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PS-07-015

Peculiarities of megakaryocytes and platelets variation in the microelementosis condition

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Background & Objectives: The aim of our study was to characterise megakaryocytes and platelets variation under the influence of heavy metal salts and determine the peculiarities of these changes in recovery period.
Methods: The laboratory rats (n=48) were used for the conduction of experimental investigation. They were divided into two groups: control – animals which drank clean water and experimental – rats which drank water with heavy metal salts (Zn, Cu, Fe, Mn, Cr and Pb). The bone marrow structure and blood parameters were studied on 30, 90, 120 and 180 day.
Results: During 90 days of intoxication the amount of megakaryocytes increased on 40%(p=0.017). There were changes of shape, size (small and giant), nuclear-cytoplasmic ratio, polysegmentation of nuclei and loss of megakaryocyte-sinusoid contacts. It was found the platelets increase by 11% in the blood. Suspending the addition of pollutants to the animal's diet was accompanied by progressive restoration of bone marrow-blood parameters. Simultaneously with disappearance of megakaryocytes morphological variations the area of thrombocytopoiesis was decreased by 28%, the thrombocytes – by 5.3%.
Conclusion: The intake of heavy metal salts in elevated concentrations provokes significant disorders in thrombocytopoiesis which leads for platelets increase in the blood. Although there was a significant improvement bone marrow-blood characteristics during recovery period, their values do not reach the indicators of the intact group animals.

PS-07-016

Myeloid/lymphoid neoplasms with eosinophilia and gene rearrangement: a report of 7 cases

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Background & Objectives: Myeloid/lymphoid neoplasms (MLNs) with eosinophilia and gene rearrangement are rare diseases characterised by myeloid and/or lymphoid proliferation, eosinophilia, and a fusion gene with constitutive tyrosine kinase (TK) activity. These disorders are responsive to TK inhibitors (TKIs) excluding FGFR1-rearranged MLNs, for which there is currently no standardised therapy.
The aim of this study is to report 7 cases of MLNs collected from 2003 to 2018.
Methods: All patients underwent bone marrow (BM) core biopsy that showed hypercellular BM, hyperplasia of eosinophilic granulopoiesis and features of myeloproliferative neoplasms (MPNs). In 4 out of 7 patients with lymphadenopathy, excisional lymph node biopsy was performed revealing a T-lymphoblastic lymphoma (T-LBL). Gene rearrangement was assessed with cytogenetic and/or molecular analysis.
Results: In 6 out of 7 cases, the fusion gene has been identified: FIP1L1-PDGFRA (2/7), ETV6-PDGFRB (2/7) and ZMYM2-FGFR1 (2/7). In one case, no currently known TK fusion genes were recognized.
Two PDGFRA-rearranged patients (one with MPN+T-LBL), two PDGFRB-rearranged patients, one FGFR1-rearranged patient (MPN+T-LBL) and the one with unidentified rearrangement (MPN+T-LBL) were treated with imatinib: all achieved complete hematologic remission except the FGFR1-rearranged patient.
The other FGFR1-rearranged patient (MPN+T-LBL) was treated with polychemotherapy and allogeneic transplantation followed by relapse.
Conclusion: Our cases confirm responsiveness of PDGFRA/B-rearranged MLNs to imatinib and possible existence of not yet known fusion TKs, which may benefit from TKIs. Identification of LBL in MLNs avoids overtreatment/nonresponse to intensive chemotherapy recommended in LBL.
FGFR1-rearranged MLNs exhibit poor prognosis without an effective targeted treatment. Recently, pemigatinib, a selective, potent inhibitor of FGFR1, has shown promising results.

PS-07-017

Next-generation sequencing-based clonality assessment of immunoglobulin gene rearrangements distinguishes relapse from second primary classical Hodgkin lymphoma

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Background & Objectives: Classical Hodgkin lymphoma (cHL) is highly curable, however relapse still occurs in up to 30% of (advanced) cHL cases. Case reports and small series have shown that some of these relapses appear to be a new primary cHL. Conventional clonality assays for cHL has thus far been hampered by low frequencies of Hodgkin and Reed-Sternberg cells and limited DNA quality obtained from formalin-fixed paraffin-embedded tissues. Within the EuroClonality-NGS Working Group, we developed a novel approach to detect immunoglobulin heavy chain (IGH*)* and k light chain (IGK) gene rearrangements. The objective of our study is to determine the clonal relationship between diagnosis and recurrent cHL to assess the incidence of second primary malignancies.
Methods: We collected 70 paired diagnosis-recurrence cHL cases including early and late recurrences. Gene-specific IGH-VJ-FR3, IGHDJ, IGK-VJ and Intron-Kde primer sets were used to perform next-generation sequencing (NGS)-based clonality analysis with Ion Torrent PGM. Bioinformatics analysis is performed with the interactive web-based immunoprofiler ARResT/Interrogate.
Results: Preliminary results of 7 paired diagnosis-relapse samples demonstrates the presence of identical clonotypes in 2 cases, while distinct clonotypes were observed in 3 other cases suggesting a second primary lymphoma. No specific clonotype were identified in either diagnosis and/or relapse of the remaining 2 samples. Additional cases of recurrent cHL have to be analysed to reveal the true incidence of clonally unrelated lymphomas in recurrent cHL.
Conclusion: This study is an important step towards establishment of NGS-based clonality assessment in clinical practice for cHL, and eventually the improvement of therapeutic management of recurrent cHL.

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Follicular lymphoma and in situ mantle cell neoplasm: a rare combination with peculiar genetic and clinical features

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Background & Objectives: Composite lymphomas are rare entities in which two or more different lymphomas coexist in the same site. Little is known about their clinical and prognostic implications. We present a