Medical Journal of Bakırköy

Med J Bakirkoy 2025;21(3):259-266
DOI: 10.4274/BMJ.galenos.2025.2024.12-2

Research

Computed Tomography Texture Analysis for Monitoring Treatment Response in Childhood Lymphomas: A Preliminary Study

Çocukluk Çağı Lenfomalarında Tedavi Yanıtının İzlenmesi için Bilgisayarlı Tomografi Doku Analizi: Bir Ön Çalışma

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ABSTRACT

Objective: This preliminary study aims to evaluate the effectiveness of computed tomography (CT) texture analysis parameters in monitoring treatment response in childhood lymphomas.

Methods: A retrospective study was conducted on 28 pediatric patients (15 with Hodgkin lymphoma and 13 with non-Hodgkin lymphoma), aged 3-16 years. CT images were acquired using a 64-detector spiral CT scanner and analyzed with OLEA research software (Olea Medical, La Ciotat, France). Regions of interest were placed on non-necrotic tumor areas in venous phase sequences.

Results: No significant age distribution difference was found between the genders, in both lymphoma groups (p=0.6). For Hodgkin lymphoma, significant texture parameters included median and gray-level non-uniformity in gray-level run-length matrix, gray-level size-zone matrix, and gray-level dependence matrix. For non-Hodgkin lymphoma, significant parameters were joint energy and sum entropy in gray-level co-occurrence matrices, zone entropy in gray-level size zone matrices, and dependence entropy in gray-level dependence matrices. Receiver operating characteristic analysis for Hodgkin lymphoma showed p-values of 0.0002-0.04, area under the curve (AUC) values of 65-78, sensitivity rates of 56-75%, and specificity rates of 58-75%. For non-Hodgkin lymphoma, significant parameters had p-values of 0.006-0.027, AUC values of 0.71-0.73, sensitivity of 47-87%, and specificity of 60-87%.

Conclusion: The study highlights the value of CT texture analysis in differentiating between Hodgkin and non-Hodgkin lymphoma in pediatric patients. By identifying significant texture parameters, this analysis method can improve diagnostic accuracy and treatment planning in childhood lymphomas.

Keywords: Texture, lymphoma, treatment

ÖZ

Amaç: Bu ön çalışma, çocukluk çağı lenfomalarında tedavi yanıtının izlenmesinde bilgisayarlı tomografi (BT) doku analizi parametrelerinin etkinliğini değerlendirmeyi amaçlamaktadır.

Gereç ve Yöntem: Üç ile on altı yaş arası 28 pediatrik hasta (15 Hodgkin lenfoma ve 13 Hodgkin olmayan lenfoma) üzerinde retrospektif bir çalışma yapıldı. BT görüntüleri 64 dedektörlü spiral BT tarayıcısı kullanılarak elde edildi ve OLEA (Olea Medical, La Ciotat, France) araştırma yazılımı ile analiz edildi. İlgi alanları, venöz faz sekanslarında nekrotik olmayan tümör alanlarına yerleştirildi.

Bulgular: Her iki lenfoma grubunda cinsiyetler arasında anlamlı yaş dağılımı farkı bulunmadı (p=0,6). Hodgkin lenfoma için önemli doku parametreleri arasında gri seviye çalışma uzunluğu matrisi, gri seviye boyut bölge matrisi ve gri seviye bağımlılık matrisinde medyan ve gri seviye homojen olmama durumu yer aldı. Hodgkin olmayan lenfoma için önemli parametreler, gri seviye eş oluşum matrisinde ortak enerji ve toplam entropi, gri seviye boyut bölge matrisinde bölge entropisi ve gri seviye bağımlılık matrisinde bağımlılık entropisi idi. Hodgkin lenfoma hastaları için alıcı işlem özellikleri eğrisi analizi, 0,0002 ile 0,04 arasında değişen p-değerleri, 65-78 eğri altında kalan alan değerleri, %56-75 duyarlılık oranları ve %58-75 özgüllük oranları gösterdi. Hodgkin olmayan lenfoma hastaları için önemli parametreler 0,006 ile 0,027 arasında p-değerleri, 0,71-0,73 eğri altında kalan alan değerleri, %47-87 duyarlılık değerleri ve %60-87 özgüllük değerleri gösterdi.

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Received: 10.12.2024
Accepted: 14.02.2025
Publication Date: 03.09.2025

Cite as: Altındaş İ, Gürhan A, Kara B, Bayramoğlu Z, Öztürk M, Köksal Y. Computed tomography texture analysis for monitoring treatment response in childhood lymphomas: a preliminary study. Med J Bakirkoy. 2025;21(3):259-266

ÖZ

Sonuç: Çalışma, pediatrik hastalarda Hodgkin ve Hodgkin olmayan lenfoma ayrımında BT doku analizinin değerini vurgulamaktadır. Önemli doku parametrelerini belirleyerek, bu analiz yöntemi çocukluk çağı lenfomalarında tanı doğruluğunu ve tedavi planlamasını iyileştirebilir.

Anahtar Kelimeler: Doku, lenfoma, tedavi

INTRODUCTION

Lymphomas rank as the third most common cancer in children, following leukemia and brain tumors (1). These malignant tumors arise from genetic abnormalities in immune system cells or their precursors and encompass a range of pathological subtypes. Lymphomas can originate from various immune system components, including B cells, T cells, and natural killer cells. Genetic alterations in these cells lead to uncontrolled cell growth and tumor formation. Lymphomas are primarily classified as Hodgkin's lymphoma (HL) and non-HL (NHL) (2). Treatment follow-up depends on factors such as the disease type, stage, and overall health of the patient. Treatments may include chemotherapy, radiotherapy, immunotherapy, and stem cell transplantation. Due to their diverse subtypes and complex structure, lymphomas pose challenges for treatment, necessitating ongoing research and clinical trials (3).

Computed tomography (CT) is a frequently used imaging technique for diagnosing and managing pediatric lymphomas. It plays a crucial role in diagnosis, staging, and follow-up by providing detailed anatomical images to evaluate the size and structure of abnormal lymph nodes. However, CT alone has limitations, such as potentially inadequate evaluation, if lymph nodes do not significantly shrink after treatment (4). Combining CT with fluoro-2-deoxy-glucose (FDG)-positron emission tomography (PET) enhances the assessment by evaluating the metabolic activity of the lymph nodes. FDG-PET is highly sensitive in detecting malignant cells through glucose metabolism measurement, which is particularly useful for diagnosing metabolically active tumors like lymphomas and monitoring treatment response. FDG-PET/CT enables early evaluation of treatment effectiveness and can identify residual disease (5). However, FDG-PET has limitations, such as the potential for false positives due to FDG retention in inflammatory and infectious processes, which can lead to diagnostic errors. Hence, FDG-PET results should be interpreted cautiously and within a clinical context (6).

CT texture analysis (CTTA) is an advanced technique that assesses tissue characteristics, including structure, microarchitecture, symmetry, and the degree of homogeneity or heterogeneity (7). This quantitative, mathematical method analyzes spatial heterogeneity in medical imaging and pixel density interrelationships. CTTA helps differentiate between benign and malignant lesions and identifies more biologically aggressive tumors. It also evaluates tissue microenvironment heterogeneity, tumor grade, cellular processes like hypoxia and angiogenesis, and genetic features such as mutation status and treatment response. Additionally, CTTA can measure fibrosis (8). Recently, CTTA has been applied to distinguish malignant from benign lymphadenopathies in children, assess metastatic versus non-metastatic lung nodules, and diagnose and grade immature teratomas (9-11). This technique improves understanding of tissue microstructure and tumor behavior, offering significant benefits in accurate diagnosis and treatment planning when used with traditional imaging methods. It also provides valuable information for evaluating treatment response and disease prognosis (12).

This study uses texture analysis parameters to assess contrast-enhanced CT scans of patients with Hodgkin and NHL before and after treatment. It will also explore the correlation between these parameters and patient treatment responses. By investigating structural and textural changes in lymph nodes and surrounding tissues, the study seeks to offer deeper insights into treatment effectiveness and identify potential predictive markers for treatment outcomes.

METHODS

Study Design and Patient Selection

This retrospective study was meticulously conducted in a single-center university hospital after obtaining approval from the Selçuk University Local Ethics Committee (approval number: 2021/175, date: 07.04.2021). The research complied with the ethical guidelines of the Declaration of Helsinki. Over twelve years, from March 2017 to March 2021, CT images of 35 patients with a pathological diagnosis of either HL or NHL were reviewed retrospectively. However, 7 patients were excluded due to artifacts, and issues with contrast-enhanced timing. Consequently, the final analysis included 28 patients, with 15 diagnosed with HL and 13 with NHL. A total of 28 mediastinal lymphadenopathy measurements were made. The CT images used in the study were sourced from the picture archiving and communication system.

Computed Tomography Examination Protocol and Imaging Analysis

Images were acquired using a 64-detector spiral CT scanner (Aera, Siemens, Erlangen, Germany) with low kilovolt peak (kVp) settings. The CT protocol included the injection of non-ionic iodinated contrast material calculated according to the patient's weight (370 mg/mL iopromide; Ultravist, Bayer Vital, Leverkusen, Germany) into an antecubital vein at a rate of 2.5 mL/sec, followed by a 50 mL saline flush at the same rate using an auto-injector (Stellant, Medtron, Saarbruecken, Germany). Thoracic images were captured 30 seconds after the contrast injection, and abdominal/pelvic images were taken 70 seconds post-contrast. Scanning parameters included a 0.6 mm collimation, a 0.5-second rotation time, and a 0.6 mm increment. Images were obtained at a tube voltage of 120 kVp, with a tube current of 180 mAs for the neck, 100 mAs for the chest, and 200-250 mAs for the abdomen. The matrix size was 512x512, with a window center of 50 and 300 and a window width of 300 and 1,500, using a soft tissue reconstruction kernel (B30f).

Computed Tomography Texture Analysis

CT images were obtained using a Toshiba CT scanner (Toshiba Medical Systems, Tokyo, Japan), and CTTA was performed using OLEA research software (Olea Medical, La Ciotat, France) by placing freehand regions of interest on non-necrotic areas of the tumor in arterial phase sequences of lymphadenopathies (Figures 1 and 2). The analysis was conducted by a researcher with 2.5 years of general radiology experience and another with 10 years of pediatric radiology experience. All data were processed in Microsoft Office Excel, and statistical analysis was conducted using SPSS (Version 21.0; IBM Corp., Armonk, NY, USA). The distribution of the data was assessed using the Kolmogorov-Smirnov test. Descriptive statistics were expressed as minimum, maximum, mean, standard deviation, and median, with variability measured by the interquartile range. The texture analysis utilized eight first-order statistical parameters (entropy, mean, median, standard deviation, skewness, kurtosis, variance, and uniformity) and eleven second-order statistical parameters. The second-order parameters included difference variance, joint energy, sum average, and sum entropy within the gray-level co-occurrence matrix (GLCOM); gray-level non-uniformity and run entropy within the gray-level run length matrix (GLRLM); zone entropy within the gray-level size zone matrix (GLSZM); contrast within the gray tone difference matrix (GTDM); and gray-level non-uniformity and dependence entropy within the gray-level dependence matrix (GLDM).

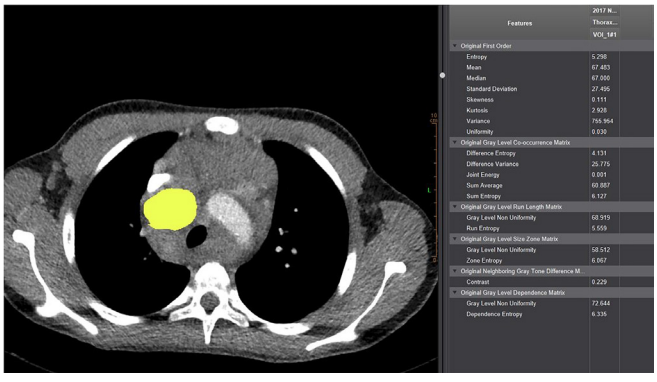

Figure 1. Axial CT image; in a patient with HL, the pre-treatment tissue analysis program monitors the results of tissue analysis of the ROI area (yellow area) and statistical parameters drawn for lymphadenopathies in the mediastinum

CT: Computed tomography, HL: Hodgkin's lymphoma, ROI: Regions of interest

Statistical Analysis

All data were processed in Microsoft Office Excel, and statistical analysis was performed using SPSS (version 21.0, IBM Corp.). The Kolmogorov-Smirnov test was used to evaluate the data distribution. Descriptive statistics were presented as minimum, maximum, mean, standard deviation, and median with the interquartile range. In texture analysis, eight first-order statistical parameters (entropy, mean, median, standard deviation, skewness, kurtosis, variance, and uniformity) and eleven second-order statistical parameters (difference variance, joint energy, sum average, sum entropy within the GLCOM, gray-level non-uniformity and run entropy within the GLRLM, gray-level non-uniformity and zone entropy within the GLSZM, contrast within the GTDM, gray-level non-uniformity and dependence entropy within the GLDM) were utilized. Wilcoxon's signed-rank test, was used to compare texture parameters for evaluating the treatment response of pathological lymph nodes in HL and NHL patients, with a p-value considered significant at <0.05.

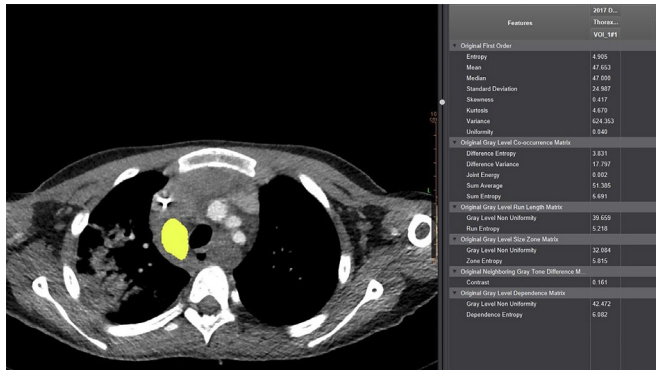

Figure 2. Axial CT image; 1 in Figure 1. In the tissue analysis program after cure chemotherapy, the results of tissue analysis of the ROI area (yellow area) and statistical parameters drawn for lymphadenopathies with shrinkage in the mediastinum are monitored

CT: Computed tomography, ROI: Regions of interest

A three-step feature selection process was used to obtain the best tissue metrics for each CT cross-section. Receiver operating characteristic (ROC) curve analysis and Pearson correlation tests were performed.

RESULTS

The study analyzed 28 patients at our center, with 15 (53%) diagnosed with HL and 13 (47%) with NHL. In the HL group, there were 8 females and 7 males, while the NHL group comprised 7 females and 6 males, with all patients aged between 3 and 16 years. The average age of female HL patients was 10, and for males, it was 11.13. In the NHL group, the average age for females was 10.38; for males, it was 13.7. Statistical analysis indicated no significant age distribution difference between males and females in HL and NHL groups (p=0.6).

Texture analysis using 19 parameters revealed statistically significant results for four parameters in differential diagnosis. For HL, the median values were gray-level non-uniformity in GLRLM, GLSZM, and GLDM. For NHL, the significant parameters were joint energy and sum entropy in GLCOM, zone entropy in GLSZM, and dependence entropy in GLDM. The median is a first-order texture feature, while gray-level non-uniformity, joint energy, sum entropy, zone entropy, and dependence entropy are second-order texture features (Tables 1 and 2).

In the ROC analysis for HL patients, the statistically significant parameters were the median and gray-level non-uniformity in GLRLM, GLSZM, and GLDM, with p-values of 0.04, 0.0002, 0.004, and 0.01, respectively. The area under the curve (AUC) for these parameters was 65, 78, 78, and 77, respectively. The sensitivity rates were 56%, 75%, 75%, and 68%, and the specificity rates were 58%, 75%, 75%, and 75%, respectively. The diagnostic accuracy values were 62%, 78%, 78%, and 77%, respectively (Table 3).

For NHL patients, the ROC analysis showed that the statistically significant parameters were joint energy and sum entropy in GLCOM, zone entropy in GLSZM, and

Table 1. Comparison of pre-and post-treatment values of CTTA parameters of HL

Hodgkin lymphoma (n=18)	**Before treatment**	**Post-treatment**	**p-value**
First-order statistical parameters	**Median (IQR)**	**Median (IQR)**	
Entropy	5.18 (5.01-5.34)	5.2 (5.09-5.41)	0.7
Mean	56.9 (52.6-70.2)	46.2 (33.6-67.4)	0.056
Median	57.5 (52.6-70.7)	48 (32.5-67)	0.04
SD	14.33 (8.73-25.7)	12.9 (10-20.4)	0.3
Skewness	-0.04 (-0.13-0.03)	0.09 (-0.04-0.5)	0.056
Kurtosis	2.96 (2.79-3.27)	2.92 (2.6-3.4)	0.57
Variance	205 (77-665)	167.6 (99.6-418)	0.37
Uniformity	0.03 (0.03-0.04)	0.03 (0.03-0.04)	0.48
Second-order statistical parameters			
Gray-level co-occurence matrix (GLCOM)			
Difference variance	35.5 (18.5-49)	18.84 (12.6-44.6)	0.44
Joint energy	0 (0-0)	0 (0-0.01)	0.058
Sum average	63.4 (60-68.3)	66.9 (53.6-74.2)	0.9
Sum entropy	5.99 (5.86-6.11)	5.84 (5.5-6.1)	0.15
Gray-level run length matrixv (GLRLM)			
Gray-level non-uniformity	24.6 (15.8-37.4)	10.56 (5.12-21.22)	0.002
Run entropy	5.43 (5.29-5.55)	5.48 (5.15-5.63)	0.68
Gray-level size zone matrix (GLSZM)			
Gray-level non-uniformity	21.2 (12.1-28.2)	8.39 (4.93-16.8)	0.004
Zone entropy	5.93 (5.74-6.1)	5.92 (5.32-6.08)	0.2
Contrast	0.4 (0.21-0.6)	0.45 (0.27-0.99)	0.1
Gray-level dependence matrix (GLDM)			
Gray-level non-uniformity	28.9 (14.5-40.6)	9.83 (5.12-22.26)	0.01
Dependence entropy	6.15 (5.96-6.34)	6.14 (5.47-6.3)	0.15

IQR: Interquartile range, HL: Hodgkin's lymphoma, CTTA: Computed tomography texture analysis, SD: Standard deviation

Table 2. Results of ROC analysis of CTTA parameters differing before and after treatment in HL

CTTA parameters	AUC	p	Cut-off value	Sensitivity	Specificity	95% CI	
						Lower limit	Upper limit
First-order statistical parameters							
Median	65	0.04	56	56	58	46	85
Gray-level run length matrixv (GLRLM)							
Gray-level non-uniformity	78	0.002	16	75	75	61	94
Gray-level size zone matrix (GLSZM)							
Gray-level non-uniformity	78	0.004	14	75	75	62	93
Gray-level dependence matrix (GLDM)							
Gray-level non-uniformity	77	0.01	20	68	75	60	94

CI: Confidence interval, AUC: Area under the curve, CTTA: Computed tomography texture analysis, ROC: Receiver operating characteristic, HL: Hodgkin's lymphoma

Table 3. Comparison of pre- and post-treatment values of CTTA parameters of NHL

Non-Hodgkin lymphoma (n=17)	Before treatment	Post-treatment	p-value
CTTA parameters	**Median (IQR)**	**Median (IQR)**	
First-order statistical parameters			
Entropy	5.27 (4.87-5.31)	5.05 (4.72-5.37)	0.33
Mean	55.9 (44.5-67.5)	53.35 (44.88-62.36)	0.6
Median	56 (41-67)	53 (44.9-62.36)	0.6
SD	13.04 (9.81-24.2)	15.4 (12.6-26.4)	0.3
Skewness	0.03 (-0.23-0.2)	0.02 (-0.2-0.28)	0.65
Kurtosis	3.1 (2.83-3.66)	2.9 (2.75-3.53)	0.9
Variance	170.1 (59.4-584.5)	236.71 (158.37-698.5)	0.28
Uniformity	0.03 (0.03-0.04)	0.03 (0.03-0.04)	0.48
Second order statistical parameters			
Gray-level co-occurence matrix (GLCOM)			
Difference variance	29.5 (22-39.7)	27 (17.8-89.2)	0.08
Joint energy	0 (0-0)	0 (0-0.1)	0.006
Sum average	62.3 (59.4-73.9)	62.67 (57.69-67.4)	0.23
Sum entropy	6 (5.8-6.11)	5.7 (5.33-5.9)	0.02
Gray-level run length matrix (GLRLM)			
Gray-level non-uniformity	14.6 (9.33-57.36)	11.8 (2.34-22.2)	0.21
Run entropy	5.51 (5.3-5.56)	5.28 (4.68-5.57)	0.07
Gray-level size zone matrix (GLSZM)			
Gray-level non-uniformity	12.54 (7.82-40.5)	10.5 (2.07-17.08)	0.25
Zone entropy	5.98 (5.76-6.08)	5.82 (5.18-5.86)	0.027
Contrast	0.37 (0.23-0.66)	0.69 (0.28-2.17)	0.11
Gray-level dependence matrix (GLDM)			
Gray-level non-uniformity	15.29 (10.5-60.48)	12.35 (2.44-24.2)	0.19
Dependence entropy	6.25 (5.99-6.34)	5.98 (5.28-6.08)	0.023

CTTA: Computed tomography texture analysis, NHL: Non-Hodgkin's lymphoma, SD: Standard deviation, IQR: Interquartile range

dependence entropy in GLDM, with p-values of 0.006, 0.02, 0.027, and 0.023, respectively. The AUC for these parameters was 0.72, 0.71, 0.73, and 0.72, respectively. The sensitivity values were 47%, 87%, 67%, and 80%, and the specificity values were 87%, 60%, 87%, and 60%, respectively. The diagnostic accuracy values were 72%, 71%, 73%, and 72%, respectively (Figures 3, 4 and Table 3b). No significant differences were found in other parameters (Table 4).

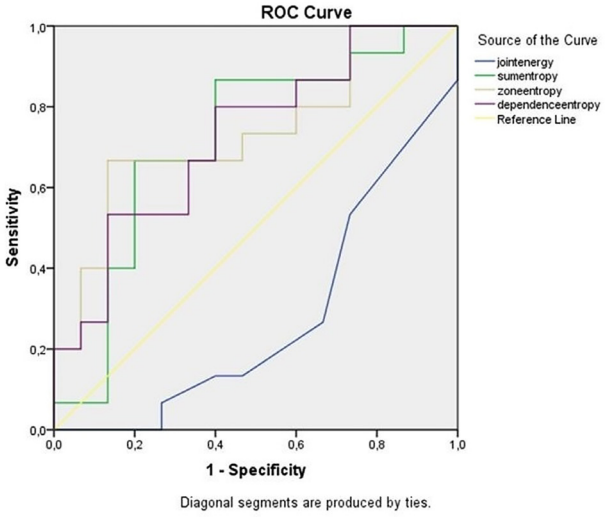

Figure 3. ROC curve of CTTA parameters differing before and after treatment in HL
CTTA: Computed tomography texture analysis, ROC: Receiver operating characteristic, HL: Hodgkin's lymphoma

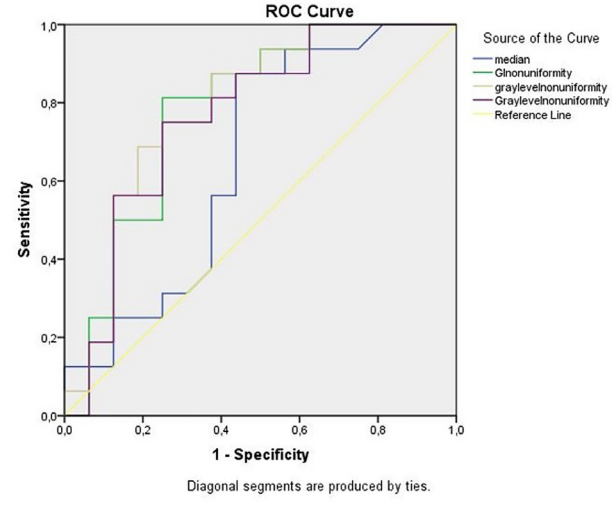

Figure 4. ROC curve of CTTA parameters differing before and after treatment in NHL
CTTA: Computed tomography texture analysis, ROC: Receiver operating characteristic, NHL: Non-Hodgkin's lymphoma

DISCUSSION

This preliminary study aimed to evaluate the efficacy of CTTA parameters in monitoring treatment response in childhood lymphomas. The results demonstrated that CTTA could effectively differentiate between HL and NHL in pediatric patients by identifying significant texture parameters. The texture analysis revealed that certain parameters significantly differed between HL and NHL, suggesting their potential role in differential diagnosis. For HL, significant parameters included the median and gray-level non-uniformity in GLRLM, GLSZM, and GLDM. These parameters reflect the heterogeneity within the tumor, which may correlate with different biological behaviors of HL. The median value in texture analysis often represents the central tendency of pixel intensity, providing insights into the overall density and structure of the tumor. Gray-level non-uniformity measures the variability of gray-levels within the tumor, indicating the degree of heterogeneity which is often higher in malignant tissues due to irregular cell growth and necrosis (13). Similarly, for NHL, significant parameters was joint energy and sum entropy in GLCOM, zone entropy in GLSZM, and dependence entropy in GLDM. Joint energy in GLCOM reflects the uniformity of pixel pairs, with lower values indicating more disorder and heterogeneity, which are characteristic of aggressive tumors. Sum entropy measures the complexity and randomness within the tumor texture, providing insights into the tumor's metabolic activity and potential aggressiveness. Zone entropy in GLSZM and dependence entropy in GLDM further quantify the spatial distribution and dependency of pixel intensities, crucial for understanding the tumor's microenvironment and potential response to treatment (14).

The ROC analysis provided further insights into the diagnostic accuracy of these texture parameters. For HL, the AUC values ranged from 65 to 78, indicating moderate to high diagnostic accuracy. The sensitivity and specificity rates were also promising, suggesting that CTTA could be a reliable tool for monitoring treatment response in HL patients. For instance, a sensitivity rate of 75% indicates that CTTA correctly identified 75% of true positive cases, while a specificity rate of 75% indicates that it detected 75% of true negative cases. These metrics are crucial for ensuring that patients receive accurate diagnoses and appropriate treatments (15). For NHL, the AUC values were slightly higher, ranging from 0.71 to 0.73, indicating a strong potential for CTTA in differentiating NHL from HL, supported by sensitivity and specificity rates. The higher AUC values for NHL suggest that the identified texture parameters are

Table 4. Results of ROC analysis of CTTA parameters differing before and after treatment in NHL

CTTA parameters	AUC	p	Cut-off value	Sensitivity	Specificity	95% CI	
						Lower limit	Upper limit
Gray-level co-occurence matrix (GLCOM)							
Joint energy	0.72	0.006	0.0	47	87	0.54	0.90
Sum entropy	0.71	0.02	5.71	87	60	0.09	0.48
Gray-level size zone matrix (GLSZM)							
Zone entropy	0.73	0.027	5.87	67	87	0.08	0.45
Gray-level dependence matrix (GLDM)							
Dependence entropy	0.72	0.023	6	80	60	0.09	0.45

CI: Confidence interval, AUC: Area under the curve, CTTA: Computed tomography texture analysis, ROC: Receiver operating characteristic, NHL: Non-Hodgkin's lymphoma

more robust in distinguishing NHL from other lymphomas, which is essential for tailoring specific treatment protocols for these patients (16).

Our findings align with previous studies that highlighted the utility of texture analysis in cancer diagnosis and treatment monitoring. For instance, Ganeshan et al. (8) demonstrated that texture analysis could differentiate between benign and malignant lung nodules by assessing the heterogeneity within the tumor. Similarly, Lubner et al. (17) showed that texture analysis could assess hepatic fibrosis by quantifying the structural changes in liver tissue. These studies support the notion that texture analysis can provide valuable information about tumor microenvironment and treatment response, reinforcing the potential of CTTA in pediatric lymphomas.

Accurately differentiating between HL and NHL using CTTA has significant clinical implications. First, it can aid in early diagnosis and appropriate treatment planning, which is crucial for improving patient outcomes. Early and accurate diagnosis allows for timely intervention, potentially reducing the disease burden and improving survival rates (12). Secondly, CTTA can provide a non-invasive method to monitor treatment response, reducing the need for repeated biopsies and invasive procedures. This is particularly important in pediatric patients, for whom minimizing radiation exposure and invasive interventions is a priority. By providing a detailed assessment of tumor heterogeneity and response to treatment, CTTA can help clinicians make informed decisions about modifying or continuing treatment regimens (11). Furthermore, CTTA's ability to evaluate tissue microenvironment heterogeneity, tumor grade, cellular processes like hypoxia and angiogenesis, and genetic features such as mutation status and treatment response, adds another layer of diagnostic precision. This comprehensive evaluation can lead to more personalized treatment plans, potentially improving the efficacy of therapeutic interventions (18,19).

Study Limitations

Despite the promising results, this study has several limitations. The sample size was relatively small, and the study was conducted at a single-center, which may limit the generalizability of the findings. Additionally, the retrospective nature of the study may introduce selection bias. Future studies with larger, multi-center cohorts are needed to validate these findings and explore the potential of CTTA in other pediatric cancers. Moreover, prospective studies could provide more robust evidence on the utility of CTTA in real-time clinical settings (3). Moreover, integrating CTTA with other imaging modalities, such as FDG-PET, could enhance the accuracy of treatment response assessment. FDG-PET provides metabolic information, while CTTA offers insights into tissue heterogeneity; combining these techniques may provide a comprehensive evaluation of the tumor. Studies have shown that FDG-PET/CT is highly sensitive in detecting malignant cells through glucose metabolism measurement, which is particularly useful for diagnosing metabolically active tumors like lymphomas and monitoring treatment response (5). However, FDG-PET has limitations, such as the potential for false positives due to FDG retention in inflammatory and infectious processes (6). Hence, combining FDG-PET with CTTA could mitigate these limitations and provide a more accurate assessment of treatment response. Additionally, advancements in artificial intelligence and machine learning could further enhance the capabilities of CTTA. Algorithms designed to analyze texture patterns could be trained to recognize subtle changes in tumor characteristics, potentially leading to earlier treatment response or resistance detection. This integration could revolutionize how we monitor and treat pediatric lymphomas, making the process more efficient and precise (9).

CONCLUSION

In conclusion, this preliminary study demonstrated that CTTA is valuable in differentiating between HL and NHL in pediatric patients. Significant texture parameters can aid in differential diagnosis and treatment response assessment. These findings suggest that CTTA can enhance diagnostic accuracy and treatment planning, providing deeper insights into treatment effectiveness and potential predictive markers for treatment outcomes. Future research should focus on validating these results in larger cohorts and integrating CTTA with other imaging modalities for a more comprehensive evaluation. Additionally, exploring the potential of CTTA in other pediatric cancers could further expand its clinical utility and improve patient care.

ETHICS

Ethics Committee Approval: This retrospective study was meticulously conducted in a single-center university hospital after obtaining approval from the Selçuk University Local Ethics Committee (approval number: 2021/175, date: 07.04.2021).

Informed Consent: Retrospective study.

FOOTNOTES

Authorship Contributions

Surgical and Medical Practices: Y.K., Concept: İ.A., Z.B., Design: İ.A., B.K., Z.B., Data Collection or Processing: A.G., B.K., Z.B., M.Ö., Analysis or Interpretation: A.G., B.K., M.Ö., Literature Search: A.G., M.Ö., Writing: M.Ö.

Conflict of Interest: No conflict of interest was declared by the authors.

Financial Disclosure: The authors declare that this study received no financial support.

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