leukemia; the blasts simultaneously expressed B-lymphoid and myeloid antigens. The patient was diagnosed with MDS-EB with blasts of myeloid lineage coexpressing a few B-lymphoid antigens with 7q and 20q abnormalities. The disease progressed to acute leukemia with blasts carrying more B-lymphoid antigens, which was immunophenotypically compatible with B-lymphoid/myeloid acute leukemia. Unlike previously reported patients whose blast populations are bilineal, our patient is the first with biphenotypic acute leukemia that progressed from MDS. The diagnosis of our patient introduces the possibility that many other types of biphenotypic acute leukemia may have gone undiagnosed and encourages hematologists to designate a specific diagnostic category for this type of disease, so that it can more readily be detected and studied in the future.

DETAIL

Subjek:	Antigens; Leukemia; Erythrocytes
Pengidentifikasi/kata kunci:	myelodysplastic syndrome; mixed phenotype acute leukemia; bilineal; biphenotypic; flow cytometry; immunohistochemistry
Judul:	Mixed Phenotype Acute Leukemia that Evolved from Myelodysplastic Syndrome with Excess Blasts
Pengarang:	Kim, Miyoung1; Dae Young Zang2; Lee, Jiwon1; Ji-Young, Park3; Chung, Yousun3; Young Kyung Lee11 Department of Laboratory Medicine, Hallym University Sacred Heart Hospital, Anyang, South Korea2 Department of Internal Medicine, Hallym University Sacred Heart Hospital, Anyang, South Korea3 Department of Laboratory Medicine, Kangdong Sacred Heart Hospital, Seoul, South Korea
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Measurement of Monoclonal Immunoglobulin Protein Concentration in Serum Protein Electrophoresis: Comparison of Automated vs Manual/Human Readings

Clavijo, Alex [1] ; Ryan, Nathan [1] ; Xu, Hongyan [2] ; Singh, Gurmukh [3 1] Department of Pathology, Medical College of Georgia at Augusta University, Augusta, GA [2] Department of Epidemiology and Bio-Statistics, Medical College of Georgia at Augusta University, Augusta, GA [3] Department of Pathology, Medical College of Georgia at Augusta University, Augusta, GA; Division of Clinical Pathology, Medical College of Georgia at Augusta University, Augusta, GA

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ABSTRAK (ENGLISH)

Background

Protein concentration of monoclonal immunoglobulin in plasma-cell myeloma/multiple myeloma provides an estimate of the tumor mass and allows for monitoring of the response to treatment. Accurate and reproducible estimates of the monoclonal immunoglobulin concentration are important for patient care.

Objective

To address the optimum method for estimation of the concentration of monoclonal immunoglobulins.

Methods

Serum protein electrophoresis and immunofixation electrophoresis were conducted by using the Helena SPIFE Touch instrument. Estimation of the protein concentration of monoclonal immunoglobulin in the gamma region by computer-assisted reading was compared with the reading by technologists and pathology residents, in 300 gels. The data were compared using *t*-testing and analysis of variance.

Results

Computer-generated readings had a consistent positive bias. The correlation coefficient of the average reading by technologists and residents with the computer generated value was 0.997. The average positive bias by the computer reading was 0.29 g per dL. The intercept on the regression analysis was 0.22 g per dL. The reading by the

computer was significantly higher than each of the human-interpreted readings. The readings by the 3 human groups were not significantly different amongst them. The main reason for the higher reading by the computer was inclusion of a greater area on the anodal size of the peak on the densitometric scan.

Conclusions

Human- and computer-interpreted readings of the protein concentration of monoclonal immunoglobulin have a high degree of correlation. The consistent positive bias by the computer reading occurred due to inclusion of a greater area of the densitometric scan on the anodal side of the peak. We suggest that vendors should adjust such computer programs to provide readings comparable to those generated by expert humans. We recommend manual delineation of the monoclonal peaks for measuring the concentration of monoclonal immunoglobulins.

DETAIL

Subjek:	Computers; Immunoglobulins; Reading; Multiple myeloma; Bias; Proteins
Pengidentifikasi/kata kunci:	plasma-cell myeloma; multiple myeloma; monoclonal immunoglobulin; densitometric scan; protein concentration; protein electrophoresis
Judul:	Measurement of Monoclonal Immunoglobulin Protein Concentration in Serum Protein Electrophoresis: Comparison of Automated vs Manual/Human Readings
Pengarang:	Clavijo, Alex1; Ryan, Nathan1; Xu, Hongyan2; Singh, Gurmukh31 Department of Pathology, Medical College of Georgia at Augusta University, Augusta, GA2 Department of Epidemiology and Bio-Statistics, Medical College of Georgia at Augusta University, Augusta, GA3 Department of Pathology, Medical College of Georgia at Augusta University, Augusta, GA; Division of Clinical Pathology, Medical College of Georgia at Augusta University, Augusta, GA
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A Novel Pathogenic CALR Exon 9 Mutation in a Patient with Essential Thrombocythemia

Jee-Soo, Lee [1] ; Ho Young Kim [2] ; Kim, Miyoung [1] ; Young Kyung Lee [1] 1 Department of Laboratory Medicine, Hallym University Sacred Heart Hospital, Anyang, South Korea 2 Department of Internal Medicine, Hallym University Sacred Heart Hospital, Anyang, South Korea

Link dokumen ProQuest

ABSTRAK (ENGLISH)

The clinical phenotypes and prognoses of *CALR*-mutant myeloproliferative neoplasms depend on the mutation type. The 2 most common mutations, type 1 (52-bp deletion) and type 2 (5-bp insertion), account for 85% of *CALR*-mutated neoplasms. The former confers a myelofibrotic phenotype, and the latter is associated with a low risk of thrombosis and an indolent clinical course. Individual case reports for patients with novel pathogenic *CALR* mutations are rare. Herein, we present the first case in the literature, to our knowledge, of a 63-year old ethnic Korean man with essential thrombocythemia who was diagnosed with a novel +1-bp frameshift mutation in *CALR*, which was predicted to exhibit a type 2–like phenotype.

DETAIL

Subjek:	Tumors; Mutation

Pengidentifikasi/kata kunci:	essential thrombocythemia; CALR mutation; type 2 mutation; frameshift; myeproliferative neoplasm; novel mutation
Judul:	A Novel Pathogenic CALR Exon 9 Mutation in a Patient with Essential Thrombocythemia
Pengarang:	Jee-Soo, Lee1; Ho Young Kim2; Kim, Miyoung1; Young Kyung Lee11 Department of Laboratory Medicine, Hallym University Sacred Heart Hospital, Anyang, South Korea2 Department of Internal Medicine, Hallym University Sacred Heart Hospital, Anyang, South Korea
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Safety Considerations in the Laboratory Testing of Specimens Suspected or Known to Contain the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)

Iwen, Peter C [1] ; Stiles, Karen L [2] ; Pentella, Michael A [3 1] Department of Pathology and Microbiology, College of Medicine, University of Nebraska Medical Center, Omaha; Nebraska Public Health Laboratory, Omaha [2] Nebraska Public Health Laboratory, Omaha [3] College of Public Health, University of Iowa, Iowa City

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DETAIL

Pengidentifikasi/kata kunci:	SARS-CoV-2; Laboratory safety; Coronavirus; COVID-19
Judul:	Safety Considerations in the Laboratory Testing of Specimens Suspected or Known to Contain the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)
Pengarang:	Iwen, Peter C1; Stiles, Karen L2; Pentella, Michael A31 Department of Pathology and Microbiology, College of Medicine, University of Nebraska Medical Center, Omaha; Nebraska Public Health Laboratory, Omaha2 Nebraska Public Health Laboratory, Omaha3 College of Public Health, University of Iowa, Iowa City
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α-1 Antitrypsin Genotype-Phenotype Discrepancy in a 42-Year-Old Man Who Carries the Null-Allele

Pavičić, Tomislav [1] ; Ćelap, Ivana [1] ; Njegovan, Milena [1] ; Kuna, Andrea Tešija [1] ; Štefanović, Mario [1] [1] Department of Clinical Chemistry, Medical School University Hospital Sestre Milosrdnice, Zagreb, Croatia

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ABSTRAK (ENGLISH)

Background

Alpha-1-antitrypsin (A1AT) deficiency is a hereditary condition caused by mutations in the SERPINA1 gene and associated with lung emphysema and liver disease. Laboratory testing in suspected A1AT deficiency involves quantifying serum A1AT concentration and identification of specific alleles by genotyping and phenotyping. The aim of this report was to present a case of the null allele carrier with consequent genotype/phenotype/concentration discrepancies and potential misclassification of the Z variant in a 42-year-old white man presenting with symptoms of chronic obstructive pulmonary disease (COPD).

Method

Serum A1AT concentration was measured using an immunoturbidimetric assay. A1AT phenotype was determined using isoelectric focusing followed with immunofixation (IEF-IF). Genotyping specifically for the S and Z allele was performed by melting curve analysis using real-time PCR and checked by an alternative PCR-RFLP method. Genotype/phenotype ambiguity and discrepancy were amended using gene sequencing.

Results

Laboratory testing revealed highly reduced A1AT concentration (less than 0.30 g/L), mild to moderate deficient genotype (Pi*Z allele: M/Z and Pi*S allele: M/M) and severe deficient Z homozygous phenotype (Pi ZZ). After repeated sampling, the same discordant results were verified by these tests. Further sequencing revealed two clinically relevant and defective variants: rs199422210 (a rare null allele) and rs28929474 (the Z allele).

Conclusion

Due to inability of genotyping kit probes to detect null/Z allele combination (which mimics the Pi ZZ phenotype), our patient was misclassified as mild to moderate deficient Pi*MZ heterozygote. In all unclear cases, whole-gene sequencing is highly recommended in order to determine definitive cause of A1AT deficiency.

DETAIL

Subjek:	Laboratories; Genotype &phenotype; Chronic obstructive pulmonary disease
Pengidentifikasi/kata kunci:	α-1 antitrypsin deficiency; genotyping error; misclassification; null allele; chronic obstructive pulmonary disease; sequencing
Judul:	α-1 Antitrypsin Genotype-Phenotype Discrepancy in a 42-Year-Old Man Who Carries the Null-Allele
Pengarang:	Pavičić, Tomislav1; Ćelap, Ivana1; Njegovan, Milena1; Kuna, Andrea Tešija1; Štefanović, Mario11 Department of Clinical Chemistry, Medical School University Hospital Sestre Milosrdnice, Zagreb, Croatia
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Precision of Fetal DNA Fraction Estimation by Quantitative Polymerase Chain Reaction Quantification of a Differently Methylated Target in Noninvasive Prenatal Testing

Blais, Jonatan [1] ; Giroux, Sylvie [2] ; Caron, André [2] ; Clément, Valérie [2] ; Rousseau, François [3] [1] Medical Biochemistry Service, Department of Laboratory Medicine, CHU (Centre hospitalier universitaire) de Québec—Université Laval, Quebec City, Quebec, Canada; Department of Molecular Biology, Medical Biochemistry, and Pathology, Faculty of Medicine, Université Laval, Quebec City, Quebec, Canada; Human and Molecular Genetics Research Unit, Research Center, CHU de Québec, Quebec City, Quebec, Canada; Medical Biochemistry Service, Department of Laboratory Medicine, CHU (Centre hospitalier universitaire) de Québec—Université Laval, Quebec City, Quebec, Canada [2] Human and Molecular Genetics Research Unit, Research Center, CHU de Québec, Quebec City, Quebec, Canada [3] Medical Biochemistry Service, Department of Laboratory Medicine, CHU (Centre hospitalier universitaire) de Québec—Université Laval, Quebec City, Quebec, Canada; Department of Molecular Biology, Medical Biochemistry, and Pathology, Faculty of Medicine, Université Laval, Quebec City, Quebec, Canada; Human and Molecular Genetics Research Unit, Research Center, CHU de Québec, Quebec City, Quebec, Canada; PEGASUS (Personalized Genomics for Prenatal Abnormalities Screening Using Maternal Blood), Quebec City, Quebec, Canada

ABSTRAK (ENGLISH)

Background

The performance of noninvasive prenatal testing (NIPT) assays is critically determined by the proportion of fetal DNA or fetal fraction (FF). Fetomaternal differential methylation of certain genomic regions has been proposed as a universal marker of fetal origin, and previous reports have suggested the use of methylation-sensitive restriction enzyme (MSRE) assays to estimate FF.

Methods

We analyzed the performance of FF estimation using an MSRE assay with duplex quantitative polymerase chain reaction (qPCR). Mixtures of genomic DNA from placental cells and from adult women were digested with 2 MSRE and FF estimates obtained, for a total of 221 pairwise treatment/control comparisons.

Results

The coefficient of variance (CV) of the MSRE assays was high, ranging from 24% to 60%. An alternative in silico FF estimation algorithm, SeqFF, displayed slightly lower variability, with a CV of 22%.

Conclusion

These results cast doubts on the usefulness of the MSRE-based assay of differentially methylated markers for FF estimation. The lack of a universal method capable of precisely estimating FF remains an incompletely solved issue.

DETAIL

Subjek:	DNA methylation; Deoxyribonucleic acid--DNA; Polymerase chain reaction
Pengidentifikasi/kata kunci:	fetal DNA; ccffDNA; fetal fraction; NIPT; methylation; MSRE; noninvasive prenatal testing; Down syndrome; next-generation sequencing
Judul:	Precision of Fetal DNA Fraction Estimation by Quantitative Polymerase Chain Reaction Quantification of a Differently Methylated Target in Noninvasive Prenatal Testing

Pengarang:	Blais, Jonatan1; Giroux, Sylvie2; Caron, André2; Clément, Valérie2; Rousseau, François31 Medical Biochemistry Service, Department of Laboratory Medicine, CHU (Centre hospitalier universitaire) de Québec—Université Laval, Quebec City, Quebec, Canada; Department of Molecular Biology, Medical Biochemistry, and Pathology, Faculty of Medicine, Université Laval, Quebec City, Quebec, Canada; Human and Molecular Genetics Research Unit, Research Center, CHU de Québec, Quebec City, Quebec, Canada; Medical Biochemistry Service, Department of Laboratory Medicine, CHU (Centre hospitalier universitaire) de Québec—Université Laval, Quebec City, Quebec, Canada2 Human and Molecular Genetics Research Unit, Research Center, CHU de Québec, Quebec City, Quebec, Canada3 Medical Biochemistry S ervice, Department of Laboratory Medicine, CHU (Centre hospitalier universitaire) de Québec—Université Laval, Quebec City, Quebec, Canada; Department of Molecular Biology, Medical Biochemistry, and Pathology, Faculty of Medicine, Université Laval, Quebec City, Quebec, Canada; Human and Molecular Genetics Research Unit, Research Center, CHU de Québec, Quebec City, Quebec, Canada; PEGASUS (Personalized Genomics for Prenatal Abnormalities Screening Using Maternal Blood), Quebec City, Quebec, Canada
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A 70-Year-Old Female with Unexpected Platelet Function Testing Results

Kim, Moon Joo [1] ; Patel, Pragna [2] ; Vyas, Niti [1] ; Leveque, Christopher [1] ; Diaz, Orlando [2] ; Salazar, Eric [1] [1] Houston Methodist Hospital, Department of Pathology and Genomic Medicine, Houston, Texas [2] Houston Methodist Hospital, Department of Neurointerventional Radiology, Houston, Texas

ABSTRAK (ENGLISH)

A 70-year-old female with a history of hypertension and left A2 segment aneurysm was scheduled for pipeline embolization device (PED) placement. Preinterventional antiplatelet prophylaxis included aspirin and ticagrelor. Unexpectedly, after 13 days of treatment, VerifyNow showed a P2Y12 reaction unit (PRU) value of 216, approximately >5 times the mean PRU of other patients on aspirin and ticagrelor. We confirmed platelet reactivity and ticagrelor resistance with light transmission aggregometry. Antiplatelet therapy was switched to prasugrel, and aspirin was continued. Eight days later, the P2Y12 reaction value (PRU) was 164. PED was placed without complications. Unlike clopidogrel, ticagrelor is a direct P2Y12 inhibitor that does not require metabolism to an active metabolite. Ticagrelor resistance is very rarely reported. To the best of our knowledge, there has been no case of ticagrelor resistance reported in the context of pre-PED placement prophylaxis.

DETAIL

Subjek:	Laboratories; Patients; Glycoproteins; Thrombosis; Angioplasty; Aneurysms; Aspirin; Hypertension; Stents; Blood platelets; Metabolism; Disease prevention; Viscoelasticity; Light; Enzymes; Metabolites; Embolization; Pipelines; Adenosine diphosphate
Pengidentifikasi/kata kunci:	aneurysm; platelet; ticagrelor; resistance; anti-platelet; coagulation
Judul:	A 70-Year-Old Female with Unexpected Platelet Function Testing Results

Pengarang:	Kim, Moon Joo1; Patel, Pragna2; Vyas, Niti1; Leveque, Christopher1; Diaz, Orlando2; Salazar, Eric11 Houston Methodist Hospital, Department of Pathology and Genomic Medicine, Houston, Texas2 Houston Methodist Hospital, Department of Neurointerventional Radiology, Houston, Texas
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Association between Small Dense Low-Density Lipoproteins and High-Density Phospolipid Content in Patients with Coronary Artery Disease with or without Diabetes

Aoua, Hanene [1] ; Nkaies, Ymène [2] ; Ali Ben Khalfallah [3] ; Sakly, Mohsen [2] ; Aouani, Ezzedine [4] ; Attia, Nebil [2] [1] Reasearch Unit 'Integrated Physiology' UR05ES02, Laboratory of Biochemistry-Human Nutrition, Faculty of Bizerta, Carthage University, Tunisia; Laboratory of Bioactive Substances, Center of Biotechnology of Borj Cedria, Tunisia; Reasearch Unit 'Integrated Physiology' UR05ES02, Laboratory of Biochemistry-Human Nutrition, Faculty of Bizerta, Carthage University, Tunisia [2] Reasearch Unit 'Integrated Physiology' UR05ES02, Laboratory of Biochemistry-Human Nutrition, Faculty of Bizerta, Carthage University, Tunisia [3] Echocardiography and Coronary Heart Disease UR6 / SP10, Cardiology Department, Hospital of Menzel Bourguiba, Tunisia [4] Laboratory of Bioactive Substances, Center of Biotechnology of Borj Cedria, Tunisia

ABSTRAK (ENGLISH)

Objective

To evaluate the phospholipid profile in total plasma, non–high-density lipoprotein (HDL), and HDL fractions. We tried to correlate the phospholipid profile to low-density lipoprotein (LDL) size, as reflected by cholesterol content in each LDL subclass.

Methods

We measured small dense LDL-C levels after heparin-magnesium precipitation and measured high-density lipoprotein phospholipid (HDL-P) levels using a colorimetric enzymatic method.

Results

The correlation of the phospholipid profile to small dense LDL-C (sdLDL-C) in patients with coronary problems showed a negative association between small dense low-density lipoprotein (sdLDL) and HDL-P ($r = -0.73$; $P = .02$). Moreover, a strong positive correlation was detected between TG and the ratio HDL-P/HDL-C ($r = 0.83$; $P < .001$).

Conclusions

HDL phospholipid has an antiatherogenic effect in coronary artery disease with or without diabetes. Further, large LDL modulation seems to be associated with diabetes rather than coronaropathy.

DETAIL

Subjek:	Cardiovascular disease; Lipoproteins; Diabetes; Coronary vessels; High density lipoprotein

Pengidentifikasi/kata kunci:	diabetes; coronary artery disease; phospholipids; high-density lipoprotein; low-density lipoprotein, cholesterol
Judul:	Association between Small Dense Low-Density Lipoproteins and High-Density Phospolipid Content in Patients with Coronary Artery Disease with or without Diabetes
Pengarang:	Aoua, Hanene1; Nkaies, Ymène2; Ali Ben Khalfallah3; Sakly, Mohsen2; Aouani, Ezzedine4; Attia, Nebil21 Reasearch Unit 'Integrated Physiology' UR05ES02, Laboratory of Biochemistry-Human Nutrition, Faculty of Bizerta, Carthage University, Tunisia; Laboratory of Bioactive Substances, Center of Biotechnology of Borj Cedria, Tunisia; Reasearch Unit 'Integrated Physiology' UR05ES02, Laboratory of Biochemistry-Human Nutrition, Faculty of Bizerta, Carthage University, Tunisia2 Reasearch Unit 'Integrated Physiology' UR05ES02, Laboratory of Biochemistry-Human Nutrition, Faculty of Bizerta, Carthage University, Tunisia3 Echocardiography and Coronary Heart Disease UR6 / SP10, Cardiology Department, Hospital of Menzel Bourguiba, Tunisia4 Laboratory of Bioactive Substances, Center of Biotechnology of Borj Cedria, Tunisia
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The Impact and Prognostic Significance of Chronic Lymphocytic Leukemia Upregulated 1 (CLLU1) Gene Expression in Patients with Chronic Lymphocytic Leukemia: A Single Center Experience

Sevinc, Mustafa [1] ; Karabulut, Aydın [2] ; Eskazan, Ahmet Emre [3] ; Suzin Catal Tatonyan [4] ; Ozbek, Ugur [5] ; Soysal, Teoman [3] [1] Department of Nephrology, Sisli Etfal Training and Research Hospital, Istanbul, Turkey [2] Vocational School of Health Services, Health Sciences University, Istanbul, Turkey [3] Division of Hematology, Department of Internal Medicine, Cerrahpasa Faculty of Medicine, Istanbul University—Cerrahpasa, Istanbul, Turkey [4] Genera Diagnostic Laboratories, Istanbul, Turkey [5] Department of Medical Genetics, Medical Faculty, Acibadem University, Istanbul, Turkey

ABSTRAK (ENGLISH)

Objectives

To determine *CLLU1* gene levels and the relationship of that gene among other prognostic parameters in patients with chronic lymphocytic leukemia.

Methods

Bone-marrow infiltration pattern, β2-microglobulin (β_2-M), cluster of differentiation (CD)38, and ZAP-70 status were recorded. *CLLU1* levels were assessed by real-time polymerase chain reaction (RT-PCR) and expressed as folds. The relationship between *CLLU1* and other known prognostic parameters was evaluated.

Results

CLLU1 expression was positive in 81 patients and negative in 3 patients. The median (interquartile range [IQR]) *CLLU1* level was 6.45 folds (3.75–16.57 folds) in patients with β_2-M normal values and 16.22 folds (3.91–62.00 folds) in patients with increased β_2-M ($P = .15$). Patients with a higher CD38 value than the median level had 3 times higher *CLLU1* levels than the other group ($P = .07$). The median (IQR) *CLLU1* level was 4.25 folds

(2.75–13.71 folds) in patients with CLL who tested negative on ZAP-70, whereas it was 49.52 folds (15.06–446.36 folds) in those who tested positive via ZAP-70 (*P* = .005).

Conclusions

CLLU1 is a specific parameter to CLL, and its level corresponds well with the ZAP-70 level.

DETAIL

Subjek:	Gene expression; Leukemia; Agent Orange; Medical prognosis
Pengidentifikasi/kata kunci:	chronic lymphocytic leukemia; chronic lymphocytic leukemia upregulated 1 gene; CLLU1; ZAP-70; prognosis, β 2 -microglobulin
Judul:	The Impact and Prognostic Significance of Chronic Lymphocytic Leukemia Upregulated 1 (CLLU1) Gene Expression in Patients with Chronic Lymphocytic Leukemia: A Single Center Experience
Pengarang:	Sevinc, Mustafa1; Karabulut, Aydın2; Eskazan, Ahmet Emre3; Suzin Catal Tatonyan4; Ozbek, Ugur5; Soysal, Teoman31 Department of Nephrology, Sisli Etfal Training and Research Hospital, Istanbul, Turkey2 Vocational School of Health Services, Health Sciences University, Istanbul, Turkey3 Division of Hematology, Department of Internal Medicine, Cerrahpasa Faculty of Medicine, Istanbul University—Cerrahpasa, Istanbul, Turkey4 Genera Diagnostic Laboratories, Istanbul, Turkey5 Department of Medical Genetics, Medical Faculty, Acibadem University, Istanbul, Turkey
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Current Practice and Regional Variability in Recommendations for Patient Preparation for Laboratory Testing in Primary Care

Salinas, Maria [1] ; López-Garrigós, Maite [2] ; Flores, Emilio [3] ; Leiva-Salinas, Carlos [4] [1] Clinical Laboratory, Hospital Universitario de San Juan, San Juan de Alicante, Spain; Department of Biochemistry and Molecular Pathology, Universidad Miguel Hernandez, Elche, Spain [2] Clinical Laboratory, Hospital Universitario de San Juan, San Juan de Alicante, Spain [3] Clinical Laboratory, Hospital Universitario de San Juan, San Juan de Alicante, Spain; Department of Clinical Medicine, Universidad Miguel Hernandez, San Juan de Alicante, Spain [4] Department of Radiology and Medical Imaging, University of Missouri Health Care, Columbia, Missouri, US

ABSTRAK (ENGLISH)

Background

Preparation of the patient for laboratory tests is crucial. Our aim was to investigate the current practice and regional variability of recommendations regarding patient preparation for laboratory testing.

Methods

A call for data was posted by email. Spanish laboratories were invited to fill out and submit a survey.

Results

Sixty-eight laboratories participated in the study. In 73% of those laboratories, fasting was always recommended regardless of the requested tests. Only one-third of the laboratories systematically recommended a 12-hour fast before the tests. In 71% of the laboratories, water intake was allowed without restrictions during the fasting period. In 57% of the laboratories, computerized order entry offered the possibility to print customized recommendations automatically in the primary care doctor's office according to the requested tests. Seventy-two percent of the laboratories agreed with the proposed recommendation.

Conclusions

There was high variability in patient preparation for laboratory testing. A significant proportion of centers did not follow international guidelines.

DETAIL

Subjek:	Laboratories; Primary care; Quality control
Ketentuan indeks bisnis:	Subjek: Quality control
Pengidentifikasi/kata kunci:	fasting; quality improvement; patient preparation; laboratory; preanalytical phase; variability
Judul:	Current Practice and Regional Variability in Recommendations for Patient Preparation for Laboratory Testing in Primary Care
Pengarang:	Salinas, Maria1; López-Garrigós, Maite2; Flores, Emilio3; Leiva-Salinas, Carlos41 Clinical Laboratory, Hospital Universitario de San Juan, San Juan de Alicante, Spain; Department of Biochemistry and Molecular Pathology, Universidad Miguel Hernandez, Elche, Spain2 Clinical Laboratory, Hospital Universitario de San Juan, San Juan de Alicante, Spain3 Clinical Laboratory, Hospital Universitario de San Juan, San Juan de Alicante, Spain; Department of Clinica l Medicine, Universidad Miguel Hernandez, San Juan de Alicante, Spain4 Department of Radiology and Medical Imaging, University of Missouri Health Care, Columbia, Missouri, US
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Basis data:	Public Health Database

Double-Edged Spike—Are SARS-CoV-2 Serologic Tests Safe Right Now?

Torres, Richard [1] ; Rinder, Henry M [1] [1] Yale University School of Medicine, Department of Laboratory Medicine

Link dokumen ProQuest

DETAIL

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Pengarang:	Torres, Richard1; Rinder, Henry M11 Yale University School of Medicine, Department of Laboratory Medicine
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The Study of SALL4 Gene and BMI-1 Gene Expression in Acute Myeloid Leukemia Patients

Rania Shafik Swelem [1] ; Elneely, Dalia Abdelmoety [1] ; Ahmed Abdel Rahman Shehata [2] [1] Department of Clinical and Chemical Pathology, Faculty of Medicine, Egypt [2] Department ofInternal Medicine (Hematology), Faculty of Medicine, Alexandria University, Egypt

ABSTRAK (ENGLISH)

Background

In acute myeloid leukemia (AML), many genes have been studied as prognostic markers. *SALL4* is expressed constitutively in human leukemia cell lines and primary AML cells. *BMI-1* is expressed highly in purified hematopoietic stem cells (HSCs), and its expression declines with differentiation.

Objective

To study the expression levels of *SALL4* and *BMI-1* and their clinical significance in patients with AML.

Methods

The study was performed with 60 patients newly diagnosed with AML and 50 control individuals. *SALL4* and *BMI-1* expression detection were performed using real-time polymerase chain reaction (PCR).

Results

The expression of *SALL4* and *BMI-1* was significantly higher in cases of AML and showed a strong association with failure to achieve complete remission (CR) or with relapse ($P = .02$, $P = .03$, respectively). In multivariate analysis, these genes were the most powerful independent predictors of poor prognosis ($P = .01$ for *SALL4*, $P = .02$ for *BMI-1*).

Conclusion

SALL4 and *BMI-1* are significant prognostic factors in AML and could be strong targets for novel types of therapy.

DETAIL

Subjek:	Gene expression; Medical prognosis; Leukemia
Pengidentifikasi/kata kunci:	AML; SALL4; BMI-1; prognosis; real-time PCR; oncogenes
Judul:	The Study of SALL4 Gene and BMI-1 Gene Expression in Acute Myeloid Leukemia Patients
Pengarang:	Rania Shafik Swelem1; Elneely, Dalia Abdelmoety1; Ahmed Abdel Rahman Shehata21 Department of Clinical and Chemical Pathology, Faculty of Medicine, Egypt2 Department ofInternal Medicine (Hematology), Faculty of Medicine, Alexandria University, Egypt
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The History of Laboratory Medicine Part 3: 1986–2004; Two Turbulent Decades

Bertholf, Roger

DETAIL

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The History of Laboratory Medicine Part 2: 1978–1985; Refocusing the Objectives

Bertholf, Roger L [1] [1] Houston Methodist Hospital, Houston, TX

DETAIL

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Expression of Blood Cells Associated CD Markers and Cardiovascular Diseases: Clinical Applications in Prognosis

Habib Haybar [1] ; Masumeh Maleki Behzad [2] ; Shahrabi, Saeid [3] ; Ansari, Narges [4] ; Najmaldin Saki [2]

[1] Atherosclerosis Research Center, Health Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran [2] Thalassemia and Hemoglobinopathy Research Center, Health Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran [3] Department of Biochemistry and Hematology, Faculty of Medicine, Semnan University of Medical Sciences, Semnan, Iran [4] Isfahan Bone Metabolic Disorders Research Center, Department of Internal Medicine, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Background

Cardiovascular diseases (CVDs) are a major cause of mortality worldwide. The results of various studies have shown that abnormality in the frequency and function of blood cells can be involved in CVD complications. In this review, we have focused on abnormalities in the expression of the CD (cluster of differentiation) markers of blood cells to assess the association of these abnormalities with CVD prognosis.

Methods

We identified the relevant literature through a PubMed search (1990–2018) of English-language articles using the terms “Cardiovascular diseases”, “CD markers”, “leukocytes”, “platelets”, and “endothelial cells”.

Results

There is a variety of mechanisms for the effect of CD-marker expressions on CVDs prognosis, ranging from proinflammatory processes to dysfunctional effects in blood cells.

Conclusion

Considering the possible effects of CD-marker expression on CVDs prognosis, particularly prognosis of acute myocardial infarction and atherosclerosis, long-term studies in large cohorts are required to identify the prognostic value of CD markers and to target them with appropriate therapeutic agents.

DETAIL

Subjek:	Blood; Medical prognosis
Pengidentifikasi/kata kunci:	cardiovascular diseases; CD markers; leukocytes; platelets; endothelial cells; prognosis
Judul:	Expression of Blood Cells Associated CD Markers and Cardiovascular Diseases: Clinical Applications in Prognosis
Pengarang:	Habib Haybar1; Masumeh Maleki Behzad2; Shahrabi, Saeid3; Ansari, Narges4; Najmaldin Saki2 1 Atherosclerosis Research Center, Health Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran2 Thalassemia and Hemoglobinopathy Research Center, Health Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran3 Department of Biochemistry and Hematology, Faculty of Medicine, Semnan University of Medical Sciences, Semnan, Iran4 Isfahan Bone Metabolic Disorders Research Center, Department of Internal Medicine, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
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Association of ABCA1 Haplotypes with Coronary Artery Disease

Fouladseresht, Hamed [1] ; Khazaee, Sahel [1] ; Zibaeenezhad, Mohammad Javad [2] ; Mohammad Hossein Nikoo [3] ; Khosropanah, Shahdad [3] ; Doroudchi, Mehrnoosh [1]

[1] Department of Immunology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran [2] Department of Cardiology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran [3] Cardiovascular Research Center, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Background

Adenosine triphosphate (ATP)–binding-cassette-transporter-A1 (ABCA1) transports cholesterol from cells into

apolipoprotein A1 to form high-density lipoprotein (HDL) cholesterol.

Methods

We investigated the frequencies of ABCA1 functional variants in 273 patients with coronary artery disease (CAD) and 261 age-matched, healthy blood donors in southwest Iran. Sequence-specific primer polymerase-chain reaction (SSP-PCR) and polymerase chain reaction–restriction fragment-length polymorphism (PCR-RFLP) were used for genotyping.

Results

Frequencies of the rs2422493-TT genotype and T-allele, rs1800976-GG genotype, and G-allele in the promoter and rs2230806-GG genotype and G allele in the exon of the *ABCA1* gene were higher in the patients. Abnormal left ventricular size and left-artery disease correlated with rs2422493-T and rs1800976-G alleles, respectively. Wall-motion abnormalities correlated with the rs1883025-G allele and rs2230806-A allele. Regarding the rs2422493/rs1800976/rs2230806/rs1883025 haplotype, T-G-G-A and T-G-A-A were more frequent in case individuals, whereas C-C-G-G was more frequent in control individuals.

Conclusions

The rs2422493-T allele and the rs1800976-G allele increase the risk of disease, as single polymorphisms and in the haplotype. The effect of the rs1883025-G allele is prominent in the haplotype, rather than individually. Considering that G allele of rs2230806 in the third place is present in both susceptible and protective haplotypes, the susceptibility haplotype can be defined as T-G-X-A.

DETAIL

Subjek:	Cardiovascular disease; Genotype &phenotype; Haplotypes; Coronary vessels; Health risk assessment
Pengidentifikasi/kata kunci:	ABCA1; coronary artery disease; rs2422493; rs1800976; rs2230806; rs1883025
Judul:	Association of ABCA1 Haplotypes with Coronary Artery Disease
Pengarang:	Fouladseresht, Hamed1; Khazaee, Sahel1; Zibaeenezhad, Mohammad Javad2; Mohammad Hossein Nikoo3; Khosropanah, Shahdad3; Doroudchi, Mehrnoosh1 1 Department of Immunology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran2 Department of Cardiology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran3 Cardiovascular Research Center, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran
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Proof of Concept for a Polyethylene Glycol/Gel Hybrid Testing Method

Delk, Alexander A [1] ; Gammon, Richard R [2 1] Immunohematology Reference Laboratory, OneBlood, Inc., Fort Lauderdale, Florida [2] Scientific Medical and Technical Administration, OneBlood, Inc., Orlando, Florida

ABSTRAK (ENGLISH)

Objective

To test a hybrid polyethylene glycol (PEG)/gel method, specifically to attempt to increase reaction strength of accidentally overdiluted anti-Co^{b} and broadly for proof of concept.

Methods

Methods were divided into 2 basic steps: sensitization and antiglobulin (AHG) testing. Sensitization was performed with PEG tubes, followed by AHG using the gel method. One wash was performed between the 2 steps. We tested 7 plasma antibody specimens.

Results

In addition to the first specimen, 6 additional antibodies were selected for detection by the PEG/gel hybrid method. Antibody reactivity was detected in all specimens tested with both methods. The PEG/gel method yielded enhanced reactivity in 3 of 7 antibodies (42.9%) and the equivalent of enhanced reactivity in 4 of 7 antibodies tested (57.1%).

Conclusion

The reactivity of diluted anti-Co^{b} (specimen 1) was increased; thus, our concept proved to be viable. The hybrid PEG/gel method showed the equivalent of enhanced or enhanced reactivity with all specimens tested and provided a stable medium.

DETAIL

Subjek:	Methods; Immunoglobulins; Polyethylene glycol
Pengidentifikasi/kata kunci:	tube; gel; immunohematology; transfusion service; blood bank
Judul:	Proof of Concept for a Polyethylene Glycol/Gel Hybrid Testing Method
Pengarang:	Delk, Alexander A1; Gammon, Richard R21 Immunohematology Reference Laboratory, OneBlood, Inc., Fort Lauderdale, Florida2 Scientific Medical and Technical Administration, OneBlood, Inc., Orlando, Florida
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Myeloperoxidase Deficiency Manifesting as Pseudoneutropenia with Low Mean Peroxidase Index and High Monocyte Count in 4 Adult Patients

Roh, Soongki [1] ; Ham, Ji Yeon [2]
; Song, Kyung Eun [2]
; Hwang, Narae [1]
; Nan Young Lee [1]

[1] Department of Laboratory Medicine, Kyungpook National University Hospital, Daegu, South Korea [2] Department of Laboratory Medicine, Kyungpook National University Hospital, Daegu, South Korea; Department of Clinical Pathology, School of Medicine, Kyungpook National University, Daegu, South

Korea

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ABSTRAK (ENGLISH)

Myeloperoxidase (MPO) deficiency, one of the most common inherited phagocyte defects, and may exist as a transient phenomenon in combination with some clinical condition. Hematological analyzer ADVIA 2120i is used to identify the different types of leukocytes based on their size and staining properties, and by mean peroxidase index (MPXI). When MPO deficiency is present, neutrophils may be incorrectly counted as monocytes with lower MPXI values. We encountered a few cases of MPO deficiency with abnormally high monocytes counts resulting in pseudoneutropenia. These abnormal reports could lead to a mistaken diagnosis of severe neutropenia, which could result in unnecessary therapy. Manual differential count exhibited the normal differential count in every case. Every case yielded a markedly low MPXI value below -20. In conclusion, we suggest that MPO deficiency must be considered in patients especially when abnormally high monocyte counts combined with low MPXI values are observed.

DETAIL

Subjek:	Laboratories; Patients; Diabetes; Medicine; Pneumonia; Neutrophils; Blood tests; Bacterial infections; Automation; Granulocytes; Neutropenia; Hematology; Stains &staining
Ketentuan indeks bisnis:	Subjek: Automation
Pengidentifikasi/kata kunci:	myeloperoxidase; pseudoneutropenia; mean peroxidase index; ADVIA 2120i; monocytosis; hematology analyzer
Judul:	Myeloperoxidase Deficiency Manifesting as Pseudoneutropenia with Low Mean Peroxidase Index and High Monocyte Count in 4 Adult Patients
Pengarang:	Roh, Soongki1; Ham, Ji Yeon2 ; Song, Kyung Eun2 ; Hwang, Narae1 ; Nan Young Lee1 1 Department of Laboratory Medicine, Kyungpook National University Hospital, Daegu, South Korea2 Department of Laboratory Medicine, Kyungpook National University Hospital, Daegu, South Korea; Department of Clinical Pathology, School of Medicine, Kyungpook National University, Daegu, South Korea
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Clinical Application of Metabolomics in Pancreatic Diseases: A Mini-Review

Wang, Gu [1] ; Zhong, Tong [2] [1] Anhui Medical University, Hefei City, China [2] Hefei First People's Hospital, Hefei City, China

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Metabolomics is a powerful new analytical method to describe the set of metabolites within cellular tissue and bodily fluids. Metabolomics can uncover detailed information about metabolic changes in organisms. The morphology of these metabolites represents the metabolic processes that occur in cells, such as anabolism, catabolism, inhomogeneous natural absorption and metabolism, detoxification, and metabolism of biomass energy. Because the metabolites of different diseases are different, the specificity of the changes can be found by metabolomics testing, which provides a new source of biomarkers for the early identification of diseases and the difference between benign and malignant states. Metabolomics has a wide application potential in pancreatic diseases, including early detection, diagnosis, and identification of pancreatic diseases. However, there are few studies on metabolomics in pancreatic diseases in the literature. This article reviews the application of metabolomics in the diagnosis, prognosis, treatment, and evaluation of pancreatic diseases.

DETAIL

Subjek:	Metabolism; Metabolites; Medical diagnosis
Pengidentifikasi/kata kunci:	metabolomics; early diagnosis; pancreatic cancer (PC); acute pancreatitis (AP); chronic pancreatitis (CP); pancreatic disease
Judul:	Clinical Application of Metabolomics in Pancreatic Diseases: A Mini-Review
Pengarang:	Wang, Gu1; Zhong, Tong21 Anhui Medical University, Hefei City, China2 Hefei First People’s Hospital, Hefei City, China
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Basis data:	Public Health Database

Persistent Rivaroxaban Effect Due to Impaired Renal Clearance and Medication Effects

Milito, Chelsea [1] ; McRae, Hannah [1] ; Victor, Adrienne [2] ; Refaai, Majed A [1] ; Schmidt, Amy E [1]
[1] Department of Pathology and Laboratory Medicine, University of Rochester Medical Center, Rochester, New York [2] Department of Hematology and Oncology, University of Rochester Medical Center, Rochester, New York

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Rivaroxaban (Xarelto; Johnson &Johnson Services, Inc) is a direct oral anticoagulant (DOAC) that works by directly inhibiting the active site of factor Xa (FXa). Rivaroxaban is metabolized and cleared via the kidney and liver. The results of various studies have shown that patients with severe renal impairment should receive reduced dosages of rivaroxaban or another anticoagulant due to impaired clearance. Although it is not required, monitoring rivaroxaban is useful in some conditions; however, the assays required for such monitoring are not readily available. Herein, we present a case of a 68-year-old Caucasian male patient who was receiving rivaroxaban (20 mg/day) for atrial flutter and had mild renal impairment. The patient was found to have increased effect of rivaroxaban due to further impairment of renal clearance caused by several renally cleared medications. This case highlights the importance of

closely examining the renal function of and medication list for a patient before starting DOACs such as rivaroxaban.

DETAIL

Subjek:	Anticoagulants; Electrocardiography
Pengidentifikasi/kata kunci:	rivaroxaban; anticoagulation; bleeding; prolonged PT; renal impairment; DOAC
Judul:	Persistent Rivaroxaban Effect Due to Impaired Renal Clearance and Medication Effects
Pengarang:	Milito, Chelsea1; McRae, Hannah1; Victor, Adrienne2; Refaai, Majed A1; Schmidt, Amy E1 1 Department of Pathology and Laboratory Medicine, University of Rochester Medical Center, Rochester, New York2 Department of Hematology and Oncology, University of Rochester Medical Center, Rochester, New York
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Individualized Correction of the Interference of Hemolysis on Glycated Albumin Determined by the Ketamine Oxidase Method

Chen, Li [1] ; Zhang, Bingfeng [2] ; Lu, Yang [2] ; Jianfang Lou [2] ; Jiang, Ye [2] ; Zhang, Shichang [1]

[1] Department of Obstetrics, First Affiliated Hospital of Nanjing Medical University, Nanjing, China [2] Department of Laboratory Medicine, First Affiliated Hospital of Nanjing Medical University, Nanjing, China

ABSTRAK (ENGLISH)

Objective

To investigate the effect of hemolysis on glycated albumin (GA) levels, as determined by the ketamine oxidase method.

Methods

GA levels and the hemolysis index were determined in nonhemolyzed serum and hemolyzed serum from corresponding patients. We developed an equation to correct the interference of hemolysis on GA, using multiple regression analysis.

Results

The degree of hemolysis was negatively correlated with GA levels (R^2 = 0.9500). A correction equation for GA (corrected GA = 2.703 × OD of hemolysis + 1.044 × measured GA −0.906) can revert GA concentrations of hemolyzed specimens to values that were not significantly different from the GA concentration of corresponding nonhemolyzed specimens. The bias of GA concentrations before and after correction was statistically significantly different (P <.01).

Conclusions

Our results indicate that the level of GA measured through the ketamine oxidase method is negatively affected by hemolysis. The individualized correction of GA results provides increased accuracy in hemolyzed specimens.

DETAIL

Subjek:	Glucose monitoring; Diabetes; Ketamine
Pengidentifikasi/kata kunci:	hemolysis; glycated albumin; interference; correction, diabetes mellitus, glucose monitoring
Judul:	Individualized Correction of the Interference of Hemolysis on Glycated Albumin Determined by the Ketamine Oxidase Method
Pengarang:	Chen, Li1; Zhang, Bingfeng2; Lu, Yang2; Jianfang Lou2; Jiang, Ye2; Zhang, Shichang1 1 Department of Obstetrics, First Affiliated Hospital of Nanjing Medical University, Nanjing, China2 Department of Laboratory Medicine, First Affiliated Hospital of Nanjing Medical University, Nanjing, China
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Investigation of JAK2V617F Mutation Prevalence in Patients with Beta Thalassemia Major

Asadi, Zari Tahannejad [1] ; Yarahmadi, Reza [2] ; Najmaldin Saki [2] ; Mohammad Taha Jalali [3] ; Ali Amin Asnafi [2] ; Tangestani, Raheleh [2] [1] Health Research Institute, Thalassemia &Hemoglobinopathy Research Center; Department of Laboratory Sciences, Faculty of Paramedicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran [2] Health Research Institute, Thalassemia &Hemoglobinopathy Research Center [3] Department of Laboratory Sciences, Faculty of Paramedicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Background

Beta (β)–thalassemia major is a genetic disorder with anemia and an increased level of erythropoietin by Janus kinase/signal transducers and activators of transcription (JAK/STAT) signaling pathway. JAK plays an important role in cell signaling, and the common mutation in the *JAK2* gene in myeloid disorders is called JAK2V617F.

Methods

A total of 75 patients with beta (β)-thalassemia major patients, including 34 males (45%) and 41 females (55%), were enrolled in this study. The presence of the JAK2V617F mutation was assessed using the amplification-

refractory mutation–polymerase chain reaction (ARMS-PCR) technique.

Results

Among the 75 patients, 14 patients (19%) tested positive and 61 patients (81%) tested negative for JAK2V617F mutation. We observed no statistically significant difference in sex, age, genotype, and JAK2V617F mutation among patients (*P*> .05). However, a significant difference between blood-transfusion frequency and JAK2V617F mutation was observed (*P* <.05).

Conclusion

Due to the low prevalence of JAK2V617F mutation in thalassemia, using a larger population of the patients to investigate this mutation in ineffective erythropoiesis can be useful.

DETAIL

Subjek:	Kinases; Mutation
Pengidentifikasi/kata kunci:	β-thalassemia; JAK2V617F; blood transfusion; erythropoiesis; mutation; ARMS-PCR
Judul:	Investigation of JAK2V617F Mutation Prevalence in Patients with Beta Thalassemia Major
Pengarang:	Asadi, Zari Tahannejad1 ; Yarahmadi, Reza2; Najmaldin Saki2 ; Mohammad Taha Jalali3; Ali Amin Asnafi2; Tangestani, Raheleh21 Health Research Institute, Thalassemia &Hemoglobinopathy Research Center; Department of Laboratory Sciences, Faculty of Paramedicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran2 Health Research Institute, Thalassemia &Hemoglobinopathy Research Center3 Department of Laboratory Sciences, Faculty of Paramedicine, A hvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
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Basis data:	Public Health Database

Balamuthia mandrillaris -Related Primary Amoebic Encephalitis in China Diagnosed by Next Generation Sequencing and a Review of the Literature

Yang, Yinan [1] ; Hu, Xiaobin [2] ; Li, Min [1] ; Dong, Xiangyu [1] ; Guan, Yuanlin [3] [1] Department of Pediatrics, Lanzhou University Second Hospital, Lanzhou, Gansu, China [2] School of Public Health, Lanzhou University, Cheng Guan District, Lanzhou, Gansu, China [3] Chief Information Officer, Hugobiotech MicrobeCode Biotechnology Co. Ltd., Xi'an, Shaanxi, China

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Background

Encephalitis is caused by infection, immune mediated diseases, or primary inflammatory diseases. Of all the

causative infectious pathogens, 90% are viruses or bacteria. Granulomatous amoebic encephalitis (GAE), caused by *Balamuthia mandrillaris*, is a rare but life-threatening disease. Diagnosis and therapy are frequently delayed due to the lack of specific clinical manifestations.

Method

A healthy 2 year old Chinese male patient initially presented with a nearly 2 month history of irregular fever. We present this case of granulomatous amoebic encephalitis caused by *B. mandrillaris*. Next generation sequencing of the patient's cerebrospinal fluid (CSF) was performed to identify an infectious agent.

Result

The results of next generation sequencing of the CSF showed that most of the mapped reads belonged to *Balamuthia mandrillaris*.

Conclusion

Next generation sequencing (NGS) is an unbiased and rapid diagnostic tool. The NGS method can be used for the rapid identification of causative pathogens. The NGS method should be widely applied in clinical practice and help clinicians provide direction for the diagnosis of diseases, especially for rare and difficult cases.

DETAIL

Subjek:	Pathogens; Encephalitis; Cerebrospinal fluid
Pengidentifikasi/kata kunci:	amoeba; Balamuthia mandrillaris; cerebrospinal fluid; child; granulomatous amoebic encephalitis; next generation sequencing
Judul:	Balamuthia mandrillaris -Related Primary Amoebic Encephalitis in China Diagnosed by Next Generation Sequencing and a Review of the Literature
Pengarang:	Yang, Yinan1; Hu, Xiaobin2; Li, Min1; Dong, Xiangyu1; Guan, Yuanlin31 Department of Pediatrics, Lanzhou University Second Hospital, Lanzhou, Gansu, China2 School of Public Health, Lanzhou University, Cheng Guan District, Lanzhou, Gansu, China3 Chief Information Officer, Hugobiotech MicrobeCode Biotechnology Co. Ltd., Xi'an, Shaanxi, China
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Paradoxical Hypercholesterolemia in an Otherwise Healthy Adult Man

Mcpherson, Peter A [1] [1] Centre for Applied Science, Belfast Metropolitan College, Belfast, Northern Ireland

ABSTRAK (ENGLISH)

Hypercholesterolemia is characterized by serum cholesterol levels greater than 5 mmol per L. However, the distribution of cholesterol among lipoprotein classes has a significant bearing on diagnosis: high–low-density lipoprotein (LDL) cholesterol suggests familial hypercholesterolemia, whereas high–high-density lipoprotein (HDL) cholesterol is associated with hyperalphalipoproteinemia. On routine screening, a 23-year-old man presented with a total cholesterol level of 7.6 mmol per L but was subsequently found to have an HDL cholesterol level of 5.6 mmol per L. The clinical picture was confounded by his use of red yeast rice extract, a popular health supplement with hypolipidemic effects. In this case individual, the use of red yeast rice extract caused a hyperlipidemic state, ostensibly through downregulation of cholesteryl ester transfer protein. This case emphasizes the extended role of laboratory medicine in complex cases of hyperlipidemia.

DETAIL

Subjek:	Lipoproteins; Cholesterol; Health risk assessment
Pengidentifikasi/kata kunci:	cholesteryl ester transfer protein; clinical chemistry; red yeast rice extract; hyperalphalipoproteinemia; herbal medicines; omega-3 fatty acids
Judul:	Paradoxical Hypercholesterolemia in an Otherwise Healthy Adult Man
Pengarang:	Mcpherson, Peter A11 Centre for Applied Science, Belfast Metropolitan College, Belfast, Northern Ireland
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Association of Serum Cholesterol Ester Transfer Protein Levels with Taq IB Polymorphism in Acute Coronary Syndrome

Amer, Noha N [1]
; Shaaban, Gamal M [2] [1] Biochemistry Department, Faculty of Pharmacy (Girls), Al Azhar University, Cairo, Egypt [2] National Heart Institute, Cairo, Egypt

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Information on the relationship between circulating cholesteryl ester transfer protein (CETP) levels and coronary heart disease (CHD) incidence (and also, therefore, acute coronary syndrome [ACS]) is conflicting. Many studies have been published concerning this relationship, most of which have incompatible results. In our study, we aimed to determine serum CETP levels in subject individuals with ACS and healthy control individuals, and the association of those levels with Taq IB polymorphism. The current study was conducted with 62 hospitalized patients who had been diagnosed with ACS and 26 controls. All subjects were selected from a previous study of which we are among the coauthors. Serum CETP levels were determined by quantitative enzyme-linked immunosorbent assay (ELISA). The mean serum CETP levels in all patients were significantly higher than those in controls. CETP TaqIB polymorphism affected serum CETP levels, with higher serum CETP for the GA genotype in both groups than in other genotypes. Although the AA genotype showed higher CETP levels than the GG genotype in patients with ACS, the GG showed higher CETP than the AA in healthy controls. Our results support an association between high serum CETP and ACS incidence. Our study helped address some of the controversies regarding the relationship of

serum CETP mass to atherosclerosis, in addition to the association of ACS occurrence with circulating CETP levels.

DETAIL

Subjek:	Cardiovascular disease; Acute coronary syndromes; Genotype &phenotype; Polymorphism; Heart attacks
Pengidentifikasi/kata kunci:	cholesterol ester transfer protein; high-density lipoprotein cholesterol; acute coronary syndrome; unstable angina; myocardial infarction; enzyme-linked immunosorbent assay
Judul:	Association of Serum Cholesterol Ester Transfer Protein Levels with Taq IB Polymorphism in Acute Coronary Syndrome
Pengarang:	Amer, Noha N1 ; Shaaban, Gamal M21 Biochemistry Department, Faculty of Pharmacy (Girls), Al Azhar University, Cairo, Egypt2 National Heart Institute, Cairo, Egypt
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Affordable, Reliable Dual-Platform Approach to Quantitating Phosphatidylserine-Exposing Platelets in Platelet Components

Noulsri, Egarit [1]
; Lerdwana, Surada [2] [1] Research Division, Mahidol University, Bangkok, Thailand [2] Division of Instruments for Research, Office for Research and Development, Faculty of Medicine, Siriraj Hospital, Mahidol University, Bangkok, Thailand

ABSTRAK (ENGLISH)

Objective

To compare the number of phosphatidylserine (PS)–exposing platelets obtained using the dual-platform approach and bead-based flow cytometry.

Methods

Platelets were enumerated using the ADVIA 2010i instrument (Siemens AG). The numbers and percentages of PS-exposing platelets in 175 platelet products were determined using a FACSCalibur flow cytometer (Becton, Dickinson and Company) and counting beads.

Results

Our results showed good correlation (r^2 = 0.96; P <.001) between the PS-exposing platelets obtained using counting beads and the dual-platform approach. The results of Bland-Altman analysis showed a bias of +46,449 cells per µL

and a limit of agreement (LOA) from −197,863 to 290,762 cells per μL. Also, 8 measurements (5.0%) revealed a number of PS-exposing platelets outside the LOA ranges. Further, 21 measurements (12.0%) revealed greater than 2-fold changes in the number of PS-exposing platelets.

Conclusions

The results suggest that the dual-platform approach is affordable and reliable for quantitating PS-exposing platelets as part of monitoring the quality of platelet products.

DETAIL

Pengidentifikasi/kata kunci:	platelet; phosphatidylserine; quantitation; flow cytometry; laboratory; transfusion
Judul:	Affordable, Reliable Dual-Platform Approach to Quantitating Phosphatidylserine-Exposing Platelets in Platelet Components
Pengarang:	Noulsri, Egarit1 ; Lerdwana, Surada21 Research Division, Mahidol University, Bangkok, Thailand2 Division of Instruments for Research, Office for Research and Development, Faculty of Medicine, Siriraj Hospital, Mahidol University, Bangkok, Thailand
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Requiem for the STAT Test: Automation and Point of Care Testing

Singh, Gurmukh [1] ; Savage, Natasha M [2] ; Gunsolus, Brandy [3] ; Foss, Kellie A [4] [1] Professor of Pathology, Shepeard Chair in Clinical Pathology, Vice Chair of Pathology, Augusta, Georgia [2] Associate Professor of Pathology, Director of Hematology and Hematopathology, Augusta, Georgia [3] Pathology Utilization Manager, Clinical Pathology, Augusta, Georgia [4] Administrative Director for Pathology Services, Medical College of Georgia at Augusta University, Department of Pathology, Augusta, Georgia

Link dokumen ProQuest

ABSTRAK (ENGLISH)

Objective

Quick turnaround of laboratory test results is needed for medical and administrative reasons. Historically, laboratory tests have been requested as routine or STAT. With a few exceptions, a total turnaround time of 90 minutes has been the usually acceptable turnaround time for STAT tests.

Methods

We implemented front-end automation and autoverification and eliminated batch testing for routine tests. We instituted on-site intraoperative testing for selected analytes and employed point of care (POC) testing judiciously. The pneumatic tube system for specimen transport was expanded.

Results

The in-laboratory turnaround time was reduced to 45 minutes for more than 90% of tests that could reasonably be ordered STAT. With rare exceptions, the laboratory no longer differentiates between routine and STAT testing. Having a single queue for all tests has improved the efficiency of the laboratory.

Conclusion

It has been recognized in manufacturing that batch processing and having multiple queues for products are inefficient. The same principles were applied to laboratory testing, which resulted in improvement in operational efficiency and elimination of STAT tests. We propose that the target for in-laboratory turnaround time for STAT tests, if not all tests, be 45 minutes or less for more than 90% of specimens.

DETAIL

Subjek:	Laboratories; Batch processing; Automation
Pengidentifikasi/kata kunci:	automation; autoverification; batch testing; intraoperative testing; paradigm shift; point of care testing; STAT test
Judul:	Requiem for the STAT Test: Automation and Point of Care Testing
Pengarang:	Singh, Gurmukh1 ; Savage, Natasha M2; Gunsolus, Brandy3; Foss, Kellie A41 Professor of Pathology, Shepeard Chair in Clinical Pathology, Vice Chair of Pathology, Augusta, Georgia2 Associate Professor of Pathology, Director of Hematology and Hematopathology, Augusta, Georgia3 Pathology Utilization Manager, Clinical Pathology, Augusta, Georgia4 Administrative Director for Pathology Services, Medical College of Georgia at Augusta University, Department of Pathology, Augusta, Georgia
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Correlation between Osteoprotegerin Levels and Antiphospholipid Syndrome Parameters

Caraiola, Simona [1] ; Dima, Alina [1]
; Jurcut, Ciprian [2] ; Jurcut, Ruxandra [3]
; Baicus, Cristian [1] ; Baicus, Anda [4] [1] Department of Internal Medicine, Carol Davila University of Medicine and Pharmacy; Department of Internal Medicine, Colentina Clinical Hospital [2] Department of Internal Medicine, Dr Carol Davila Central University Emergency Military Hospital [3] Department of Cardiology, Prof Dr CC Iliescu Institute of Cardiovascular Diseases [4] Immunology Laboratory, University Emergency Hospital, Bucharest, Romania

ABSTRAK (ENGLISH)

Objective

To identify the osteoprotegerin (OPG) correlates with antiphospholipid syndrome (APS) parameters.

Methods

Our cohort included 40 patients with primary APS disease associated with systemic lupus erythematosus (SLE) (mean age, 43.7 years; 87% female). Data on cardiovascular risk factors and specific clinical events in APS were collected. Then we tested OPG and 10 criteria and noncriteria antiphospholipid antibodies (aPLs) on preserved specimens in all cases.

Results

A total of 26 patients (65%) had high serum OPG levels. Patients with high OPG were mostly overweight. In patients with SLE, the OPG levels were associated with anti–double-stranded DNA (anti-dsDNA) and anti-Sm titers. However, we did not find significant correlations of the OPG with any of the 10 aPLs tested. Also, we found no relationship regarding venous APS events.

Conclusion

In APS, high OPG levels are not linked to serum aPL expression.

DETAIL

Pengidentifikasi/kata kunci:	osteoprotegerin; antiphospholipid syndrome; cardiovascular risk; stroke; thrombosis; systemic lupus erythematosus
Judul:	Correlation between Osteoprotegerin Levels and Antiphospholipid Syndrome Parameters

Pengarang:	Caraiola, Simona1; Dima, Alina1 ; Jurcut, Ciprian2; Jurcut, Ruxandra3 ; Baicus, Cristian1; Baicus, Anda41 Department of Internal Medicine, Carol Davila University of Medicine and Pharmacy; Department of Internal Medicine, Colentina Clinical Hospital2 Department of Internal Medicine, Dr Carol Davila Central University Emergency Military Hospital3 Department of Cardiology, Prof Dr CC Iliescu Institute of Cardiovascular Diseases4 Immunology Laboratory, University Emergency Hospital, Bucharest, Romania
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Human Epididymis Protein 4 as an Indicator of Acute Heart Failure in Patients with Chronic Kidney Disease

Huang, Ying [1] ; Jiang, Hong [1] ; Zhu, Lihua [1] [1] Department of Cardiology, Renmin Hospital, Wuhan, China; Cardiovascular Research Institute of Wuhan University, Wuhan, China

ABSTRAK (ENGLISH)

Background

Cardiovascular disease (CVD) is the leading cause of death in patients with chronic kidney disease (CKD).

Objective

To assess whether human epididymis protein 4 (HE4) can be useful in diagnosing acute heart failure (AHF) in patients with CKD.

Methods

A cohort of 139 Han nationality female patients with CKD who were hospitalized at Renmin Hospital of Wuhan University, Wuhan, China from January 2015 through November 2017 were included.

Results

Multivariable linear regression analysis showed that HE4 levels were significantly associated with N-terminal pro b-type natriuretic peptide (NT-proBNP) after adjustment of kidney function and other confounding factors. In the multivariate logistic regression analysis, HE4 was independently associated with AHF in patients with CKD (odds ratio, 2.120; 95% confidence interval, 1.034–4.344; $P = .04$). Moreover, according to the optimal cutoff value of 639.6 pmol per L, the area under the curve, sensitivity, and specificity of HE4 were 0.729, 74.2%, and 76.8%, respectively.

Conclusions

During hospitalization, HE4 maybe an useful indicator for diagnosing AHF in patients with CKD.

DETAIL

Subjek:	Regression analysis; Kidney diseases; Heart failure; Medical diagnosis
Pengidentifikasi/kata kunci:	human epididymis protein 4; acute heart failure; chronic kidney disease; marker; diagnostic value; multivariate analysis
Judul:	Human Epididymis Protein 4 as an Indicator of Acute Heart Failure in Patients with Chronic Kidney Disease
Pengarang:	Huang, Ying1; Jiang, Hong1; Zhu, Lihua11 Department of Cardiology, Renmin Hospital, Wuhan, China; Cardiovascular Research Institute of Wuhan University, Wuhan, China
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Cardiomyopathy in Thalassemia: Quick Review from Cellular Aspects to Diagnosis and Current Treatments

Ghanavat, Majid [1] ; Habib Haybar [2] ; Seyed Mohammad Sadegh Pezeshki [3] ; Shahjahani, Mohammad [3] ; Jodat, Hosein [3] ; Elyasi, Milad [3] ; Najmaldin Saki [4]

[1] Child Growth &Development Research Center, Isfahan University of Medical Sciences, Isfahan, Iran [2] Atherosclerosis Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran [3] Thalassemia &Hemoglobinopathy Research Center, Health Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran [4] Thalassemia &Hemoglobinopathy Research Center, Health Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran; Child Growth &Development Research Center, Isfahan University of Medical Sciences, Isfahan, Iran

ABSTRAK (ENGLISH)

Background

Cardiomyopathic manifestations induced by continuous blood transfusion are the leading cause of death among patients with thalassemia major (TM). Despite introduction of chelation therapy, heart failure after cardiomyopathic manifestations is still a major threat to patients.

Methods

We performed a search of relevant English-language literature, retrieving publications from the PubMed database and the Google Scholar search engine (2005–2018). We used “thalassemia major”, “cardiomyopathy”, “iron overload”, “cardiac magnetic resonance T2” “chelation therapy”, and “iron burden” as keywords.

Results

The results of the studies we found suggest that cardiac hepcidin is a major regulator of iron homeostasis in cardiac tissue. Unlike previous assumptions, the heart appears to have a limited regeneration capability, originating from a small population of hypoxic cardiomyocytes.

Conclusions

Oxygen levels determine cardiomyocyte gene-expression patterns. Upregulation of cardiac hepcidin in hypoxia preserves cardiomyocytes from forming out of reactive oxygen species catalyzed by free cellular iron in cardiomyocytes. Using the limited regeneration capacity of cardiac cells and gaining further understanding of the cellular aspects of cardiomyopathic manifestations may help health care professionals to develop new therapeutic strategies.

DETAIL

Subjek:	Cardiomyopathy; Chelation therapy; Cardiomyocytes; Medical diagnosis
Pengidentifikasi/kata kunci:	thalassemia major; cardiomyopathy; iron overload; cardiac magnetic resonance T2; chelation therapy; iron burden
Judul:	Cardiomyopathy in Thalassemia: Quick Review from Cellular Aspects to Diagnosis and Current Treatments
Pengarang:	Ghanavat, Majid1; Habib Haybar2; Seyed Mohammad Sadegh Pezeshki3 ; Shahjahani, Mohammad3; Jodat, Hosein3; Elyasi, Milad3; Najmaldin Saki4 1 Child Growth &Development Research Center, Isfahan University of Medical Sciences, Isfahan, Iran2 Atherosclerosis Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran3 Thalassemia &Hemoglobinopathy Research Center, Health Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran4 Thalassemia &Hemoglobinopathy Research Center, Health Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran; Child Growth &Development Research Center, Isfahan University of Medical Sciences, Isfahan, Iran
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Farahani, H., Alaee, M., Amri, J., Mahmoud-Reza Baghinia, & Rafiee, M. (2020). Serum and saliva concentrations of biochemical parameters in men with prostate cancer and benign prostate hyperplasia. Labmedicine, 51(3), 243-251. doi:https://doi.org/10.1093/labmed/lmz053

Objectives To find suitable biomarkers for diagnosis of prostate cancer (PC) in serum and saliva; also, to evaluate the diagnostic efficacy of saliva in patients with PC. Methods This case-control study included 20 patients with PC and 20 patients with benign prostatic hyperplasia (BPH). Blood and saliva were collected from the participants and centrifuged. Serum and supernatant saliva were used for biochemical analysis. We evaluated serum and salivary levels of urea, creatinine, prostate-specific antigen (PSA), creatine kinase BB (CK-BB), zinc, β-2 microglobulin (B2M), and melatonin. Also, we used Mann-Whitney U testing, Spearman correlation coefficients, and receiver operating characteristic (ROC) analysis to evaluate the data. Results Serum and salivary concentrations of urea, creatinine, PSA, CK-BB, zinc, and B2M were significantly higher in patients with PC, compared with the BPH group ($P < .05$). However, serum and salivary concentrations of melatonin were significantly lower in patients with PC, compared with BPH group ($P < .05$). In both groups, salivary concentrations of all markers were lower ($P < .05$), compared with those values in serum. We observed positive correlation between serum and salivary concentrations of all markers studied ($P < .05$). Conclusion From the data, we conclude that investigation using saliva specimens is a noninvasive, simple, and effective tool for screening of biochemical parameters.

Kaplan, A., Gabert, K. A., & Yazer, M. H. (2020). Unexpectedly weak anti-B in 2 group O pediatric patients on parenteral nutrition and disease specific supplemental enteral feeds. Labmedicine, 51(3), 296-300. doi:https://doi.org/10.1093/labmed/lmz057

Anti-A and anti-B antibodies are naturally occurring and develop from exposure to intestinal bacteria after age 4 to 6 months. In the laboratory, strong agglutination with A1 and B cells, or B cells only and A1 cells only, on reverse typing in a healthy person with immunocompetence is expected for patients with ABO types O, A, and B, respectively. However, absent or weak anti-A and anti-B antibodies can be observed in some clinical scenarios, such as patients with immunodeficiencies, newborns, elderly patients, and patients who have recently received bone marrow transplants. In this article, we report the cases of 2 pediatric patients with group O blood type who were receiving total parenteral nutrition (TPN) and disease-specific enteral feeds and who have strong anti-A and absent/weak anti-B.

Q&A with dr paul phillip sher, editor in chief 1986-2004. (2020). Labmedicine, 51(3), 234-235. doi:https://doi.org/10.1093/labmed/lmaa020

Chang-Hun, P., Yun, J. W., Hyun-Young, K., Ki-O, L., Sun-Hee, K., & Hee-Jin, K. (2020). Myelodysplastic Syndrome/Myeloproliferative neoplasm with ring sideroblasts and thrombocytosis with cooccurrent SF3B1 and MPL gene mutations: A case report and brief review of the literature. Labmedicine, 51(3), 315-319. doi:https://doi.org/10.1093/labmed/lmz076

Background Myelodysplastic syndrome/myeloproliferative neoplasm with ring sideroblasts and thrombocytosis (MDS/MPN-RS-T) is a new disease entity in the current WHO classification. Genetically, 60%–90% of cases have mutations in SF3B1, strongly associated with RS, and more than half of them cooccur with JAK2 V617F. This report describes the rare case of MDS/MPN-RS-T with SF3B1 mutation cooccurring with an MPL mutation. Methods We report a 79-year-old man who was referred because of generalized edema. Peripheral blood testing showed macrocytic anemia and thrombocytosis, and bone marrow analysis demonstrated dyserythropoiesis with RS and increased megakaryocytes. A molecular study was performed to detect SF3B1 mutations and recurrent mutations in MPN disease (JAK2 V617F/exon 12, CALR gene exon 9, and MPL gene exon 10 mutations). Results The molecular study revealed SF3B1 K666T and MPL W515R mutations, while BCR-ABL1 or JAK2 V617F/exon 12 and CALR mutations were all negative. Conclusion This is a rare case of concomitant SF3B1 and MPL mutations in MDS/MPN-RS-T.

Kulkarni, S., Piraino, D., Strauss, R., Proctor, E., Waldman, S., King, J., & Selby, R. (2020). The cost of pre-analytical errors in INR testing at a tertiary-care hospital laboratory: Potential for significant cost savings. Labmedicine, 51(3), 320-324. doi:https://doi.org/10.1093/labmed/lmz062

Background Preanalytical errors account for most laboratory errors. Although the frequencies of preanalytical errors are well characterized in the literature, little is known regarding the costs of these errors to the laboratory. Objective To analyze costs associated with preanalytical errors associated with the international normalized ratio (INR) test. Methods We performed a retrospective analysis of INR requests associated with preanalytical error codes from January 2009 through September 2013. Preanalytical error types were those related to order entry (no specimen collected) and those unrelated to order entry (insufficient specimen quantity or specimen-integrity concerns). We calculated the cost of analysis of a specimen and the cost of investigating errors. Results During the study period, there were 557,411 INR requests, 13.1% of which were associated with a preanalytical error code. The total annual cost of INR testing was USD $379,222.50. Investigation and reporting of preanalytical errors not related to order entry represented 10.5% of our annual INR testing budget (USD $39,939.00). Conclusions Minimizing preanalytical errors has the potential to result in significant cost savings.

Kim, M., Dae, Y. Z., Lee, J., Ji-Young, P., Chung, Y., & Young, K. L. (2020). Mixed phenotype acute leukemia that evolved from myelodysplastic syndrome with excess blasts. Labmedicine, 51(3), 288-295. doi:https://doi.org/10.1093/labmed/lmz054

Myelodysplastic syndrome (MDS) that evolves into acute leukemia with blasts of mixed phenotypes has rarely been reported and has no distinct diagnostic category. Herein, we describe a 79-year-old Korean female patient with MDS–excess blasts (MDS-EB) that evolved into acute leukemia; the blasts simultaneously expressed B-lymphoid and myeloid antigens. The patient was diagnosed with MDS-EB with blasts of myeloid lineage coexpressing a few B-lymphoid antigens with 7q and 20q abnormalities. The disease progressed to acute leukemia with blasts carrying more B-lymphoid antigens, which was immunophenotypically compatible with B-lymphoid/myeloid acute leukemia. Unlike previously reported patients whose blast populations are bilineal, our patient is the first with biphenotypic acute leukemia that progressed from MDS. The diagnosis of our patient introduces the possibility that many other types of biphenotypic acute leukemia may have gone undiagnosed and encourages hematologists to designate a specific diagnostic category for this type of disease, so that it can more readily be detected and studied in the future.

Clavijo, A., Ryan, N., Xu, H., & Singh, G. (2020). Measurement of monoclonal immunoglobulin protein concentration in serum protein electrophoresis: Comparison of automated vs Manual/Human readings. Labmedicine, 51(3), 252-258. doi:https://doi.org/10.1093/labmed/lmz055

Background Protein concentration of monoclonal immunoglobulin in plasma-cell myeloma/multiple myeloma provides an estimate of the tumor mass and allows for monitoring of the response to treatment. Accurate and reproducible estimates of the monoclonal immunoglobulin concentration are important for patient care. Objective To address the optimum method for estimation of the concentration of monoclonal immunoglobulins. Methods Serum protein electrophoresis and immunofixation electrophoresis were conducted by using the Helena SPIFE Touch instrument. Estimation of the protein concentration of monoclonal immunoglobulin in the gamma region by computer-assisted reading was compared with the reading by technologists and pathology residents, in 300 gels. The data were compared using t-testing and analysis of variance. Results Computer-generated readings had a consistent positive bias. The correlation coefficient of the average reading by technologists and residents with the computer generated value was 0.997. The average positive bias by the computer reading was 0.29 g per dL. The intercept on the regression analysis was 0.22 g per dL. The reading by the computer was significantly higher than each of the human-interpreted readings. The readings by the 3 human groups were not significantly different amongst them. The main reason for the higher reading by the computer was inclusion of a greater area on the anodal size of the peak on the densitometric scan. Conclusions Human- and computer-interpreted readings of the protein concentration of monoclonal immunoglobulin have a high degree of correlation. The consistent positive bias by the computer reading occurred due to inclusion of a greater area of the densitometric scan on the anodal side of the peak. We suggest that vendors should adjust such computer programs to provide readings comparable to those

generated by expert humans. We recommend manual delineation of the monoclonal peaks for measuring the concentration of monoclonal immunoglobulins.

Jee-Soo, L., Ho, Y. K., Kim, M., & Young, K. L. (2020). A novel pathogenic CALR exon 9 mutation in a patient with essential thrombocythemia. Labmedicine, 51(3), 306-309. doi:https://doi.org/10.1093/labmed/lmz064

The clinical phenotypes and prognoses of CALR-mutant myeloproliferative neoplasms depend on the mutation type. The 2 most common mutations, type 1 (52-bp deletion) and type 2 (5-bp insertion), account for 85% of CALR-mutated neoplasms. The former confers a myelofibrotic phenotype, and the latter is associated with a low risk of thrombosis and an indolent clinical course. Individual case reports for patients with novel pathogenic CALR mutations are rare. Herein, we present the first case in the literature, to our knowledge, of a 63-year old ethnic Korean man with essential thrombocythemia who was diagnosed with a novel +1-bp frameshift mutation in CALR, which was predicted to exhibit a type 2–like phenotype.

Iwen, P. C., Stiles, K. L., & Pentella, M. A. (2020). Safety considerations in the laboratory testing of specimens suspected or known to contain the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Labmedicine, 51(3), 239-242. doi:https://doi.org/10.1093/labmed/lmaa018

Pavičić, T., Ćelap, I., Njegovan, M., Kuna, A. T., & Štefanović, M. (2020). α-1 antitrypsin genotype-phenotype discrepancy in a 42-year-old man who carries the null-allele. Labmedicine, 51(3), 301-305. doi:https://doi.org/10.1093/labmed/lmz059

Background Alpha-1-antitrypsin (A1AT) deficiency is a hereditary condition caused by mutations in the SERPINA1 gene and associated with lung emphysema and liver disease. Laboratory testing in suspected A1AT deficiency involves quantifying serum A1AT concentration and identification of specific alleles by genotyping and phenotyping. The aim of this report was to present a case of the null allele carrier with consequent genotype/phenotype/concentration discrepancies and potential misclassification of the Z variant in a 42-year-old white man presenting with symptoms of chronic obstructive pulmonary disease (COPD). Method Serum A1AT concentration was measured using an immunoturbidimetric assay. A1AT phenotype was determined using isoelectric focusing followed with immunofixation (IEF-IF). Genotyping specifically for the S and Z allele was performed by melting curve analysis using real-time PCR and checked by an alternative PCR-RFLP method. Genotype/phenotype ambiguity and discrepancy were amended using gene sequencing. Results Laboratory testing revealed highly reduced A1AT concentration (less than 0.30 g/L), mild to moderate deficient genotype (Pi*Z allele: M/Z and Pi*S allele: M/M) and severe deficient Z homozygous phenotype (Pi ZZ). After repeated sampling, the same discordant results were verified by these tests. Further sequencing revealed two clinically relevant and defective variants: rs199422210 (a rare null allele) and rs28929474 (the Z allele). Conclusion Due to inability of genotyping kit probes to detect null/Z allele combination (which mimics the Pi ZZ phenotype), our patient was misclassified as mild to moderate deficient Pi*MZ heterozygote. In all unclear cases, whole-gene sequencing is highly recommended in order to determine definitive cause of A1AT deficiency.

Blais, J., Giroux, S., Caron, A., Clément, V., & Rousseau, F. (2020). Precision of fetal DNA fraction estimation by quantitative polymerase chain reaction quantification of a differently methylated target in noninvasive prenatal testing. Labmedicine, 51(3), 279-287. doi:https://doi.org/10.1093/labmed/lmz068

Background The performance of noninvasive prenatal testing (NIPT) assays is critically determined by the proportion of fetal DNA or fetal fraction (FF). Fetomaternal differential methylation of certain genomic regions has been proposed as a universal marker of fetal origin, and previous reports have suggested the use of methylation-sensitive restriction enzyme (MSRE) assays to estimate FF. Methods We analyzed the performance of FF estimation using an MSRE assay with duplex quantitative polymerase chain reaction (qPCR). Mixtures of genomic DNA from placental cells and from adult women were digested with 2 MSRE and FF estimates obtained, for a total of 221 pairwise treatment/control comparisons. Results The coefficient of variance (CV) of the MSRE assays was high, ranging from 24% to 60%. An alternative in silico FF estimation algorithm, SeqFF, displayed slightly lower variability, with a CV of 22%. Conclusion These results cast doubts on the usefulness of the MSRE-based assay of differentially methylated

markers for FF estimation. The lack of a universal method capable of precisely estimating FF remains an incompletely solved issue.

Kim, M. J., Patel, P., Vyas, N., Leveque, C., Diaz, O., & Salazar, E. (2020). A 70-year-old female with unexpected platelet function testing results. Labmedicine, 51(3), 310-314. doi:https://doi.org/10.1093/labmed/lmz070

A 70-year-old female with a history of hypertension and left A2 segment aneurysm was scheduled for pipeline embolization device (PED) placement. Preinterventional antiplatelet prophylaxis included aspirin and ticagrelor. Unexpectedly, after 13 days of treatment, VerifyNow showed a P2Y12 reaction unit (PRU) value of 216, approximately >5 times the mean PRU of other patients on aspirin and ticagrelor. We confirmed platelet reactivity and ticagrelor resistance with light transmission aggregometry. Antiplatelet therapy was switched to prasugrel, and aspirin was continued. Eight days later, the P2Y12 reaction value (PRU) was 164. PED was placed without complications. Unlike clopidogrel, ticagrelor is a direct P2Y12 inhibitor that does not require metabolism to an active metabolite. Ticagrelor resistance is very rarely reported. To the best of our knowledge, there has been no case of ticagrelor resistance reported in the context of pre-PED placement prophylaxis.

Aoua, H., Nkaies, Y., Ali, B. K., Sakly, M., Aouani, E., & Attia, N. (2020). Association between small dense low-density lipoproteins and high-density phospolipid content in patients with coronary artery disease with or without diabetes. Labmedicine, 51(3), 271-278. doi:https://doi.org/10.1093/labmed/lmz067

Objective To evaluate the phospholipid profile in total plasma, non–high-density lipoprotein (HDL), and HDL fractions. We tried to correlate the phospholipid profile to low-density lipoprotein (LDL) size, as reflected by cholesterol content in each LDL subclass. Methods We measured small dense LDL-C levels after heparin-magnesium precipitation and measured high-density lipoprotein phospholipid (HDL-P) levels using a colorimetric enzymatic method. Results The correlation of the phospholipid profile to small dense LDL-C (sdLDL-C) in patients with coronary problems showed a negative association between small dense low-density lipoprotein (sdLDL) and HDL-P ($r = -0.73$; $P = .02$). Moreover, a strong positive correlation was detected between TG and the ratio HDL-P/HDL-C ($r = 0.83$; $P < .001$). Conclusions HDL phospholipid has an antiatherogenic effect in coronary artery disease with or without diabetes. Further, large LDL modulation seems to be associated with diabetes rather than coronaropathy.

Sevinc, M., Karabulut, A., Eskazan, A. E., Suzin, C. T., Ozbek, U., & Soysal, T. (2020). The impact and prognostic significance of chronic lymphocytic leukemia upregulated 1 (CLLU1) gene expression in patients with chronic lymphocytic leukemia: A single center experience. Labmedicine, 51(3), 259-264. doi:https://doi.org/10.1093/labmed/lmz058

Objectives To determine CLLU1 gene levels and the relationship of that gene among other prognostic parameters in patients with chronic lymphocytic leukemia. Methods Bone-marrow infiltration pattern, β2-microglobulin (β 2-M), cluster of differentiation (CD)38, and ZAP-70 status were recorded. CLLU1 levels were assessed by real-time polymerase chain reaction (RT-PCR) and expressed as folds. The relationship between CLLU1 and other known prognostic parameters was evaluated. Results CLLU1 expression was positive in 81 patients and negative in 3 patients. The median (interquartile range IQR]) CLLU1 level was 6.45 folds (3.75–16.57 folds) in patients with β 2-M normal values and 16.22 folds (3.91–62.00 folds) in patients with increased β 2-M ($P = .15$). Patients with a higher CD38 value than the median level had 3 times higher CLLU1 levels than the other group ($P = .07$). The median (IQR) CLLU1 level was 4.25 folds (2.75–13.71 folds) in patients with CLL who tested negative on ZAP-70, whereas it was 49.52 folds (15.06–446.36 folds) in those who tested positive via ZAP-70 ($P = .005$). Conclusions CLLU1 is a specific parameter to CLL, and its level corresponds well with the ZAP-70 level.

Salinas, M., López-Garrigós, M., Flores, E., & Leiva-Salinas, C. (2020). Current practice and regional variability in recommendations for patient preparation for laboratory testing in primary care. Labmedicine, 51(3), e32-e37. doi:https://doi.org/10.1093/labmed/lmz092

Background Preparation of the patient for laboratory tests is crucial. Our aim was to investigate the current practice and regional variability of recommendations regarding patient preparation for laboratory testing. Methods A call for data was posted by email. Spanish laboratories were invited to fill out and submit a survey. Results Sixty-eight laboratories participated in the study. In 73% of those laboratories, fasting was always recommended regardless of the requested tests. Only one-third of the laboratories systematically recommended a 12-hour fast before the tests. In 71% of the laboratories, water intake was allowed without restrictions during the fasting period. In 57% of the laboratories, computerized order entry offered the possibility to print customized recommendations automatically in the primary care doctor's office according to the requested tests. Seventy-two percent of the laboratories agreed with the proposed recommendation. Conclusions There was high variability in patient preparation for laboratory testing. A significant proportion of centers did not follow international guidelines.

Torres, R., & Rinder, H. M. (2020). Double-edged Spike—Are SARS-CoV-2 serologic tests safe right now? Labmedicine, 51(3), 236-238. doi:https://doi.org/10.1093/labmed/lmaa025

Rania, S. S., Elneely, D. A., & Ahmed Abdel, R. S. (2020). The study of SALL4 gene and BMI-1 gene expression in acute myeloid leukemia patients. Labmedicine, 51(3), 265-270. doi:https://doi.org/10.1093/labmed/lmz056

Background In acute myeloid leukemia (AML), many genes have been studied as prognostic markers. SALL4 is expressed constitutively in human leukemia cell lines and primary AML cells. BMI-1 is expressed highly in purified hematopoietic stem cells (HSCs), and its expression declines with differentiation. Objective To study the expression levels of SALL4 and BMI-1 and their clinical significance in patients with AML. Methods The study was performed with 60 patients newly diagnosed with AML and 50 control individuals. SALL4 and BMI-1 expression detection were performed using real-time polymerase chain reaction (PCR). Results The expression of SALL4 and BMI-1 was significantly higher in cases of AML and showed a strong association with failure to achieve complete remission (CR) or with relapse (P = .02, P = .03, respectively). In multivariate analysis, these genes were the most powerful independent predictors of poor prognosis (P = .01 for SALL4, P = .02 for BMI-1). Conclusion SALL4 and BMI-1 are significant prognostic factors in AML and could be strong targets for novel types of therapy.

Bertholf, R. (2020). The history of laboratory medicine part 3: 1986–2004; two turbulent decades. Labmedicine, 51(3), 225-233. doi:https://doi.org/10.1093/labmed/lmaa014

Bertholf, R. L. (2020). The history of laboratory medicine part 2: 1978–1985; refocusing the objectives. Labmedicine, 51(2), 109-113. doi:https://doi.org/10.1093/labmed/lmaa004

Haybar, H., Masumeh, M. B., Shahrabi, S., Ansari, N., & Saki, N. (2020). Expression of blood cells associated CD markers and cardiovascular diseases: Clinical applications in prognosis. Labmedicine, 51(2), 122-142. doi:https://doi.org/10.1093/labmed/lmz049

Background Cardiovascular diseases (CVDs) are a major cause of mortality worldwide. The results of various studies have shown that abnormality in the frequency and function of blood cells can be involved in CVD complications. In this review, we have focused on abnormalities in the expression of the CD (cluster of differentiation) markers of blood cells to assess the association of these abnormalities with CVD prognosis. Methods We identified the relevant literature through a PubMed search (1990–2018) of English-language articles using the terms "Cardiovascular diseases", "CD markers", "leukocytes", "platelets", and "endothelial cells". Results There is a variety of mechanisms for the effect of CD-marker expressions on CVDs prognosis, ranging from proinflammatory processes to dysfunctional effects in blood cells. Conclusion Considering the possible effects of CD-marker expression on CVDs prognosis, particularly prognosis of acute myocardial infarction and atherosclerosis, long-term studies in large cohorts are required to identify the prognostic value of CD markers and to target them with appropriate therapeutic agents.

Fouladseresht, H., Khazaee, S., Zibaeenezhad, M. J., Mohammad, H. N., Khosropanah, S., & Doroudchi, M. (2020). Association of ABCA1 haplotypes with coronary artery disease. Labmedicine, 51(2), 157-168. doi:https://doi.org/10.1093/labmed/lmz031