lymph nodes, and adhesions were found on exploratory laparotomy. Small-bowel segments and appendix were resected. A prolonged hospital course ensued postoperatively with death due to multiple complications.
Results (if a Case Study enter NA): The intestinal wall was grossly thickened with no discrete masses and microscopically had extensive infiltrates of small- to intermediate-sized, mature, minimally pleomorphic, CD3+/CD4- / CD5-/CD7+/CD8+/CD10-/CD20-/CD30-/CD56+/ EBER-ISH- T-lymphocytes, focally infiltrating into the epithelium. Ascitic fluid cytology had small lymphocytes, CD2+/CD3+/CD4-/CD5-/CD10-/CD7+/CD8+/CD25-/ CD30-/CD56+ /TCRαβ+/TCRγδ- by flow cytometry immunophenotyping. A diagnosis of MEITL was rendered based on these findings.
Conclusion: MEITL is rare, aggressive, unassociated with celiac disease and usually seen in Asian and Hispanic populations. It presents with non-specific GI symptoms of abdominal pain, perforation, diarrhea, weight loss and intestinal obstruction underscoring the need for a high index of suspicion. Upper GI endoscopy has a limited role since involvement of small-bowel, specifically jejunum, is common. The evolving capsule endoscopy techniques may help in an early diagnosis. Due to limited literature, optimal treatment is unclear and various strategies using chemotherapy, surgery and stem-cell transplant have been tried with variable outcomes.

An Unusual Hematologic Manifestation in a COVID-19 Patient Treated with COVID-19 Convalescent Plasma.

C. Andrzejewski,[1] S.R. Chakraborty,[1] L. Stoddart,[1] V. Johari[1]; [1]Pathology, UMass Medical School-Baystate Health, Springfield, Massachusetts, UNITED STATES

Introduction/Objective: A subset of Chronic Lymphocytic Leukemia (CLL) patients with COVID-19 may manifest rapid elevations in lymphocyte counts and poor clinical outcomes. Here we report our observations regarding this unusual hematologic manifestation in a CLL patient after he experienced a COVID-19 convalescent plasma (CCP) transfusion reaction.
Methods/Case Report: 56-year-old A Rh- male with stable, treatment-naive CLL (13q deletion positive) diagnosed three years prior was admitted for COVID-19 hypoxia. Before developing COVID-19, baseline white blood cell (WBC) count was stable (~ 64 K/ mm3). Due to worsening hypoxia he was treated with an ARh+ High Titer CCP unit, Remdesivir, tocilizumab, and dexamethasone. The Blood Bank was notified of a possible CCP reaction and performed its standard workup which was adjudicated to be a febrile TACO reaction. During this evaluation it was noted that the patient's WBC count had initially decreased to 46 K/ mm3, but rose on HD 3, to 78.4 K/mm3 and by discharge on HD 10 had increased to 200 K/ mm3. Flow cytometry revealed a B cell CLL immunophenotype. Post discharge day (PDD) 6 he developed herpes zoster. On post-discharge day (PDD) 7 his WBC count was 124K/mm3. By PDD 77 his WBC count had returned to baseline (~50 K/mm3).
Results (if a Case Study enter NA): NA
Conclusion: The pt's initial drop in his WBC count followed by a gradual rise has been observed in patients with severe COVID-19 independent of CCP infusion. Lymphocytosis in a subset of CLL patients with COVID-19 has been reported (termed "COVID-19 Induced Lymphocytosis" (CIL)) and, in contrast to our patient with an improved outcome, has been associated with severe/fatal outcomes. Of note these other patients did not receive CCP. Mechanisms related to CIL are unknown. Such poor clinical outcomes heighten the need for further studies of CIL. The role of CCP in affecting this process, if any, also merits further clarification.

Molecular findings in bone marrow samples of myeloid sarcoma

J. Khan,[1] M. Nassiri[1]; [1]Department of Pathology and Lab Medicine, Indiana University School of Medicine, Indianapolis, Indiana, UNITED STATES

Introduction/Objective: Myeloid sarcoma is a rare extramedullary manifestation of acute myeloid leukemia. There are very few studies regarding molecular findings in myeloid sarcoma or their associated myeloid leukemia
Methods/Case Report: We evaluated cases of myeloid sarcoma with concurrent or prior bone marrow studies diagnosed as acute myeloid leukemia, from 2014 to 2021. We searched our Anatomic pathology information system for the terms 'myeloid sarcoma' or 'leukemia cutis'. Out of 58 cases of myeloid sarcoma, ten had next generation sequencing studies (FoundationOne Heme) performed on bone marrow aspirate. Results-There were 7 male and 3 female patients. Age range was from 1-79 yrs. Myeloid sarcoma involved the skin (n=7) or soft tissue (n=3). Most common mutated genes were KMT2A/MLL (n=4, all translocations/fusions) followed by AXL1 (n=3), TP53 (n=3), NRAS (n=2), TET2 (n=2) and CEPBA (n=2). KMT2A fusion partners were MLLT1/ENL (n=1), MLLT3 (n=1), and MLLT10/AF10 (n=2). In all except for one case that harbored KMT2A/MLL fusions, karyotype also showed translocation of KMT2A. Only one case had both an AXL stop codon and a KMT2A translocation, otherwise AXL1/CEBPA mutated cases and KMT2A/MLL mutated cases were mutually exclusive. Other mutated genes were PHF6, BRCA2, DNMT3A, NPM1, RAD21, CBL, KMD6A, and NF1; each found in one case.
Results (if a Case Study enter NA): Our result support the notion of higher risk of myeloid sarcoma in KMT2A and

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