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ORIGINAL PAPER

ASSOCIATION BETWEEN BIOCHEMICAL PARAMETERS, OXIDATIVE DAMAGE MARKERS, AND UNFAVOURABLE CYTOGENETIC ABERRATIONS IN CHRONIC LYMPHOCYTIC LEUKAEMIA

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Abstract

Introduction. Chronic lymphocytic leukaemia (CLL) is the most common type of leukaemia in adults and is characterised by marked phenotypic heterogeneity and variable risk profiles.
The objective of the study was to investigate the association between markers of oxidative damage and unfavourable cytogenetic aberrations in the context of routinely used biochemical parameters in patients with CLL.
Material and methods. A total of 39 individuals were enrolled and divided into three groups: 10 healthy controls, 11 asymptomatic untreated CLL patients, and 18 patients receiving targeted therapy (venetoclax or ibrutinib). Serum prooxidant status was assessed using the d-ROMs test. Serum levels of protein carbonyls, advanced oxidation protein products (AOPP), and 8-hydroxy-2'-deoxyguanosine (8-OHdG) were measured by enzyme-linked immunosorbent assay.

Résumé

Association entre les paramètres biochimiques, les marqueurs de dommages oxydatifs et les auberrations cytogénétiques défavorables dans la leucémie lymphoïde chronique

Introduction. La leucémie lymphoïde chronique (LLC) est la leucémie la plus fréquente chez l'adulte. Elle se caractérise par une hétérogénéité phénotypique marquée et des profils de risque variables.
L'objectif de l'étudea été d'évaluer l'association entre les marqueurs de dommages oxydatifs et les aberrations cytogénétiques défavorables dans le contexte des paramètres biochimiques couramment utilisés chez les patients atteints de LLC.
Matériel et méthodes. Au total, 39 personnes ont été recrutées et réparties en trois groupes: 10 témoins sains, 11 patients atteints de LLC asymptomatique

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Results. Serum triglyceride levels were significantly higher in patients receiving targeted therapy compared to controls (p=0.003) and were also higher in patients with del(17p) than in those with del(11q) (p=0.019). Total cholesterol concentrations were increased in patients on targeted therapy compared to controls (p=0.016). No statistically significant differences were observed in oxidative damage markers between CLL patients and controls. However, serum protein carbonyl levels were significantly higher in patients harbouring del(17p) compared to those without this aberration (p=0.013).
Conclusions. Elevated serum protein carbonyl levels in CLL patients with del(17p) may contribute to more unfavourable clinical outcomes in these patients Alterations in lipid parameters, including higher triglyceride and lower total cholesterol levels, suggest disease-related specificity in lipid metabolism. Larger studies are required to validate the combined use of oxidative stress markers and cytogenetic abnormalities for predicting disease progression.

Keywords: oxidative stress, chromosome abberations, lipid metabolism, chronic lymphocytic leukaemia.

List of abbreviations
ANOVA –analysis of variance
AOPP – advanced oxidation protein products
ATM – ataxia-telangiectasia mutated
CI – confidence interval
CLL – chronic lymphocytic lleukemia
del (11q) – deletions of the long arm of chromosome 11
del(17p) – deletion of the short arm of chromosome 17
DNA – deoxyribonucleic acid
d-ROM – derivatives-reactive oxygen metabolites
8-oxo-dG – 8-oxo-2'-deoxyguanosine
ELISA – enzyme-linked immunosorbent assay
FISH – fluorescence in situ hybridization
HOOH – hydrogen peroxide
IQR – interquartile range
LYM – lymphocytes
MDA – malondialdehyde
OS – oxidative stress
PC – protein carbonyls
p53 – tumor protein 53
ROS – reactive oxygen species
SD – standard deviation
TG– triglycerides
TP53 – tumour protein p53
WBC– white blood cells

Résultats. Les taux sériques de triglycérides étaient significativement plus élevés chez les patients recevant un traitement ciblé que chez les témoins (p=0.003) et étaient également plus élevés chez les patients présentant une délétion 17p que chez ceux présentant une délétion 11q (p=0.019). Les concentrations de cholestérol total étaient plus élevées chez les patients sous traitement ciblé que chez les témoins (p=0.016). Aucune différence statistiquement significative n'a été observée entre les patients atteints de LLC et les témoins en ce qui concerne les marqueurs de dommages oxydatifs. Cependant, les taux sériques de protéines carbonylées étaient significativement plus élevés chez les patients présentant une délétion 17p que chez ceux ne présentant pas cette aberration (p=0.013).
Conclusions. Des taux élevés de protéines carbonylées sériques chez les patients atteints de LLC présentant une délétion 17p pourraient contribuer à des résultats cliniques moins favorables chez ces patients. Les modifications des paramètres lipidiques, notamment des taux plus élevés de triglycérides et plus faibles de cholestérol total, suggèrent une spécificité liée à la maladie dans le métabolisme lipidique. Des études à plus grande échelle sont nécessaires pour valider l'utilisation combinée des marqueurs de stress oxydatif et des anomalies cytogénétiques pour prédire la progression de la maladie.

Mots-clés: stress oxydatif, aberrations chromosomiques, métabolisme lipidique, leucémie lymphoïde chronique.

Introduction

Chronic lymphocytic leukaemia (CLL) is the most common form of leukaemia in adults and is characterised by the accumulation of dysfunctional lymphocytes in the bone marrow, lymphoid organs, and peripheral blood[1]. Distinctive features of the disease include its heterogeneous phenotypic expression and highly variable clinical course, ranging from an asymptomatic state to chronic relapsing disease and,

less frequently, transformation into aggressive lymphoma.

Published data indicate that CLL progression is associated with an increased frequency of cytogenetic aberrations[2]. At least one chromosomal deletion is detected in approximately 80% of untreated patients, while a combination of two or more chromosomal abnormalities is reported in 23% of cases[3]. Certain chromosomal aberrations, such as del(17p) and del(11q), are considered predictors of poor clinical outcome[4]. The del(17p) aberration often results in the loss of the tumour protein p53 (TP53) gene, which plays a key role in the control of DNA damage, whereas del(11q) affects the ataxia-telangiectasia mutated (ATM) gene, which is essential for DNA repair. Identification of these chromosomal abnormalities is used for patient risk stratification and therapeutic decision-making. However, the presence or absence of molecular genetic aberrations alone is not sufficient for reliable prediction of individual risk profiles[3].

Tumour microenvironment support and T-cell dysfunction have long been recognised as key mediators of disease progression, together with the high degree of epigenetic heterogeneity underlying the diversity of CLL subtypes. Data accumulated in recent years have drawn attention to the role of metabolic reprogramming of CLL cells, which contributes to their increased proliferation and survival[5]. Metabolic reprogramming is associated with the activity of certain tumour suppressor regulators, particularly TP53 and ATM[6]. However, the relationship between chromosomal abnormalities leading to functional alterations in these genes and the routinely used panel of biochemical parameters has not been sufficiently studied[1].

According to several authors, oxidative stress (OS) is considered to play a role in the aetiology and progression of CLL[7]. OS represents a state of imbalance between processes generating reactive oxygen species (ROS) and those responsible for their elimination[8]. Overproduction of reactive oxygen metabolites that exceeds the capacity of the antioxidant defence system leads to oxidative damage of macromolecules and disruption of cellular signalling. Significantly higher concentrations of lipid peroxidation products[2,8,9], markers of protein oxidation[10,11], and oxidative DNA damage[9] have been observed in biological tissues and fluids of CLL patients. Elevated blood oxidative capacity has also been reported in newly diagnosed patients[4]. Furthermore, studies suggest that oxidative stress may contribute to genetic instability in CLL; however, its role in the acquisition of specific cytogenetic aberrations remains unclear[12].

The objective of the study was to investigate potential relationships among routine biochemical parameters, early and late products of oxidative damage, and unfavourable gene aberrations in patients with chronic lymphocytic leukaemia. Given the chronic and incurable nature of the disease, identification of a set of prognostic factors is important to enable more effective prediction and treatment.

Materialand methods

Study population

The study included a total of 39 individuals, divided into three groups: 10 healthy volunteers, 11 asymptomatic untreated patients with CLL, and 18 patients receiving targeted therapy (Venetoclax or Ibrutinib). Patient recruitment and screening were conducted between November 2024 and May 2025 at the Haematology Clinic of Dr Georgi Stranski University Hospital, Pleven, Bulgaria.

The inclusion criteria for the control group were clinically healthy individuals aged 50 years or older, with no family history of haematological or malignant diseases. The inclusion criteria for the patient groups were age over 18 years and a confirmed diagnosis of B-cell CLL, meeting established diagnostic criteria, with no history of previous treatment. Patient stratification was based on physical examination, imaging diagnostics, and standard laboratory tests. Disease stage was determined using the Binet staging system.

All participants were informed in advance about the objectives and procedures of the study and provided written informed consent. The study protocol was approved by the Ethics Committee of the Medical University of Pleven (approval no. 780/14.06.2024).

Biochemical blood analysis

Peripheral venous blood was collected from fasting participants into EDTA-containing vacutubes (10 mL; VWR, Austria). Samples were used for complete blood count analysis and for the determination of total cholesterol, triglycerides, and β2-microglobulin using standard laboratory methods.

Immunophenotyping of lymphocytes by flow cytometry

Immunophenotyping of peripheral blood lymphocytes was performed to confirm the diagnosis, using a panel of monoclonal antibodies against CD45, CD5, CD19, CD20, CD22, CD23, CD38, CD11a, CD49d, CD29, and CD200 (Immunostep).

Cytogenetic analysis

Fluorescence in situ hybridisation (FISH) analysis was carried out on interphase nuclei isolated from peripheral blood cells, according to the standard protocol of Vysis (Vysis®; Abbott Molecular). Locus-specific DNA probes were used to detect deletions involving

Table 1. Demographic, biochemical, and clinical characteristics of the study subjects

Indicators	*Patients*			*Control*
	All (n=29)	*Untreated* (n=11)	*Treated* (n=18)	(n=10)
Age [years], mean ± SD	66.6±2.0	69.8±2.7	64.7±2.6	57.4±2.9
Male sex, n (%)	15 (52)	5 (41)	10 (56)	3 (30)
Vascular risk factors				
Diabetes mellitus type 2, n (%)	3 (10)	1 (9)	2 (11)	
Hypertension, n (%)	19 (66)	9 (82)	10 (56)	
Binet staging system				
Stage A, n (%)	19 (66)	11 (100)	8 (44)	
Stage B+C, n (%)	10 (34)	0 (0)	10 (56)	
β2-microglobulin elevated (>2.4 or 3.1 mg/L), n(%)	14(64)	3(50)	11(69)	
WBC (×10^9/L), median (25^{th}-75^{th} percentile)	36.0 (21.5 – 52.5)	35.0 (23.0 – 45.0)	35.0 (20.0 – 86.3)	6.6 (5.8 – 7.3)
LYM (×10^9/L), median (25^{th}-75^{th} percentile)	33.0 (20.5 – 50.5)	33.0 (26.0 – 38.0)	38.5 (20.0 – 86.8)	2.0 (1.8 – 2.3)
Glucose, median (25^{th}-75^{th} percentile)	5.0 (5.0 – 6.9)	5.0 (5.0 – 7.1)	5.2 (4.6 – 6.8)	5.1 (4.3 – 5.2)
Triglycerides [mmol/L], mean ± SD	1.65 ± 0.59	1.41 ± 0.49	1.81 ± 0.61	1.09 ± 0.45
Total cholesterol [mmol/L], mean ± SD	5.28 ± 4.90	5.48 ± 4.89	5.17 ± 4.63	6.10 ± 5.63

Legend. LYM – lymphocytes; SD – standard deviation; WBC – white blood cells

the TP53, ATM, and DLEU1genes: Vysis TP53/CEP17 FISH Probe Kit, Vysis ATM/CEP11 FISH Probe Kit, and Vysis D13S319/13q34 FISH Probe Kit.

Determination of oxidative damage markers in serum

In parallel with routine laboratory tests, venous blood samples were obtained from fasting participants for serum separation. Serum samples were stored at –80°C until analysis. Oxidative damage markers were measured using colourimetric and enzyme-linked immunosorbent assay (ELISA)methods, performed in accordance with the manufacturers' instructions.

Prooxidant status of serum

Serum prooxidant status was assessed photometrically using the d-ROMs Test (Diacron International). This assay measures total hydroperoxide levels, including those derived from amino acids, peptides, nucleic acids, and hydrocarbons. Results are expressed in relative units (U.CARR), corresponding to 100 mg H_2O_2/mL.

Protein carbonyls

Protein carbonyl concentration, as a marker of protein oxidation, was determined in serum using an enzyme-linked immunosorbent ELISA with the OxiSelect™ Protein Carbonyl ELISA Kit (Elabscience). Results are expressed as mg/g protein.

Advanced oxidation protein products (AOPP)

Serum levels of advanced oxidation protein products (AOPP) were measured by ELISA using the Human Advanced Oxidation Protein Products ELISA Kit (Cloud-Clone Corp). Results are presented in μmol/L.

8-OHdG

Serum levels of 8-hydroxy-2'-deoxyguanosine (8-OHdG), a marker of oxidative DNA damage, were determined by ELISA using the 8-Hydroxydeoxyguanosine ELISA Kit (Elabscience). Results are expressed as mg/mL serum.

Statistical analysis

Statistical analysis was performed using the Statistical Package for the Social Sciences version 12.0 (SPSS Inc., Chicago, IL, USA). Continuous variables are presented as mean ± standard deviation or median (25^{th}–75^{th} percentile), depending on data distribution. Normality was assessed using the Shapiro–Wilk test. Differences between groups were analysed using Student's *t*-test or one-way ANOVA for normally distributed data, and the Mann–Whitney U test or Kruskal–Wallis test for non-normally distributed data. A p value < 0.05 was considered statistically significant.

Results

Basic characteristics of the study subjects

Demographic, clinical, and biochemical characteristics of the study participants, together with commonly accepted risk factors for oxidative stress, are summarised in Table 1. Of the 29 patients included in the study, 15 were men. The mean age of the control group was 57.4±2.9 years, whereas the mean age of the patient group was 66.6±2.0 years.

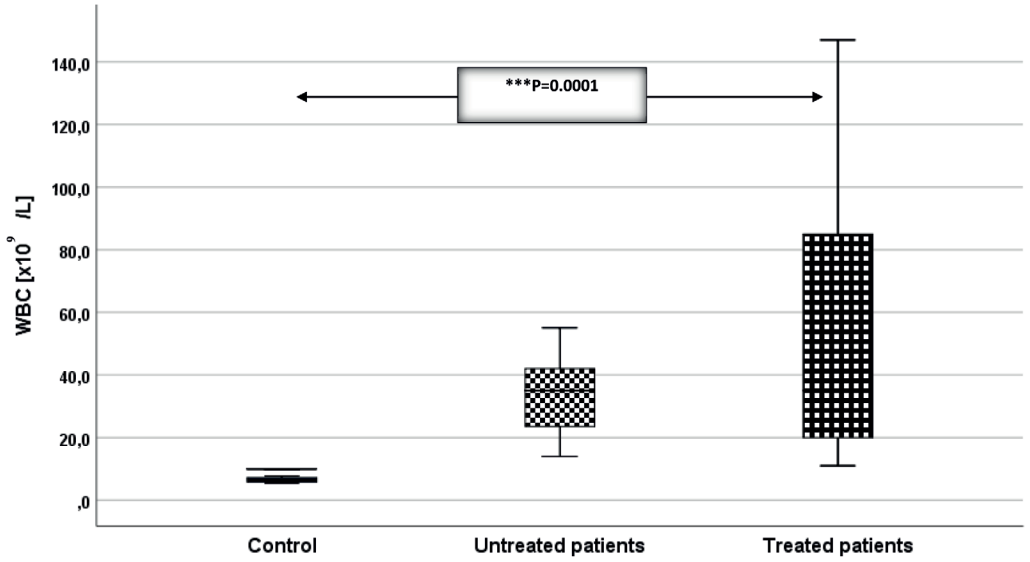


Fig. 1. Total leukocyte count by study groups. Data are presented as median (IQR).
The box represents IQR, the line within the box indicates the median, and whiskers extend to 1.5 × IQR.
Abbreviations: IQR – interquartile range; WBC – white blood cells.

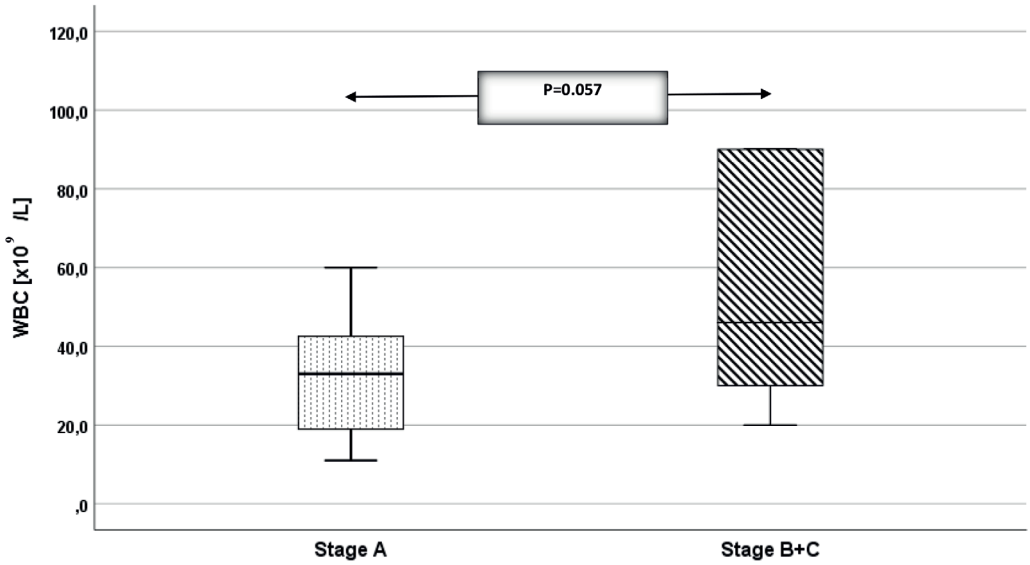


Fig. 2. Total leukocyte count according to disease stage. Data are presented as median (IQR).
The box represents IQR, the line within the box indicates the median, and whiskers extend to 1.5 × IQR.
The clinical stage was established in accordance with the Binet staging criteria.
Abbreviations: IQR – interquartile range; WBC – white blood cells.

Arterial hypertension was present in 66% of patients, and type 2 diabetes mellitus in 10%. Overall, 73% of patients had at least one concomitant disease. Staging according to the modified Binet classification showed that all asymptomatic, untreated patients were classified as stage A. Among treated patients, 44% were in stage A, while 56% were in stages B and C.

Biochemical blood indicators

Total white blood cell (WBC) count was a significant parameter among the studied groups (Kruskal–Wallis H=22.017, df=2, p=0.0001). Considerable variability in WBC counts was observed among patients receiving therapy (Fig. 1).A tendency toward higher total WBC counts was observed in patients with more advanced disease (Binet stages B+C compared to stage A); however, this difference did not reach statistical significance (Mann–Whitney U, z=–1.905, p = 0.057) (Fig. 2).

Mean triglyceride levels were significantly higher in patients compared with the control group (Student's t-test, t_{35}=–2.579, p=0.014) (Fig. 3). When analysed by subgroup, statistical significance was

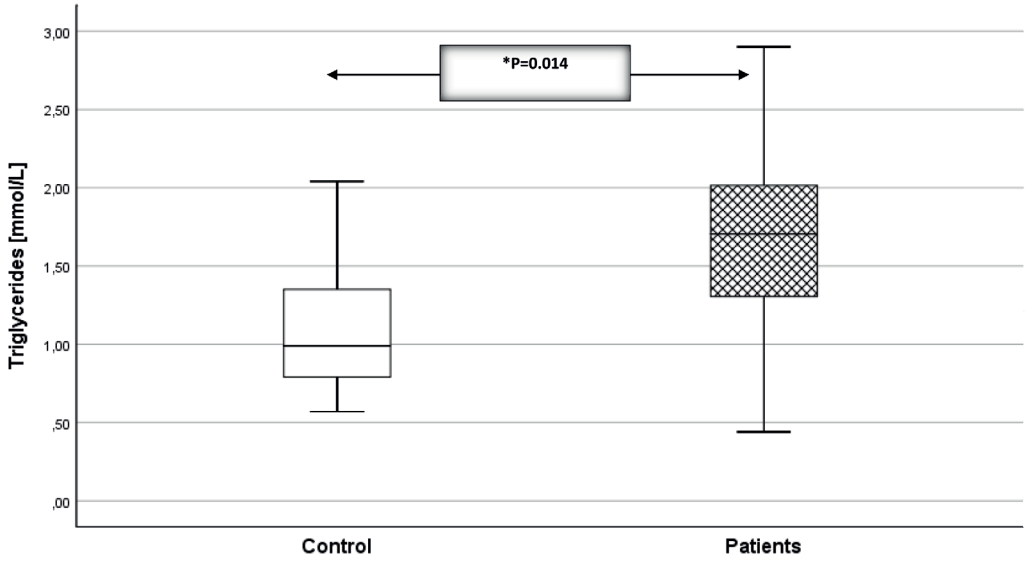


Fig. 3. Triglyceride levels in patients and controls. Data are presented as median (IQR).
The box represents IQR, the line within the box indicates the median, and whiskers extend to 1.5 × IQR.
Abbreviation: IQR – interquartile range.

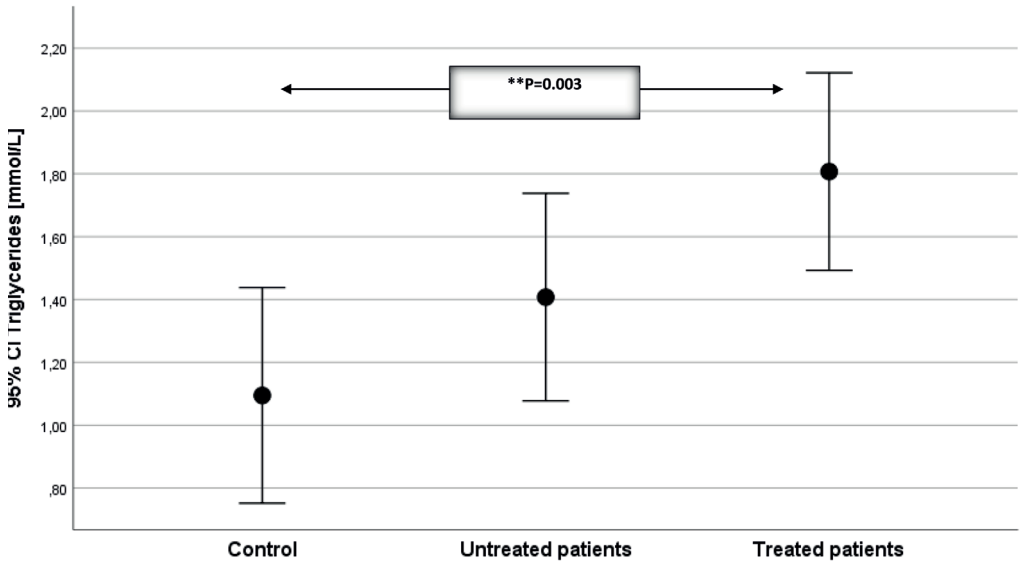


Fig. 4. Triglyceride levels by study groups. Values are expressed as mean with 95% confidence interval.
Abbreviation: CI – confidence interval

observed only between treated patients and controls (ANOVA, F=5.716, p=0.022; LSD post hoc test, p=0.003) (Fig. 4).

Arterial hypertension was associated with triglyceride levels (F=3.250, p=0.05). A significant difference in triglyceride concentration was observed between patients with hypertension and the control group (p=0.043) (Fig. 5). In addition, mean triglyceride levels were significantly higher in patients with del(17p) compared with those carrying del(11q) (Student's t-test, t_6=3.184, p=0.019) (Fig. 6).

Total cholesterol concentration was significantly higher in healthy controls than in patients with CLL (Student's t-test, t_{37}=–2.391, p=0.022) (Fig. 7). When analysed by group, this difference remained significant only between controls and treated patients (ANOVA, F=3.216, p=0.05; LSD post hoc test, p=0.016) (Fig. 8).

Products of oxidative damage

The concentrations of selected markers of oxidative damage to lipids, proteins, and DNA are presented in Table 2.

No statistically significant differences in oxidative damage markers were observed between patients and controls.

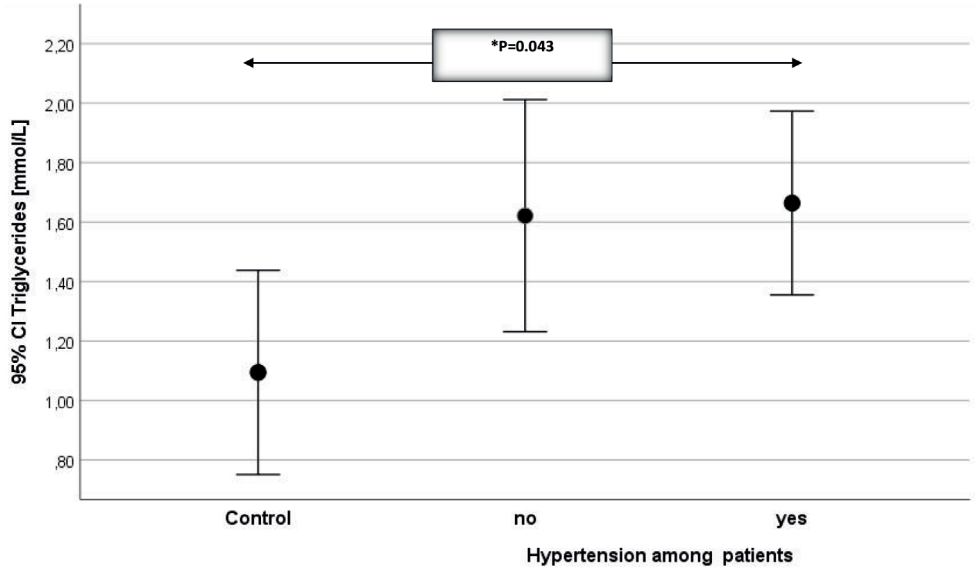


Fig. 5. Comparison of triglyceride levels by hypertension comorbidity. Values are expressed as mean with 95% confidence interval. *Abbreviation:* CI – confidence interval.

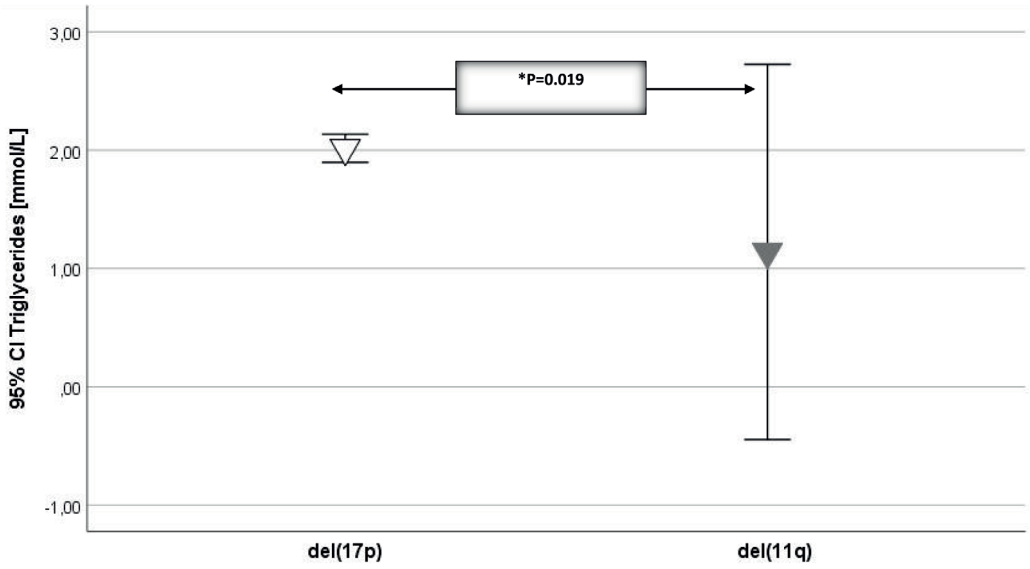


Fig. 6. Effect of cytogenetic aberrations on triglyceride concentration. Values are expressed as mean with 95% confidence interval. *Abbreviations:* del(11q) – deletion of the long arm of chromosome 11; del(17p) – deletion of the short arm of chromosome 17; CI – confidence interval.

Table 2. Levels of biomarkers of oxidative damage

Markers of oxidative damage	*Patients*			*Control*
	All (*n = 29*)	*Asymptomatic* (*n = 11*)	*Treated* (*n = 18*)	(*n = 10*)
Prooxidant status of serum [mg HOOH/dL], mean ± SD	27.61 ± 25.750	28.50 ± 25.24	27.00 ± 24.52	23.82 ± 20.39
AOOP [µmol/L], median (25^{th}-75^{th} percentile)	775 (480–1055)	936 (823–1154)	701 (489–967)	1028 (823–1154)
Protein carbonils [pmol/g protein], median (25^{th}-75^{th} percentile)	0.86 (0.37–1.56)	0.88 (0.36–1.50)	0.80 (0.37–1.67)	1.32 (0.96–1.43)
8-OHdG [g/L], median (25^{th}-75^{th} percentile)	14.39 (10.00–29.40)	23.86 (8.00–34.02)	13.32 (8.88–21.87)	18.70 (11.71–50.93)

Legend. AOPP – advanced oxidation protein products; 8-OHdG –8-hydroxy-2'-deoxyguanosine

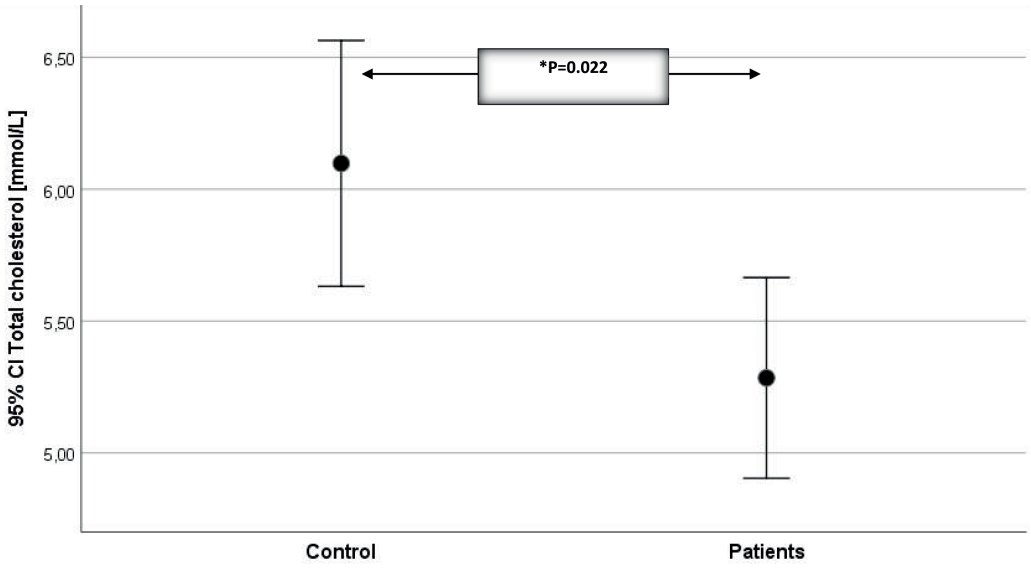


Fig. 7. Cholesterol levels in patients and controls. Values are expressed as mean with 95% confidence interval. *Abbreviation:* CI – confidence interval.

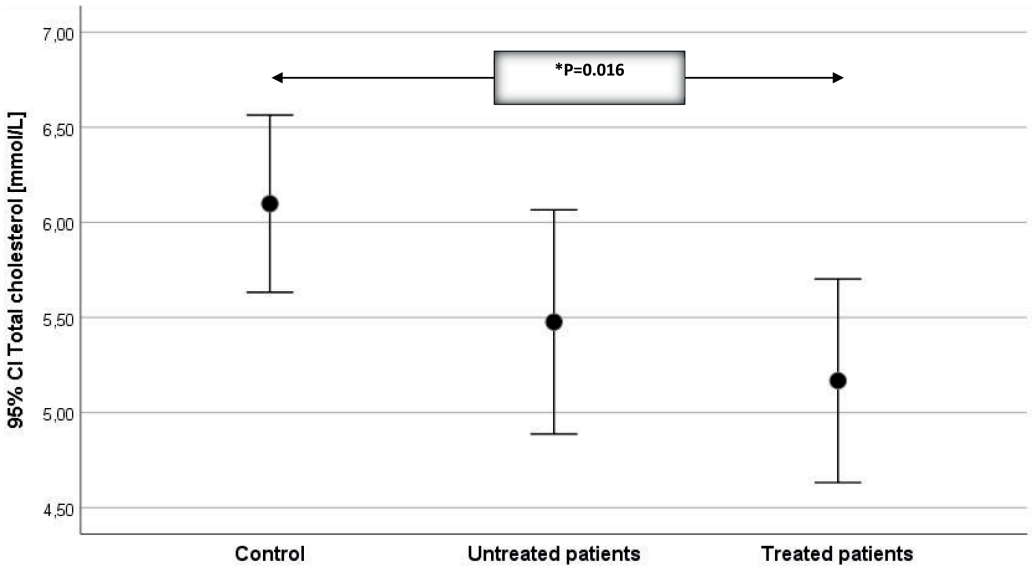


Fig. 8. Cholesterol levels by study groups. Values are expressed as mean with 95% confidence interval. *Abbreviation:* CI – confidence interval.

However, serum protein carbonyl levels were significantly higher in patients carrying the del(17p) chromosomal aberration compared with patients without this deletion (Mann–Whitney U, z=–2.4925, p=0.013) (Fig. 9).

Discussion

The key findings of the present study, in line with the stated objective, include significantly higher serum triglyceride levels in patients with del(17p) compared with those harboring del(11q), as well as elevated serum protein carbonyl levels in patients with del(17p) relative to patients without this aberration. These differences define distinct lipid profiles in the two high-risk cytogenetic groups and likely reflect more pronounced metabolic disturbances and a more aggressive disease course in patients with del(17p) compared to those with del(11q).

Deletion of 17p is known to be associated with loss of function of TP53, whereas deletion of 11q involves ATM gene. These genetic alterations may underlie differences in CLL pathogenesis between the two subgroups[25]. Accumulating evidence indicates that both TP53 and ATM play key roles in regulating the metabolic reprogramming of CLL cells during

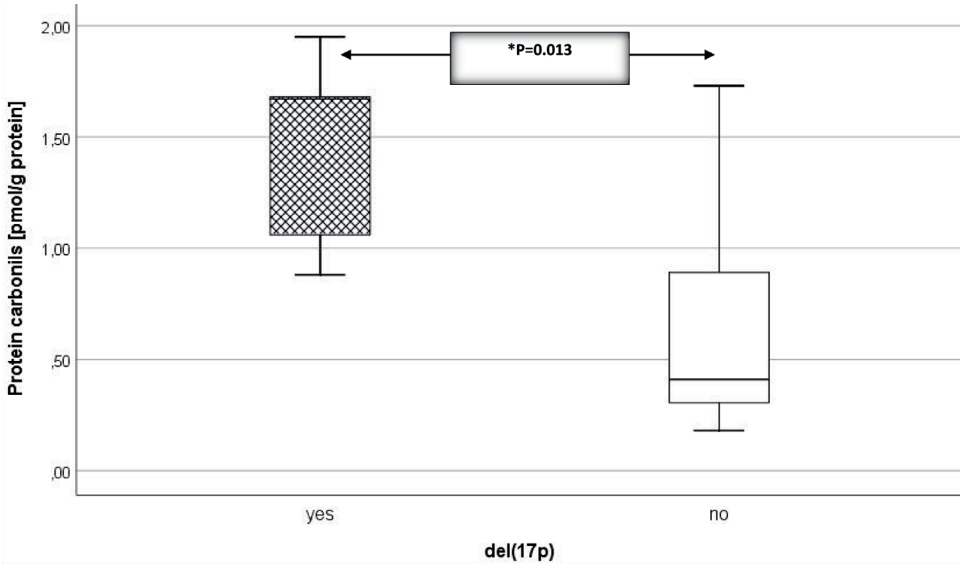


Fig. 9. Effect of del(17p) on serum protein carbonyl levels of CLL patients. Data are presented as median (IQR). |The box represents IQR, the line within the box indicates the median, and whiskers extend to 1.5 × IQR.
Abbreviations: del(17p) – deletion of the short arm of chromosome 17; IQR – interquartile range.

disease progression[6]. Nevertheless, the relationship between specific chromosomal aberrations and biochemical markers of lipid metabolism in CLL remains insufficiently explored.

While earlier studies have shown no significant difference in serum triglyceride levels between newly diagnosed CLL patients and healthy individuals[14,15], our findings reveal significantly elevated triglyceride levels in CLL patients. These results are consistent with those reported by Zaini et al.[16]. The observed increase may be indicative of impaired lipid metabolism resulting from an imbalance between triglyceride synthesis and utilization.

From a clinical perspective, elevated triglyceride levels are associated with increased cardiovascular risk, and arterial hypertension is one of the most common contributing factors[17]. A cumulative analysis demonstrated that arterial hypertension is present in 47–66% of patients at the time of CLL diagnosis, while its incidence after treatment initiation is relatively low (4%)[18]. Consistent with these observations, our findings revealed a statistically significant difference in triglyceride levels between hypertensive CLL patients and controls, indicating that hypertension may contribute to altered lipid metabolism in CLL.

The significant difference in triglyceride concentrations between patients undergoing treatment and the control group raises the possibility that targeted therapies in CLL may contribute to changes in lipid profiles. Previous reports suggest that Bruton tyrosine kinase inhibitors may affect lipoprotein metabolism, potentially leading to alterations in serum lipid parameters[19].

Although serum triglyceride levels are not used as stand-alone diagnostic parameters in CLL due to their variability and limited specificity, lipid parameters–particularly cholesterol–have gained attention for their prognostic relevance. Studies have shown that the addition of serum cholesterol levels to the CLL-IPI index improves its prognostic performance[20]. Lower total cholesterol at diagnosis has been linked to adverse outcomes, while higher post-treatment levels may reflect improved therapeutic response[20].

Consistent with prior reports[14,15], our findings indicate a tendency toward lower total cholesterol levels in CLL patients compared with healthy individuals, although statistical significance was observed only in treated patients. Reduced cholesterol levels in CLL have been attributed to altered expression of genes regulating lipoprotein hydrolysis, synthesis, and uptake by CLL cells, resulting in changes in circulating lipid levels[15,21]. Importantly, the complex interplay of metabolic pathways in CLL limits straightforward interpretation of lipid profile alterations.

In the present study, markers of both early and late oxidative damage–PC, AOPP, 8-oxo-dG, and serum prooxidant capacity–were measured to evaluate oxidative stress in CLL patients. No significant differences were detected between patients and the control group. These results differ from several reports in the literature demonstrating higher serum levels of PC[22,23], AOPP[24], and prooxidant capacity[4] in CLL patients compared with healthy volunteers.

Analysis of cytogenetic subgroups revealed significantly elevated serum protein carbonyl levels in patients harboring del(17p) compared with those lacking

this aberration. This increase likely reflects enhanced oxidative damage resulting from loss of p53 function, a key regulator of DNA and protein repair pathways[25]. Disruption of these mechanisms promotes genetic instability, which may further amplify OS and aggravate cellular damage. Accordingly, del(17p) is consistently recognized as the cytogenetic abnormality associated with the poorest clinical prognosis[25].

Although the interplay between OS and cytogenetic abnormalities in CLL remains incompletely characterized, accumulating evidence indicates higher systemic pro-oxidant capacity in patients with adverse chromosomal alterations, particularly del(17p) and del(11q), compared with those exhibiting normal FISH profiles[4]. In line with these findings, increased oxidative stress has been reported in patients with del(17p) relative to those without del(11q), del(13q), or trisomy 12, as reflected by elevated serum malondialdehyde levels[2,9].

Consistent with previous reports, patients with CLL exhibited significantly higher leukocyte counts compared with the control group[14,15,27]. Our data further indicate a trend toward increased peripheral blood leukocyte counts in patients with more advanced disease stages (B and C) relative to those with early-stage disease (A). This observation may be of clinical relevance, as it potentially reflects a more aggressive disease phenotype in patients with intermediate and advanced stages.

Nevertheless, it should be emphasized that elevated white blood cell counts alone do not invariably predict adverse clinical outcomes and should be interpreted in conjunction with other clinical and biological parameters[27].

Conclusions

Patients with CLL exhibit altered serum triglyceride and total cholesterol levels compared with healthy controls, indicating disturbances in lipid metabolism. The observation of higher triglyceride concentrations in patients with del(17p) compared with those harboring del(11q), together with increased serum protein carbonyl levels relative to patients without del(17p), suggests a less favorable clinical profile associated with this cytogenetic subgroup. Our results indicate that del(17p) CLL is characterized by distinct metabolic and oxidative stress features that may underlie its unfavorable clinical behavior.

However, the present study is limited by sample size and design and does not allow definitive conclusions regarding the associations between biochemical parameters, markers of oxidative damage, and the chromosomal aberrations del(17p) and del(11q). Larger, well-designed studies are warranted to clarify these relationships and to determine their potential prognostic and clinical significance.

Author Contributions

V.S.P., M.L.A. and M.A.A. participated in the conception and design of the study, analysis of the data; M.A.A., V.R.V, S.O.B. and T.H.L. recorded the data and made computer analysis of recorded parameters; M.L.A. made statistical analysis and presented figures, M.L.A., V.S.P and V.R.V. wrote the manuscript. All the authors have read and agreed with the final version of the article.

Compliance with Ethics Requirements

"The authors declare no conflict of interest regarding this article"

"The authors declare that all the procedures and experiments of this study respect the ethical standards in the Helsinki Declaration of 1975, as revised in 2008(5), as well as the national law. Informed consent was obtained from all the patients included in the study"

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References

1. Hallek M. Chronic lymphocytic leukemia: 2025 update on the epidemiology, pathogenesis, diagnosis, and therapy. *American Journal of Hematology* 2025;100(3):450–480.
2. Zhevak T, Shelekhova T, Chesnokova N, et al. The relationship between oxidative stress and cytogenetic abnormalities in B-cell chronic lymphocytic leukemia. *Experimental and Molecular Pathology* 2020;11(116):104524.
3. Mollstedt J, Mansouri L, Rosenquist R. Precision diagnostics in chronic lymphocytic leukemia: Past, present and future. *Frontiers in Oncology* 2023;13:11464-86.
4. D'Arena G, Seneca E, Migliaccio I, et al. Oxidative stress in chronic lymphocytic leukemia: still a matter of debate. *Leukemia & Lymphoma* 2018; 60(4):867–875.
5. Hacken TE, Eichhorst B. Updates on the biology of chronic lymphocytic leukemia: introductory editorial. *Seminars in Hematology* 2024;61(3):139-141.
6. Nie Y, Yun X, Zhang Y, Wang X. Targeting metabolic reprogramming in chronic lymphocytic leukemia. *Expeperental Hematology and Oncology* 2022;11(1):39.
7. Tannoury M, Garnier D, Susin SA, Bauvois B. Current status of novel agents for the treatment of B cell malignancies: What's coming next? *Cancers* 2022;14(24):6026.
8. Ortin X, Giraltb M, Romeub M, et al. Oxidative stress in patients with early-stage chronic lymphocytic leukemia, assessment and correlation with prognostic factors. *Journal in Hematology* 2012;1(4-5):77-88.
9. Collado R, Ivars D, Oliver I, et al. Increased oxidative damage associated with unfavorable cytogenetic subgroups in chronic lymphocytic leukemia. *BioMed Research International* 2014:686392-7.

10. Chaudhary P, Janmeda P, Docea AO, et al. Oxidative stress, free radicals and antioxidants: potential crosstalk in the pathophysiology of human diseases. *Frontiers in Chemistry* 2023;11(6):158-198.
11. Jové M, Mota-Martorell N, Pradas I, Martín-Gari M, Ayala V, Pamplona R. The advanced lipoxidation end-product malondialdehyde-lysine in aging and longevity. *Antioxidants* 2020;9(11):11-32.
12. Puiggros A, Blanco G, Espinet B. Genetic abnormalities in chronic lymphocytic leukemia: where we are and where we go. *Biomedical Research International* 2014;435983.
13. Parrales A, Iwakuma T. p53 as a regulator of lipid metabolism in cancer. *International Journal of Molecular Sciences* 2016;17(12):2074.
14. Sakashita M, BydlowskiP. Chamone A, et al. Plasma kinetics of an artificial emulsion resembling cholesterol levels and chronic lymphocytic leukemia. *Journal of the National Medical Association Chylomicrons in Patients with Chronic Lymphocytic Leukemia. Ann Hematol* 2016; 79(12):687e690.
15. Yavasoglu I, Sargin G, Yilmaz F, et al. Cholesterol levels in patients with chronic lymphocytic leukemia. *Jornal of the National Medical Association* 2017;109(1):23-27.
16. Zaini RG, Dahlawi H, Althobyani A, Alzhrani A, AlqahtaniF, Althubaiti M. Cholesterol and triglyceride abnormalities in newly diagnosed patients with acute and chronic leukaemia.*International Review of Basic and Applied Sciences* 2022;10(1):57-62.
17. Goto K. Triglyceride, an independent risk factor for new-onset hypertension: aperspective. *Endocrine, Metabolic & Immune Disord Drug Targets* 2023;23(12):1483-1490.
18. Ferrajoli A, Follows G, Marmor Y, et al. Cumulative review of hypertension in patients with chronic lymphocytic leukemia treated with acalabrutinib. *Haematologica* 2025;110(3):744-748.
19. Galitzia A, Maccaferri M, Mauro FR, Murru R, Marasca R. Chronic lymphocytic leukemia: management of adverse events in the era of targeted agents. *Cancers (Basel)* 2024;16(11):1996.
20. Gao R, Du K, Liang J, et al. Low serum cholesterol level is a significant prognostic factor that improves CLL-IPI in chronic lymphocytic leukaemia. *Internatiol Journal of Molecular Scinces* 2023;24(8):7396.
21. Stefaniuk P, Onyszczuk J, Szymczyk A, Podhorecka M. Therapeutic options for patients with TP53 deficient chronic lymphocytic leukemia: narrative review. *Cancer Management of Research* 2021;13:1459–1476.
22. Musolino C, Allegra A, Alonci A, et al. Carbonyl group serum levels are associated with CD38 expression in patients with B chronic lymphocytic leukemia. *Clinical Biochemistry* 2011;44(17-18):1487-90.
23. Sabry SA, El-Senduny FF, Abousamra NK, Salah El-Din M, Youssef MM. Oxidative stress in chronic lymphocytic leukemia patients leads to activation of Th9 cells: an experimental and comprehensive survey. *Immunological Medicine* 2020;43(1):36–46.
24. Gangemi S, Allegra A, Aguennouz M, et al. Relationship between advanced oxidation protein products, advanced glycation end products, and s-nitrosylated proteins with biological risk and MDR-1 polymorphisms in patients affected by B-chronic lymphocytic leukemia. *Cancer Invest* 2012;30(1):20-6.
25. Xu B, Maimaitijiang A, Nuerbiyamu D, Su Z, Li W. The multifaceted role of p53 in cancer molecular biology. Insights for precision diagnosis and therapeutic breakthroughs. *Biomolecules* 2025;15(8):1088.
26. Döhner H, Stilgenbauer S, Döhner K, Bentz M, Lichter P. Chromosome aberrations in B-cell chronic lymphocytic leukemia: reassessment based on molecular cytogenetic analysis. *Journal of Molecular Medicine* 1999; 77(2):266-81.
27. Silverman JA, Franssen E, Buckstein R, Imrie KR. The development of marked elevation in white blood cell count does not predict inferior outcome in chronic lymphocytic leukemia. *Leukemia & Lymphoma* 2002;43(6):1245-51.