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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; $\beta$= 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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