restriction, suggests true biclonality. High-risk cytogenetic alterations such as TP53 gain further contribute to an aggressive disease course, as noted in previous reports (Gentry et al., 2013; Haidary et al., 2022)

References:

Gentry AE, et al. Biclonal myeloma: Two independent clones or clonal evolution? Archives of Pathology & Laboratory Medicine. 2013;137(8):1110-3.

Haidary AM, et al. Biclonal plasma cell neoplasms: A case series and review of the literature. Clinical Lymphoma, Myeloma & Leukemia. 2022;22(9):e748–e754.

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BIOMARCADORES INflAMATÓRIOS NA AVALIAÇÃO DA GRAVIDADE DA ANEMIA DE DOENÇA CRÔNICA: UMA REVISÃO INTEGRATIVA

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Introdução: Anemia de Doença Crônica (ADC) apresenta elevada prevalência, é uma condição clínica comum em distúrbios infecciosos, inflamatórios ou doenças neoplásicas. Ocorre como consequência da resposta inflamatória persistente, que leva à ativação de macrófagos e à liberação de citocinas como IL-6 e TNF-α, as quais bloqueiam a liberação de ferro e reduzem a resposta à eritropoetina, mecanismos que, associados a sobrevida das hemácias, culminam em uma resposta medular inadequada e deficiência funcional de ferro. Nesse contexto, a integração entre marcadores inflamatórios e os parâmetros hematológicos pode aprimorar o diagnóstico e o manejo clínico dessa patologia. **Objetivos:** Analisar como os marcadores inflamatórios (hepcidina, ferritina, IL-6 e TNF-α) contribuem para o diagnóstico diferencial e monitoramento da anemia de doença crônica (ADC). **Material e métodos:** Trata-se de uma revisão integrativa da literatura. Foram utilizados os descritores “anemia de doença crônica” e “biomarcadores inflamatórios”. A busca foi realizada nas bases de dados SciELO e PubMed, no período entre os anos de 2002 e 2023, nos idiomas português e inglês, incluiu-se os artigos disponíveis online e na íntegra. **Discussão e conclusão:** Resultados: Os estudos incluídos analisaram pacientes com diversas condições crônicas associadas à ADC, como Lúpus Eritematoso Sistêmico (LES), doença renal crônica (DRC) e artrite reumatóide. No LES, observou-se um aumento significativo nas concentrações de ferritina, correlacionando com o estado inflamatório e a ADC. Em pacientes com DRC, os níveis elevados de hepcidina têm sido atribuídos não apenas à redução de sua eliminação pelos rins, mais também ao aumento de sua produção estimulado pela resposta inflamatória característica desse quadro. Em pacientes com artrite reumatóide, maioria dos estudos, os biomarcadores inflamatórios se correlacionam de forma significativa com a fisiopatologia e a gravidade da ADC. **Discussão:** Os biomarcadores possuem grande potencial na avaliação da gravidade e evolução da anemia de doença crônica. A citocina inflamatória IL-6 estimula a produção de hepcidina, hormônio que regula o metabolismo do ferro, quando elevada inibe a ferroportina, proteína que libera ferro dos macrófagos e enterócitos para a circulação. Como consequência, o ferro fica retido nos estoques corporais, levando a uma deficiência funcional de ferro. Esse mecanismo eleva os níveis de ferritina, , que também atua como marcador inflamatório. Ao contrário da anemia ferropriva, em que a ferritina está reduzida, na ADC ela se apresenta aumentada, o que auxilia no seu diagnóstico diferencial. Os valores elevados de TNF-α são um marcador de estado inflamatório, ao inibir a proliferação de células eritroides na medula óssea e reduzir a resposta à eritropoetina, intensificando o quadro anêmico em doenças inflamatórias. **Conclusão:** Evidenciou que os biomarcadores inflamatórios hepcidina, IL-6, ferritina e TNF- α, associados com a patologia de base, desempenham papel fundamental no diagnóstico diferencial e no monitoramento da gravidade da anemia de doença crônica. Essa integração entre biomarcadores pode aprimorar o manejo clínico da ADC, auxiliando na estratificação de risco e na tomada de decisão terapêutica.

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CLINICAL SIGNIfiCANCE OF INTERPRETING INCIDENTAL GENETIC FINDINGS IN ONCOHEMATOLOGICAL KARYOTYPE STUDIES

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Introduction: Karyotyping, widely used in various clinical settings, is a fundamental tool for identifying genetic aberrations of either germline or somatic origin. In the diagnosis of hematologic neoplasms, it serves as a solid foundation for investigations in suspected cases of acute and chronic leukemias, myelodysplastic syndromes, among others. However, when analyzing the complete genomic content of an individual, incidental findings may arise. Even when the sample analyzed has high diagnostic value — such as bone marrow — it is possible, albeit rarely, for the identified alterations to be of germline origin, not necessarily associated with a neoplastic process. These findings become particularly relevant given the lack of systematic genomic screening in the general population, which may lead to the unexpected identification of previously unknown constitutional variants. **Objectives:** To identify and describe constitutional cytogenetic abnormalities unrelated to hematologic neoplasms in patients referred for oncohematological karyotyping. **Material and methods:** Over a nine-month period, a total of 3,822 oncohematological karyotype tests were performed at Flow Diagnósticos. For this study, individuals were selected based on complementary tests — such as immunophenotyping and bone marrow morphology — that did not show significant abnormalities. Bone

marrow samples were processed for oncohematological karyotyping as part of the routine diagnostic workup for suspected neoplasms. To clarify the origin of certain findings, a second karyotype was performed using phytohemagglutinin stimulation, aimed at constitutional genetic analysis. Comparison of the two tests enabled a better understanding of the nature of the identified genetic aberration. **Results:** In five patients, cytogenetic abnormalities were found involving the sex chromosomes (X and Y). One patient presented a structural alteration consistent with a Robertsonian translocation. Additionally, 14 individuals were referred to the laboratory with previously identified constitutional abnormalities, with trisomy 21 being the most frequent and well-documented finding in the literature. In total, 0.4% of the individuals referred for oncohematological karyotyping exhibited genetic aberrations unrelated to hematologic malignancies. **Discussion and conclusion:** Clinical investigation of suspected hematologic disorders requires an integrated analysis of bone marrow samples, including cell morphology, immunophenotyping, and karyotyping. It is the combination of these tests that allows for a more accurate and reliable diagnostic approach in identifying hematologic neoplasms. In the cases analyzed, all genetic alterations were confirmed to be germline, exhibiting a non-clonal profile, often representing incidental findings. Proper interpretation of these variants — supported by consultation of public databases describing known aneuploidies and classical chromosomal abnormalities — is essential for correct clinical classification. The trained assessment by a qualified professional is equally important. Accurate characterization of these findings was crucial for guiding clinical decision-making and avoiding unnecessary treatments aimed at non-neoplastic genetic alterations.

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COMPARATIVE EffECTIVENESS OF HEMATOLOGISTS WITH LARGE LANGUAGE MODELS IN HEMATOLOGIC DIAGNOSIS

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Introduction: Artificial intelligence (AI) use is rising and may benefit healthcare. Text-trained Large language model (LLM) seem to interpret images, but proof of accurate medical-image analysis is still scarce. **Objectives:** Primary objective: compare the diagnostic accuracy of a human expert vs four LLMs. **Material and methods:** We selected 3 - 10 images of microscopy fields to test 3 clinical situations. All images were derived from peripheral blood (PB) or bone marrow (BM) films, stained with WG and obtained with a cell phone camera. Ten test questions were developed based on the images. The images and questions were sent to a Hematologist and the following LLMs: ChatGPT 4.0 (CGPT4) and o3 (CGPTo3), Gemini Flash 2.5 (GF), and Claude Sonnet 4.0 (CS). Question type 1 sought to measure the machines' ability to evaluate images. Question type 2 provided a biased clinical context to test for confirmatory bias. Question type 3 provided a correct clinical context, aiming to obtain a correct diagnosis. The responses were compared to the standard response using a Likert scale as follows: 0 (no or incorrect answer); 1 point (correct answer with incorrect suggestions); 2 points (correct answer with or without suggestions). Considering the 10 questions, the score could vary from 0 to 20 points. **Results:** Images from 3 clinical situations (ClinSit) were tested, with the third clinical situation having two parts. ClinSit 1: pics of 10 fields of PB images of B-ALL at 1000x magnification. ClinSit 2: pics of 6 fields of BM images of multiple myeloma at 1000x magnification. ClinSit 3: BM images of acute myeloid leukemia at diagnosis and after treatment. At diagnosis, 3 pics of BM images at 1000x magnification were used, whereas after treatment, 9 images were used (magnification 100 × to 1000 ×). The overall score (maximum 20 points) was 18 for the Hematologist, 8 for CGPT4, 11 for CGPTo3, 16 for GF and 12 for CS. Regarding the image-specific questions: Hematologist scored 8/8, CGPT4 and o3 3/8, GF and CS 6/8. Confirmation bias questions: Hematologist scored 6/6, CGPT4 3/6, CGPTo3 and CS 2/6, and GF 4/6. Diagnostic questions: Hematologist scored 4/6, CGPT4 2/6, CS 4/6, and the CGPTo3 and GF models 6/6. **Discussion and conclusion:** We present a proof of concept: LLM AI as a potential hematology image analyst. We observed that machines could interpret these images, achieving a score of 8 to 16 (maximum 20), lower than the experienced hematologist (18/ 20). To date, there is no robust data that LLM AI can provide reliable answers based on images. For descriptive image analysis, the two CGPT models (4.0 and o3) performed worse than GF and CS, suggesting that the latter are more reliable for image interpretation. Carefully designed prompts can improve the accuracy of AI generated content. When using a partially correct context but a biased question, the different machine models were unable to maintain response coherence. This is a known flaw in these systems, which can have undesirable consequences. The physician's only incorrect answer was in scenario 3, question 3, possibly due to image quality. The performance of GF and CGPTo3 in type 3 questions was surprising. Limitations include small sample/physician numbers, expert-selected images, and ongoing model advances that may now surpass our results. Despite their text focus, LLMs may aid image analysis with open-ended prompts, but decision-making errors are still possible.

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COMPARATIVO DOS PARÂMETROS PRÉ E PÓS TRANSFUSIONAIS PARA ANÁLISE DA RESPOSTA À TRANSFUSÃO.

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