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Unsupervised machine learning techniques are employed to understand patterns and behaviors of variables in databases. Multiple Correspondence Analysis (MCA), an extension of correspondence analysis, can be used to verify the association of categorical variables and their categories. In this study, we evaluated the relationship between clinical-demographic variables of 154 patients with nodal peripheral T-cell lymphoma (PTCL) to understand how these variables relate to the unfavorable clinical outcome, death. **Methodology:** MCA was used to reduce the dimensionality of the real world database by creating two dimensions, 1 and 2, which were subsequently categorized into group 1 and group 2. Dimension 1, comprising ECOG, IPI, treatment, overall response, remission, and bone marrow transplant, represented about 30% of the total observed variance. Survival analysis was conducted to assess the association between these groups and overall survival (OS) and mortality rate. **Results:** The categories of dimension 1, group 1 and group 2, were associated with OS and mortality rate, with group 1 being associated with 5.5 months (95% CI: 2.70 − 8.40) of OS, while group 2 had a survival time of 277.20 months (95% CI: 91.21 − 463.12). Moreover, the mortality rate in group 1 was 87% (n = 67) and in group 2 it was 36% (n = 28) ($p < 0.001$). The risk of death for group 1 was 11.11 times (95% CI: 9.75-18.30; β= 2.41; $p < 0.001$). **Discussion:** These findings indicate a significant disparity in survival outcomes based on the clinical-demographic profiles of the patients. Group 1, characterized by poorer clinical indicators, exhibited substantially shorter OS and higher mortality rates. The ability of MCA to effectively reduce dimensionality while preserving the clinical relevance of the variables underscores its utility in identifying key prognostic factors. **Conclusion:** The MCA technique was effective in reducing the dimensionality of the database, maintaining the clinical characteristics of the variables robustly for use in Cox regression. This approach can aid in the identification of high-risk patient groups and inform treatment strategies aimed at improving clinical outcomes.

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IDENTIFICATION, QUANTIFICATION, AND MONITORING OF CIRCULATING TUMOR DNA IN PERIPHERAL BLOOD IN PATIENTS WITH DIFFUSE LARGE B-CELL LYMPHOMA USING THE Z-SCAN TECHNIQUE

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Introduction: Circulating free DNA (cfDNA), particularly circulating tumor DNA (ctDNA), has emerged as a pivotal tool for diagnosis, response assessment, and monitoring of various malignancies. However, in most cancers, it has yet to be incorporated into clinical practice due to the lack of reproducible and widely accessible methodological standardization. In this context, numerous studies have been conducted to achieve such standardization. The purpose of this study was to evaluate the quantification of cfDNA and the identification of plasma ctDNA using the Z-scan technique in patients with diffuse large B-cell lymphoma (DLBCL). **Methods:** Peripheral blood samples were prospectively collected from DLBCL patients at diagnosis, after the fourth treatment cycle, and at the end of R-CHOP-like treatment. Simultaneously, samples from healthy individuals matched by sex and age were collected. After obtaining cfDNA, its concentration was assessed using Nanodrop, Qubit, Bioanalyzer, and Z-scan equipment. The results were compared and correlated with the clinical characteristics of the patients. **Results:** From January 2018 to December 2022, 54 DLBCL patients were recruited, with a median age of 58 years (ranging from 21 to 91 years), 33 (62.9%) of whom were female. The overall response rate of the cohort was 68.52%, with a median follow-up of 24.6 months, showing an overall survival of 32 months and event-free survival of six months. The concentrations of cfDNA varied significantly among the different reading methodologies used. The peak-to-valley distance (Theta values - Θ) of cfDNA from patients at diagnosis (mean of 0.438) obtained in the Z-scan was statistically distinct between the control group (background) and patients at different collection points. The peak-to-valley distance (Θ) of cfDNA samples collected at diagnosis was higher than that of the control group (background), p = 0.068, those collected after cycle 4 (mean 0.33), p = 0.016, and after treatment completion (mean 0.33), p = 0.0005. Several cut-off points for "Θ" were tested to identify the best discriminatory value between DLBCL and healthy control, with a sensitivity of 64.71% (95% CI: 50.99% to 76.37%) and specificity of 86.61% (95% CI: 62.86% to 93.02%) for $\Theta > 0.406$. No correlations were found between "Θ" values and the clinical and demographic characteristics of the patients. **Conclusion:** The Z-Scan technique was able to distinguish DLBCL patients from healthy controls, as well as samples obtained during and after treatment from those collected before the start of anti-lymphoma therapy. We hypothesize that this discrimination was possible because the Z-scan technique may have been capable of distinguishing ctDNA from cfDNA.

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TRANSPLANTE ALOGÊNICO DE CÉLULAS TRONCO HEMATOPOIÉTICAS COMO ÚNICO TRATAMENTO CURATIVO PARA DOENÇA LINFOPROLIFERATIVA T/NK HIDROA VACINIFORME-LIKE EBV POSITIVO: UM RELATO DE CASO

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Objetivo: Demonstrar alternativa de tratamento curativo de um caso raro de doença linfoproliferativa T/NK hidroa vaciniforme-like EBV positivo. **Materiais e métodos:** O tipo de estudo adotado compreende em um relato de caso cujos dados são provenientes de revisão do prontuário e revisão de literatura. **Resultados:** Paciente masculino, iniciou seguimento com equipe de dermatologia aos 18 anos em 2014 para investigação de lesões linfomatóides papulosas em membros, com evolução para crostas, associado a febre. Biópsia inicialmente sugeria hipóteses de púrpura de Hennoch-Schoinlein e vasculite de médios vasos onde iniciou tratamento com corticóide e metotrexato, sem resposta. Realizada nova biópsia de pele com laudo de lesão linfoproliferativa de células T, encaminhado então a equipe da hematologia. Apresentava anemia hemolítica, hepatoesplenomegalia e linfonodomegalias cervicais e inguinais. Tratado com III ciclos do esquema CHOEP seguido de interferon, sem resposta. Nova biópsia com achados sugestivos de doença linfoproliferativa T hidroa vaciniforme-like EBV positivo, indicando tratamento com com prednisona, metotrexato, ciclosporina e talidomida, progredindo doença com edema de face periorbital e conjuntival e novas lesões de pele. Devido manutenção de PCR EBV positivo iniciado tratamento com bortezomibe e ganciclovir, com progressão. Realizado tratamento com GEMOX e Doxorrubicina lipossomal enquanto aguardava transplante alogênico de células tronco hematopoiéticas (Alo-TCTH). Realizou transplante com doador do REDOME, HLA idêntico e EBV positivo em 03/2024, fonte de sangue periférico, com condicionamento FLU(160)+BU(2)+ATG. No D+28 apresentou PCR para EBV do sangue negativo e melhora significativa do aspecto de lesões cutâneas. Apresentou DECH aguda de pele grau II, magic I, confirmadas por biópsia, resistente a corticóide com necessidade de introdução de segunda linha, Ruxolitinib e troca de imunossupressão devido nefrotoxicidade. Atualmente se encontra assintomático, em desmame de imunnossupressão com ruxolitinibe e micofenolato, apresentando apenas lesões cicatriciais de pele. Avaliação de doença e do enxerto pós transplante de 06/2024 com quimêra completa e mantendo PCR para EBV negativo. **Discussão:** A doença linfoproliferativa T/NK hidroa vaciniforme-like é um distúrbio linfoproliferativo raro relacionado ao EBV, mais comum em crianças podendo ser relatado em adultos, sendo a maioria em países asiáticos e latino-americanos. Manifesta-se inicialmente com pápulas que evoluem com crostas e cicatrizes principalmente em face e membros que geralmente pioram com a exposição solar. Alguns casos se apresentam com febre, linfoadenopatia, edema facial, perda de peso e hepatoesplenomegalia. Foi relatado que o adulto tem doença mais agressiva e que o edema facial e altas cargas séricas do EBV pode estar associado a um mau prognóstico. Atualmente não existe protocolo de tratamento definitivo e os pacientes geralmente são tratados com antivirais, corticosteróides, imunossupressores, imunomoduladores, quimioterapia e radioterapia,com relatos descritos de pouco efeito ou efeito temporário. Existem relatos de pacientes que receberam Alo-TCTH que alcançaram remissão completa e estão vivos sem doença. **Conclusão:** O tratamento dos pacientes com doença linfoproliferativa T/NK hidroa vaciniforme-like EBV positivo deve depender do curso da doença e o Alo-TCTH deve ser a escolha para pacientes recidivados e refratários devido ao fraco efeito da quimioterapia.

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ANALYSIS OF THE EXPRESSION PATTERN OF CELL CYCLE AND TUMOR SENESCENCE REGULATORY GENES IN HTLV-1 CARRIERS AND ADULT T-CELL LEUKEMIA/LYMPHOMA PATIENTS

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Introduction: Infection with Human T-Lymphotropic Virus Type 1 (HTLV-1) is endemic in various regions worldwide. Brazil has an estimated 800,000 to 2.5 million infected individuals. This virus is associated with a broad spectrum of clinical manifestations, ranging from asymptomatic infection to severe diseases such as tropical spastic paraparesis/HTLV-1-associated myelopathy (HAM/TSP) and adult T-cell leukemia/lymphoma (ATLL). Both conditions are linked to high morbidity and mortality. HTLV-1 can infect and alter the function of immune system cells, particularly CD4+ T lymphocytes, causing abnormalities in genes involved in cellular senescence, proliferation, and apoptosis. This study aimed to evaluate the differential expression of genes regulating senescence and cellular proliferation in asymptomatic HTLV-1 carriers. **Methods:** Peripheral blood samples were collected from healthy individuals (controls), asymptomatic HTLV-1 carriers, and ATLL patients. Gene expression analysis was performed using RNA extracted from CD4 + T lymphocytes separated by magnetic microbeads. The extracted RNA was converted into cDNA for quantitative real-time polymerase chain reaction (qRT-PCR). **Results:** A total of 32 asymptomatic HTLV-1 carriers, 30 healthy controls, and 7 ATLL cases were analyzed (N = 69). Of the 32 asymptomatic HTLV-1 carriers, 22 (68.8%) were female; in the control group, 16 (53.3%) were female, and in the ATLL group, 5 (71.4%) were female. The age of asymptomatic HTLV-1 carriers ranged from 20 to 87 years (median 58 years), from 31 to 66 years (median 52 years) in the control group, and from 43 to 79 years (median 64 years) in the ATLL group. Three (43%) patients were classified as having smouldering ATLL, and 1 (14.3%) as acute ATLL. The genes CDKN1A, PIK3CA, and RBL2 were underexpressed in asymptomatic HTLV-1 carriers. ATLL patients exhibited underexpression of CDKN1A and overexpression of COL3A1. **Conclusion:** Asymptomatic HTLV-1 carriers showed underexpression of CDKN1A, PIK3CA, and RBL2 in CD4+ T lymphocytes. CDKN1A was also significantly underexpressed in ATLL. Asymptomatic carriers and ATLL patients did not