Table 4. Risk factors for second solid cancers among >1 year survivors after hematopoietic stem cell transplantation

Solid cancer	Risk factor	Number of patients with second cancer	RR	95% CI	*P*-value
All second solid cancers[a]		249			
	Total body irradiation	151	0.9	0.7–1.1	0.294
	Chronic GVHD				
	Limited type	45	1.4	1.0–1.9	0.087
	Extensive type	93	1.8	1.4–2.4	<0.001
	Age at transplant (years)				
	16–29	45	1.0		
	30–39	46	1.6	1.0–2.4	0.042
	40–49	68	2.5	1.7–3.7	<0.001
	50–59	71	5.5	3.7–8.2	<0.001
	60 or older	19	7.9	4.4–14.1	<0.001
Oral cancer[b]		64			
	Total body irradiation	38	1.0	0.8–1.3	0.957
	Chronic GVHD				
	Limited type	10	1.4	0.6–2.9	0.440
	Extensive type	29	2.9	1.6–5.1	<0.001
Esophageal cancer[b]		41			
	Total body irradiation	22	0.6	0.3–1.1	0.108
	Chronic GVHD				
	Limited type	7	2.1	0.8–5.9	0.151
	Extensive type	25	5.3	2.4–11.8	<0.001
Colon cancer[b]		26			
	Total body irradiation	12	0.5	0.2–1.2	0.144
	Chronic GVHD				
	Limited type	6	1.7	0.6–4.9	0.353
	Extensive type	10	1.6	0.6–4.2	0.329
	Grade 2–4 acute GVHD	12	2.0	0.9–4.4	0.101
Skin cancer[b]		13			
	Total body irradiation	12	1.2	0.8–1.6	0.377
	Chronic GVHD				
	Limited type	6	5.8	1.4–23.9	0.016
	Extensive type	2	1.8	0.3–8.9	0.500

RR, relative risk; CI, confidence interval; TBI, total body irradiation; GVHD, graft-versus-host disease.
[a]Stratified for primary disease (acute myeloid leukemia, acute lymphoblastic leukemia, chronic myeloid leukemia, and other).
[b]Stratified for primary disease (acute myeloid leukemia, acute lymphoblastic leukemia, chronic myeloid leukemia, and other) and patient age groups (<19, 20–29, 30–39, 40–49, 50–59, and >60). Adjusted for patient age as a continuous variable.

The incidence of secondary solid tumors in our study was similar to those in previously reported large studies [8, 9, 12, 13]. Rizzo et al. [12] reported that the incidence of secondary solid cancers among 28 874 transplant recipients and 85 583 person-years at risk was 1% at 10 years and 2.2% at 15 years, which were very similar to our results using the same statistical method for cumulative incidence, while treating death before secondary solid tumor as a competing risk. Majhail et al. [13] reported that the incidence of secondary solid cancers after HSCT using non-TBI, busulfan-cyclophosphamide conditioning was also ~1.2% at 10 years. The oral cavity was the most prominent high-risk cancer site compared with the general population, as in previous reports [8, 9, 12, 13]. Despite regional and racial differences in cancer incidence and cancer sites in the general population, the impact of HSCT on secondary cancer was similar.

In previous studies, TBI was reported to be a significant risk factor for the development of secondary cancer, but significant differences were not found in our study [7, 8, 10, 12, 23]. The subjects in this study were adult recipients, which may explain the different findings. Conditioning with radiation was reported to be associated with the development of secondary solid cancer in recipients at a younger age at transplant [12]. Moreover, a recent long-term follow-up analysis of patients who were transplanted after myeloablative doses of busulfan and cyclophosphamide without TBI found a similar increased incidence of secondary solid cancers as previous reports [13].

An older recipient age at transplant was a significant risk factor for the development of secondary solid tumor, as in previous studies [9, 13]. This result was not surprising since it is also the case in the general population. However, it is important to note that older patients are at higher risk of developing

secondary cancer and to promote patient education and preventive practices, since there has been a dramatic increase in the number of transplant recipients who are more than 50 years of age at transplant over the past decade. In comparison with the general population, younger patients were at a higher risk of developing a solid tumor. Several high-risk cancer sites (esophagus, liver, and bronchus/lung) in younger group did have only one observed cases, therefore, these results should not be emphasized and need to be confirmed in other studies. These sites were found to be significant because the expected numbers in general population for these sites were extremely small.

Although this study included a large number of recipients and a large number of person-years of follow-up, there are limitations. The follow-up years for older recipients were still limited, and therefore we may find a higher incidence of and risk of secondary solid cancers among recipients who are 50 years of age or older at transplant in the future. Second limitation involves possible under-reporting by recipients to transplant centers or by transplant centers to the registry. Until recently, transplant recipients have received only limited information regarding screening or the prevention of secondary solid cancers. Another limitation of this analysis was lack of central pathology review for secondary solid tumors. JSHCT data collection does not include the submission of specimen or pathology report. Since this study included transplants from 1990, central pathology review was difficult to perform at the time of analyses. In addition, limiting secondary tumors to centrally diagnosed tumors would decrease the number of identified secondary tumors; therefore, secondary solid tumors were identified as reported from transplant centers.

In conclusion, recipients of allogeneic hematopoietic stem cell transplant had a significantly higher risk of developing secondary solid cancers than the general population. Older recipients are at higher risk of developing secondary solid tumors, as in the general population. Lifelong screening is important for high-risk organ sites, especially for oral, pharynx, and esophageal cancers in recipients with active, or a history of, chronic GVHD.

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disclosure

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ORIGINAL ARTICLE

Allogeneic transplantation for primary myelofibrosis with BM, peripheral blood or umbilical cord blood: an analysis of the JSHCT

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To determine whether a difference in donor source affects the outcome of transplantation for patients with primary myelofibrosis (PMF), a retrospective study was conducted using the national registry data on patients who received first allogeneic hematopoietic cell transplantation (HCT) with related BM ($n=19$), related PBSCs ($n=25$), unrelated BM ($n=28$) or unrelated umbilical cord blood (UCB; $n=11$). The 5-year OS rates after related BM, related PBSC and unrelated BM transplantation were 63%, 43% and 41%, respectively, and the 2-year OS rate after UCB transplantation was 36%. On multivariate analysis, the donor source was not a significant factor for predicting the OS rate. Instead, performance status (PS) $\geqslant 2$ (vs PS 0–1) predicted a lower OS ($P=0.044$), and RBC transfusion $\geqslant 20$ times before transplantation (vs transfusion $\leqslant 9$ times) showed a trend toward a lower OS ($P=0.053$). No advantage of nonmyeloablative preconditioning regimens in terms of decreasing nonrelapse mortality or increasing OS was found. Allogeneic HCT, and even unrelated BM and UCB transplantation, provides a curative treatment for PMF patients.

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Keywords: idiopathic myelofibrosis; hematopoietic SCT; donor source; engraftment; survival

INTRODUCTION

Primary myelofibrosis (PMF) is a clonal stem cell disorder characterized by anemia, BM fibrosis, progressive splenomegaly, constitutional symptoms and a significant risk of evolution into acute leukemia.[1,2] The median age at diagnosis is ~65 years, with a median survival of ~5 years after diagnosis, depending on the presence or absence of clinically defined prognostic factors, such as those defined by the International Prognostic Scoring System (IPSS), Dynamic IPSS and Dynamic IPSS plus.[3–5] No available conventional drug therapies for PMF have been shown to prolong survival. Palliative therapeutic options include agents such as hydroxyurea, prednisone, EPO, androgens, thalidomide and lenalidomide, and nonpharmacological approaches such as blood transfusion, splenic irradiation and splenectomy.[6,7] The impact of new agents, such as Janus kinase 2 (JAK2) inhibitors, pomalidomide and histone deacetylase inhibitors, on the long-term management of PMF is under investigation.[7,8] The only known curative therapy for PMF is allogeneic hematopoietic cell transplantation (HCT).[9]

The largest retrospective study of PMF patients undergoing allogeneic BM or PBSC transplantation reported OS of 30–40% at 5 years after transplantation with nonrelapse mortality (NRM) of 24–43% at 1 year after transplantation.[10] The prospective study in patients with PMF or secondary myelofibrosis to evaluate a nonmyeloablative preconditioning regimen followed by mainly PBSC transplantation achieved an OS of 51% at 5 years after transplantation with NRM of 16% at 1 year after transplantation.[11] The issues of the choice of stem cell source, the choice of conditioning regimen and the timing of transplantation are currently under debate.[6–9,12,13]

To determine whether a difference in stem cell source affects the outcome of HCT for PMF patients, a retrospective study was conducted using the national registry data on patients who received first allogeneic HCT in Japan with BM, PBSCs or umbilical cord blood (UCB).

PATIENTS AND METHODS

Patients

Clinical data for patients with PMF who received first allogeneic HCT in Japan were extracted from the Transplant Registry Unified Management Program (TRUMP) system, which is a registry of the outcomes of Japanese transplant patients.[14] Patients who had progressed to myelofibrosis from polycythemia vera, essential thrombocythemia, leukemia or other disease were excluded. This study was approved by the Data Management Committee of the Japan Society for Hematopoietic Cell Transplantation (JSHCT) and by the ethics committee of the Nagoya University School of Medicine (no. 2012–0270).

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respectively. For patients with PS ⩾2 ($n=16$), NRM at 2 years was 77% (45–92%), and NRM at 5 years was not evaluable because of lack of patients alive beyond 5 years after transplantation.

OS

OS rates at 2 and 5 years after transplantation were 63% (95% CI, 38–80%) and 63% (38–80%) in related BM, 48% (28–66%) and 43% (23–61%) in related PBSC and 41% (21–59%) and 41% (21–59%) in unrelated BM transplantations, respectively (Figure 3). The OS rate at 2 years after unrelated UCB transplantation was 36% (11–63%), and the OS rate at 5 years after UCB transplantation was not evaluable because of a lack of patients alive beyond 5 years after transplantation (longest follow-up, 48 months). There was no significant difference among stem cell donor sources ($P=0.15$).

Cox's proportional hazards model was used with all clinical features listed in Table 1, and the final multivariate model is shown in Table 2. After adjustment by PS and frequency of RBC transfusion, which were significant on univariate analysis, donor source was not a significant factor for predicting OS. Instead, PS ⩾2 predicted a lower OS rate, and RBC transfusion ⩾20 times before transplantation showed a trend toward a lower OS. We confirmed that there was no significant difference in the frequencies of PS ⩾2 between patients receiving different stem cell sources (2 of 13 related BM, 6 of 24 related PBSC, 5 of 27 unrelated BM and 3 of 6 unrelated UCB transplantations; $P=0.30$). Similarly, we confirmed that there was no significant difference in the frequencies of RBC transfusion ⩾20 times between patients receiving different stem cell sources (2 of 8 related BM, 5 of 18 related PBSC, 8 of 20 unrelated BM and 2 of 5 unrelated UCB transplantations; $P=0.80$).

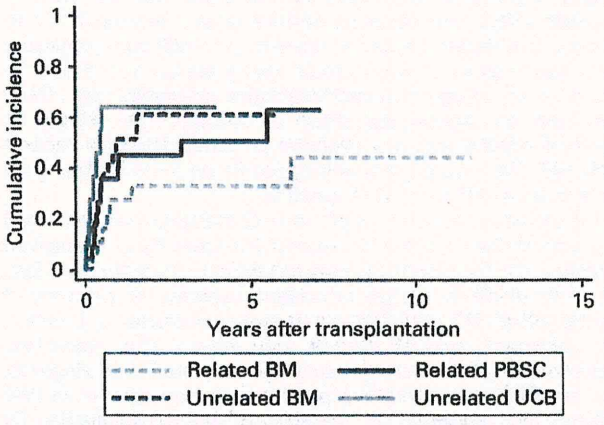

Figure 2. NRM after transplantation in PMF patients. Cumulative incidences of NRM after related BM (gray and dash line), related PBSC (black and solid line), unrelated BM (black and dash line) and unrelated UCB (gray and solid line) transplantations are shown.

Causes of death

The causes of death after transplantation are summarized in Table 3. For patients after related donor transplantation ($n=23$), the most common cause of death was primary disease ($n=9$, 39%), followed by infection ($n=4$, 17%) and organ failure ($n=3$, 13%). For patients after unrelated donor transplantation ($n=22$), the most common causes of death were infection ($n=7$, 32%) and organ failure ($n=7$, 32%), followed by GVHD ($n=3$, 14%), and only 1 patient (5%) died of primary disease.

DISCUSSION

The present study confirmed 5-year OS of 63%, 43% and 41% after related BM, related PBSC and unrelated BM transplantations, respectively. These results are comparable to previous reports in which long-term survival rates in patients with PMF or secondary myelofibrosis were 30–67% after transplantation.[10,11,21–26] This is the first report of UCB transplantation for more than 10 patients with PMF, and a 2-year OS of 36% was confirmed.

Several investigators have examined factors to predict outcomes after allogeneic HCT for PMF patients. The largest retrospective study of PMF patients from the CIBMTR demonstrated that Karnofsky score of <90% and the presence of blasts in peripheral blood, but not donor source, predicted lower disease-free survival of patients who had received BM or PBSC transplantation from related or unrelated donors.[10] Other retrospective studies including both PMF and secondary myelofibrosis demonstrated negative predictors for OS of higher patient age, nonchronic phase disease, RBC transfusion >20 times, increased comorbidity score, intermediate-2 and high scores of the Dynamic IPSS and non-HLA-matched sibling donor.[11,21,24,26,27] In the present study, multivariate analysis demonstrated that PS ⩾2 predicted a lower OS and that RBC transfusion ⩾20 times before transplantation showed a trend toward a lower OS (Table 2). Unexpectedly, the stem cell source was not a significant factor for OS. One possibility is that a significant association between stem cell source and OS was not detected because of a lack of statistical power, namely, the small

Table 2. Significant factors in multivariate analyses for nonrelapse mortality and OS after transplantation

	Nonrelapse mortality HR (95% CI)	*P-value*	*Overall survival* HR (95% CI)	*P-value*
Performance status at transplant				
0–1	1.0		1.0	
⩾2	3.36 (1.42–7.95)	0.006	2.67 (1.03–6.95)	0.044
Frequency of RBC transfusion[a]				
⩽9	NA		1.0	
10–19	NA		0.48 (0.97–2.36)	0.37
⩾20	NA		2.42 (0.99–5.93)	0.053
Donor source				
Related BM	1.0		1.0	
Related PBSCs	2.43 (0.73–8.07)	0.15	3.86 (0.81–18.44)	0.091
Unrelated BM	3.58 (1.07–12.01)	0.039	3.13 (0.66–14.79)	0.15
Unrelated umbilical cord blood	2.71 (0.49–14.86)	0.25	3.79 (0.60–23.91)	0.16

Abbreviations: CI = confidence interval; HR = hazard ratio; NA = not applicable.
[a]Frequency of RBC transfusion before transplantation.

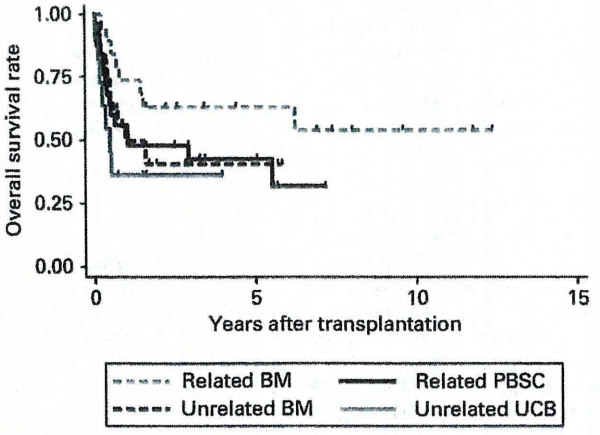

Figure 3. OS rates after transplantation in PMF patients. OS rates after related BM (gray and dash line), related PBSC (black and solid line), unrelated BM (black and dash line) and unrelated UCB (gray and solid line) transplantations are shown.

Table 3. Causes of death

	Related BM, n (%)	*Related PBSC, n (%)*	*Unrelated BM, n (%)*	*Unrelated UCB, n (%)*
Primary disease	2 (25)	7 (46)	1 (7)	0
Infection	1 (13)	3 (20)	6 (40)	1 (14)
Interstitial pneumonitis	2 (25)	0	1 (7)	0
ARDS	0	0	1 (7)	0
GVHD	1 (13)	1 (7)	2 (13)	1 (14)
Organ failure	1 (13)	2 (13)	3 (20)	4 (58)
Graft failure	1 (13)	0	0	0
Bleeding	0	1 (7)	1 (7)	0
Other	0	1 (7)	0	1 (14)
Total	8 (100)	15 (100)	15 (100)	7 (100)

Abbreviations: ARDS = acute respiratory distress syndrome; UCB = umbilical cord blood.

number of patients in each group, and the short-term follow-up. In particular, the number of patients with UCB transplantation was very small, and therefore, careful interpretation of these data is required. Further analysis with data including more patients undergoing UCB transplantation is required in order to determine the effect of UCB transplantation on outcomes of PMF patients. Another possibility is that the HCT outcome for PMF patients is more adversely affected by the deterioration in a patient's systemic condition as a consequence of multiple transfusions of blood and so on, rather than by the difference in stem cell sources.

In practice, UCB transplantation may be avoided in the treatment of PMF patients because of delayed engraftment and a higher probability of graft failure.[9] The present study demonstrated that UCB transplantation was significantly associated with a lower probability of hematopoietic recovery in comparison with related BM transplantation (Figure 1). The incidences of neutrophil recovery at 60 days and platelet recovery at 1 year were 82% and 44% for UCB transplantation, respectively. In a recent report of nonmyeloablative UCB transplantation for 14 patients with myelofibrosis, including 1 patient with PMF and 13 patients with secondary myelofibrosis, the incidences of neutrophil recovery at 60 days and platelet recovery at 100 days were 93% and 43%, respectively.[28] Thus, careful management is required for PMF patients, especially in the early period after unrelated UCB transplantation.

NRM was 30–60% (Figure 2), which is higher than in previous studies from large, well-known transplant center(s).[22–24,26,27,29–32] This may be explained by the large number of the participating centers, the heterogeneity of patients' clinical features and the fact that 18% of patients were ⩾60 years in the present study.

Nonmyeloablative preconditioning regimens have advantages of less NRM and a broader applicability in elderly patients and may, therefore, be appropriate for PMF patients. After small studies demonstrated the feasibility of allogeneic HCT with nonmyeloablative preconditioning for myelofibrosis,[33–35] Kröger *et al.*[11] prospectively treated 103 patients with PMF or post essential thrombocythemia and post polycythemia vera myelofibrosis with BU and fludarabine-based nonmyeloablative preconditioning. They reported encouraging 1-year NRM of 16% and 5-year OS of 67%. The Swedish group compared results from 10 patients undergoing nonmyeloablative transplant with 17 patients undergoing myeloablative transplant for secondary myelofibrosis. NRM was lower in the nonmyeloablative group than in the myeloablative group (10% vs 30%). With a median follow-up of 55 months, 9 (90%) of 10 patients undergoing nonmyeloablative transplant and 9 (55%) of 16 patients undergoing myeloablative transplant survived.[36] In contrast, the present study could not find any advantage of nonmyeloablative preconditioning in terms of decreasing NRM or increasing OS (Table 2). Other retrospective studies, including a large study ($n = 289$), also did not find any favorable affect with nonmyeloablative preconditioning.[10,22,24] In retrospective studies, drugs and doses of preconditioning regimens were heterogeneous, which could partly explain the failure to detect an advantage of nonmyeloablative preconditioning. There has been no randomized study to compare the efficacy of nonmyeloablative and myeloablative preconditioning for patients with PMF. The advantage of nonmyeloablative preconditioning for patients with PMF remains in question.

The molecular assessment of the *JAK2* mutation was performed in a very limited number of patients (six cases for pretransplant mutation and four cases for post transplant mutation). Therefore, we were unable to analyze association between the presence of pretransplant *JAK2* mutation and transplant outcomes or between the minimum residual disease and relapse after transplant. However, the present study clearly demonstrated that allogeneic BM and PBSC transplantations provide long-term survival for PMF patients and suggested the feasibility of UCB transplantation for PMF patients. Given the constant improvement in supportive care for transplant patients and the beginning of the use of molecular targeted therapy for myelofibrosis, the NRM and relapse rates may be further decreased. Allogeneic HCT should be considered in the treatment plan for PMF patients. The indications for allogeneic HCT in PMF patients have to be defined in a future study.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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APPENDIX

Institutes participating in this study: Japanese Red Cross Asahikawa Hospital; Hokkaido University Hospital; Sapporo Medical University Hospital; Sapporo Hokuyu Hospital; Akita University Hospital; Iwate Medical University; Tohoku University Hospital; Fukushima Medical University Hospital; Nagaoka Red Cross Hospital; Gunmaken Saiseikai Maebashi Hospital; Tsukuba Memorial Hospital; Chiba University Hospital; Kameda Medical Center; National Defense Medical College Hospital; Saitama Medical Center, Jichi Medical University; Keio University Hospital; Tokyo Metropolitan Cancer and Infectious diseases Center, Komagome Hospital; Toranomon Hospital; National Cancer Center Hospital; Tokyo Women's Medical University Hospital; Institute of Medical Science, University of Tokyo; Nippon Medical School Hospital; Kanagawa Cancer Center; Yokohama City University Medical Center; Nagano Red Cross Hospital; Shinshu University Hospital; Toyama Prefectural Central Hospital; Kurobe City Hospital; Kanazawa University Hospital; Shizuoka General Hospital; Japanese Red Cross Shizuoka Hospital; Hamamatsu University Hospital; Hamamatsu Medical Center; Anjo Kosei Hospital; Fujita Health University Hospital; Japanese Red Cross Nagoya Daiichi Hospital; Japanese Red Cross Nagoya Daini Hospital; Meitetsu Hospital; Nagoya University Hospital; Nara Medical University Hospital; Tenri Hospital; Takanohara Central Hospital; Kyoto University Hospital; Kyoto-Katsura Hospital; Osaka Red Cross Hospital; Osaka Medical Center for Cancer and Cardiovascular Diseases; Takatsuki Red Cross Hospital; Seichokai Fuchu Hospital; Kinki University Hospital; Wakayama Medical University Hospital; Hyogo College of Medicine; Institute of Biomedical Research and Innovation; Kurashiki Central Hospital; Okayama Medical Center; Hiroshima Red Cross Hospital & Atomic-bomb Survivors Hospital; Shimane Prefectural Central Hospital; Yamaguchi University Hospital; Ehime University Hospital; Ehime Prefectural Central Hospital; Kochi Medical School Hospital; Kitakyushu Municipal Medical Center; University of Occupational and Environmental Health; Kyushu Cancer Center; Kyushu Medical Center; Kyushu University Hospital; Kurume University Hospital; Ryukyu University Hospital.

Leukemic evolution of donor-derived cells harboring *IDH2* and *DNMT3A* mutations after allogeneic stem cell transplantation

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Although allogeneic stem cell transplantation is effective for the treatment of leukemia with poor prognosis, some such treated individuals experience disease relapse at various times after transplantation. Chimerism analysis of the relapsed disease has revealed infrequent cases in which the malignant cells originate from the donor and not from the initial leukemic clones.[1,2] Such donor cell leukemia (DCL) is often refractory to further treatment, with a mean overall survival for the affected patients of only 32.8 months.[2]

We recently described a 47-year-old Japanese man with acute myeloid leukemia (AML) who underwent a transplantation of peripheral blood stem cells (PBSCs) from his HLA-matched brother.[3] Although the allogeneic transplantation was successful, AML again became apparent in the patient 27 months later and chimerism analysis revealed that the leukemia was DCL. Genomic DNA was isolated and subjected to whole-exome sequencing from specimens of the initial AML (containing 70% myeloblasts, referred to as sample P1), the first complete remission after chemotherapy (sample P2), the first relapse (containing 24% myeloblasts; sample P3), donor PBSCs (sample D1), DCL at 27 months after allogeneic transplantation (containing 6% myeloblasts, sample D2) and DCL at 36 months after transplantation (containing 71% myeloblasts, sample D3).

Exome sequencing yielded a total of ~84.7 million, ~31.6 million, ~73.5 million, ~44.3 million and ~53.2 million unique, high-quality, paired-end reads for samples P1, P2, P3, D1 and D3, respectively (Supplementary Information). Although chimerism analysis for short tandem repeats had indicated that D3 was derived from D1 clones,[3] we further examined this possibility in a genome-wide manner. As demonstrated in Supplementary Figure 1a, the allele frequency of single-nucleotide polymorphisms (SNPs) detected in our data sets was highly concordant between P1 and P2 (Pearson's correlation coefficient (r) of 0.978) as well as between P1 and P3 ($r = 0.986$), suggesting that these three samples originate from a single individual. However, as expected, the concordance dropped substantially for the P1 and D3 pair ($r = 0.628$). In contrast, the concordance between D1 and D3 was high ($r = 0.983$), suggesting that the relapsed leukemia after transplantation was indeed derived from the donor cell. Of note, the allele frequency of SNPs showed only a low level of concordance ($r = 0.285$) between P1 and a cell line (KCL22)[4] derived from an unrelated Japanese patient with chronic myeloid leukemia (Supplementary Figure 1b). The correlation coefficient of 0.628 for P1 and D3 thus indicated that the patient and donor siblings share a substantial number of SNPs.

We next searched for somatic nonsynonymous mutations among the leukemic samples. For P1 and P3, we used P2 as a paired normal control. Given that D3 was shown to be derived from D1, we used the latter as the germline control for the former. Through our computational pipeline (Supplementary Information), nine missense mutations and two out-of-frame insertions/deletions (indels) were detected for P1, two missense mutations for P3 and nine missense mutations and one out-of-frame indel for D3 (Table 1). As described previously,[3] a 4-bp deletion of *CEBPA* was present in the initial AML but absent from the DCL. Similarly,

Table 1. Confirmed somatic mutations in the specimens analyzed

Specimen	*Gene symbol*	*GenBank accession no.*	*Nucleotide change*	*Amino-acid change*	*Mutation ratio (%)*				
					P1	*P2*	*P3*	*D1*	*D3*
P1	*ACSL5*	NM_016234	c.280G>A	p.V94I	40.6	0.0	30.6	0.0	0.0
	ANO4	NM_178826	c.2441C>T	p.S814L	42.3	0.0	16.7	0.0	0.0
	APOB	NM_000384	c.9175C>T	p.R3059C	32.8	0.0	7.4	0.0	0.0
	BANK1	NM_017935	c.222C>G	p.N74K	36.4	0.0	9.2	0.0	0.0
	CCDC88C	NM_001080414	c.3748G>A	p.E1250K	36.4	0.0	0.0	0.0	0.0
	FAM178B	NM_001122646	c.81G>A	p.M27I	41.2	0.0	25.0	0.0	0.0
	GABRB2	NM_021911	c.1009C>T	p.R337C	44.8	0.0	14.5	0.0	0.0
	JAK3	NM_000215	c.2570T>C	p.L857P	40.8	0.0	0.0	0.0	0.0
	SPATA31D1	NM_001001670	c.3793C>T	p.R1265C	36.6	0.0	6.7	0.0	0.0
	CEBPA	NM_004364	c.319_322delGACT	p.D107Tfs	63.6	0.0	10.0	0.0	0.0
	STAG2	NM_001042750	c.219_220insCG	p.H73Rfs	100.0	0.0	27.6	0.0	0.0
P3	*ACSL5*	NM_016234	c.280G>A	p.V94I	40.6	0.0	30.6	0.0	0.0
	NTNG2	NM_032536	c.1348G>T	p.G450C	0.0	0.0	37.5	0.0	0.0
D3	*CCDC168*	NM_001146197	c.11761G>C	p.D3921H	0.0	0.0	0.0	0.0	55.6
	GAL3ST1	NM_004861	c.1086G>T	p.M362I	0.0	0.0	0.0	0.0	32.6
	IDH2	NM_002168	c.419G>A	p.R140Q	0.0	0.0	0.0	7.1	50.0
	MYO7B	NM_001080527	c.635G>A	p.R212H	0.0	0.0	0.0	0.0	45.8
	NFATC1	NM_172390	c.736G>A	p.V246I	0.0	0.0	0.0	0.0	48.6
	PSMB8	NM_004159	c.637C>T	p.P213S	0.0	0.0	0.0	0.0	40.9
	TCAIM	NM_173826	c.668C>G	p.S223C	0.0	0.0	0.0	0.0	70.0
	TMEM132D	NM_133448	c.481G>A	p.A161T	0.0	0.0	0.0	0.0	35.3
	UBA2	NM_005499	c.419G>A	p.G140E	0.0	0.0	0.0	0.0	47.4
	DNMT3A	NM_153759	c.449delT	p.V150Gfs	0.0	0.0	0.0	8.7	61.1
	NRAS[a]	NM_002524	c.38G>A	p.G13D	0.0	0.0	0.0	0.0	18.4

[a]Below the threshold in the initial screening.

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none of the identified somatic mutations were shared between the initial AML and DCL, providing further support for the distinct nature of the two leukemias.

Given that P3 contains only 24% myeloblasts, our computational pipeline could not accurately detect all of the associated somatic mutations. Indeed, most of the somatic mutations found in P1 (such as those in *ANO4*, *APOB*, *BANK1*, *STAG2* and *CEBPA*) were still present in P3 at lower frequencies (Table 1) but were not isolated in our pipeline analysis for P3. Lowering the threshold for somatic calls, however, increased the number of pseudopositive mutations in all specimens. We therefore applied the 30% threshold for mutation calls to all analyses. Of note, our data still indicate that P3 is not completely identical to P1. Nonsynonymous mutations of *CCDC88C* and *JAK3* detected in P1 were thus absent in P3, whereas a mutation of *NTNG2* was newly apparent in P3, suggestive of a clonal evolution in P3 divergent from the original P1 clones.

Surprisingly, whereas most somatic mutations detected in D3 were not present in D1, our results suggested that IDH2(R140Q) and DNMT3A(V150Gfs) were already present in the healthy donor at a low frequency (Table 1). Polymerase chain reaction (PCR)-based cloning of the genomic fragments and Sanger sequencing for *IDH2* and *DNMT3A* from D1 indeed confirmed the presence of the corresponding mutations in 2 (2.3%) out of 87 DNA clones and 1 (1.1%) out of 93 clones, respectively (Supplementary Figure 2). Furthermore, although the mutation rate (18.4%) was below the threshold of the present study, the oncogenic mutation NRAS(G13D)[5] in D3 (Table 1) was confirmed by Sanger sequencing of the corresponding genomic DNA (Supplementary Figure 2).

We then verified these infrequent mutations by sequencing the corresponding DNA fragments at extra-high coverage (hundreds of thousand times) with the use of a next-generation sequencer. The D2 sample, which contains only 6% myeloblasts, was also examined in this analysis. We confirmed that 1.6% (5.96×10^3 mutant reads out of 3.67×10^5 total reads at the corresponding nucleotide position) and 2.1% (1.24×10^4 out of 6.01×10^5 reads) of D1 cells already harbored the IDH2(R140Q) and DNMT3A(V150Gfs) mutations, respectively (Figure 1a). These mutations were not detected in the primary AML (P1 to P3). Whereas the *NRAS* mutation was not detected in D1, it became apparent in D2 and D3 at a frequency similar to that of the *IDH2* mutation. In addition, the *JAK3* mutation present in P1 was no longer evident at the relapsed stage P3.

On the basis of the genetic mutation profiles identified in the present case, we propose the following scheme for disease progression (Figure 1b). Given the high frequency of *STAG2* and *CEBPA* mutations in the primary AML, the 2-bp insertion in *STAG2* on the X chromosome (with there being only one copy of *STAG2* per cell in the male patient) as well as the heterozygous 4-bp deletion in *CEBPA* may characterize the founding clone of the original leukemia, with subsets of this clone subsequently acquiring additional oncogenic hits such as JAK3(L857P). The disappearance of *JAK3* and *CCDC88C* mutations in P3 suggests that the leukemic subclones harboring these mutations were sensitive to the initial chemotherapy.

The molecular pathogenesis of DCL has been unclear and may differ among cases. For instance, germline predisposition to cancer, such as the Li-Fraumeni syndrome or Bloom syndrome, may be shared between recipients and related donors.[6] However, in the present case, mutations in *IDH2* and *DNMT3A* were detected only in the donor, not in the primary AML, rendering this scenario unlikely. Alternatively, occult leukemia may already be present in the donor blood system and is inadvertently transmitted to the recipient.[7] In such cases, however, leukemia usually emerges in the donor soon after transplantation. Our donor, in contrast, has not developed any hematologic malignancy at 10 years after the donation of his PBSCs.

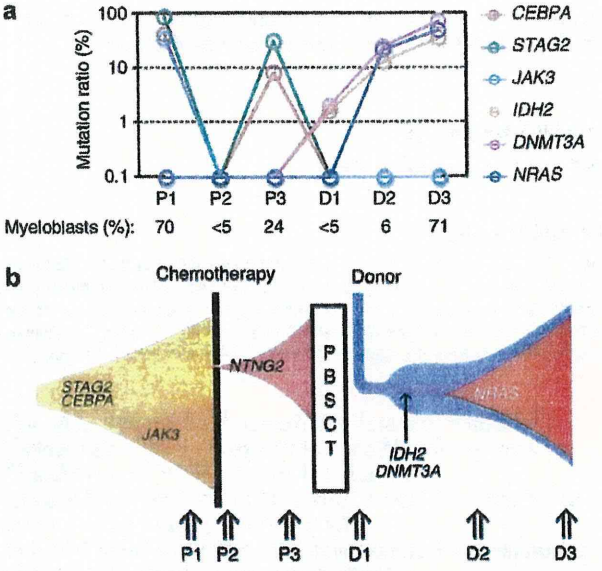

Figure 1. Genomic analysis of AML samples and donor PBSCs. (**a**) Genomic mutations corresponding to CEBPA(D107Tfs), STAG2(H73Rfs), JAK3(L857P), IDH2(R140Q), DNMT3A(V150Gfs) and NRAS(G13D) were examined by targeted deep sequencing in genomic DNA prepared from samples P1, P2, P3, D1, D2 and D3. The ratio of mutant reads to all reads at the corresponding position is shown as a percentage, with mutation frequencies of <0.1% being considered as 0.1% in the graph. The percentage of myeloblasts in each sample is indicated below the graph. (**b**) Founding clones of the primary AML harbored nonsynonymous mutations of *STAG2* and *CEBPA* and gave rise to subclones harboring a *JAK3* mutation. Whereas the latter cell population was sensitive to the initial chemotherapy, a subclone positive for an *NTNG2* mutation emerged from the former population and gave rise to relapse. All of these leukemic clones were successfully eradicated by peripheral blood stem cell transplantation (PBSCT). PBSCs of the donor, however, contained a small clonal population of cells positive for *IDH2* and *DNMT3A* mutations that eventually gave rise to AML on acquisition of additional mutations including NRAS(G13D).

Our present data therefore strongly suggest that apparently healthy individuals may harbor preleukemic subclones in their blood system (Figure 1b). Indeed, somatic mutations of *TET2* and *DNMT3A* were recently identified in clonal blood cells from one healthy elderly individual.[8] Furthermore, the *IDH2* and *DNMT3A* mutations identified in the present study may have had a specific role in the initiation of leukemia, given that mutations in the epigenetic modifiers including TET1/2, IDH1/2 and DNMT3A have been identified as early genetic events in AML progression.[9,10] Such mutations are indeed among the most frequently detected somatic alterations in AML.[11] These observations raise an important concern as to how 'appropriate' donors should be chosen, especially given that the incidence of DCL is increasing with the prevalence of molecular analysis for donor/recipient chimerism.[2] Prospective studies of whether and how examination of preleukemic subclones should be incorporated into the donor selection process for stem cell transplantation are thus warranted.

Furthermore, in our case, the oncogenic mutation NRAS(G13D) was likely a driver for leukemia progression, given that the frequency of this mutation was almost identical to that of the *IDH2* mutation in the D2 and D3 specimens. In contrast to the absence of leukemia in the donor, DCL rapidly developed in the recipient after transplantation in association with the accumulation of additional genetic hits, possibly as a result of a growth-promoting condition of the bone marrow after transplantation and due to a

defective immune surveillance resulting from the immunosuppressive treatment to control graft-versus-host disease.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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Supplementary Information accompanies this paper on the Leukemia website (http://www.nature.com/leu)

Cytogenetics and outcome of infants with acute lymphoblastic leukemia and absence of *MLL* rearrangements

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Acute lymphoblastic leukemia (ALL) in infants less than 1 year of age is rare and the biological features are different from ALL in older children.[1] Infant ALL is characterized by a high frequency of rearrangements of the *MLL* gene (*MLL*-R) and heterogeneous outcome. However overall, their event-free survival (EFS) is much worse than older children with ALL.[1–5] A large collaborative trial, Interfant-99, demonstrated improved outcome, while characterizing definitively the independent prognostic variables in infant ALL.[6] While cytogenetic data are reported within individual infant ALL clinical trials, the numbers are typically small and many reports are less detailed for those patients without *MLL* gene rearrangements (*MLL*-G). However, it was previously suggested that *MLL*-G had an important predictive influence on outcome.[7,8] These observations were later confirmed in Interfant-99,[6] in which *MLL*-G patients showed a threefold reduced risk of an event compared with *MLL*-R patients, although all *MLL*-G patients were grouped together into a single category. To better understand the association of different chromosomal abnormalities and outcome among *MLL*-G infants, here we have carried out detailed cytogenetic investigation of two infant ALL trials: Interfant-99 and Children's Oncology Group (COG)-P9407.

Patients were 365 days old or less with newly diagnosed ALL without a rearrangement of the *MLL* gene enrolled to Interfant-99 (May 1999–December 2005; $n=110$) and COG-P9407 (June 1996–October 2006; $n=52$).[6,9] Individual study groups obtained ethical approval, and treating physicians obtained informed consent from parents or guardians. The presence of *MLL* gene rearrangements was excluded using fluorescence *in situ* hybridization (FISH), reverse transcription (RT)-PCR and/or Southern blotting, as previously reported.[6] Each national study group provided patient data, including cytogenetics, FISH and molecular results. EFS and overall survival (OS) were calculated from the date of trial enrolement to the date of the first event (induction failure, relapse, second malignancy or death) or last follow-up. Median follow-up time was 7 years.

Among 162 *MLL*-G patients, no cytogenetic data were available for 34 (21%), resulting in a success rate of 79%. An abnormal karyotype was detected in 90/128 (70%) patients with a successful cytogenetic result (Supplementary Table 1) with the remainder classified as normal based on the presence of at least 10 (but usually 20) normal metaphases. They were categorized according to cytogenetic risk group as previously defined for childhood ALL.[10] Compared with childhood ALL (1–18 years) using data from the UKALL97/99 treatment trial,[10] the frequency of good risk cytogenetic abnormalities among *MLL*-G infants was significantly lower (12 vs 60%, $P<0.01$), whereas the frequency of poor risk abnormalities (excluding *MLL* translocations) was similar (8 vs 10%). Although *ETV6–RUNX1* fusion is present in 25% of childhood ALL, we found no *ETV6–RUNX1* cases among the 75 patients tested by FISH or RT-PCR. High hyperdiploidy (HeH) was the most

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ORIGINAL ARTICLE

Risk factors and organ involvement of chronic GVHD in Japan

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Few studies have evaluated the risk factors for chronic GVHD and organ involvement associated with different graft types, including unrelated cord blood (U-CB). We retrospectively studied 4818 adult patients who received their first allogeneic transplantation and survived for at least 100 days. The incidence of chronic GVHD at 2 years was 37%. The following factors were associated with the development of chronic GVHD: female donor/male recipient, CMV-Ab seropositivity, matched related peripheral blood grafts vs matched related BM grafts, no *in vivo* T-cell depletion and the occurrence of grade II–IV acute GVHD. Among these factors, the association with acute GVHD occurrence was consistently significant across donor subtypes. The use of U-CB was not associated with chronic GVHD, but was associated with a low incidence of extensive chronic GVHD. Chronic GVHD patients who had received U-CB transplants showed less frequent involvement of the oral cavity (28% vs 55%), eye (12% vs 26%), liver (20% vs 44%), lung (11% vs 25%) and joint (0% vs 6%) than those with matched related BM grafts. In conclusion, we found that U-CB transplants were associated with a low incidence of extensive chronic GVHD and less frequent involvement of the oral cavity, eye, liver, lung and joints.

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Keywords: chronic GVHD; unrelated cord blood; acute GVHD; risk factors

INTRODUCTION

Chronic GVHD is a serious complication that affects the survival and quality of life of long-term survivors after allogeneic hematopoietic SCT.[1–3] Various pre- and post-transplant risk factors associated with chronic GVHD have been identified, mostly in transplantations using BM and PBSC grafts from related or unrelated donors.[2,3] Several studies have reported a history of acute GVHD to be a strong risk factor that is consistently associated with chronic GVHD development.[4–8] Other identified risk factors include the following: female donor and male recipient,[4,6] use of PBSC grafts,[6,9–13] older patient,[4,6–8] older donor,[6,7] transplantation from a mismatched or unrelated donor,[5,6,14] diagnosis of CML[4,7,8] and absence of anti-thymocyte globulin (ATG) use.[15]

The number of unrelated cord blood (U-CB) transplantations performed has rapidly increased during the past decade. However, few studies have compared the incidences and risk factors of chronic GVHD and its organ-specific symptoms in adult patients receiving U-CB and other available grafts, including related or unrelated BM/PBSC grafts.[16,17] Therefore, we conducted a retrospective study using national registry data involving 4818 patients who underwent allogeneic transplantation. This study aimed to evaluate the incidence and risk factors of chronic GVHD, and the prevalence of chronic GVHD organ involvement in patients who received transplantation using various types of graft, including U-CB.

MATERIALS AND METHODS

Data collection

Data for 54072 patients who had received auto-SCT or allo-SCT by December 31, 2009 were provided by the Transplant Registry Unified Management Program (TRUMP).[18] We included 4993 adult patients who had: (1) received allogeneic transplantation for hematologic malignancies; (2) received their first SCT; (3) used the same questionnaire form involving chronic GVHD organ involvement (skin, oral cavity, eye, liver, lung, joint, intestine/genitals and other manifestations; 2006–2009 for transplantations using BM or PBSC grafts and 2007–2009 for transplantations using U-CB units); (4) achieved neutrophil engraftment; (5) survived for at least 100 days; and (6) received the following: (a) a related BM or PBSC graft (R-BM/PB), (b) an unrelated BM (U-BM) or (c) a single U-CB unit. Donation of peripheral blood by unrelated volunteers was permitted for the first time in Japan in 2011. The following patients were excluded: (1) patients who received *ex vivo* T-cell-depleted grafts ($n = 26$) and (2) patients who lacked data on acute or chronic GVHD ($n = 149$). Thus, 4818 patients were included in this study, which was approved by the TRUMP Data Management Committees and by the institutional review board of the Nagoya University Graduate School of Medicine, where this study was performed.

Histocompatibility

Histocompatibility data for the HLA-A, HLA-B and HLA-DR loci were obtained through reports acquired from the institution where the transplantation was performed or from the cord blood bank. HLA

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