

## Original Article

### The Impact of Pre-transplant Cell-free DNA Levels on Leukemia Relapse and Transplant Related Complications in Allogeneic Hematopoietic Stem Cell Transplant Recipients

#### Yeğin et al. Impact of cfDNA on Transplant Outcome

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**Background:** Cell free DNA (cfDNA), which may be considered as “liquid” biopsy, may serve as a diagnostic and prognostic marker not only in hematological malignancies but in solid tumors as well.

**Aims:** The aim of this study is to investigate the prognostic role of pre-transplant cfDNA levels in allogeneic hematopoietic stem cell transplant (allo-HSCT) recipients.

**Study Design:** This study is a retrospective cohort study.

**Methods:** A total of 177 allo-HSCT recipients [ median age: 36(16-66) years; male/female: 111/66] with an initial diagnosis of acute leukemia were included in the study. Cell free DNA was extracted from pre-transplant serum samples using the MagNA Pure Compact Nucleic Acid Isolation Kit I with the MagNA Pure Compact instrument (Roche Diagnostics, Penzberg, Germany).

**Results:** A positive correlation was demonstrated between cfDNA and age ( $p=0.018$ ;  $r=0.177$ ). Pre-transplant cfDNA levels were found to be lower in bcr-abl (+) patients ( $p=0.001$ ), whilst an adverse correlation was indicated between cfDNA and bcr-abl levels ( $p=0.001$ ;  $r=-0.531$ ). Akut lymphoblastic leukemia patients with bcr-abl positivity ( $p=0.001$ ) or abnormal cytogenetics ( $p=0.038$ ) represented significantly lower pre-transplant cfDNA levels. Cell free DNA levels were lower in patients who developed sinusoidal obstruction syndrome ( $p=0.035$ ). In terms of long term complications, acute myeloid leukemia patients who experienced post-transplant relapse had significantly lower pre-transplant cfDNA levels ( $p=0.024$ ). Overall survival was not statistically different between high- and low-cfDNA groups (45.2% vs 22.5;  $p=0.821$ ).

**Conclusion:** In general, lower serum levels of pre-transplant cfDNA seem to be associated with transplant related morbidities and may be considered as an adverse prognostic factor for allo-HSCT recipients.

**Keywords:** acute lymphoblastic leukemia, acute myeloid leukemia, allogeneic hematopoietic stem cell transplantation, cell free DNA

Hematological malignancies may be considered as “liquid” tumors, since the primary involved sites are bone marrow and lymphoid tissues, along with neoplastic cells circulating in the peripheral blood (1). The amount of cell free deoxyribonucleic acid (cfDNA) was found to be increased in patients with hematological malignancies besides a variety of solid tumors. Circulating cfDNA may sustain genetic characteristics of the tumor as cancer specific mutations were demonstrated in the circulating cfDNA of akut myeloid leukemia (AML) and myelodysplastic syndrome (MDS) patients. In addition, tumor associated micro-ribonucleic acids (RNA) were identified in the peripheral blood of lymphoma patients (2,3). Circulating cfDNA, which may be described as “liquid” biopsy, is currently introduced as a diagnostic marker as it provides a typical representation of tumor genetic profile and has a feasible role in minimal residual disease (MRD) determination which makes it a potential predictor of prognosis (2,4-7).

Cell free DNA is composed of extracellular DNA fragments which are released from the cells as a result of necrosis or apoptosis. In healthy individuals, cfDNA is a product of physiological hematopoietic cell cycle

including myeloid and lymphoid apoptotic cells, whereas in cancer patients, only a small amount of total cfDNA is originated from neoplastic cells. The wide range of this circulating tumor DNA fraction, which differs between 0.01% and 60% of total cfDNA, depends on several tumoral features including volume, stage, vascularization, proliferation and apoptosis rate (1,2,4,7-9).

To date, the predictor role of cfDNA was demonstrated in a wide spectrum of malignancies including hematological disorders such as AML, MDS and lymphoid neoplasms (2). In particular, this study was performed in order to evaluate the potential prognostic role of pre-transplant cfDNA levels in the development of transplant related complications and survival in allogeneic hematopoietic stem cell transplantation (allo-HSCT) recipients.

#### **MATERIAL AND METHODS**

The study cohort was composed of 177 acute leukemia patients who underwent allo-HSCT. Participants were classified into two subgroups for comparable statistical analysis, which were denominated as high and low-cfDNA groups, based on median cfDNA level which was considered to be 8.5(3.7-56.6) ng/□L. Patient demographics and transplant characteristics are represented in Table 1 & 2.

Pre-transplant serum samples were stored at -80°C until the assay. Cell free DNA was obtained from the serum based on the manufacturer's instructions using MagNA Pure Compact Nucleic Acid Isolation Kit I and instrument (Roche Diagnostics, Penzberg, Germany). Four hundred microliters of serum specimen were used as the starting volume and the nucleic acids were eluted in 100 µL of the supplied elution buffer. Cell free DNA concentration, which is expressed in ng/µL, was measured at 260 nm and the purity was measured using the 260/280 ratio by Thermo Scientific™ NanoDrop Lite Spectrophotometer.

Median pre-transplant cfDNA level was found to be 8.5(3.7-56.6) ng/□L whereas simultaneous measurement of white blood cell (WBC) count yielded a median of 4.6(0.3-17.7)×10<sup>9</sup>/L in the whole population. As WBC counts may interfere with cfDNA analysis, we performed a comparative analysis and did not find any significant statistical correlation between cfDNA levels and WBC counts. White blood cell counts were similar in high- and low-cfDNA groups, therefore additional processing such as logarithmic transformation was not required for statistical analysis.

#### **Statistical analysis**

All 177 subjects had valid cfDNA data with a mean serum level of 9.576 ng/□L. Based on a standard deviation of 5.857, the standard error was estimated to be 0.440. The lower and upper boundaries of the 95% confidence interval (CI) were identified to be between 8.707 and 10.444 (p<0.001). The 95% CIs for cumulative survival were determined to be between -8.325 and 10.483 (p=0.821). The statistical power of the study was indicated to be 95.23% on post hoc analysis.

Shapiro Wilk test was performed for normality analysis. Parametric and non-parametric tests were used in case of normal and abnormal distribution respectively. For normal distributed groups, equality and homogeneity of variances were analysed by Levene's test through One Way Anova and Student T Tests. Comparison of continuous variables was performed by Student T test for normal distribution, whereas Mann Whitney U and Kruskal Wallis tests were used for abnormal distributed parameters. Categorical variables were analyzed by Chi-square test. Correlations were determined by Pearson and Spearman tests for normal and abnormal distributed data respectively. Survival analysis was performed using Kaplan Meier test. Cox regression and log rank tests were used for the assessment of risk factors which were significantly associated with survival. The statistical threshold for significance was considered to be p<0.05 on SPSS 22.0 programme (SPSS Inc, Chicago, IL, USA).

#### **Ethical Standards**

The study was certified by the institutional ethics board of Gazi University Faculty of Medicine (Date: 12.02.2018; Number: 106). The procedures in the study were consistent with the Helsinki declaration and informed consents were taken from all participants.

#### **RESULTS**

Median cfDNA levels did not statistically differ in terms of gender, primary diagnosis, extramedullary leukemia, cytogenetics including fms like tyrosine kinase 3 (FLT3), nucleophosmin (NPM-1), AML1-ETO (RUNX1/RUX1T1), inv16 (CBFB/MYH11) and complex karyotype, pre-transplant disease status, development of mucositis, peri-engraftment infections, cytomegalovirus (CMV) reactivation, thrombotic microangiopathy (TMA), graft versus host disease (GvHD) and relapse (p>0.05). Early and late transplant complications are detailed in Table 3.

Patients who represented bcr-abl positivity had significantly lower cfDNA levels than bcr-abl (-) patients [ 7.5(5.4-12.1) vs 9.5(7-13.4) ng/□L; p=0.001] . A negative correlation was identified between bcr-abl status and cfDNA amount (p=0.001; r=-0.531). Patients with sinusoidal obstruction syndrome (SOS) had lower levels of cfDNA compared to patients who did not develop SOS [ 7.7(4.7-15.3) vs 8.8(5.2-56.6) ng/□L; p=0.035] . In addition, a tendency to SOS was observed in patients who had lower pre-transplant cfDNA levels (p=0.049). There was an adverse relationship between cfDNA amount and SOS development (p=0.035; r=-0.163). Cytomegalovirus reactivation was also more frequent in patients with lower pre-transplant cfDNA levels, without statistical significance (p=0.065).

Peri-transplant infections were evaluated in 153 patients. Febrile neutropenia was demonstrated in 134 patients (87.6%). Thirty seven patients (27.6%) had catheter related infections, 19 patients (14.2%) bloodstream infections, 15 patients (11.2%) urinary tract infections, 11 patients (8.2%) had pneumonia and 21 patients (15.7%) had other types of infections. In a total of 31 patients (23.1%) the site of infection or microbiological documentation were not identified. Seven patients developed invasive fungal infection. Any significant association was not indicated between cfDNA levels and infectious complications.

Median age was identified to be higher in high-cfDNA group compared to low-cfDNA group [41(18-65) years vs 29(16-66) years;  $p=0.03$ ]. There was a positive correlation between age and pre-transplant cfDNA levels ( $p=0.018$ ;  $r=0.177$ ). Neutrophil and platelet engraftment days, chimerism values, frequency of SOS, mucositis, TMA, infectious morbidity, hemorrhagic cystitis, acute/chronic GvHD and post-transplant relapse were not significantly different among high- and low-cfDNA groups ( $p>0.05$ ). The total number of febrile days were fewer in patients with high cfDNA levels than low-cfDNA group [2(0-15) days vs 3(0-18) days;  $p=0.073$ ]. In the subgroup analysis of AML patients, significantly lower pre-transplant cfDNA levels were observed in the course of post-transplant relapse when compared to those who stayed in remission [8(5.2-11.5) vs 9.6(3.7-14.5) ng/ $\mu$ L;  $p=0.024$ ] (Figure 1). No significant association was observed between cfDNA levels and cytogenetical features including complex karyotype and the mutational status of FLT3, NPM-1, AML1-ETO (RUNX1/RUX1T1) and inv16 (CBFB/MYH11).

In acute lymphoblastic leukemia (ALL) group, bcr-abl (+) patients had significantly lower pre-transplant cfDNA levels than bcr-abl (-) patients [7.5(5.4-12.1) vs 9.7(7-13.4) ng/ $\mu$ L;  $p=0.001$ ] (Figure 2). Similarly, cfDNA levels were found to be lower in patients who represented with abnormal cytogenetics compared to patients with normal karyotype [7.9(5.4-12.5) vs 10.1(7-13.4) ng/ $\mu$ L;  $p=0.038$ ]. Sinusoidal obstruction syndrome was observed more frequent in the low-cfDNA group ( $p=0.019$ ).

Overall survival (OS) was 15.3% in the whole population at the the end of 14.6(0.2-160.9) months of follow-up. Overall survival was not statistically different between high- and low-cfDNA groups (45.2% vs 22.5%;  $p=0.821$ ) (Figure 3).

In univariate Cox regression analysis; primary diagnosis ( $p=0.042$ ), pre-transplant disease status ( $p=0.004$ ), SOS ( $p<0.001$ ), acute GvHD ( $p=0.001$ ), chronic GvHD ( $p<0.001$ ) and relapse ( $p<0.001$ ) were shown to have significant impact on OS. The significance was confirmed for primary diagnosis ( $p=0.042$ ), SOS ( $p<0.001$ ), acute GvHD ( $p=0.001$ ), chronic GvHD ( $p=0.009$ ) and post-transplant relapse ( $p=0.003$ ) in multivariate Cox regression analysis. Pre-transplant cfDNA levels did not represent any significant impact on OS ( $p>0.05$ ).

## DISCUSSION

In this study, the prognostic role of pre-transplant cfDNA levels was investigated in allo-HSCT recipients with acute leukemia. A significant association was identified between cfDNA and age. Pre-transplant cfDNA levels were lower in bcr-abl (+) patients indicating an adverse correlation between cfDNA and bcr-abl levels. Acute lymphoblastic leukemia patients with bcr-abl positivity or abnormal cytogenetics represented significantly lower pre-transplant cfDNA levels. Cell free DNA levels were found to be lower in patients with SOS. In terms of long term complications, AML patients who represented post-transplant relapse had significantly lower pre-transplant cfDNA levels. Overall survival was not statistically different between high- and low-cfDNA groups. In general, lower serum levels of pre-transplant cfDNA seem to be associated with transplant related morbidities and may be considered as an adverse predictor of prognosis in allo-HSCT recipients.

The amount of cfDNA ranges between 10 to 100 ng/mL in healthy individuals and may be influenced by age, gender, food intake and diurnal variations. It can circulate as a single molecule or in a complex with cellular or non-cellular components in order to act as a signaling molecule. Besides several physiological states such as pregnancy and physical activity, pathological conditions including inflammation and autoimmune diseases may represent with elevated cfDNA levels. In cancer, cfDNA levels may be increased up to 1000 ng/mL which draws attention to an association between cfDNA levels and tumor burden (1,4,8,10-13). A previously reported association between age and cfDNA was confirmed in our study. Teo et al showed a remarkable consistence between nucleosome signals of cfDNA and redistribution of heterochromatin which has a role in cellular senescence and aging. In this perspective, cfDNA may be designated as a biomarker of age or a predictor of health status (14).

Circulating tumor DNA analysis requires distinctive attention due to its molecular properties including low concentration and high fragmentation rate as well as contamination potential with genomic DNA. It is essential to improve the methodologies of cfDNA based analysis as the appropriate source of cfDNA and technical details of sample processing have not been clarified (9). Serum levels of cfDNA are found to be 2-24 times more than plasma levels as a result of the contamination of genomic DNA which is considered as a product of WBC lysis during serum processing. As serum cfDNA levels are expected to be more variable than plasma levels, it was suggested that higher serum cfDNA levels may represent an indirect tumor-related process, whereas plasma levels may be a better indicator of in vivo circulating DNA (4-6,9,15,16). Alongside WBC count there are several factors which may affect cfDNA analysis such as individualized variations, diurnal rhythm, inflammatory responses and physical stimuli (1). Although sample preference would be considered as an

eventual limitation for the present study, we did not mean to discriminate the impact of WBCs on the entire process, considering the potential role of leukocytes in the leukemia microenvironment. From a global perspective, cfDNA may not only be a tumoral or genetic predictor, but also an indicator of inflammation and cytokine stimulation which is well known to be closely associated with leukocyte activation. The diversity in the methodologies of cfDNA analysis, compared to polymerase chain reaction or next generation sequencing, may be considered as a possible explanation for the contradictory results with the previous studies (5,17,18). Serum cfDNA levels were found to be incompatible with plasma levels in the previous reports. In a study by Thijssen et al which was performed in patients with colorectal cancer, serum cfDNA was significantly associated with the liver metastasis whereas plasma cfDNA was predictive for the recurrence (15). In concordance with our results, cfDNA levels were shown to be decreased in the sera of rheumatoid arthritis (RA) patients. On the contrary, several studies also stated elevated serum or plasma cfDNA levels in RA patients. Besides the physiopathological diversity of underlying autoimmune disorders and distinct stages of disease activity at the time of sampling, the role of the heterogeneous methods which were used in sample collection/processing, cfDNA extraction and quantification should be emphasized. This point of view, mainly based on the lack of uniformity and standardization of cfDNA analysis, may lead to a distinct perspective which may particularly elucidate the predictor impact of lower cfDNA levels in the present study (11-13).

Several studies underlined the predictor role of cfDNA in endotheliopathies which shows a significant association of cfDNA with endothelial markers including syndecan-1 and thrombomodulin (19,20). Endothelial dysfunction, which is indicated to be the major underlying physiopathological mechanism of SOS, may be a reasonable explanation for the association of SOS and pre-transplant cfDNA levels in the current study. However, the predictive role of lower cfDNA levels as well as its negative correlation with SOS require further evaluation. Sample preference and insufficient number of patients with SOS may partially help to elucidate the contradictory results. Simultaneous measures of cfDNA may be more informative for the clarification of the predictive role of cfDNA in the course of SOS.

Several infectious and inflammatory conditions may represent with elevated cfDNA levels which were shown to be correlated with disease severity and mortality (21,22). In addition, cfDNA was found to be associated with the degree of inflammation in viral infections (23). In consideration with these preliminary data, the insignificant association of cfDNA with CMV reactivation may earn further verification.

Cell free DNA levels were found to be elevated in various hematological disorders. High levels of cfDNA and DNA integrity index represented a lower probability of progression free survival in diffuse large B cell lymphoma (DLBCL) patients (8). Cell free DNA levels were shown to be increased in lymphoma patients and correlated with advanced age and stage, poor prognosis, B symptoms and lactate dehydrogenase levels (4,6,24). The amount of cfDNA was also higher in myeloma patients which was shown to be associated with progressive disease (4,25,26).

Several studies reported high cfDNA levels in acute leukemia patients. Cytogenetic and molecular abnormalities such as FLT3 and NPM-1 were identified in cfDNA, suggesting a feasible role for cfDNA in predicting AML prognosis and treatment indications (4). Gao et al found that not only cfDNA concentrations but also DNA integrity index were found to be elevated in patients with acute leukemia compared to healthy individuals. As DNA integrity index was shown to be correlated with disease status, its clinical utility for MRD assessment may also be considered (27). We did not observe any significant association of cfDNA with AML mutational status, however the adverse correlation of cfDNA with bcr-abl levels and abnormal cytogenetics in ALL patients should be confirmed with large and prospective studies.

Chimerism analysis may be performed in cfDNA in allo-HSCT recipients. Furthermore, as chimerism analysis of cfDNA was shown to predict early relapse in patients with hematological malignancies, monitoring allo-HSCT survivors with cfDNA could be feasible in predicting early relapse (28,29). Lymphoma patients were shown to have detectable cfDNA prior to progression after allo-HSCT (30). The impact of lower cfDNA levels on post-transplant relapse in AML patients requires further verification as well as its statistically insignificant impact on OS which may be associated with inadequate number of patients.

In conclusion, cfDNA, which can be considered as a non-invasive and repeatable analysis of genetic profiles, may serve a potential for diagnosis and prognosis assessment (2,7). Nevertheless, several issues remain to be solved including standardization of sample collecting, processing and lack of comparability due to inconsistent thresholds (7). We need further understanding of the biological features of cfDNA in order to determine its true physiological role.

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<b>TABLE 1. Patient and Disease Characteristics</b>	
<b>Age</b> [ median(range)] (years)	36 (16-66)
<b>Gender</b> [ n (%) ] (male/female)	111/66
<b>Diagnosis</b> [ n (%) ]	
Acute myeloid leukemia	99 (55.9)
Acute lymphoblastic leukemia	74 (41.8)
Mixed phenotype acute leukemia	3 (1.7)
Blastic plasmacytoid dendritic cell neoplasm	1 (0.6)
Therapy related acute leukemia	-
<b>Extramedullary disease</b> [ n (%) ]	17 (9.6)
<b>CNS involvement</b> [ n (%) ]	5 (2.8)
<b>Cytogenetics</b> [ n (%) ] (n=76)	
Normal	32 (42.1)
Abnormal	44 (57.9)
Complex Karyotype	10 (22.7)
Other	34 (77.3)
<b>FLT3 Mutational Status for AML</b> [ n (%) ] (n=19)	
Positive	-
Negative	19 (100)
<b>NPM-1 Mutational Status for AML</b> [ n (%) ] (n=20)	
Positive	13 (65)
Negative	7 (35)
<b>AML1-ETO (RUNX1/RUX1T1) for AML</b> [ n (%) ] (n=26)	
Positive	11 (42.3)
Negative	15 (57.7)
<b>Inv16 (CBFB/MYH11) for AML</b> [ n (%) ] (n=21)	
Positive	1 (4.8)
Negative	20 (95.2)
<b>Bcr-abl</b> [ n (%) ] (n=39)	
Positive	17 (43.6)
Negative	22 (56.4)

AML: acute myeloid leukemia, CNS: central nervous system, FLT3: fms like tyrosine kinase 3, NPM-1: nucleophosmin

<b>TABLE 2. Transplant characteristics</b>	
<b>Time to transplant</b> [ median(range)] (months)	5.6 (1-125.1)
<b>Pre-transplant disease status</b> [ n (%)]	
Complete remission	154 (87)
Partial remission	6 (3.4)
Refractory	17 (9.6)
<b>Donor type</b> [ n (%)]	
Related	144 (81.4)
Unrelated	30 (16.9)
Haploidentical	3 (1.7)
<b>HLA match status</b> [ n (%)]	
Full-matched	149 (84.2)
Mismatched	28 (15.8)
<b>Graft type</b> [ n (%)]	
Bone marrow	-
Peripheral blood	177 (100)
<b>Conditioning regimen</b> [ n (%)]	
Myeloablative	160 (90.4)
Reduced intensity	17 (9.6)
<b>Total body irradiation</b> [ n (%)]	68 (38.4)
<b>GvHD Prophylaxis</b> [ n (%)]	
Cyclosporine A + methotrexate	161 (91)
Cyclosporine A + mycophenolate mofetil	13 (7.3)
Cyclosporine A + methotrexate + ATG	3 (1.7)
<b>Defibrotide prophylaxis</b> [ n (%)]	36/177
<b>Number of febrile days</b> [ median(range)]	3 (0-18)
<b>Infused CD34<sup>+</sup> cells</b> [ median(range)] (10 <sup>6</sup> /kg)	4.4 (0.8-7.3)
<b>Neutrophil engraftment</b> [ median(range)] (days)	16 (0-30)
<b>Platelet engraftment</b> [ median(range)] (days)	14 (0-67)
ATG: antithymocyte globulin, GvHD: graft versus host disease	

<b>TABLE 3. Early and Late Complications</b>	
<b>Sinusoidal obstruction syndrome</b> [ n(%)]	41(23)
<b>Grade</b> [ median(range)]	1(0-4)
<b>Mucositis</b> [ n(%)]	163(92.1)
<b>Grade</b> [ median(range)]	2(1-4)
<b>Pre-engraftment infections</b> [ n(%)]	134(75.7)
<b>Thrombotic microangiopathy</b> [ n(%)] (in the first 100 days)	11(6.2)
<b>CMV reactivation</b> [ n(%)] (in the first 100 days)	51(28.8)
<b>Viral hemorrhagic cystitis</b> [ n(%)] (in the first 100 days)	25(14.1)
<b>Acute GvHD</b> [ n(%)]	71(40.1)
<b>Grade</b> [ median(range)]	2(1-4)
<b>Onset</b> [ median(range)] (days)	50(7-372)
<b>Sites</b> [ n(%)]	
Skin	36(50.7)
Liver	3(4.2)
Gastrointestinal tract	14(19.7)
More than one site	18(25.4)
<b>Chronic GvHD</b> [ n(%)]	67(37.8)
<b>Post-transplant lymphoproliferative disorder</b> [ n(%)]	1(0.6)
<b>Secondary malignancy</b> [ n(%)]	2(1.1)
<b>Graft failure</b> [ n(%)]	2(1.1)
<b>Relapse</b> [ n(%)]	63(35.6)
<b>Post-transplant day of relapse</b> [ median(range)]	117(30-1460)
CMV: cytomegalovirus, GvHD: graft versus host disease	

**Figure Legends:**

**FIG. 1.** Pre-transplant cfDNA levels were significantly lower in acute myeloid leukemia patients who experienced post-transplant relapse compared to the patients who stayed in remission (p=0.024).

**FIG. 2.** Pre-transplant cfDNA levels were significantly lower in bcr-abl(+) acute lymphoblastic leukemia patients compared to bcr-abl(-) patients (p=0.001).

**FIG. 3.** Overall survival was not statistically different between high- and low-cfDNA groups (45.2% vs 22.5%; p=0.821).