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DAFTAR ISI

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

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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.

Unexpectedly Weak Anti-B in 2 Group O Pediatric Patients on Parenteral Nutrition and Disease Specific Supplemental Enteral Feeds

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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.

Dokumen 3 dari 18

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

Dokumen 4 dari 18

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

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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.

Dokumen 5 dari 18

The Cost of Pre-Analytical Errors in INR Testing at a Tertiary-Care Hospital Laboratory: Potential for Significant Cost Savings

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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.

Dokumen 6 dari 18

Mixed Phenotype Acute Leukemia that Evolved from Myelodysplastic Syndrome with Excess Blasts

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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.

Measurement of Monoclonal Immunoglobulin Protein Concentration in Serum Protein Electrophoresis: Comparison of Automated vs Manual/Human Readings

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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.

Dokumen 8 dari 18

A Novel Pathogenic CALR Exon 9 Mutation in a Patient with Essential Thrombocythemia

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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.

Dokumen 9 dari 18

Safety Considerations in the Laboratory Testing of Specimens Suspected or Known to Contain the Severe Acute Respiratory Syndrome Coronavirus 2

(SARS-CoV-2)

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α-1 Antitrypsin Genotype-Phenotype Discrepancy in a 42-Year-Old Man Who Carries the Null-Allele

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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.

Precision of Fetal DNA Fraction Estimation by Quantitative Polymerase Chain Reaction Quantification of a Differently Methylated Target in Noninvasive Prenatal Testing

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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.

Dokumen 12 dari 18

A 70-Year-Old Female with Unexpected Platelet Function Testing Results

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Link dokumen ProQuest

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.

Dokumen 13 dari 18

Association between Small Dense Low-Density Lipoproteins and High-Density Phospolipid Content in Patients with Coronary Artery Disease with or without Diabetes

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Link dokumen ProQuest

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.

Dokumen 14 dari 18

The Impact and Prognostic Significance of Chronic Lymphocytic Leukemia Upregulated 1 (CLLU1) Gene Expression in Patients with Chronic Lymphocytic Leukemia: A Single Center Experience

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Link dokumen ProQuest

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.

Dokumen 15 dari 18

Current Practice and Regional Variability in Recommendations for Patient Preparation for Laboratory Testing in Primary Care

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Link dokumen ProQuest

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.

Dokumen 16 dari 18

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

Dokumen 17 dari 18

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

Link dokumen ProQuest

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.

Dokumen 18 dari 18

The History of Laboratory Medicine Part 3: 1986–2004; Two Turbulent Decades

Bertholf, Roger

Link dokumen ProQuest

Daftar Pustaka

Citation style: APA 6th - Annotated with Abstracts - American Psychological Association, 6th Edition

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.