Table 5 Candidate genes close to the positive microsatellite markers

Marker	Position	Distance	Neighboring gene	Description	Function
Donor allele					
D22S283	22q12.3	172 kb	MYH9	Myosin, heavy chain 9, nonmuscle	Cytoskelton
D22S0141i	22q12.3	Intron 3	CACNG2	Calcium cannel, voltage dependent, gamma-2 subunit	Cell signaling
Recipient allele					
D22S0021i	22q13.2	10 kb	EP300	E1A binding protein, 300 KD	Transcription
D22S0199i	22q13.2	40 kb	TCF20	Transcription factor 20	Transcription
D22S0222i	22q13.33	45 kb	ARSA	Arylsulfatase A	Enzyme
Mismatching allele					
D22S0267i	22q11.21	Intron 3	PEX26	Peroxisome biogenesis factor 26	Protein degradation
D22S0152i	22q11.23	20 kb	FLJ31568	Hypothetical protein	Unknown
D22S0145i	22q11.23	Intron 4	KIAA0376	Hypothetical protein	Unknown
Z66750	22q12.1	10 kb	EMID1	BMI domain containing protein 1	Unknown
D22S0085i	22q12.3	Intron 7	LARGE	Acetyl glucosaminyltransferase-like protein	Unknown
D22S0220i	22q12.3	Intron 8	TOM1	Target of myb 1	Immuno regulation
D22S683	22q12.3	20 kb	APOL3	Apolipoprotien L-III	Lipid metabolism
D22S0197i	22q13.33	10 kb	FLJ44385	Hypothetical protein	Unknown

different genes (Vo and Goodman 2001). The p300 protein, together with the adenovirus serotype 5 E1A, has been reported to regulate the NKG2D ligand, NK cell lysis, and tumor rejection (Routes et al. 2005). In addition, p300-binding domains are known to interact with STAT1, 2, and 3, which play an important role in cytokine signal transduction (Pfitzner et al. 2004). Therefore, the p300 gene might be associated haplotypically with the D22S0021i marker, which has both a protective and risk allele for aGVHD (Table 3). These facts, together with our association results, strongly suggest that the loci at position 22q12–13 could affect the development of aGVHD. Whereas three of these positive markers are located 10 kb to 45 kb from any of the known genes, the positive microsatellite marker D2250141i is located within intron 3 of the CACNG2 gene that encodes the calcium channel, voltage dependent, gamma-2 subunit (Table 5). This protein appears to interact with neural proteins (Black and Lennon 1999; Chen et al. 2000), and it might have a role in neurological complications arising from aGVHD (Sostak et al. 2003).

We found eight microsatellite markers that were significantly different between the aGVHD-free group and the aGVHD group when matched or mismatched between the recipient and donor groups. Three of the eight markers, D22S0267i, D22S0220i, and D22S683, are considered to be protective because they were more often mismatched in the severe aGVHD group (OR>1), suggesting the existence of one or more protective candidate genes in close vicinity. Two of these markers, D22S0220i and D22S683, were approximately 780 kb apart (D22S0085i and D22S0220i) with another three markers (Z67524, D22S0132i, and D22S0075i) located between them that showed a positive trend ($P<0.1$) of association (Fig. 1). Interestingly, Gubarev et al. (1996) reported the localization of a gene encoding mHa on 22q12.3 in close vicinity to our significant markers by using T-cell clone and linkage-analysis. This report, which used different methods from our genome-wide approach, therefore strongly supports our results.

The highly significant protective microsatellite marker D22S0220i is located within intron 8 of the gene TOM1. The specific function of this gene has not yet been determined, but Tom1 may be a negative regulator of interleukin-1 and tumor necrosis factor-induced signaling pathways (Yamakami and Yokosawa 2004), and, therefore, affect aGVHD. D22S0220i is also located near to the HMOX1 gene (NCBI Gene ID 3162) that encodes the heme oxygenase (decycling) 1 protein. This association is biologically significant because HMOX1 (alias HO-1) is known to be a protective protein with anti-inflammatory and antiapoptotic properties (Willis et al. 1996; Brouard et al. 2002). Moreover, induction of HMOX1 in recipient mice of a BMT model resulted in a reduction in aGVHD and improved survival (Gerbitz et al. 2004). Therefore, HMOX1 is an excellent protective candidate gene for further aGVHD association studies specifically at the level of gene SNP analysis.

Another potential protective microsatellite marker D22S683 is located ~172.2 kb from the MYH9 gene (MIM 160775) and the Epstein syndrome locus (MIM 153650). The MYH9 mutations are known to result in the autosomal dominant giant-platelet disorders such as the May–Hegglin anomaly, the Fechtner syndrome, and the Sebastian syndrome (Seri et al. 2000). In addition, the MYH9 or the motor protein non-muscle heavy chain II A has been associated with the chemokine receptor CXCR4 in the T cell (Rey et al. 2002) and with the modulation of T cell motility (Jacobelli et al.

2004). Considering that one of the alleles of the microsatellite marker D22S283 is located within 172.2 kb of the MYH9 gene of the transplantation donors that were positively associated with aGVHD, then it can be envisaged that a neighboring SNP may affect the donor T cell behavior in a protective role against the occurrence and/or maintenance of aGVHD.

The five 'disease-negative' markers shown in Table 4 were associated with a risk of aGVHD because they were more often mismatched in aGVHD grade 0 group (OR<1) than the aGVHD group. This result seems to be paradoxical when considering the concept of a minor antigen mismatch, but it suggests that some gene products might need to be mismatched to prevent the development of disease. For example, it has been reported that the killer cell immunoglobulin-like receptor ligand (KIR-ligand), when mismatched between the donor and recipient, is associated with improved survival after stem cell transplantation for acute myeloid leukemia (Ruggeri et al. 2002). In this regard, the product of an unknown gene located near the 'disease-negative' microsatellite markers, when mismatched between donor and recipient, might help to prevent the development of aGVHD in a way that is analogous to the unique KIR-ligand mismatch involved with the NK-KIR biological system in response to transplantation (Malmberg et al. 2005).

To identify the candidate genes that are located within close vicinity to the significant microsatellite markers, we searched the human genome sequence deposited at NCBI for locations and annotations of genes in both directions of the microsatellite markers (Table 5). Interestingly, many of the genes that we identified near the associated markers, such as MYH9, CACNG2, EMID1, LARGE, and TCF20, have proximal STAT1- and STAT2-binding sites. Many DNA binding sites for STAT1 and STAT2 have been identified distributed across chr 22 in interferon-treated cells (Hartman et al. 2005). The STAT family proteins mediate transcriptional responses to many cytokines and are a useful system for studying inducible gene regulation. In addition, APOL3, EMID1, and LARGE exhibit IFN-sensitive expression changes. Considering the complex roles of cytokines, such as IFN, in the aGVHD occurring phase after BMT, the cytokine inducible candidate genes may play an important role in aGVHD.

The results of our study are largely dependant upon the hypothesis that microsatellite markers in LD will reveal an association between polymorphisms and the functional risk conferred by the variants or relevant genes so that certain marker alleles will be over represented in the aGVHD donors or patients compared with the GVHD-free donors or recipients (Ohashi and Tokunaga 2003; Zapata et al. 2001). In this study, we used 155 microsatellite markers whose spacing average was about 200 kb on the basis of the knowledge accumulated from a large number of recent data that the average length of LD between disease susceptible SNPs and nearby microsatellite alleles is ≥100 kb (Abecasis et al. 2001; Keicho et al. 2000; Oka et al. 1999; Ota et al. 1999). Although the LD pattern is variable between different regions of human genome depending on several factors such as allele frequency, mutation and recombination, and ethnic population, the 200 kb interval between markers is likely to be of sufficient distance for LD coverage of chr 22 in this study.

The multiple testing issues and the restricted sample size of our study limit the statistical power to find conclusive evidence of association particularly in the case of susceptibility genes with minor effects. It is statistically possible that at a probability level of less than 0.05 that 1 in 20 of our markers will represent false positives. We have analyzed 155 different microsatellite markers for association with aGVHD, and therefore, we could expect about eight false positive markers distributed randomly across the 40 Mb of the long arm of chr 22. Of the 13 microsatellite markers that were significantly different between the GVHD-free group and the GVHD severe group, the location of three of the markers, D22S0220i, D22S683, and D22S283, were relatively close to each other, which increases the probability that they represent a true association. Moreover, this GVHD susceptibility locus, from D22S0220i and D22S283, spans approximately 1 MB of genomic sequence and contains at least 14 candidate genes, including TOM1 and HMOX1 and MYH9, near the APOL1 to APOL6 gene cluster (Fig. 1).

In conclusion, we used 155 microsatellite markers distributed across the long arm of chr 22 and the 'genome-wide approach' in this genetic association study of aGVHD to identify and map potential aGVHD susceptibility and resistant regions on the basis of a small number of significant markers. It now remains to use the "candidate gene approach" and investigate the SNPs and haplotypes of the candidate genes, such as TOM1, HMOX, MCM5, and MYH9, which are located closely to the most significant microsatellite markers.

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ORIGINAL ARTICLE

Significance of additional high-dose cytarabine in combination with cyclophosphamide plus total body irradiation regimen for allogeneic stem cell transplantation

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The combination of cyclophosphamide (CY) and total body irradiation (TBI) has been used as a standard conditioning regimen for allogeneic transplantation. Several studies showed an advantage of adding high-dose cytarabine (HDCA) to this regimen. To clarify the significance of additional HDCA, we conducted a retrospective multicenter study and compared the clinical results of these two regimens. From June 1985 to March 2003, 219 patients with hematological malignancies underwent allogeneic transplantation after conditioning with CY + TBI 12Gy ($n = 73$) or CA + CY + TBI 12Gy ($n = 146$). Engraftment, overall survival, transplant-related mortality (TRM), relapse rate and incidence of graft-versus-host disease (GVHD) were compared according to risks and donors. Addition of HDCA had no impact on the relapse rate in all subgroups, and it was associated with lower TRM among standard-risk patients after related transplantation, and with higher TRM and worse survival among standard-risk patients after unrelated transplantation. The incidence of acute GVHD was not significantly different between the two regimens, and HDCA resulted in a higher incidence of chronic GVHD among standard-risk patients after related transplantation. In summary, addition of HDCA is not beneficial for high-risk patients, and is not recommended for standard-risk patients receiving unrelated transplantation.

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Introduction

For allogeneic stem cell transplantation, the conditioning regimen is one of the most important factors. The combination of cyclophosphamide (CY) and total body irradiation (TBI) has been used as a standard conditioning regimen for myeloablative hematopoietic stem cell transplantation.[1–4] Intensification of the conditioning regimen using high-dose cytarabine (HDCA) has been investigated as possibly reducing disease relapse in hematological malignancies. Some studies are encouraging additional HDCA,[5–11] whereas others are reporting more toxicity using HDCA particularly on the heart and lung.[12–16] Our previous preliminary report did not show any significant differences between CY + TBI and CA + CY + TBI in a small cohort.[17]

To clarify the significance of additional HDCA, we conducted a retrospective multicenter study of 219 patients, and compared the clinical results of these two regimens. We confirmed that addition of HDCA neither did improve overall survival, nor reduce the relapse rate.

Patients and methods

Patients, conditioning regimen and GVHD prophylaxis
From June 1985 to March 2003, a total of 219 patients with various hematological malignancies from 13 institutes

underwent allogeneic stem cell transplantation after conditioning with either CY + TBI ($n = 73$) or CA + CY + TBI ($n = 146$). CY was given at a dose of 60 mg/kg once daily intravenously (i.v.) on days −5 and −4 (total dose 120 mg/kg), CA at a dose of 2 g/m^2 twice daily i.v. over 3 h on day −6 and 2 g/m^2 once daily i.v. over 3 h on days −5 and −4 (total dose 8 g/m^2) and TBI at a dose of 300 cGy fractions twice daily on days −2 and −1 (total dose 12 Gy). Seven institutions used only one regimen, either CY + TBI or CA + CY + TBI. The other six institutions used both regimens at the same time. There were no consistent indications for either regimen in any institution. Donors were HLA-fully-matched related donors or HLA-fully-matched unrelated donors. GVHD prophylaxis consisted of either cyclosporine (CsA) and short-term methotrexate (sMTX) or taclorimus (FK) and sMTX.

Statistical analysis

Engraftment, overall survival, transplant-related mortality (TRM), relapse rate and incidence of graft-versus-host disease (GVHD) were compared between the two regimens in each subgroup, which was defined according to risk (standard or high) and donor (related or unrelated). TRM was defined as mortality owing to any cause other than relapse or disease progression. Standard-risk patients are defined as those with acute myeloblastic leukemia (AML) or acute lymphoblastic leukemia (ALL) in first complete remission, chronic myelogenous leukemia (CML) in first chronic phase, or myelodysplastic syndromes (MDS) as refractory anemia (RA) or refractory anemia with ringed sideroblasts (RARS). High-risk patients were those with AML or ALL in subsequent complete remission, in relapse or of induction failure, Philadelphia-chromosome-positive ALL, CML in subsequent chronic phase, accelerated phase or blastic phase or MDS as RAEB or overt leukemia with MDS. The χ^2 test and Fisher's exact test were used for comparison of the two groups. Overall survival was calculated using the Kaplan–Meier method and *P*-values were calculated using the log-rank test. Cumulative incidence curves for TRM and relapse, with or without death, were constructed, reflecting time to relapse and time to TRM as competing risks. *P*-values were calculated at the fixed point in time as reported by Klein *et al.*[18] Univariate and multivariate analyses were performed using the Cox proportional hazard regression model, and variables were selected using stepwise method. A two-sided *P*-value of less than 0.05 was considered significant. Data were analyzed as of March 2003.

Results

Patient characteristics

Patient characteristics of each subgroup are summarized in Table 1. One hundred and twenty-seven patients received transplantation from a related donor whereas 92 received from an unrelated donor. GVHD prophylaxis consisted of CsA + sMTX in 182 patients and FK + sMTX in 37 patients. FK was used in one patient after related transplantation in 1999, and in 36 patients after unrelated

Table 1 Patient characteristics

Risk	*Standard*				*High*			
Donor	*Related*		*Unrelated*		*Related*		*Unrelated*	
Conditioning	*CY + TBI(19)*	*CA + CY + TBI(71)*	*CY + TBI(24)*	*CA + CY + TBI(40)*	*CY + TBI(14)*	*CA + CY + TBI(23)*	*CY + TBI(16)*	*CA + CY + TBI(12)*
Median age (range)	29 (20–50)	33 (16–53)	33 (18–54)	31 (17–50)	39 (24–51)	9 (16–44)	27 (15–48)	31 (16–50)
Sex, F/M	6/13	25/46	8/16	15/25	3/11	8/15	3/13	6/6
Diagnosis								
AML	5	26	2	4	5	6	3	3
ALL	8	18	4	16	3	10	9	4
CML	4	26	15	19	4	5	1	5
MDS	2	1	3	1	2	2	3	0
P-value[a]	0.25		0.09		0.31		0.41	
GVHD prophylaxis								
CsA + sMTX	18	71	10	26	14	23	11	9
FK + sMTX	1	0	14	14	0	0	5	3
P-value	0.48		0.12		—		1.0	

Abbreviations: ALL = acute lymphoblastic leukemia; AML = acute myeloblastic leukemia; CA = cytarabine; CML = chronic myelogenous leukemia; CY = cyclophosphamide; CsA = cyclosporine; FK = taclorimus; MDS = myelodysplastic syndromes; sMTX = short-term methotrexate; TBI = total body irradiation.
[a]Myeloid malignancy vs lymphoid malignancy.

transplantation since 1996. All stem cell sources were from bone marrow except for three patients who received peripheral blood stem cell transplantation from a related donor. Diagnosis and GVHD prophylaxis did not differ significantly between conditioning regimens in each subgroup. The median follow-up period of survivors was 979 days (range 31–4704 days).

Engraftment

All evaluable patients achieved sustained engraftment (an absolute neutrophil count of $>0.5 \times 10^9$/l for three consecutive days) in both regimens.

Overall survival

Overall survival did not differ significantly in any patient between the two regimens (58 vs 56% at 3 years, $P=0.90$) (Figure 1a). Addition of HDCA resulted in significantly worse survival among standard-risk patients after unrelated transplantation (45 vs 81% at 3 years, $P=0.02$) (Figure 1b), whereas it resulted in comparable survival among standard-risk patients after related transplantation (80 vs 60% at 3 years, $P=0.27$).

No significant differences were observed among high-risk patients (40 vs 40% at 3 years, $P=0.48$ among patients after related transplantation; and 11 vs 28% at 3 years, $P=0.93$ among patients after unrelated transplantation).

TRM and hazard analysis for TRM

TRM did not differ significantly in any patient between the two regimens (28 vs 32% at 3 years, $P=0.56$). Addition of HDCA was associated with significantly lower TRM among standard-risk patients after related transplantation (7.8 vs 35% at 3 years, $P=0.027$) (Figure 2a), whereas it resulted in higher TRM among standard-risk patients after unrelated transplantation (51 vs 19% at 3 years, $P=0.0082$) (Figure 2b).

No significant differences were observed among high-risk patients (22 vs 16% at 3 years, $P=0.65$ among patients after related transplantation; and 69 vs 58% at 3 years, $P=0.64$ among patients after unrelated transplantation).

Univariate analysis among standard-risk patients after related transplantation showed that addition of HDCA, female patients, age over 40 and GVHD prophylaxis with CsA + sMTX were significant factors affecting TRM. Addition of HDCA remained a significant factor on multivariate analysis (relative risk = 0.18; confidence interval, 0.052–0.63) (Table 2a). Univariate analysis among standard-risk patients, after unrelated transplantation, showed that addition of HDCA and GVHD prophylaxis

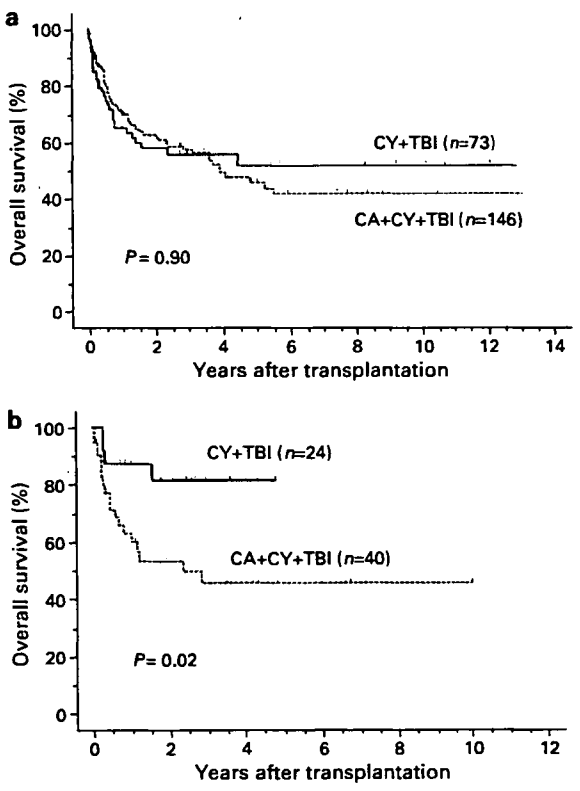

Figure 1 Overall survival. (a) No significant differences were observed between CA + CY + TBI and CY + TBI ($P=0.90$) in all patients. (b) CA + CY + TBI resulted in significantly worse survival than CY + TBI among patients who received transplantation from unrelated donors ($P=0.02$).

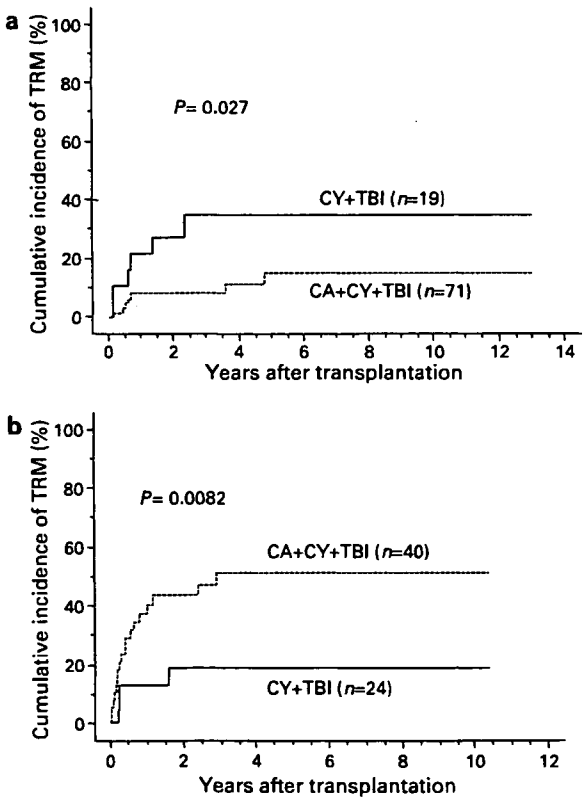

Figure 2 Cumulative incidence of TRM in patients with standard-risk disease. (a) CA + CY + TBI resulted in significantly lower TRM than CY + TBI among patients who received transplantation from related donors ($P=0.027$). (b) CA + CY + TBI resulted in significantly higher TRM than CY + TBI among patients who received transplantation from unrelated donors ($P=0.0082$).

Table 2 Prognostic factors affecting TRM

Variables	*Unfavorable factors*	*Univariate*		*Multivariate*[a]	
		Hazard ratio (CI)	P-*value*	*Hazard ratio (CI)*	P-*value*
(a) Related standard risk					
Conditioning	CA + CY	0.32 (0.11–0.94)	0.038	0.18 (0.052–0.63)	0.0070
Sex	Female	3.3 (1.1–10)	0.039	7.0 (2.0–25)	0.0030
Female to male	Yes	0.95 (0.29–3.1)	0.94		
Disease	Other than CML (CP)	1.4 (0.44–4.7)	0.55		
Age	>40	3.8 (1.2–12)	0.020	8.4 (2.4–30)	0.0010
GVHD prophylaxis	CsA + sMTX	0.12 (0.016–0.98)	0.047	0.53 (0.051–5.5)	0.59
Transplant year	~1996	1.9 (0.50–7.0)	0.35		
(b) Unrelated standard risk					
Conditioning	CA + CY	3.2 (1.1–9.3)	0.038	2.7 (0.90–8.1)	0.078
Sex	Female	0.70 (0.27–1.8)	0.45		
Female to male	Yes	0.74 (0.22–2.5)	0.63		
Disease	Other than CML (CP)	1.1 (0.46–2.5)	0.88		
Age	>40	1.1 (0.41–2.7)	0.93		
GVHD prophylaxis	CsA + sMTX	2.6 (1.0–6.6)	0.048	2.2 (0.84–5.6)	0.11
Transplant year	~1996	0.88 (0.29–2.6)	0.82		

Abbreviations: CA = cytarabine; CI = confidence interval; CML = chronic myelogenous leukemia; CsA = cyclosporine; CY = cyclophosphamide; sMTX = methotrexate.
[a]Final model.

of CsA + sMTX were significant factors influencing TRM. On multivariate analysis, addition of HDCA was associated with a trend for increased TRM (relative risk = 2.7; CI, 0.90–8.1) (Table 2b).

Relapse rate

Relapse rate did not differ between the two regimens (20 vs 13% at 3 years, $P = 0.23$). Addition of HDCA was not associated with any significant differences as to relapse rate in any subgroups (18 vs 5.6% at 3 years, $P = 0.085$ among standard-risk patients after related transplantation; 2.8 vs 0% at 3 years, $P = 0.31$ among standard-risk patients after unrelated transplantation; 51 vs 47% at 3 years, $P = 0.81$ among high-risk patients after related transplantation; and 17 vs 13% at 3 years, $P = 0.81$ among high-risk patients after unrelated transplantation).

Graft-versus-host disease

Results are summarized in Table 3. The incidence of grade II–IV acute GVHD did not differ between the two regimens in any subgroup. Addition of HDCA was associated with a significantly higher incidence of chronic limited and extensive GVHD among standard-risk patients after related transplantation (40/69 vs 5/19, $P = 0.029$).

Table 3 Incidence of acute and chronic GVHD

Risk	*Standard*		*High*	
Donor	*Related*	*Unrelated*	*Related*	*Unrelated*
Acute GVHD (II–IV)				
CY + TBI	6/19	6/24	3/11	8/14
CA + CY + TBI	9/71	11/40	6/22	6/11
P-value	0.11	1.0	1.0	0.78
Chronic GVHD				
CY + TBI	5/19	11/21	7/10	3/6
CA + CY + TBI	40/69	15/34	7/19	6/8
P-value	0.029	0.75	0.13	0.58

Abbreviations: CA = cytarabine; CY = cyclophosphamide; GVHD = graft-versus-host disease; TBI = total body irradiation.

Discussion

We examined a total of 219 patients, which is the largest series in the literature. Aurer and Gale[19] reviewed modified conditioning regimens in 1991, and failed to detect any major improvements in the overall survival with any of the new regimen. Although intensification of the conditioning regimen with HDCA is one of the approaches designed to improve outcome, particularly for high-risk hematological malignancies,[20–24] our retrospective analysis did not show any improvement in overall survival in any subgroups. In addition, no significant reduction in relapse rate was observed in any subgroups, suggesting that anti-leukemic activity may not be intensified by HDCA.

Many of the previous studies reported the superior anti-leukemic activity of HDCA for high-risk disease. Champlin *et al.*,[9] for example, showed that HDCA had good anti-leukemic activity before transplantation. Riddell *et al.*[21] reported a low relapse rate of 14% with the higher dose of CA (36 g/m^2), but an accurate relapse rate could not be fully evaluated because the day 100 TRM was as high as 50%. Mineishi *et al.*[22] reported a lower relapse rate of 11% after related transplantation compared to the 51% in our study. However, of 55 patients, 18 patients with AML/ALL with cytogenetic abnormalities in first remission were classified as high risk in their study. The difference in the definition of high-risk patients may be one reason for the lower relapse rate. In addition, the higher dose of CA (18 g/m^2) in their study may explain the lower relapse rate. Jillella *et al.*[10] also reported a similar outcome, but almost three-quarters of the patients had standard-risk disease. Woods

et al.[6] and Minami *et al.*[17] demonstrated a high relapse rate of 50–75% even with HDCA after related transplantation for high-risk disease. The dose effect of HDCA on anti-leukemic activity should be explored, but it may be offset by the increased toxicity reported in many earlier studies.

Interestingly, however, addition of HDCA was associated with lower TRM among standard-risk patients after related transplantation, and with higher TRM among standard-risk patients after unrelated transplantation. Thus, we performed multivariate analyses to clarify the factors affecting TRM, and confirmed that addition of HDCA still remained as a prognostic factor. Although the effects of the differences in unevaluable factors, such as supportive care, in each institute cannot be fully excluded, additional HDCA may play a role in the reduction of TRM after related transplantation. In contrast, a trend for increased TRM with HDCA after unrelated transplantation is reasonable. TRM is reported to be higher after unrelated than after related transplantation,[25,26] and intensification of the conditioning regimen increases TRM after unrelated transplantation.[27]

Intensity of conditioning is reported to modify the incidence of both acute and chronic GVHD,[28] but its effect on chronic GVHD is controversial.[29] Addition of HDCA was further associated with a significant increase in chronic GVHD among patients with standard-risk disease after related transplantation, but it was not associated with acute GVHD. Thus, other factors such as management of immunosuppresion may also have affected the incidence of chronic GVHD in our series.

In summary, addition of HDCA is not beneficial for patients with high-risk disease. It is not recommended for patients with standard-risk disease who will receive transplantation from unrelated donors because of increased TRM and decreased survival. It may be beneficial for patients with standard-risk disease who will receive transplantation from a related donor. Although the number of patients in this subgroup is somewhat small, such differences could not have emerged without underlying facts. Therefore, further studies are warranted to verify our results in this subgroup.

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Allogeneic Bone Marrow Transplantation from Unrelated Human T-Cell Leukemia Virus-I–negative Donors for Adult T-Cell Leukemia/Lymphoma: Retrospective Analysis of Data from the Japan Marrow Donor Program

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ABSTRACT

Allogeneic hematopoietic stem cell transplantation (allo-HSCT) from an HLA-matched related donor has been suggested to improve the poor prognosis of adult T-cell leukemia/lymphoma (ATLL). However, the infusion of HTLV-I–infected cells from HTLV-I–positive related donors could lead to the development of donor-derived ATLL under immunosuppressive conditions. Although most ATLL patients lack a suitable HLA-matched related donor and require an HTLV-I–negative unrelated donor, little information is currently available regarding the outcome of unrelated bone marrow transplantation (UBMT) for ATLL. To evaluate the role of UBMT in treating ATLL, we retrospectively analyzed data from 33 patients with ATLL treated by UBMT through the Japan Marrow Donor Program (JMDP). Overall survival (OS), progression-free survival, and cumulative incidence of disease progression and progression-free mortality at 1 year after UBMT were 49.5%, 49.2%, 18.6%, and 32.3%, respectively. Multivariate analysis identified recipient age as an independent prognostic factor for OS ($P = .044$). Patients age ≥50 years who showed nonremission at transplantation tended to have higher rates of treatment-related mortality. Our observations suggest that UBMT could represent a feasible treatment option for ATLL patients and warrant further investigation based on these risk factors.

KEY WORDS

Adult T-cell leukemia/lymphoma • Allogeneic hematopoietic stem cell transplantation • Unrelated donor • Graft-versus-adult T-cell leukemia/lymphoma

INTRODUCTION

Adult T-cell leukemia/lymphoma (ATLL) is a peripheral T-cell neoplasm caused by human T-cell leukemia virus type I (HTLV-I) [1,2]. ATLL is generally classified into 4 clinical subtypes based on clinical and laboratory features: acute, chronic, smoldering, and lymphoma type. Clinically, acute- and lymphoma-type ATLL show an aggressive course, with tumor

burden, severe hypercalcemia, multiorgan failure, and poor performance status. ATLL has an extremely poor prognosis, with a median survival of about 6 months for the acute type and about 10 months for the lymphoma type; these patients are usually highly immunocompromised and develop various opportunistic infections. [3] Furthermore, their tumor cells are usually resistant to conventional chemotherapies, because overexpression of multidrug-resistance genes leads to intrinsic drug resistance. [4,5] Intensified chemotherapy [6,7] and autologous stem cell transplantation [8] likewise have failed to improve the prognosis. Thus, alternative treatment strategies for ATLL are needed.

Some cases of successful treatment with allogeneic stem cell transplantation (allo-HSCT) from an HLA-matched related donor have been reported, and a graft-versus-ATLL (GvATLL) effect has been implicated for improving treatments outcomes in transplant patients undergoing transplantation for ATLL. [9–11] However, more than 2/3 of patients with ATLL lack HLA-matched related donors. Furthermore, approximately 2/3 of the siblings of patients with ATLL are HTLV-I carriers [12], and allo-HSCT from an HTLV-I–positive donor may carry a risk of promoting the development of ATLL through the addition of a new HTLV-I load on the immunocompromised host. [13,14] Although most ATLL patients lack a suitable HLA-matched related donor and require an unrelated donor to benefit from allo-HSCT, few reports are available concerning the results of unrelated donor bone marrow transplantation (UBMT) for ATLL [9,11,15–18], and the number of patients in these few reports has been too small on which to base any solid conclusions. Therefore, to clarify the feasibility and efficacy of UBMT from an HTLV-I-negative donor for ATLL, we retrospectively analyzed registered data and clinical outcomes of UBMT for ATLL through the Japan Marrow Donor Program (JMDP).

PATIENTS AND METHODS

Patients and Transplantation Procedure

The subjects of this retrospective study consisted of 33 patients with ATLL (acute type, n = 20; lymphoma type, n = 7; not described, n = 6) who received UBMT from a donor mediated and recruited through the JMDP between September 1999 and January 2004. The clinical indications for UBMT were determined by each individual institution. The median time from diagnosis of ATLL to UBMT was 8 months (range, 5–28 months). At the time of transplantation, 13 patients were in complete remission (CR), 2 patients were in partial remission (PR), and 14 patients were in nonremission (NR); disease status at the time of transplantation was not described in 4 patients. CR status was reported in detail for 13 patients, with 11 patients in first CR (CR1) and 2 patients in second CR (CR2) (Table 1). All unrelated donors were HTLV-I antibody–negative. Serologic typing for HLA-A, -B, and -DR was performed using a standard 2-stage complement-dependent test of microcytotoxicity. [19] Alleles at the HLA-A, -B, and -DRB1 loci were identified by high-resolution DNA typing as described previously. [20] Serologic typing revealed that 22 patients were matched at the HLA-A, -B, and -DR loci. Four patients were mismatched at 1 HLA-DR locus, and 1 patient was mismatched at 2 loci of HLA-A and -DR. DNA typing revealed that 13 patients were matched at HLA-A, -B and -DRB1 loci. Ten patients were mismatched at 1 locus; 9 patients were mismatched at the HLA-DRB1 locus, and the remaining patient was mismatched at 1 HLA-A locus. Another 4 patients were mismatched at 2 loci. HLA typing data were not described in 6 patients. Patient and donor characteristics are summarized in Table 2.

Table 1. *Patient characteristics*

Characteristic	Value
Median age at transplantation, years (range)	49 (range, 24–59)
Sex, n	
Male	18
Female	15
Performance status, n	
0–1	21
2–4	4
ND	8
Subtypes of ATLL, n	
Acute	20
Lymphoma	7
ND	6
Disease status at transplantation, n	
CR or PR	15
NR	14
ND	4
Duration from diagnosis to UBMT, n	
Within 1 year	21
Beyond 1 year	11
ND	1
Conditioning, n	(TBI-containing, 22; non-TBI-containing, 11)
CST	27
RIST	6
Cell dose, n	
$< 3.0 \times 10^8$/kg	16
$\geq 3.0 \times 10^8$/kg	14
ND	3
GVHD prophylaxis, n	
CsA + MTX	13
TCR + MTX	20

ND indicates not described; CR, complete remission; PR, partial remission; NR, nonremission; UBMT, unrelated bone marrow transplantation; TBI, total body irradiation; CST, conventional stem cell transplantation; RIST, reduced-intensity stem cell transplantation; GVHD, graft-versus-host disease; CsA, cyclosporine; MTX, methotrexate; TCR, tacrolimus.

Table 2. *Patient and donor characteristics*

Characteristic	Value
HLA-A, -B, and -DRB1 allele mismatches, n	
0	13
1	10
2	4
ND	6
Sex of donor/patient, n	
Male/male	13
Female/female	8
Female/male	5
Male/female	7
Extent of ABO match, n	
Match	19
Minor mismatch	4
Major mismatch	7
Major/minor	2
ND	1

ND indicates not described.

Transplantation was performed according to the protocol of each institution; therefore, conditioning regimens and prophylaxis against graft-versus-host disease (GVHD) differed among patients. Conditioning regimens were myeloablative in 27 patients; total body irradiation (TBI) was incorporated in 22 patients. Reduced-intensity conditioning regimens were used in 6 patients. GVHD prophylaxis included cyclosporine (n = 13) and tacrolimus (n = 20) combined with methotrexate. All recipients received bone marrow transplantation, which was not manipulated.

Assessment of Engraftment, GVHD, Survival, and Progression-Free Mortality

The day of sustained engraftment was defined as the first of 3 consecutive days with an absolute neutrophil count exceeding 0.5×10^9/L. Acute GVHD was diagnosed and graded according to the standard criteria described previously. [21,22] Chronic GVHD was evaluated according to standard criteria [23] in patients who survived more than 100 days after transplantation. Overall survival (OS) was defined as the duration (in days) from transplantation to death from any cause. Progression-free survival (PFS) was defined as days from transplantation to disease progression or death from any cause. Progression-free mortality was defined as death without disease progression.

Data Management and Statistical Considerations

Data were collected by the JMDP using a standardized report form. Follow-up reports were submitted at 100 days, 1 year, and every subsequent year after transplantation. The cumulative incidence of disease progression and progression-free mortality were evaluated using Gray's method, [24] considering each other risk as a competing risk. OS and PFS were estimated using the Kaplan-Meier method. Potential confounding factors considered in the analysis were age, sex, disease status, duration from diagnosis to transplantation, Eastern Cooperative Oncology Group (ECOG) performance status, [25] conditioning regimen, number of bone marrow cells transplanted, and presence of grade II–IV acute GVHD. Proportional hazard modeling was used to evaluate any influence of these factors on OS, treating development of acute GVHD as a time-dependent covariate. Factors associated with at least borderline significance ($P < .05$) in univariate analyses were subjected to multivariate analyses using backward-stepwise proportional hazards modeling. P values $P < .10$ were considered statistically significant.

RESULTS

Engraftment and GVHD

Transplantation outcomes are summarized in Table 3. The median number of cells transplanted was 2.44×10^8 nucleated cells/kg of recipient body weight (range, $0.58–3.58 \times 10^8$ nucleated cells/kg of recipient body weight). Five patients (15%) died within 20 days. Neutrophil engraftment was achieved in 28 patients. Late graft failure occurred in 1 of these 28 patients, although the patient showed engraftment on

Table 3. *Transplantation outcome*

	Value
Alive/dead, n	19/14
Median follow-up for survivors, days (range)	139 (87–600)
Cause of death	
Progression, n	2
Death without progression, n	9
Median days after transplantation (range)	32 (10–71)
Late graft failure, n	1
GVHD, n	1
Infection, n	3
TMA, n	2
VOD, n	1
Arrhythmia, n	1
Not described, n	3
Disease progression, n	5
Median days after transplantation (range)	122 (61–223)
Engraftment, n	
Engraftment	28
Death within 20 days	5
Late graft failure	1
Acute GVHD, n	
None	3
Grade I	8
Grade II	12
Grade III	3
Grade IV	2
Chronic GVHD, n	
None	14
Limited	1
Extensive	3

GVHD indicates graft-versus-host disease; TMA, thrombotic microangiopathy; VOD, venooculusive disease.

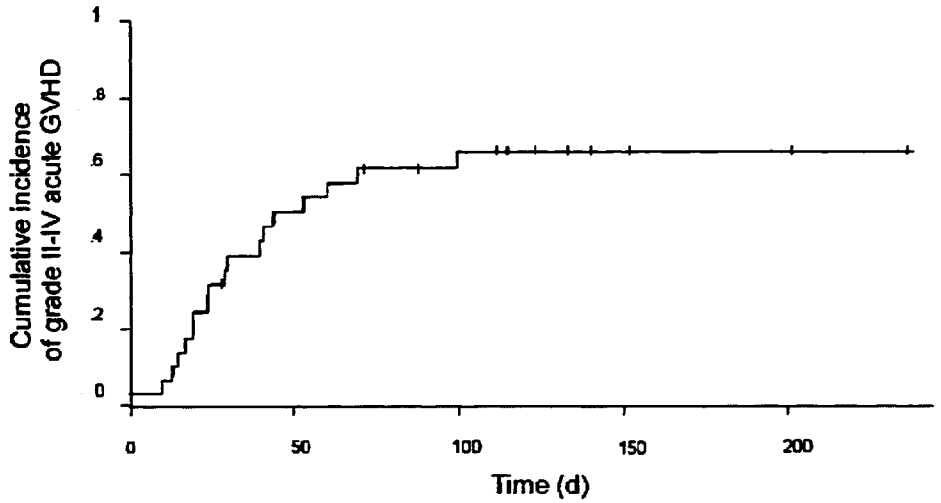

Figure 1. Cumulative incidence of grade II–IV acute GVHD in patients who achieved neutrophil engraftment.

day 14. Acute GVHD developed in 25 of the 28 patients who achieved engraftment (89%): grade I GVHD in 8 patients, grade II in 12 patients, grade III in 3 patients, and grade IV in 2 patients. The cumulative incidence of grade II–IV acute GVHD was 61% (Figure 1). Chronic GVHD developed in 4 of 18 patients, with limited disease in 1 patient and extensive disease in the other 3 patients.

Survival and disease progression

The 1-year OS and PFS were 49.5% (95% confidence interval [CI], 31.2%–78.5%) and 49.2% (95% CI, 33.6%–72.1%), respectively (Figure 2). Disease progression was observed in 5 patients, and the median number of days from transplantation to disease progression was 122 (range, 61–223 days). As of the last follow-up, 14 deaths had been reported. Primary cause of death was disease progression in 2 patients and was not described in 3 patients, but the other 9 deaths were not due to disease progression (see Table 3). Primary causes of transplantation-related death within 100 days after transplantation were late graft failure in 1 patient, GVHD in 1 patient, infection in 3 patients (with methicillin-resistant *Staphylococcus aureus*–positive sepsis in 1 patient and pulmonary infection in 2 patients), thrombotic microangiopathy (TMA) in 2 patients, veno-occlusive disease (VOD) in 1 patient, and arrhythmia in 1 patient.

Univariate and Multivariate Analyses for OS

Pretransplantation and posttransplant factors were calculated for OS (Table 4). In univariate analyses, OS was not significantly associated with sex, duration from diagnosis to transplantation, ECOG performance status, conditioning regimen, number of bone marrow cells transplanted, or presence of grade II–IV acute GVHD. On the other hand, patient age and disease status at transplantation were identified as significant independent risk factors. In multivariate analyses, only patient age at transplantation was identified as exerting a significant independent risk impact on OS (≥50 years vs <50 years; relative risk, 3.47; 95% CI, 1.03–11.6; $P = .044$). Disease status at transplantation exerted a marginally significant impact on OS (NR vs CR or PR; relative risk, 3.17; 95% CI, 0.96–10.5; $P = .059$) (Figure 3).

Influence of Pretransplantation Factors on Disease Progression and Progression-Free Mortality

The cumulative incidence of disease progression and progression-free mortality at 1 year were 18.6% and 32.3%, respectively (Figure 4). To clarify how age and disease status at transplantation affected OS, we evaluated the relationship between these factors and the incidence of progression-free mortality. The cumulative incidence of progression-free mortality was significantly higher in patients age ≥50 years at transplantation (50% vs 18%; $P = .048$; Figure 5A). NR at transplantation exerted a marginally significant effect on increased progression-free mortality (54% vs 20%; $P = .070$; Figure 5B).

DISCUSSION

This study analyzed the data and evaluated treatment outcomes for 33 patients with ATLL who received UBMT. Two important findings were identified regarding UBMT for ATLL. First, UBMT from HTLV-I–negative donors for ATLL represents a feasible treatment. Second, recipient age (≥50 years) and NR disease status at transplantation were independent risk factors for OS, and patients with ATLL displaying these risk factors tended to exhibit higher frequencies of treatment-related mortality.

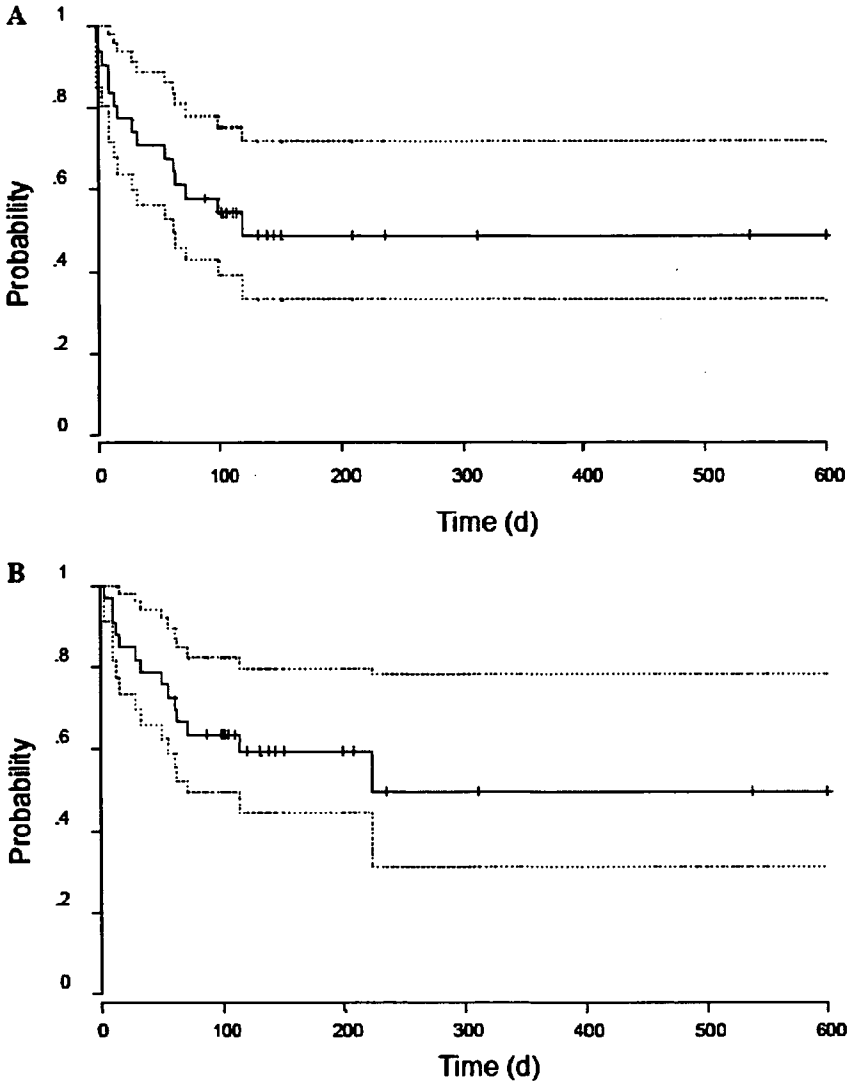

Figure 2. Probability of progression-free survival (A) and overall survival (B) after unrelated bone marrow transplantation for adult T-cell leukemia/lymphoma. Dashed lines represent 95% confidence intervals.

Table 4. *Prognosis factors in univariate and multivariate analyses*

	Univariate		Multivariate	
	Relative risk (95% CI)	P	Relative risk (95% CI)	P
Age ≥50 versus <50 years	4.03 (1.23–13.3)	.022	4.03 (1.23–13.3)	.022
Male versus female	0.97 (0.34–2.80)	.95		
PS 0–1 versus 2–4	0.44 (0.11–1.70)	.23		
NR versus CR or PR	3.37 (1.03–11.0)	.044		.059
UBMT within 1 year versus beyond 1 year	0.54 (0.15–2.00)	.35		
RIST versus CST	0.71 (0.19–2.59)	.60		
TBI versus non-TBI	1.35 (0.45–4.04)	.59		
Cell dose < 3.0 × 10^8/kg versus ≥ 3.0 × 10^8/kg	0.98 (0.31–3.05)	.97		
GVHD II–IV present versus absent	1.91 (0.50–7.26)	.34		

CI indicates confidence interval; PS, performance status; NR, nonremission; CR, complete remission; PR, partial remission; UBMT, unrelated bone marrow transplantation; RIST, reduced-intensity stem cell transplantation; CST, conventional stem cell transplantation; TBI, total body irradiation; GVHD, graft-versus-host disease.

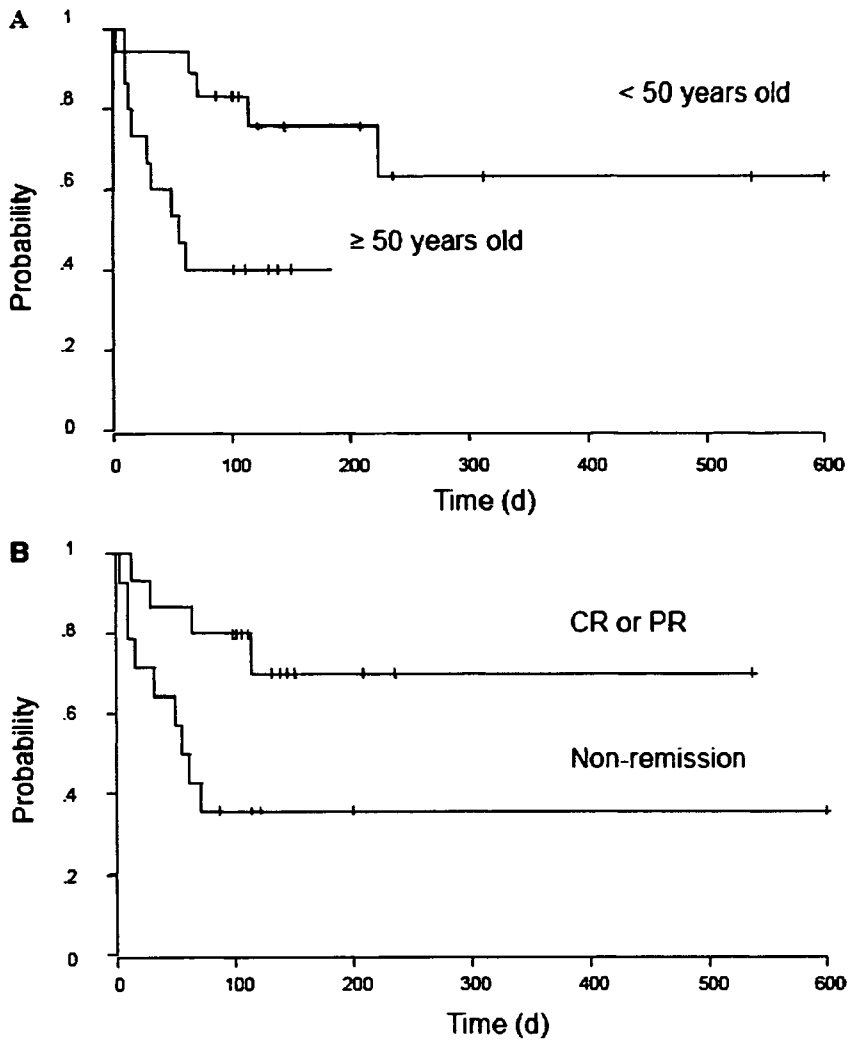

Figure 3. Overall survival according to pretransplantation factors, age (A) and disease status at transplantation (B).

ATLL has an extremely poor prognosis, with projected 2- and 4-year survival rates of 16.7% and 5.0% for the acute type and 21.3% and 5.7% for the lymphoma type, respectively. [3] Neither intensified chemotherapy nor autologous stem cell transplantation have improved the prognosis. Encouraging results for allo-HSCT for ATLL from HLA-matched related donors have been reported by several groups; thus, allo-HSCT may improve the poor prognosis of ATLL. However, the number of patients in most reports has been too small to allow evaluation of the efficacy of allo-HSCT for ATLL. The present results were derived from a large number of patients who underwent transplantation (33 patients) performed through the JMDP. Longer follow-up is, of course, needed to confirm the curative potential of allo-HSCT for ATLL. However, the good survival rates noted here suggest that allo-HSCT is an effective treatment for ATLL, and that patients with ATLL will benefit from allo-HSCT through HTLV-I–negative unrelated donors, because the OS and PFS rates at 1 year after UBMT were 49.5% and 49.2%, respectively. Compared with the results for patients with non-Hodgkin's lymphoma in the National Marrow Donor Program, the incidence of grade III–IV acute GVHD in the present study was low (18% vs 30%). [26] The outcome in the present study appears to be favorable, possible due to the lower incidence of grade III–IV acute GVHD. This observation is compatible with previous studies showing a lower incidence of acute GVHD in Japanese patients compared with Western patients, which might reflect the less diverse genetic background of in the Japanese population. [27,28]

Frequency of relapse after transplantation differs between autologous and allo-HSCT for ATLL. The use of high-dose chemotherapy with autologous HSCT has been reported in only 9 patients, all of whom relapsed or died from transplantation-related mortality. [8] In contrast, the cumulative incidence of

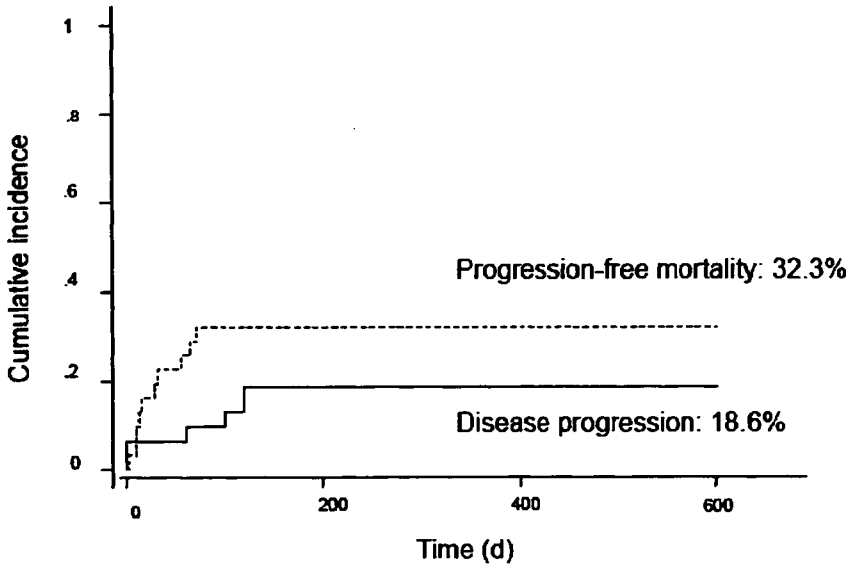

Figure 4. Cumulative incidence of disease progression (—) and progression-free mortality (---) after transplantation.

disease progression was lower after UBMT in this study. Interestingly, patients with ATLL displaying acute or chronic GVHD reportedly did not relapse. [9] In another report, patients with ATLL who relapsed after allo-HSCT reachieved CR after tapering or discontinuation of immunosuppressive agents and donor lymphocyte infusions. [10,11] Reactivation in tax-specific CD8-positive cytotoxic T lymphocytes (CTLs), which has been recently shown in patients with ATLL after allo-HSCT, may indicate a potential contribution of CTLs to anti-ATLL immunity and induction of a GvATLL effect. [29] These results strongly suggest that a GvATLL effect could work on some patients with ATLL to prevent relapse after allo-HSCT. In the present study, neither univariate nor multivariate analysis showed a survival benefit for acute GVHD. We were unable to analyze the relationship between chronic GVHD and relapse, because of the low number of patients with chronic GVHD. In fact, the number of patients may have been insufficient to confirm GvATLL in this study. On the other hand, the absence of benefit from GVHD in preventing relapse suggests that a GvATLL effect could occur in patients with ATLL after allo-HSCT without clinically obvious GVHD. [11]

Transplantation-related mortality was a significant problem in this study. Five patients (15%) died within 20 days, from infection in 3 patients and TMA in 2 patients. Nine patients (27%) died within 100 days, due to infection in 3 patients, TMA in 2 patients, and VOD in 1 patient. Patients with ATLL might have an increased risk of frequent opportunistic infection, because they have an associated T-cell immunodeficiency. Furthermore, ATLL is usually systemic in distribution, and the accumulated organ damages as a result of repeated cytotoxic chemotherapy seen in patients before transplantation may have contributed to the onset of TMA. In univariate and multivariate analysis, recipient age (≥50 years) and NR disease status at transplantation represented significant risk factors for OS. The multivariate analyses were limited by the small number of patients in each subgroup; however, patients displaying these risk factors tended to have a higher rate of treatment-related mortality than patients without these factors, and it can be assumed that these risk factors have a significant relationship with outcome clinically. In this study, mostly myeloablative conditioning regimens were used before transplantation. Given that conventional allo-HSCT is designed to eradicate tumor cells with myeloablative intensity using maximally tolerated doses of high-dose chemotherapy and radiotherapy, the desirable effects often may be offset by overwhelming toxicity in patients age ≥50 years. Moreover, the number of patients with ATLL who are eligible for allo-HSCT with myeloablative conditioning is limited, because the typical patient with ATLL has a relatively advanced age at presentation (about 60 years). To reduce treatment-related mortality, allo-HSCT with reduced-intensity conditioning offers a new treatment option for patients with ATLL who are ineligible for allo-HSCT with myeloablative conditioning due to advanced age or medical infirmity. [30,31] Okamura et al [32] reported on 16 patients age > 50 years with ATLL who underwent allo-HSCT with reduced-intensity conditioning from HLA-matched related donors and found that treatment-related mortality was acceptable and that allo-HSCT with reduced-intensity conditioning was a feasible treatment for ATLL. Given these findings, UBMT

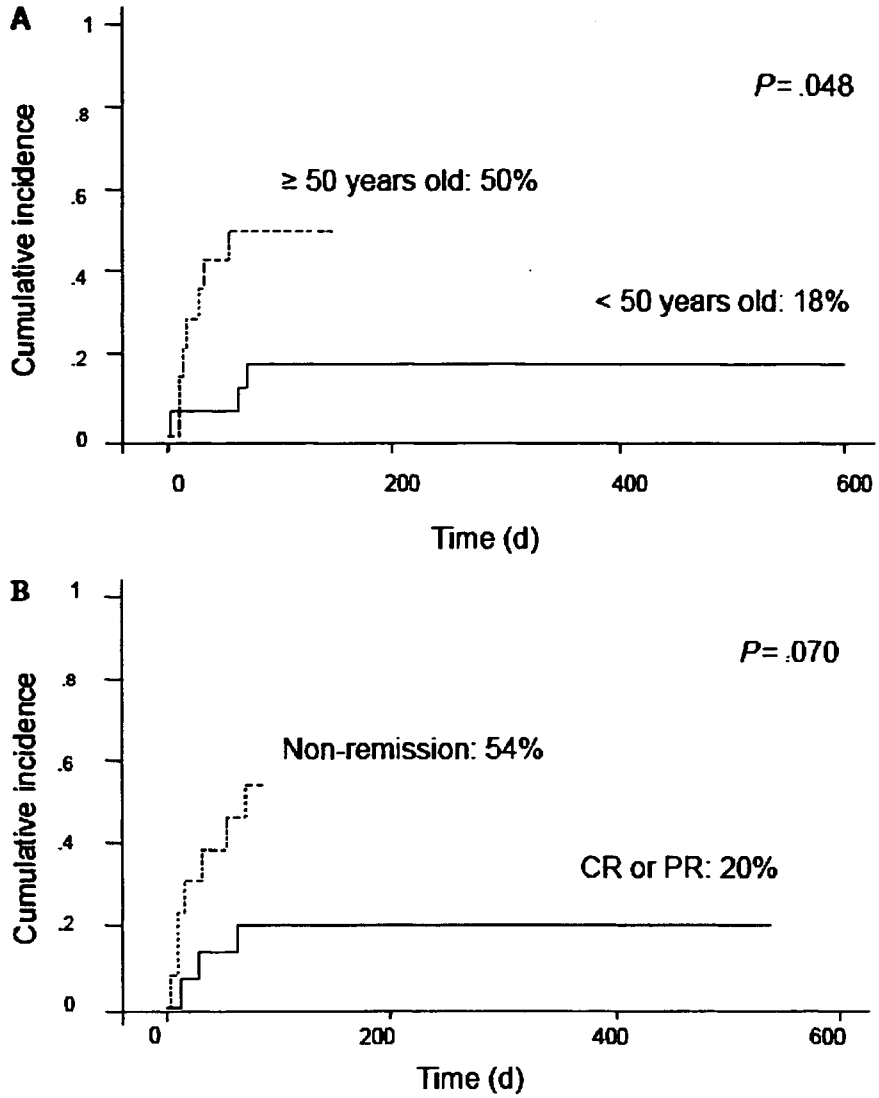

Figure 5. Cumulative incidence of progression-free mortality grouped according to pretransplantation factors, age (A) and disease status at transplantation (B).

with reduced-intensity conditioning should be considered for elderly patients with ATLL.

Another concern related to allo-HSCT for ATLL involves the use of HTLV-1–positive carrier donors. About 2/3 of siblings of patients with ATLL are HTLV-I carriers. From the perspective of HTLV-I–positive donor risk, granulocyte colony–stimulating factor (G-CSF) can reportedly stimulate the proliferation of ATLL cells [33], and HTLV-I–positive donors may be at increased risk of developing ATLL due to the administration of G-CSF in the setting of allogeneic peripheral blood stem cell transplantation. From the perspective of patients with ATLL, allo-HSCT from an HTLV-I–positive donor may carry a risk of HTLV-I–associated disease after allo-HSCT [34] or a risk of promoting the future development of ATLL due to the new HTLV-I load on immunocompromised recipients [13,14]. On the other hand, to date there is no evidence in the JMDP or the literature that ATLL can develop from infected HTLV-I–negative donor cells due to the HTLV-I load of the recipient. The HTLV-I proviral load dramatically decreased to an undetectable level after transplantation, especially after transplantation from HTLV-I–negative donors. [18, 32] This decreased HTLV-I proviral load was observed after both myeloablative and reduced-intensity conditioning. Transplantation from an HTLV-I–positive donor is reportedly associated with a higher frequency of relapse compared with transplantation from an HTLV-I–negative donor. [11] Therefore, the uninfected normal donor T cells might overwhelm infected HTLV-I recipient T cells due to a GvATLL response and might act as an antiviral therapy. However, an HTLV-I–positive do-

nor might avoid clonal expansion of HTLV-I–infected T lymphocytes after allo-HSCT through the provision of cytotoxic T cells. Thus, it is currently difficult to determine whether an HTLV-I–positive or–negative donor should be selected. Longer follow-up is needed to resolve this issue. In the meantime, a prudent clinical attitude toward both HTLV-I–positive donors and recipients with ATLL is warranted.

In conclusion, allo-HSCT from an HTLV-I–negative unrelated donor appears to be an feasible alternative treatment for patients with ATLL for whom an HLA-matched related donor is unavailable. Further prospective controlled studies are needed to assess the efficacy of allo-HSCT for ATLL and to define the clinical indications of allo-HSCT for ATLL, taking into account donor selection, the conditioning regimen, and the prognostic factors identified in this study.

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APPENDIX: PARTICIPATING INSTITUTIONS

The following centers in Japan participated in this study: Hokkaido University Hospital, Sapporo University Hospital, Sapporo Hokuyu Hospital, Japanese Red Cross Asahikawa Hospital, Asahikawa Medical College Hospital, Hirosaki University Hospital, Tohoku University Hospital, Yamagata University Hospital, Akita University Hospital, Fukushima Medical College, National Cancer Center Central Hospital, Institute of Medical Science at the University of Tokyo, Toho University Hospital, Omori Hospital, Tokyo Metropolitan Komagome Hospital, Nihon University Hospital, Itabashi Hospital, Jikei University Hospital, Keio University Hospital, Tokyo Medical College Hospital, Tokyo Medical and Dental University Hospital, Tokyo University Hospital, Yokohama City University Hospital, Kanagawa Children's Medical Center, Kanagawa Cancer Center, Tokai University Hospital, St Marianna University Hospital, Chiba University Hospital, Chiba Children's Hospital, Matsudo Municipal Hospital, Kameda General Hospital, Saitama Children's Medical Center, Saitama Cancer Center Hospital, Saitama Medical School Hospital, Ibaraki Children's Hospital, Jichi Medical School Hospital, Dokkyo University Hospital, Fukaya Red Cross Hospital, Saiseikai Maebashi Hospital, Gunma University Hospital, Niigata University Hospital, Niigata Cancer Center Hospital, Shinshu University Hospital, Saku Central Hospital, Hamamatsu University Hospital, Hamamatsu Medical Center, Shizuoka General Hospital, Shizuoka Children's Hospital, Japanese Red Cross Nagoya First Hospital, Nagoya Daini Red Cross Hospital, Meitetsu Hospital, Nagoya University Hospital, Nagoya Ekisaikai Hospital, National Nagoya Hospital, Aichi Medical School Hospital, Nagoya City University Hospital, Showa Hospital, Anjo Kousei Hospital, Fujita Health University Hospital, Mie University Hospital, Kanazawa University Hospital, Kanazawa Medical University Hospital, Toyama Prefectural Central Hospital, Fukui Medical School Hospital, Shiga University of Medical Science, Center for Adult Disease in Osaka, Kinki University Hospital, Osaka University Hospital, Osaka Medical Center and Research Institute for Maternal and Child Health, Matsushita Memorial Hospital, Hyogo College of Medicine Hospital, Hyogo Medical Center for Adults, Kobe City General Hospital, Kobe University Hospital, Kyoto University Hospital, Kyoto Prefectural University of Medicine Hospital, Social Insurance Kyoto Hospital, Tottori Prefectural Central Hospital, Tottori University Hospital, Hiroshima Red Cross Hospital and Atomic-Bomb Survivors Hospital, Yamaguchi University Hospital, Ehime Prefectural Central Hospital, Okayama National Hospital, Kurashiki Central Hospital, Kyushu University Hospital, Harasanshin General Hospital, Hamanomachi General Hospital, National Kyushu Cancer Center, St Mary's Hospital, Kokura Memorial Hospital, Saga Prefectural Hospital, Nagasaki University Hospital, Miyazaki Prefectural Hospital, Kumamoto National Hospital, Kumamoto University Hospital, Oita Medical University Hospital, Kagoshima University Hospital, and Imamura Bun-in Hospital.

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