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blood advances

Cytokine profiling in 128 patients with transient abnormal myelopoiesis: a report from the JPLSG TAM-10 trial

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Key Points

- Unsupervised consensus clustering of cytokine profiles in 128 patients with TAM identified groups at higher risk for early death.
- Measurement of levels of cytokine provides valuable information for patients with TAM that may help determine therapeutic interventions.

Transient abnormal myelopoiesis (TAM) occurs in 10% of neonates with Down syndrome (DS). Although most patients show spontaneous resolution of TAM, early death occurs in ~20% of cases. Therefore, new biomarkers are needed to predict early death and determine therapeutic interventions. This study aimed to determine the association between clinical characteristics and cytokine levels in patients with TAM. A total of 128 patients with DS with TAM enrolled in the TAM-10 study conducted by the Japanese Pediatric Leukemia/Lymphoma Study Group were included in this study. Five cytokine levels (interleukin-1b [IL-1b], IL-1 receptor agonist, IL-6, IL-8, and IL-13) were significantly higher in patients with early death than in those with nonearly death. Cumulative incidence rates (CIRs) of early death were significantly associated with high levels of the 5 cytokines. Based on unsupervised consensus clustering, patients were classified into 3 cytokine groups: hot-1 (n = 37), hot-2 (n = 42), and cold (n = 49). The CIR of early death was significantly different between the cytokine groups (hot-1/2, n = 79; cold, n = 49; hot-1/2 CIR, 16.5% [95% confidence interval (CI), 7.9-24.2]; cold CIR, 2.0% [95% CI, 0.0-5.9]; P = .013). Furthermore, cytokine groups (hot-1/2 vs cold) were independent poor prognostic factors in the multivariable analysis for early death (hazard ratio, 15.53; 95% CI, 1.434-168.3; P = .024). These results provide valuable information that cytokine level measurement was useful in predicting early death in patients with TAM and might help to determine the need for therapeutic interventions. This trial was registered at UMIN Clinical Trials Registry as #UMIN000005418.

Introduction

Transient abnormal myelopoiesis (TAM), also known as transient leukemia or transient myeloproliferative disorder, is a unique clonal myeloproliferation characterized by immature megakaryoblasts. It occurs in

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The full-text version of this article contains a data supplement.

10% of neonates with Down syndrome (DS).[1] Although most patients show spontaneous resolution of TAM without therapeutic interventions, ~20% of TAM cases result in early death (death within 9 months), and ~20% of the survivors develop acute megakaryoblastic leukemia within 4 years.[2-6] Our previous reports showed that high white blood cell (WBC) count (≥100 × 10^9/L), systemic edema, low birth weight, preterm birth at <37 weeks of gestational age, and elevated direct bilirubin level >5 mg/dL were associated with early death.[2-6] Low-dose cytarabine (LDAC) is a common therapy for TAM. It has been reported that LDAC should be considered for patients with life-threatening symptoms and risk factors associated with early death.[7] Additionally, it has been reported that the LDAC intervention rate was adversely associated with the early death rate.[2] However, further studies are needed to determine the criteria for consensus therapeutic intervention.

Previous reports showed that cytokine levels are associated with liver failure, which is a cause of early death in patients with TAM.[8] Thus, cytokine levels can be new biomarkers to predict early death in patients with TAM. However, no large cohort data are available for cytokine analyses in patients with TAM. Thus, this study aimed to determine the association between clinical characteristics and cytokine levels in patients with TAM by analyzing 128 patients with DS with TAM enrolled in the TAM-10 prospective observational study conducted by the Japanese Pediatric Leukemia/Lymphoma Study Group (JPLSG).

Methods

Patients

A total of 167 neonates diagnosed with TAM were prospectively registered in the TAM-10 study between May 2011 and February 2014 conducted by the JPLSG of the Japan Children's Cancer Group. The TAM-10 study was registered with the University Hospital Medical Information Network (UMIN) Clinical Trials Registry

Table 1. Clinical characteristics of 128 patients with TAM

	All patients, N = 128	Patients with early death, n = 14	Patients without early death, n = 114	*P* value*
Sex (male:female)	64:64	9:5	55:59	.396
Median gestational age (range), wk	37 (29-40)	34 (29-38)	37 (31-40)	**.003**
Median birth weight (range), g	2588 (1438-3714)	2249 (1438-3044)	2624 (1598-3714)	**.035**
Median age at diagnosis (range), d	0 (0-8)	0 (0-8)	0 (0-8)	.854
Congenital heart disease, n (%)	87 (68)	5 (36)	82 (72)	**.012**
Other congenital abnormally, n (%)	14 (11)	2 (14)	12 (11)	.651
Chromosomal status, n				
Trisomy 21:mosaic trisomy 21:normal karyotype	126:1:1	14:0:0	112:1:1	1.000
Median WBC count at diagnosis (range), ×10^9/L	48.3 (4.7-478.7)	157.3 (14.3-238.5)	44.3 (4.7-478.7)	**.006**
Median blasts percentage in PB at diagnosis (range), %	41 (1-96)	60 (5-95)	37 (1-96)	.057
Direct bilirubin, median (range), mg/dL	0.8 (0-12.3)	1.0 (0.3-5.6)	0.7 (0-12.3)	.134
Hepatomegaly, median (range)†, cm	3 (0-8)	5 (0-8)	2 (0-7)	**.043**
Systemic edema, n (%)	26 (20)	11 (79)	15 (13)	**<.001**
Organ hemorrhage, n (%)	12 (9)	4 (29)	8 (7)	**.027**
Therapeutic interventions, n (%)	60 (47)	11 (79)	49 (43)	**.021**
LDAC, n (%)	46 (36)	6 (43)	40 (35)	.586
Exchange blood transfusion, n (%)	16 (13)	4 (29)	12 (11)	.076
Systemic steroid therapy, n (%)	24 (19)	8 (57)	16 (14)	**<.001**
Classification of *GATA1* mutation				
High-expression type mutation, n (%)	57 (45)	6 (43)	51 (45)	1.000
Low-expression type mutation, n (%)	58 (45)	6 (43)	52 (46)	1.000
Unclassified mutation, n (%)	12 (9)	2 (14)	10 (9)	.620
Negative, n (%)	1 (1)	0	1 (1)	1.000
Events‡, n (%)	42 (33)	14 (100)	28 (25)	**<.001**
Early deaths (age <9 mo), n (%)	14 (11)	14 (100)	0 (0)	**<.001**
Later phase deaths (after 9 mo), n (%)	5 (4)	0 (0)	5 (4)	1.000
Leukemia development, n (%)	23 (18)	0 (0)	23 (20)	.073

Bold indicates $P < 0.05$.
PB, peripheral blood.
**P* value was evaluated between patients with early death vs patients without nonearly death using Fisher exact test or Mann-Whitney *U* test.
†Under costal margin.
‡Events were defined by death or leukemia development.

(http://www.umin.ac.jp/ctr/index.htm, number UMIN000005418). The details of the eligibility criteria and the central review system, including the *GATA1* mutation analysis, are shown in the previous report.[2] Clinical data and sample collections in the clinical trials were approved by the institutional review boards of each participating institution. Written informed consent was obtained from all patients' parents/guardians. This study was conducted in accordance with the principles of the Declaration of Helsinki and approved by the ethical review board of the JPLSG. Cytokine levels were analyzed in 128 of the 167 patients for whom serum samples were available in the early postnatal period (days 0-8). A comparison of clinical characteristics between 128 and 39 patients with or without available samples, respectively, is shown in supplemental Table 1.

Cytokine analysis

Serum concentrations of the following 27 cytokines were determined using the Bio-Plex cytokine assay (Bio-Rad, Hercules, CA), measured using a Luminex System (Austin, TX), and quantified using Bio-Plex software (Bio-Rad).[9] The details of 27 cytokines are described in supplemental Table 2. Serum samples were frozen at −80°C immediately after collection and stored until analysis. Each sample was analyzed twice. The mean values of measurements were used as representative values for each subject.

Statistical analysis

Optimal cutoff values for biomarkers were determined using the Youden index of the receiver operator characteristic curve based on logistic regression analyses. The association between the covariates and early death (<9 months of age) was evaluated in univariable and multivariable Cox proportional hazard models using the stepwise Akaike information criterion method. Between-group comparisons were performed using the Mann-Whitney *U* test or Fisher exact test, as appropriate. Differences in cytokine levels between groups were determined using the Mann-Whitney *U* test. A correction for multiple testing was performed using the Benjamini-Hochberg method with the threshold *P* value set at $< .05$.

Cluster analysis was performed by 2-step unsupervised consensus clustering of 27 cytokine variables. Five cytokines (interleukin-2 [IL-2], IL-12, IL-15, IL-17, and RANTES) with missing values in ≥10 patients were excluded from subsequent analyses (supplemental Figure 1A). Details of missing values for the remaining 22 cytokines are shown in supplemental Figure 1B-C. Missing values of 22 cytokines were imputed using the random forest-based algorithm, missForest.[10] The features were log-standardized for data preprocessing. For sensitivity analyses, cluster analyses were also performed on the data set complemented with different imputation methods based on the k-nearest neighbor (kNN) and principal

Table 2. Serum concentrations (pg/mL) of cytokines between patients with TAM with or without a high WBC count

	Patients with a high WBC count*, n = 29	Patients without a high WBC count, n = 99	*P* value†
IL-1b, median (range)	3.13 (1.42-325.2)	2.49 (0.63-3662)	**.005**
IL-1ra	211.6 (19.71-868.1)	116.0 (8.85-9285)	.064
IL-4	4.06 (1.69-10.43)	3.79 (0.89-32.97)	.698
IL-5	2.295 (0.11-16.44)	2.47 (0.06-20.88)	.625
IL-6	117.9 (8.49-1537.9)	33.70 (1.75-6851)	**.003**
IL-7	31.67 (4.91-613.2)	12.10 (0.97-184.5)	**.007**
IL-8	93.43 (19.42-8350)	44.97 (8.81-37418)	**.023**
IL-9	26.71 (2.46-130.8)	21.89 (1.26-250.6)	.225
IL-10	14.69 (5.36-260.5)	11.62 (1.56-170.6)	.066
IL-13	19.84 (1.01-123.0)	8.980 (0.58-199.2)	**.029**
Eotaxin	176.7 (48.34-2265)	148.4 (12.50-892.0)	.090
PDGF-bb	5610 (300.0-18523)	4459 (61.75-18489)	.060
Basic FGF	60.79 (16.31-935.3)	47.42 (6.77-254.3)	.079
G-CSF	65.73 (25.02-7232)	55.71 (9.39-1770)	.078
GM-CSF	173.8 (47.04-851.1)	132.0 (6.05-1836)	.081
IFN-r	93.31 (16.52-597.9)	74.79 (10.22-6328)	.606
IP-10	2011 (296.0-18554)	1742 (70.84-18686)	.602
MCP-1(MCAF)	617.2 (86.33-4051)	195.8 (31.28-10398)	**.020**
MIP-1a	7.710 (0.53-759.1)	6.640 (0.71-565.6)	.460
MIP-1b	380.7 (121.7-4387)	280.1 (59.98-50908)	.229
TNF-a	50.40 (21.43-362.8)	40.81 (10.23-1029)	.216
VEGF	112.6 (12.17-1974)	76.85 (8.27-4490)	.083

Bold indicates $P < 0.05$.

G-CSF, granulocyte colony-stimulating factor; GM-CSF, granulocyte-macrophage colony-stimulating factor; MCAF, monocyte chemotactic and activating factor; MCP-1, monocyte chemoattractant protein-1; MIP, macrophage inflammatory protein; PDGF, platelet-derived growth factor; TNF-a, tumor necrosis factor-alpha; VEGF, vascular endothelial growth factor.

*A high WBC count was defined as $>100 \times 10^9$ cells per liter.

†*P* value was evaluated using the Mann-Whitney *U* test, followed by the Benjamini-Hochberg method used as a correction for multiple testing.

Table 3. Serum concentrations (pg/mL) of cytokines between patients with TAM with or without early death

	Patients with early death, n = 14	Patients without early death, n = 114	*P* value*
IL-1b, median (range)	4.435 (1.94-351.1)	2.630 (0.63-3662)	**.031**
IL-1ra	372.1 (101.9-1544)	122.0 (8.85-9285)	**.007**
IL-4	4.690 (1.69-9.35)	3.725 (0.89-32.97)	.178
IL-5	5.210 (0.26-20.88)	2.140 (0.06-17.35)	.232
IL-6	222.9 (23.55-1537)	37.43 (1.75-6851)	**.022**
IL-7	31.30 (4.43-613.2)	12.86 (0.97-301.1)	.081
IL-8	217.1 (28.92-8350)	45.87 (8.81-37418)	**.004**
IL-9	34.92 (2.46-110.2)	23.43 (1.26-250.6)	.335
IL-10	28.38 (1.85-260.5)	11.71 (1.56-170.6)	.069
IL-13	22.80 (3.52-173.5)	9.045 (0.58-199.2)	**.037**
Eotaxin	178.2 (46.17-2265)	150.4 (12.50-892.0)	.424
PDGF-bb	5755 (300.0-18523)	4568 (61.75-18489)	.434
Basic FGF	60.28 (19.26-935.3)	49.75 (6.77-254.3)	.261
G-CSF	58.34 (25.63-7232)	56.40 (9.39-1770)	.354
GM-CSF	141.7 (59.65-851.1)	138.1 (6.05-1836)	.750
IFN-r	106.4 (26.36-597.9)	74.79 (10.22-6328)	.329
IP-10	1360 (195.7-17268)	1857 (70.84-18686)	.604
MCP-1(MCAF)	658.6 (93.37-4051)	292.3 (31.28-10398)	.222
MIP-1a	7.79 (2.63-759.1)	6.660 (0.53-565.6)	.347
MIP-1b	454.5 (116.8-50908)	283.8 (59.98-40790)	.185
TNF-a	63.46 (21.97-362.8)	40.66 (10.23-1029)	.065
VEGF	105.7 (12.17-1974)	76.85 (8.27-4490)	.275

Bold indicates $P < 0.05$.

G-CSF, granulocyte colony-stimulating factor; GM-CSF, granulocyte-macrophage colony-stimulating factor; MCAF, monocyte chemotactic and activating factor; MCP-1, monocyte chemoattractant protein-1; MIP, macrophage inflammatory protein; PDGF, platelet-derived growth factor; TNF-a, tumor necrosis factor-alpha; VEGF, vascular endothelial growth factor.

*P value was evaluated using the Mann-Whitney U test, followed by the Benjamini-Hochberg method used as a correction for multiple testing.

component analysis (PCA; supplemental Figure 1D-E).[11] In addition, complete data analysis was performed on 43 patients without missing data for all 27 cytokines.

All statistical analyses were performed using EZR software version 1.36 (Saitama Medical Center, Jichi Medical University, Saitama, Japan)[12] and R Version 4.3.2 with "naniar," "Consensus ClusterPlus,"[13] "ComplexHeatmap," and "ggplog2" packages. A 2-tailed P value $< .05$ was considered statistically significant. Details and other information on statistical analysis are described in supplemental Methods.

Results

Patient characteristics

Table 1 shows the clinical characteristics and laboratory findings of 128 patients with TAM. The median values of gestational age, body weight at birth, WBC count, and percentage of blasts at diagnosis were 37 weeks (range, 29-40), 2588 g (range, 1438-3714), 48.3 × 10^9/L (range, 4.7 × 10^9/L to 478.7 × 10^9/L), and 41% (range, 1%-96%), respectively. Of the 128 patients, 87 (68%) had congenital heart disease, and 14 (11%) had other congenital abnormalities. Trisomy 21 was observed in 126 patients (98%), trisomy 21 mosaicism in 1 patient (1%), and a normal karyotype in 1 patient (1%). Systemic edema was observed in 26 patients (20%) and organ hemorrhage in 12 patients (9%). Somatic *GATA1* gene mutations were confirmed in 127 patients (99%) using Sanger and/or next-generation sequencing. One patient with undetectable *GATA1* mutations had flow cytometry markers ($CD7^+$/$CD117^+$/$CD56^+$), consistent with a TAM phenotype. The expression type of *GATA1* mutations was determined based on a previous report.[2] High-expression mutations were observed in 57 patients (45%), whereas low-expression mutations were observed in 58 patients (45%). Of the 128 patients, 46 (36%) received LDAC.

Of the 128 patients, 20 (16%) died, and early death (<9 months of age) occurred in 14 (11%). The causes of early death were as follows: multiple organ failure (n = 5), liver failure (n = 1), respiratory failure (n = 3), sepsis (n = 1), congenital heart disease (n = 1), and other reasons (n = 3; supplemental Table 3). Cumulative incidence rate (CIR) of early death at 9 months was 11.0% (95% confidence interval [CI], 5.3-16.2), and the leukemia development rate at 4 years was 20.9% (95% CI, 12.9-28.2; supplemental Figure 2). The early death group had a significantly lower gestational age (P = .003), lower birth weight (P = .035), higher WBC counts (P = .006), higher rate of organ hemorrhage (P = .012), and higher rate of systemic edema ($P < .001$) than the nonearly death group, which are poor prognostic factors associated with early death (Table 1). The median values and ranges of the 27 cytokines and the number of subjects for each cytokine are shown in supplemental Table 2. Five cytokines (IL-2, IL-12, IL-15, IL-17, and RANTES) with missing values in ≥10 patients were excluded from subsequent analyses (supplemental Figure 1A).

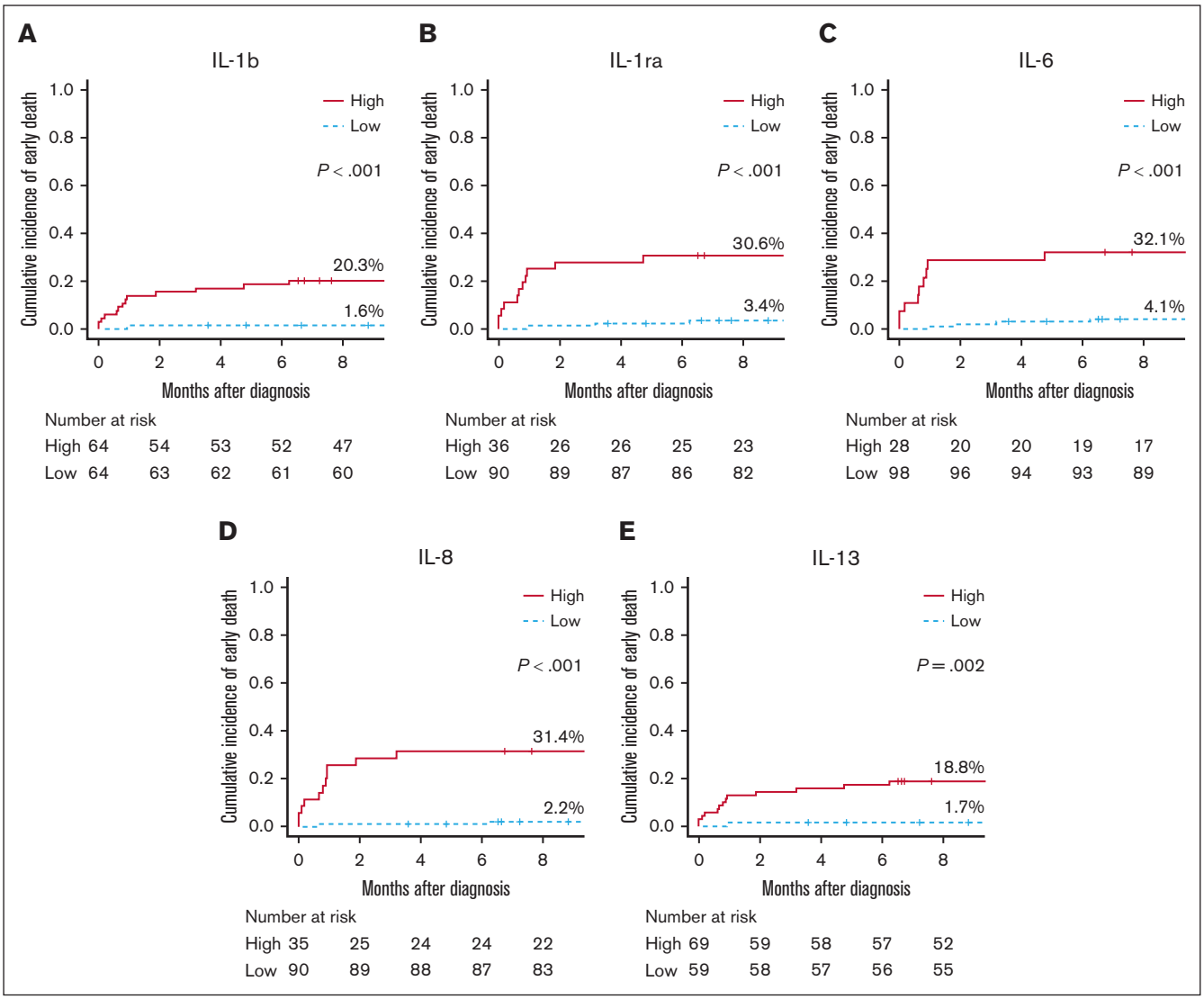

Figure 1. Cytokine levels are valuable markers for predicting early death in patients with TAM. (A) CIR of early death between patients with TAM with high and low levels of IL-1b (high, n = 64; low, n = 64; CIR, 20.3% [95% CI, 9.8-29.6] vs 1.6% [95% CI, 0.0-4.6]; $P < .001$); (B) high and low levels of IL-1ra (high, n = 36; low, n = 90; CIR, 30.6% [95% CI, 13.8-44.1] vs 3.4% [95% CI, 0.0-7.0]; $P < .001$); (C) high and low levels of IL-6 (high, n = 28; low, n = 98; CIR, 32.1% [95% CI, 12.4-47.4] vs 4.1% [95% CI, 0.0-8.0]; $P < .001$); (D) high and low levels of IL-8 (high, n = 35; low, n = 90; CIR, 31.4% [95% CI, 14.2-45.2] vs 2.2% [95% CI, 0.0-5.3]; $P < .001$); and (E) high and low levels of IL-13 (high, n = 69; low, n = 59; CIR, 18.8% [95% CI, 9.1-27.6] vs 1.7% [95% CI, 0.0-4.9]; $P < .001$).

Relation between cytokine levels and clinical characteristics

The comparison between 29 patients with a high WBC count ($\geq 100 \times 10^9$ cells/L, a poor prognostic factor in patients with TAM) and 99 patients without a high WBC count for 22 cytokine levels showed that the levels of 6 cytokines (IL-1b, IL-6, IL-7, IL-8, IL-13, and monocyte chemoattractant protein-1b) were significantly higher in patients with high WBC counts (Table 2). The association between expression types of *GATA1* mutations and 22 cytokine levels is shown in supplemental Table 4. Six cytokines (IL-4, eotaxin, platelet-derived growth factor-BB, basic fibroblast growth factor, macrophage inflammatory protein 1β, and tumor necrosis factor α) were significantly higher in the high *GATA1* expression group than in the low *GATA1* expression group.

Furthermore, the correlation between cytokine levels and hepatomegaly and serum markers of liver fibrosis (procollagen type III peptide, type IV collagen, and hyaluronic acid) was evaluated (supplemental Table 5). The serum levels of several cytokines, especially IL-13 ($r = 0.35$; $P < .05$) and eotaxin ($r = 0.35$; $P < .05$), were correlated with hepatomegaly. Additionally, 5 cytokines (IL-6, IL-9, eotaxin, interferon-gamma-induced protein-10, and macrophage inflammatory protein 1β) were positively correlated with 2 liver fibrosis markers. Cytokine levels were compared in patients with or without leukemia development (n = 23 vs n = 105), and no

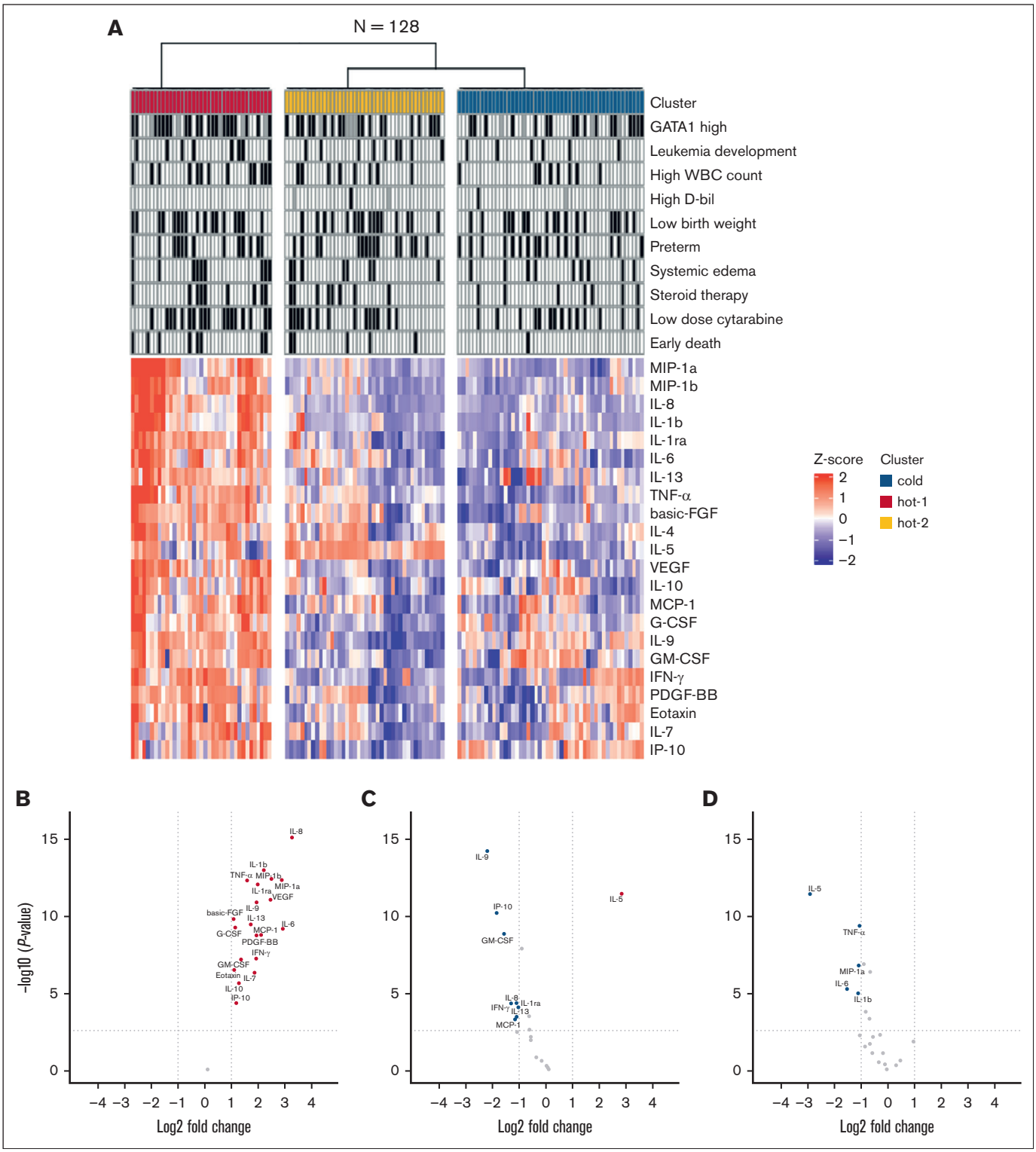

Figure 2. Total of 128 patients with TAM are classified into 3 groups by an unsupervised consensus clustering analysis based on cytokine profiling. (A) Based on unsupervised clustering, patients were classified into 3 cytokine groups (hot-1 [n = 37], hot-2 [n = 42], and cold groups [n = 49]). Missing data (1.1%) in 22 cytokines were imputed using the missForest method. Black boxes indicate each clinical feature. Gray boxes indicate patients with no data. (B-D) The mean cytokine differences (x-axis) and the negative log10-transformed statistical *P* value (y-axis) between hot-1 group and other groups (B), hot-2 group and other groups (C), cold group and other groups (D) are shown in the volcano plot.

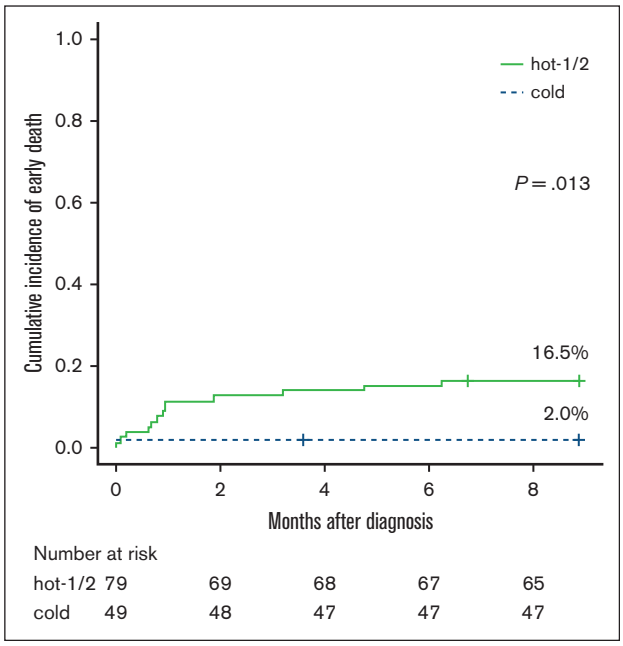

Figure 3. Cytokine group is significantly associated with the early death rate in patients with TAM. The CIR of early death in patients with TAM between cytokine hot-1/2 and cold groups (hot-1/2, n = 79; cold, n = 49; hot-1/2 CIR, 16.5% [95% CI, 7.9-24.2]; cold CIR, 2.0% [95% CI, 0.0-5.9]; $P = .013$).

cytokine showed significant differences between the 2 groups (supplemental Table 6).

Strong association between cytokine levels and early death

Cytokine levels were compared between the early death (n = 14) and nonearly death groups (n = 114). The levels of 5 cytokines (IL-1b [$P = .031$], IL-1ra [$P = .007$], IL-6 [$P = .022$], IL-8 [$P = .004$], and IL-13 [$P = .037$]) were significantly higher in the early death group than in the nonearly death group (Table 3). The optimal cytokine cutoff points of IL-1b, IL-1ra, IL-6, IL-8, and IL-13 were determined as 2.9 pg/mL, 256.0 pg/mL, 141.0 pg/mL, 102.0 pg/mL, and 9.2 pg/mL, respectively, to predict early death using receiver operator characteristic curves, which yielded the highest sum of sensitivity and specificity (supplemental Figure 3). The CIR of early death was significantly associated with higher levels of these 5 cytokines (Figure 1). Additionally, in a subgroup analysis restricted to 99 patients with low WBC counts ($<100 \times 10^9$/L), high levels of these 5 cytokines were significantly associated with early death (supplemental Figure 4).

An unsupervised clustering analysis was performed using the values of 22 cytokines. Missing values (1.1%; supplemental Figure 1B) were computationally imputed using the missForest method. The patients were divided into 3 groups: hot-1 (n = 37), hot-2 (n = 42), and cold (n = 49) (Figure 2A). The hot-1 group showed high inflammatory cytokine levels, including IL-8, IL-6, and IL-1β (Figure 2B). The hot-2 group was characterized by elevated IL-5 levels (Figure 2C). The cold group did not show any significant cytokine elevation (Figure 2D). The clinical characteristics of the 3 groups are described in supplemental Table 7. The CIR of early death was significantly different between the cytokine groups (hot-1/2, n = 79; cold, n = 49; hot-1/2 CIR, 16.5% [95% CI, 7.9-24.2]; cold CIR, 2.0% [95% CI, 0.0-5.9]; $P = .013$). The cytokine hot-1/2 groups showed significantly higher early mortality than the cytokine cold group (Figure 3; supplemental Figure 5). For sensitivity analyses, cluster analyses were conducted on data sets complemented using other imputation methods: kNN and PCA (supplemental Figure 6A-B). In addition, complete data analysis was performed for 43 patients without missing data for 27 cytokines (supplemental Figure 6C). The reproducibility of the 3 identified clusters was high while using the missForest-imputed data set as a reference; the concordance rates with the kNN, PCA, and complete data analysis were 0.94, 0.99, and 0.95, respectively (supplemental Figure 1D-E).

The univariable analysis showed that the following covariates were correlated with early death: cytokine group, gestational age, organ hemorrhage, systemic edema, congenital heart disease, high WBC counts in peripheral blood, systemic steroid therapy, and hepatomegaly (supplemental Table 8). The multivariable analysis was performed in 2 models using factors extracted using the stepwise Akaike information criterion method, which were identified as significantly different in univariable analysis. The multivariable analysis (model 1), without incorporating cytokine group, identified the following independent risk factors for early death: high WBC counts (hazard ratio [HR], 3.450; 95% CI, 1.127-10.56; $P = .030$), systemic edema (HR, 13.76; 95% CI, 3.784-50.06; $P < .001$), hepatomegaly (HR, 3.375; 95% CI, 1.108-10.28; $P = .032$), and congenital heart disease (HR, 0.294; 95% CI, 0.096-0.903; $P = .033$); and the multivariable analysis (model 2), incorporating cytokine group, showed that cytokine hot-1/2 groups was an independent prognostic factor (HR, 15.53; 95% CI, 1.434-168.3; $P = .024$; Table 4).

Discussion

A total of 22 cytokine levels were analyzed in 128 patients with DS with TAM who were enrolled in the TAM-10 prospective observational study to determine the association between cytokine levels and clinical characteristics. Five cytokines (IL-1b, IL-1ra, IL-6, IL-8, and IL-13) were significantly associated with early death. Furthermore, an unsupervised clustering analysis based on the 22 cytokine levels generated 3 groups (cytokine hot-1, hot-2, and cold). The cytokine hot-1/2 groups showed significantly higher early death rates than the cytokine cold group.

The univariable analysis showed a strong association between the cytokine hot-1/2 groups and early death (HR, 8.509; 95% CI, 1.113-65.05), and a multivariable model incorporating cytokine group (model 2) identified the cytokine hot-1/2 groups as an independent prognostic factor. These findings indicate that the cytokine group is a potent prognostic factor for TAM and may outperform the traditional clinical prognostic factor, WBC count.

The IL-1 family consists of proinflammatory cytokines such as IL-1b and anti-inflammatory cytokines such as IL-1ra.[14] IL-1b is a potent proinflammatory cytokine, originally identified as an endogenous thermogenic agent, and IL-1ra is an acute phase protein secreted by the liver in response to inflammatory stimuli and can inhibit signal transduction.[15] It has been reported that patients with TAM who died early had significantly elevated levels of both IL-1b and IL-1ra. However, IL-1ra is considered much less effective than agonists,

Table 4. Multivariable Cox regression analyses of early death

Covariates	Number	Multivariable analysis: model 1 without incorporating cytokine group		Multivariable analysis: model 2 incorporating cytokine group	
		HR (95% CI)	*P* value	HR (95% CI)	*P* value
Cytokine group					
Cold	49	Exclusion		(1)	**.024**
Hot-1/2	79			15.53 (1.434-168.3)	
Systemic edema					
No	102	(1)	**<.001**	(1)	**<.001**
Yes	26	13.76 (3.784-50.06)		19.24 (4.787-77.30)	
Congenital heart disease					
No	41	(1)	**.033**	(1)	**.012**
Yes	87	0.294 (0.096-0.903)		0.174 (0.044-0.681)	
WBC					
$<100 \times 10^9$ /L	99	(1)	**.030**	(1)	.607
$\geq 100 \times 10^9$ /L	29	3.450 (1.127-10.56)		1.383 (0.401-4.770)	
Hepatomegaly					
<5 cm	100	(1)	**.032**	(1)	**.006**
≥5 cm	28	3.375 (1.108-10.28)		5.839 (1.639-20.80)	
Akaike information criterion		102.4		96.17	
Likelihood ratio		40.00 ($P < .001$)		48.21 ($P < .001$)	

Bold indicates $P < 0.05$.

requiring up to 1000-fold excess IL-1ra to inhibit IL-1 signaling.[16] These findings suggest that the observed IL-1ra elevation is a secondary event, and IL-1 signaling is activated in patients with severe TAM. IL-6 promotes B and T lymphocyte differentiation and immunoglobulin G production.[17,18] Furthermore, IL-6 has been reported to be involved in cancer cell proliferation via STAT3 activation[19] and promote cancer cell migration and invasion.[20-22] Shitara et al[23] reported a case of severe TAM that showed IL-6 elevation in the pericardial fluid. Targeted therapy with cytokine antagonists, such as anakinra and canakinumab, which inhibit IL-1 signaling, and tocilizumab, which inhibits IL-6, have already been approved and demonstrated clinical efficacy for the treatment of hypercytokinemia in various diseases. These cytokine antagonists are expected to be evaluated in clinical studies as a potential future treatment for hypercytokinemia in severe TAM.

The correlation between cytokine levels and other clinical features was evaluated, except for early death. This study revealed that no cytokine levels were associated with leukemia development. Only the flow cytometric minimal residual disease positivity has been reported to be a valuable marker for predicting leukemia development.[2,24] These results implied that it might be difficult to predict leukemia development from any data at the time of diagnosis. Furthermore, the association between cytokine levels and *GATA1* expression type was investigated. The results showed that 7 cytokine levels were significantly associated with the *GATA1* expression type. All 7 cytokine levels were higher in patients in the *GATA1* high-expression group than in those in the *GATA1* low-expression group. Kanezaki[25] reported that the mutation types of *GATA1* affected the amount of the mutant, and the *GATA1* expression type significantly affected the TAM phenotype. The study findings might imply that the *GATA1* high-expression type caused high levels of their cytokines.

This study has several limitations. First, this study included patients enrolled in the JPLSG TAM-10 study, and clinical samples immediately after diagnosis for cytokine measurement in 23% (39 patients) were unavailable and could not be included in the analysis. Most clinical characteristics did not show significant differences between patients with and without cytokine information; however, WBC counts at diagnosis, blast rates, and percentage of patients receiving LDAC were significantly higher in cases with cytokine information (supplemental Table 1). Second, of the 27 cytokines measured, the percentage of deficient values for 22 cytokines used in the analysis was only 1.1% (supplemental Figure 1B); however, 5 cytokines were deficient in >10% of cases and had to be excluded from subsequent analyses. Moreover, we performed a complete data analysis of 43 cases for which we had data for all 27 cytokines and found consistent results (supplemental Figure 1D-E). Third, the dosage and intervention criteria of LDAC were not standardized, although a relatively high percentage (36%) of patients were treated with LDAC as per the policy of the participating centers. Fourth, the clinical significance of cytokine profiling analysis has not been validated due to the absence of a validation cohort. This limitation is largely unavoidable given the rarity of TAM and the scarcity of international prospective studies in this field. However, we plan to re-evaluate the cytokine profiling analysis in the future using clinical samples from patients enrolled in our ongoing prospective clinical trial (jRCTs041190063).

In conclusion, this study showed that cytokine profiling provides supportive information along with previous clinical prognostic

factors such as WBC count as a biomarker for predicting early death and may contribute to precision medicine for patients with TAM.

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Authorship

Contribution: G.Y. conducted the study, analyzed the data, and wrote the manuscript; Y.H. designed and conducted the study, led the project, and wrote the manuscript; Y.T. and H.M. wrote the manuscript and analyzed the data; A.S., N.S., T. Kaburagi, T.D., T. Kawai, and Y.Y. analyzed the data; T.I. performed statistical analyses; H.T. performed the research and bioinformatics analysis; Y.T. wrote the manuscript; K.T. and E.I. performed the *GATA1* mutation analysis; K.W. collected clinical samples and data; and all authors critically reviewed and revised the manuscript.

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