Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.
The laboratory plays an important role in detecting these pathologies, and the protocol established between Clinical Analysis and Haematology allows for the early diagnosis of these patients and more rapid implementation of the necessary clinical actions.

doi: 10.1016/j.cca.2022.04.742

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T255

Acquired Hemophilia A during pregnancy: A case report

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Background-aim

Acquired hemophilia A (AHA) is a rare disease, mediated by an immune process, in which autoantibodies are developed in the coagulation cascade against factor VIII. This causes alterations in the hemostatic functions, which can trigger serious bleeding that compromise the patient’s life.

The incidence of this condition is approximately 1-1.5 cases per million people, although this increases in pregnant women and in the post-partum period as well as in both sexes at 68-70 years of age.

Methods

Describing a clinical case of AHA during pregnancy.

Results

A 34 year old pregnant woman attended the hospital for a gynecological check-up. When the lab performed a basic coagulation, which had previously presented normals values, the revised values were: prothrombin time (PT) of 9.9 seconds (s), prothrombin time 100% (>60%), INR 0.87 (0.8-1.2), and activated partial prothrombin time (APPT) of 40.1 s (>60%). The platelet values were normal.

On detecting this value, it was decided to extend the coagulation study, the elongated APPT (39.8s) was confirmed and the mixture test with normal plasma was also performed, obtaining a baseline APPT of 28.3s, 28.6s at one hour, 29.3s at two hours and 30.4s at three hours. Because of abnormal values, the following parameters were studied: Factor VIII 10.7% (50-150), Factor IX 96.2% (65-150), Factor X 57.2% (70-150), Factor XII 119.1% (50-150), lupus anticoagulant 21.3s, 28.3s, 28.6s at one hour, 29.3s at two hours and 30.4s at three hours. The platelet values were normal.

Conclusions

This pathology is characterized by the appearance of bleeding in patients with no prior history of it, and who have characteristic laboratory profile, namely a prolonged APPT, normal thrombin and prothrombin time, a normal platelet count, low levels of Factor VIII and the presence of antibodies against this factor.

The treatment aims to either increase the factor VIII, in which case recombinant factor VIII and/or desmopressin is used; or to eradicate the inhibitor, using immunosuppressants.

doi: 10.1016/j.cca.2022.04.743

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T256

Evaluation of coagulation function by rotation thromboelastometry in critically ill patients with severe Covid-19 Pneumonia

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Background-aim

Critically ill patients with COVID-19 pneumonia suffered both high thrombotic and bleeding risk. The effect of SARS-CoV-2 on coagulation and fibrinolysis is not well known.

Methods

Retrospective cohort study including 84 patients, during 16 months, divided into two groups: patients with severe SARS-Cov-2 pneumonia (group 1, N=42) and patients with severe non-COVID-19 pneumonia (group 2, N=42). We evaluated coagulation standard parameters (hemoglobin, platelet count and conventional laboratory coagulation tests) in group 1 vs group 2 and coagulation standard parameters on day of admission (T0) and 10 (T10) days after admission to ICU and coagulation function using rotational thromboelastometry (ROTEM) in patients with severe SARS-Cov-2 pneumonia.

Results

84 patients were enrolled into the study. Similar results in conventional laboratory coagulation tests were detected in group 1 and group 2: prothrombin time (15.14s vs 14.76s, p=0.212), international normalized ratio (1.21 vs 1.19, p=0.112), activated partial thromboplastin time (32.17s vs 25.52s, p=0.06), fibrinogen level (6.15 mg/dl vs 3.39 mg/dl, p=0.208), hemoglobin (11.81 g/dl vs 11.20 g/dl, p=0.139) and platelet count (208.98x103/ul vs 288.74 x103/ul, p=0.123). However, a statistically significant difference was observed in the D-dimer count (2442.11 ng/ml vs 370 ng/ml, p=0.03). In addition, statistically significant increase in D-dimer count during Intensive Care Unit (ICU) stay (T0=2442.11 ng/ml vs T10=8564.39 ng/ml, p=0.000) in group 1 were detected. Finally, blood thromboelastometry profiles were consistent with hypercoagulability characterized by higher clot strength (MCF or maximum clot firmness close to upper limit in FIBTEM test, MCF median value = 25.9 mm). Clotting time presented normal results in INTEM (163.41 s) and EXTEM (68.74 s). No sign of secondary hyperfibrinolysis were found during the study period. In six patients a deep vein thrombosis and in six patients a thromboembolic event. Eighteen patients (43%) died during hospitalization due to coagulopathy produced by SARS-Cov-2 pneumonia.

Conclusions

The results observed in our study support hypercoagulability in a severe inflammatory state, rather than a Consumption Coagulopathy.
(DIC) state. More studies are needed to better understanding of coagulopathy produced in patients with severe COVID-19 pneumonia.

doi: 10.1016/j.cca.2022.04.744

T257

Blood coagulation testing and hematological features of thalassemia carriers in pregnant
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Background-aim

The incidence rate of thalassemia in Guangxi is very high, and the carriers of the thalassemia gene are also very numerous. In this study, we focused on the coagulation function and hematological parameters of pregnant women with thalassemia gene.

Methods

In this study, the prothrombin time(PT), international normalized ratio(INR), activated partial thromboplastin time(APTT), thrombin times(TT), fibrinogen(FIB), D-dimer(DD), red blood cells count(RBC), hemoglobin(Hb), haematocrit(Hct), mean corpuscular volume (MCV), mean corpuscular hemoglobin (MCH), mean corpuscular hemoglobin concentration(MCHC) and red cell distribution width (RDW) parameters of 460 pregnant women were collected and analyzed, including 49 cases in group -/\langle\langle, 49 cases in group \langle\langle/\langle, 114 cases in group \langle\langle/\langle, 5 cases in group \langle\langle/\langle, 7 cases in group \langle\langle/\langle, 28 cases in group \langle\langle/\langle, 105 cases in group \langle\langle/\langle, 103 cases in normal group.

Results

APTT was significantly prolonged in the \langle\langle/\langle group(p<0.01). RBC of each group of \langle-thalassemia was significantly higher than that of the normal group(p<0.01), MCV and MCH were significantly lower (p<0.01). Compared with the normal group, RBC, Hb, Hct, MCV, MCH, MCHC and RDW parameters in the \langle\langle/\langle and \langle\langle/\langle group were statistically significant(p<0.01). MCV, MCH can be used as a promising indicator to distinguish group \langle\langle/\langle, \langle\langle/\langle, and sensitivity and specificity are more than 0.9.

Conclusions

In \langle\langle/\langle group, the APTT prolonged significantly, and the hematological parameters changed significantly. Abnormal red blood cells can increase the risk of thrombosis, so pregnant women with thalassemia gene should take precautions.

doi: 10.1016/j.cca.2022.04.745

T258

Investigation of genetic biomarkers associated with low platelet count in normal karyotype acute myeloid leukemia
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Background-aim

Acute myeloid leukemia (AML) is associated with the risk of bleeding due to systemic coagulopathy and the disease-related lack of platelets. Leukemic blasts could alter platelet activation in vitro in previous report. The aim of the study is comprehensive investigation of genetic biomarkers contributing to low platelet count in normal karyotype AML (NK-AML).

Methods

Among 200 AML cases from The Cancer Genome Atlas, 37 NK-AML with no known driver mutations were enrolled in this study. Among them, AMLs with platelet count < 100 \times 10^9/L (N = 24) were classified as platelet-decreased AML (PD-AML) and the others (N = 13) as control. Using the RNA-seq expression data, differentially expressed gene (DEG) analysis and pathway analysis was done. Using the result of DEG, biomarker performance test for predicting PD-AML was done through ROC curve analysis.

Results

In DEG analysis, 175 genes were differentially expressed in normal karyotyped PD-AML. Among them, most differentially expressed genes were CHIH3 (p=0.0003), CSF1R (p=0.0007), HTR3E (p=0.0015), CILP2 (p=0.0023), and LOC64685 (p=0.0028). DEGs were enriched in pathways including GPCR-related signalings, Cytokine-cytokine receptor interaction, cytokines and inflammatory response, JAK STAT molecular variation 1, C-type lectin receptors, and bone remodeling signalings with statistical significance. Based on the biomarkers which were selected through the DEG analysis and functional review, area under curve was up to 0.947 in performance evaluation of biomarkers for predicting PD-AML.

Conclusions

Comprehensive description for cell signaling pathways related with low platelet count in NK-AML was presented in this study. Putative biomarkers which could predict the decreased platelet status and the bleeding tendency in NK-AML were suggested and evaluated. We believe the result of study would contribute to advances in precision medicine and the effective AML treatment.

doi: 10.1016/j.cca.2022.04.746

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Clinica Chimica Acta 530 (2022) S163–S188