(ligand–ligand analysis) in unrelated T cell–replete HLA-A, -B, and -DR serologically matched bone marrow transplantation without preadministration of antithymocyte globulin (ATG) (n = 1790) through the Japan Marrow Donor Program (JMDP) [5]. Other UR-HSCT studies have documented either adverse or beneficial effects of KIR ligand incompatibility on transplantation outcome [6-14].

Candidate factors possibly accounting for this discrepancy include T cell depletion, *KIR* genotype of patients and donors, sample size, ethnicity, number and source of stem cells, ATG preadministration, graft-versus-host disease (GVHD) prophylaxis, and diseases. Associations between *KIR* genotype and clinical outcome have been reported in both related HLA-identical transplantation [15-22] and unrelated transplantation settings [10,23-27]. However, the contribution of the *KIR* genotype to KIR ligand compatibility has not yet been well defined. Preadministration of ATG in the conditioning regimen both reduces stem cell rejection by host lymphocytes and prevents GVHD by donor-derived lymphocytes, as the drug remains in the patient's blood for several weeks after transplantation and affects residual donor mature lymphocyte activity and reconstitution of the lymphocyte repertoire from donor stem cells [28]. Earlier UR-HSCT studies have demonstrated the need for ATG administration to gain the beneficial effect of NK cell alloreactivity [7], whereas an adverse effect of KIR-L-MM has been reported in both a non-ATG preadministration study [6] and ATG preadministration studies [8,9]; however, a direct comparison of the ATG-administration and ATG-nonadministration groups in a single large cohort has never been performed. Such a study is desirable for a precise evaluation of the effect of ATG on KIR-L-MM.

In this study, patients with hematologic malignancy cases who received uniform GVHD prophylaxis were retrospectively selected from patients undergoing unrelated bone marrow transplantation through the JMDP. All cases were HLA-A, -B, and -DR serologically matched (ie, including HLA-A, -B, and -DR allele-mismatched pairs as well as HLA-Bw4 and HLA-A3 and -A11 KIR ligand matched and HLA-C-KIR ligand matched and mismatched pairs) and mostly uniform with regard to ethnicity and transplantation regimens [29,30]. In these cases, the effects of *KIR* genotype, KIR ligand compatibility, and ATG administration status on transplantation outcomes were analyzed to resolve the discrepant findings regarding the effects of KIR-L-MM.

PATIENTS AND METHODS

Patient and Cohort Selection Criteria

A cohort (n = 1489) was selected from among patients undergoing unrelated bone marrow transplantation between 1993 and 2000 through the JMDP. Characteristics of the patients and donors are summarized in Table 1. A source of hematopoietic stem cells of all transplantations were from T cell–replete and HLA-A, -B, and -DR serologically matched bone marrow. Patients with hematologic malignancies, including 401 cases of acute myelogenous leukemia (AML), 438 cases of acute lymphoblastic leukemia (ALL), 451 cases of chronic myelogenous leukemia (CML), 137 cases of myelodysplastic syndrome (MDS), and 62 cases of malignant lymphoma (non-Hodgkin lymphoma) were analyzed. GVHD prophylaxis other than the combination of cyclosporine and short-term methotexate (the most common treatment reported in the JMDP [68.1%]) was excluded. Ninety-four patients with preadministered ATG were included and analyzed separately or together with the nonadministered cases. Standard risk for relapse was defined as the status of first complete remission (CR) of AML or ALL, first chronic phase (CP) of CML at transplantation, or refractory anemia (RA) in MDS. High risk was defined as a more advanced status than standard risk in AML, ALL, CML, and MDS. All patients were preconditioned with a myeloablative regimen, and 1204 patients received total body irradiation (TBI)-containing regimens, whereas 285 received non–TBI-containing regimens. The final clinical survey of these patients was performed as of

Table 1. *Patient characteristics and matching of HLA allele between patient and donor*

	All patients	C-match	C-mismatch KIR-L-MM-G	C-mismatch KIR-L-M
Analyzed number	1489	1013	81	395
AML	401	286	17	98
ALL	438	306	24	108
CML	451	296	25	130
MDS	137	82	14	41
Malignant lymphoma	62	43	1	18
Patient age	26	27	25	27
Donor age (90 high risk)	34	35	35	34
Sex match	57	56.6	59.3	57.5
TBI	80.9	81	79	80.8
Status of leukemia (% high risk)	55.1	53.5	70	56
HLA-allele mismatch, %				
A	18.5	14.2	28.4	27.6
B	9.1	3.5	25.9	20.1
C	32	0	100	100
DRB1	18.9	15.5	32.1	24.8
DQB1	22	18.7	28.4	29.1
DPB1	71.3	74.8	82.7	76.7
ATG+	94	56	11	27
ATG−	1395	957	70	368
Donor *KIR 2DS2* analyzed	233	83	80	70
Patient–donor *16 KIR* type analyzed	187	70	55	62

June 1, 2005. The mean and range for clinical follow-up were 2914 days and 1639-4597 days, respectively. A part of the subject population (leukemia treated with cyclosporine and short-term methotexate; n = 1210) was overlapped with that reported in our previous study [5]. Written informed consent was obtained from all patients and donors, and the study design was approved by the institutional review boards of the Japanese Red Cross Tokyo Metropolitan Blood Center, the Aichi Cancer Center, and the JMDP.

HLA and KIR Ligand Typing and Compatibility Characterization of Patient–Donor Pairs

HLA-A, -B, -C, -DR, -DQ, and *-DP* alleles of all patients and donors were retrospectively determined by DNA typing as described previously [5]. For analysis of GVHD and leukemia relapse, *HLA* allele mismatch among donor–patient pairs was defined as the patient's alleles not being shared by the donor. KIR ligand specificity of the HLA-C antigen was determined according to the amino acid residues of the HLA-C allele. C1 ligand specificity consists of Asn 80 (Cw1, w3, w7, w8, and others); C2 specificity consists of Lys 80 (Cw2, w4, w5, w6, and others). In the cohort (patients and donors, n = 2978), the numbers of C1C1, C1C2, and C2C2 were 2555 (85.8%), 399 (13.4%), and 24 (0.81%), respectively. HLA-C mismatched pairs (n = 476) were divided into KIR ligand mismatch in the GVH direction (KIR-L-MM-G) (n = 81) and KIR ligand match in the GVH direction (KIR-L-M) (n = 395). KIR-L-MM-G was defined as the donor's KIR ligand for HLA-C not being shared by the patient's ligand. KIR-L-M included ligand match and ligand mismatch in the host-versus-graft (HVG) rejection direction. The combinations of KIR ligands in KIR-L-MM-G were as follows: C1C1 (patient)–C1C2 (donor), 78 (96.2%); C2C2–C1C2, 1 (1.2%); C1C1–C2C2, 2 (2.5%); and C2C2–C1C1, 0.

KIR Genotyping and Profile Analysis

KIR genotyping was performed using genomic DNA from patient and donor, and the presence of the 16 *KIR* genes (*2DL1, 2DL2, 2DL3, 2DL4, 2DL5, 2DS1, 2DS2, 2DS3, 2DS4, 2DS5, 3DL1, 3DL2, 3DL3, 3DS1, 2DP1,* and *3DP1*) was determined by the polymerase chain reaction sequence-specific primer (PCR-SSP) method [31] with minor modifications [32]. Pairs of all of KIR-L-MM-G (n = 81) cases and also KIR-L-M from HLA-C mismatch cases were selected, and HLA-C–matched cases were randomly selected as controls for the comparison. From the 260 pairs analyzed, all 16 *KIR* types of both patients and donors were successfully obtained in only 187 pairs, because of either insufficient quantity or quality of DNA. These data were used for evaluating *KIR* gene frequency and performing statistical analyses (Table 1). For the KIR-L-MM-G donor *2DS2* analysis, 46 cases, in which donor *2DS2* status was obtained, were added (for a total of 233 cases). KIR haplotype A is defined as carrying a single activating *KIR* gene, *2DS4*; KIR haplotype B has additional activating *KIR* genes [33].

Definition of Transplantation-Related Events

The occurrence of acute GVHD (aGVHD) was evaluated according to grading criteria in patients who survived for more than 8 days after transplantation, as described previously [30].

Statistical Analysis

Statistical analysis was performed as described previously [5]. All analyses were conducted using STATA version 8.2 (STATA Corp, College Station, TX). Overall survival (OS) rate was assessed using the Kaplan-Meier product limit method. Cumulative incidence of aGVHD and leukemia relapse were assessed as described previously [5] to eliminate the effects of competing risks. The competing events regarding aGVHD and relapse were defined as death without aGVHD and death in remission (treatment related mortality), respectively. For each endpoint, a log-rank test was applied to assess the impact of the factor of interest. Multivariate analysis by Cox proportional hazard models was applied to assess the impact of KIR ligand compatibility, donor *KIR* genotype, and ATG administration along with potential confounders. Confounders considered were HLA-A, -B, -DR, -DQ, and -DP matching (GVH direction), sex (donor–patient pairs), patient age (linear), donor age (linear), type of disease, risk of leukemia relapse (standard and high, leukemia only analyzed), number of cells transplanted (linear), and preconditioning (TBI vs non-TBI). The number of nucleated cells before the manipulation of bone marrow was replaced with the number of cells transplanted. P values $< .05$ were considered statistically significant. Adjustment of P values for multiple comparison was done because of an a priori hypothesis that activating KIR would interact with the cognate ligand and transduce a stimulatory signal only when the inhibitory signal was inactive.

RESULTS

Adverse Effects of KIR Ligand Incompatibility

We first confirmed the effects of KIR-L-MM in the newly selected cohort in this study (Table 1). The cumulative incidence of aGVHD and OS are shown in Figure 1. KIR-L-MM-G showed a significantly higher incidence of grade III-IV aGVHD (41.1%; 95% confidence interval [CI] = 29.5%-51.9%) compared with KIR-L-M in HLA-C–mismatched patients (29.7%; 95% CI = 25.2%-34.3%; P = .032). A similar trend was seen in grade II-IV aGVHD (data not shown). In addition, in

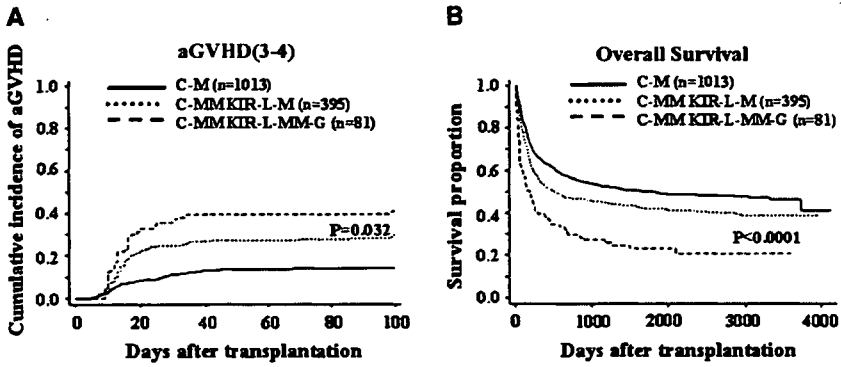

Figure 1. Effects of KIR ligand mismatch on transplantation outcome. Cumulative incidence of acute GVHD (grade III-IV) (A) and overall survival (B) by matching of KIR ligands in the GVHD direction. The directions of HLA-C mismatching were GVH and/or HVG. All patients were analyzed. The solid line represents HLA-C match (CM), the thin dotted line represents HLA-C mismatch KIR ligand match in the GVHD direction (C-MM KIR-L-M), and the thick dotted line represents HLA-C mismatch KIR ligand mismatch in the GVH direction (C-MM KIR-L-MM-G). The log-rank test was applied between CMM KIR-L-MM-G and CMM KIR-L-M.

Table 2. *Multivariate analysis of the effects of KIR ligand matching, donor KIR genotype, and ATG preadministration*

			aGVHD 3-4		aGVHD 2-4		Relapse		OS	
Group	Confounders	Subject number	HR (95%CI)	P value	HR (95%CI)	P value	HR (95%CI)	P value	HR (95%CI)	P value
A	HLA-C (HCX) matched	1013	1.00(reference)		1.00(reference)		1.00(reference)		1.00(reference)	
	HLA-C-MM (HCX) and KIR-L-MM-G	81	3.08(2.05-4.62)	<.001	1.76(1.28-2.43)	.001	1.27(0.73-2.22)	.403	1.93(1.47-2.53)	<.001
	HLA-C-MM (HCX) and KIR-L-M	395	2.00(1.54-2.61)	<.001	1.47(1.23-1.77)	<.001	0.58(0.41-0.81)	.001	1.17(0.99-1.37)	.065
	ATG (yes vs no)	94 vs 1395	0.56(0.31-0.99)	.047	0.63(0.43-0.93)	.019	1.01(0.60-1.71)	.957	1.23(0.92-1.65)	.158
B	KIR-L (MM-G vs M)	80 vs 70	1.36(0.76-2.44)	.304	1.32(0.81-2.15)	.258	2.16(0.89-5.24)	.087	1.60(1.05-2.44)	.027
	Donor KIR genotype (2DS2 + vs −)	28 vs 122	1.96(1.01-3.80)	.045	1.62(0.92-2.85)	.095	0.78(0.24-2.47)	.666	1.04(0.62-1.74)	.889

Adjusted for HLA-A, -B, -DR –DQ, DP(GVH direction), age, donor age, donor-recipient sex pattern, disease, TBI, and risk.
Group A: all pairs, n=1489; group B: HLA-C-mismatched and donor *2DS2*-typed n=150.

HLA-C–mismatched patients, KIR-L-MM-G had a lower 5-year OS rate (23.2%; 95% CI = 14.6%-32.9%) than KIR-L-M (41.8%; 95% CI = 36.9%-46.7%; $P < .0001$). Multivariate analysis (Table 2, group A [n = 1489]) also demonstrated the strong adverse effects of KIR-L-MM-G in HLA-C mismatch on aGVHD (grade III-IV GVHD: hazard rate [HR] = 3.08, $P < .001$; grade II-IV GVHD: HR = 1.76, $P = .001$) and on OS (HR = 1.93; $P < .001$), but not on relapse (HR = 1.27; $P = .40$). Allele mismatches of *HLA-A*, *-B*, *-DR*, *-DQ*, and *-DP* loci of the patient and donor were considered confounders in the analysis; consequently, the observed KIR-L-MM-G effects in HLA-C mismatch were adjusted for other HLA disparities. These adverse effects of KIR-L-MM-G on aGVHD and OS were consistent with those found in our previous study [5]. Consequently, we further analyzed the factors responsible for the effects of KIR-L-MM-G on transplantation outcome using this cohort.

KIR Genotypes and Profiles of Patients and Donors

The selected patients and donors were analyzed using the PCR-SSP method for genotyping 16 different *KIR* genes. Data for 187 pairs were obtained, including 55 cases of KIR-L-MM-G and 62 cases of KIR-L-M in HLA-C mismatch and 70 cases of HLA-C match (Table 1). Table 3 shows the frequency of each *KIR* gene and the KIR profiles of patients and donors, demonstrating no significant differences between the patients and donors. The frequency of each *KIR* was similar to that of the healthy Japanese population [32-34]. Nearly half of the patients had only haplotype A.

Donor *KIR2DS2* Exacerbated aGVHD in KIR-L-MM-G

To statistically evaluate the possible involvement of *KIR* genotype in the adverse effects of KIR-L-MM-G, we investigated the particular combinatory

Table 3. *KIR genotype analysis of patient and donor of the cohort (n = 374)*

Haplotype	Profile	2DL1	2DL2	2DL3	2DL4	2DL5	2DS1	2DS2	2DS3	2DS4	2DS5	3DL1	3DL2	3DL3	3DS1	2DP1	3DP1	Patient Number	Patient Frequency	Donor Number	Donor Frequency	KIR number** Inhibitory	KIR number** Activating	KIR number** Total
A	#1	+	−	+	+	−	−	−	−	+	−	+	+	+	−	+	+	95	0.51	92	0.49	6	1	7
B	#2	+	−	+	+	+	+	−	−	+	+	+	+	+	+	+	+	24	0.13	35	0.19	7	4	11
B	#3	+	+	+	+	−	+	+	−	+	−	+	+	−	+	+	+	13	0.07	9	0.05	7	2	9
B	#4	+	+	+	+	+	−	−	+	+	−	+	+	+	+	+	+	12	0.06	4	0.02	7	4	11
B	#5	+	+	+	+	+	+	−	−	−	+	−	+	+	+	+	+	8	0.04	8	0.04	6	3	9
B	#6	+	−	+	+	−	−	−	−	+	−	+	+	−	+	+	+	6	0.03	5	0.03	6	0	6
B	#7	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	+	6	0.03	5	0.03	8	6	14
B	#8	+	−	+	+	+	+	−	−	+	+	+	+	+	+	+	+	4	0.02	3	0.02	7	3	10
B	#9	+	+	+	+	+	+	+	+	+	−	+	+	+	+	+	+	4	0.02	3	0.02	8	5	13
B	#10	+	+	+	+	+	+	+	+	−	+	−	+	+	+	+	+	2	0.01	2	0.01	7	5	12
	Others*																	13	0.07	21	0.11			
	Patient		0.16		1.00	0.38	0.37	0.17	0.17	0.88	0.25	0.94	1.00	1.00	0.35	1.00	1.00							
Frequency	Donor		0.14	0.98	1.00	0.41	0.39	0.16	0.14	0.87	0.32	0.93	1.00	0.99	0.37	0.99	1.00							
	Total		0.15	0.99	1.00	0.39	0.38	0.16	0.15	0.87	0.28	0.93	1.00	1.00	0.36	0.99	1.00							

* Combined profiles < 1% frequency; ** Not include pseudo-gene.

effects of donor *KIR* genotype and patient cognate KIR ligand type (receptor-ligand analysis). For the inhibitory KIR, we attempted to examine the combination of a particular ligand in the patient and absence of the cognate inhibitory *KIR* gene in the donor. But with regard to HLA-C-KIR ligand specificity, almost all individuals were positive for both C1 and C2 inhibitory KIRs (*2DL2* and/or *2DL3*, and *2DL1*, respectively; Table 3); therefore, there was no mismatch between patient KIR ligand and donor inhibitory *KIR* genotype combination or vice versa. In contrast, activating *KIR* genotypes were quite variable among individuals, and mismatch (ie, reactive) combinations of activating KIR with its presumed ligand (*2DS1* with C2 and *2DS2* with C1, respectively) were present.

For activating KIR, the combination of a particular ligand in the patient and presence of the cognate-activating KIR but absence of the corresponding inhibitory KIR in the donor was selected and analyzed. This choice was based on dominance of the inhibitory signal over the cognate-activating signal [35,36]. The corresponding activating donor *KIR* genotypes to patients C1C1 and C2C2 in KIR-L-MM-G were *2DS2* and *2DS1*, respectively. However, the frequency of C2C2 in the JMDP cases was too low (only 1 case in this study) to permit statistical evaluation. As shown in Figure 2, donor *2DS2*-positive cases in KIR-L-MM-G had a significantly higher incidence of aGVHD (grade III-IV GVHD, 70.9% [95% CI = 40.0%-87.9%]; grade II-IV GVHD, 78.6% [95% CI = 47.2%-92.5%]) compared with the donor *2DS2*-negative cases (grade III-IV GVHD, 33.6% [95% CI = 22.0%-45.7%]; grade II-IV GVHD, 54.4% [95% CI = 40.8%-66.1%]; $P = .012$ and .029, respectively). This was not true for KIR-L-M cases, however. These results suggest that the adverse effects of KIR-L-MM-G depend on combinations of the donor-activating *KIR* genotype and cognate patient ligand C1.

To explore the possibility of the neighboring activating *KIR* loci being the primary factor in outcomes because of possible linkage disequilibrium, we next investigated the associations between other *KIR* genotypes and transplantation outcomes. No other activating *KIR*, but inhibitory *2DL2* (located adjacent to and tightly linked with *2DS2*) showed a significant association with the incidence of aGVHD (data not shown). No significant associations between donor *2DS2* with relapse or OS in KIR-L-MM-G could be observed (Figures 2C and D, respectively).

Multivariate analysis (Table 2; group B [n = 150]) demonstrated that the donor *2DS2* was a possible risk factor for grade III-IV aGVHD in HLA-C–mismatched cases (HR = 1.96; $P = .045$). The same trend was observed for grade II-IV GVHD (HR = 1.62; $P = .095$). We also tested the currently proposed model for the *KIR* genotype effects on HSCT outcomes (donor *KIR* gene numbers [10,16,18,26,37], comparison of

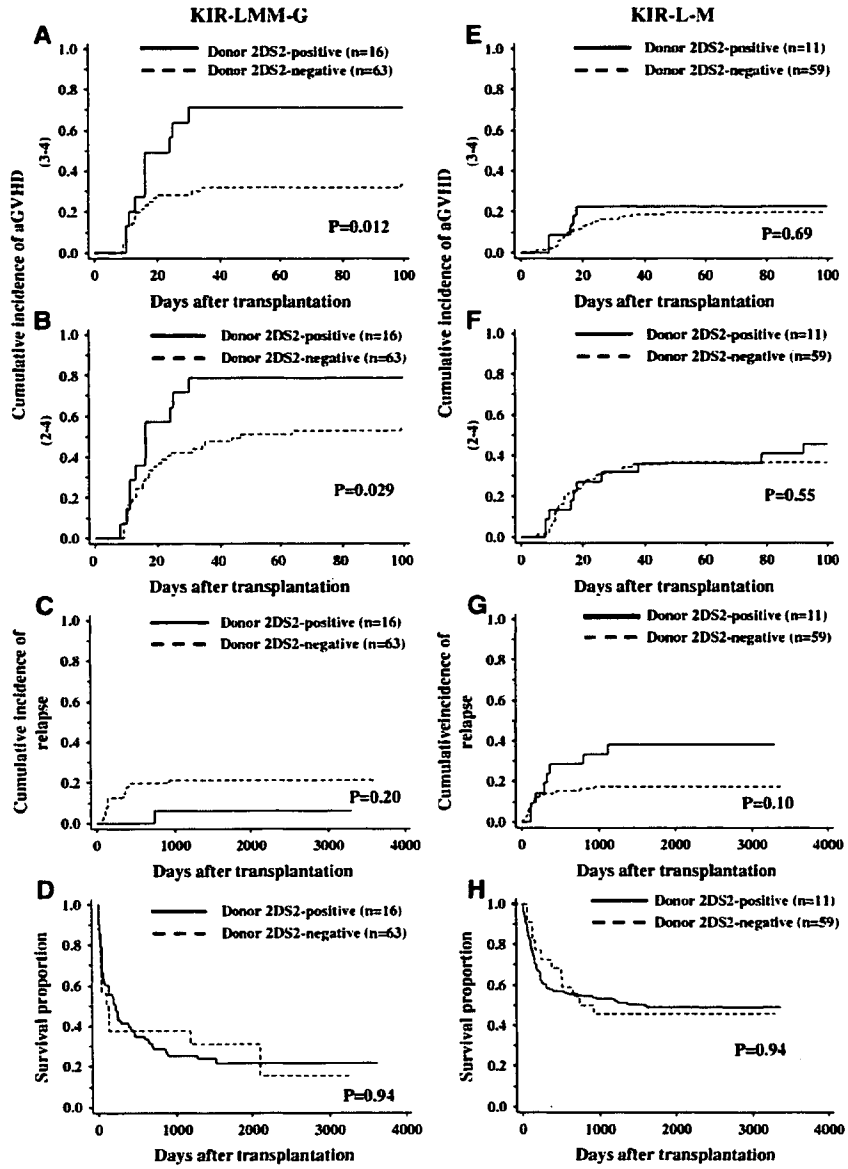

Figure 2. Effects of donor *KIR2DS2* in KIR ligand mismatch on transplantation outcome: Cumulative incidence of aGVHD, relapse, and overall survival with presence or absence of donor *KIR2DS2* gene in HLA-C-mismatched patients. Grade III-IV GVHD (A and E), grade 2-4 GVHD (B and F), relapse (C and G), and overall survival (D and H) with KIR-L-MM-G (A-D) or KIR-L-M (E-H) cases were analyzed. The solid line represents donor *KIR2DS2*-positive; the dotted line, donor *KIR2DS2*-negative.

KIR genotype and profile between patient and donor [receptor–receptor analysis] [17,19,25], compatibility score [24], ligand homozygosity in patients [21,27,38,39], and "missing ligand" effect [3,11,13,40,41]), and found no significant associations in this cohort (data not shown).

ATG Preadministration Ameliorates the Adverse Effects of KIR-L-MM-G on aGVHD and OS

In our previous study [5], the incidence of aGVHD was high in KIR-L-MM-G, where all cases did not involve ATG administration in the conditioning regimen, which is common in the JMDP cases. In the present study, we included rare ATG-administered cases (n = 94) in the analysis and evaluated the effects of ATG administration on KIR-L-MM-G. We found no significant differences in most of the parameters between the ATG-administered and non–ATG-administered groups, except for patient average age (18 years vs 27 years). Multivariate analysis (Table 2; group A [n = 1489]) indicated that ATG administration was a risk-reducing factor for severe aGVHD (grade III-IV

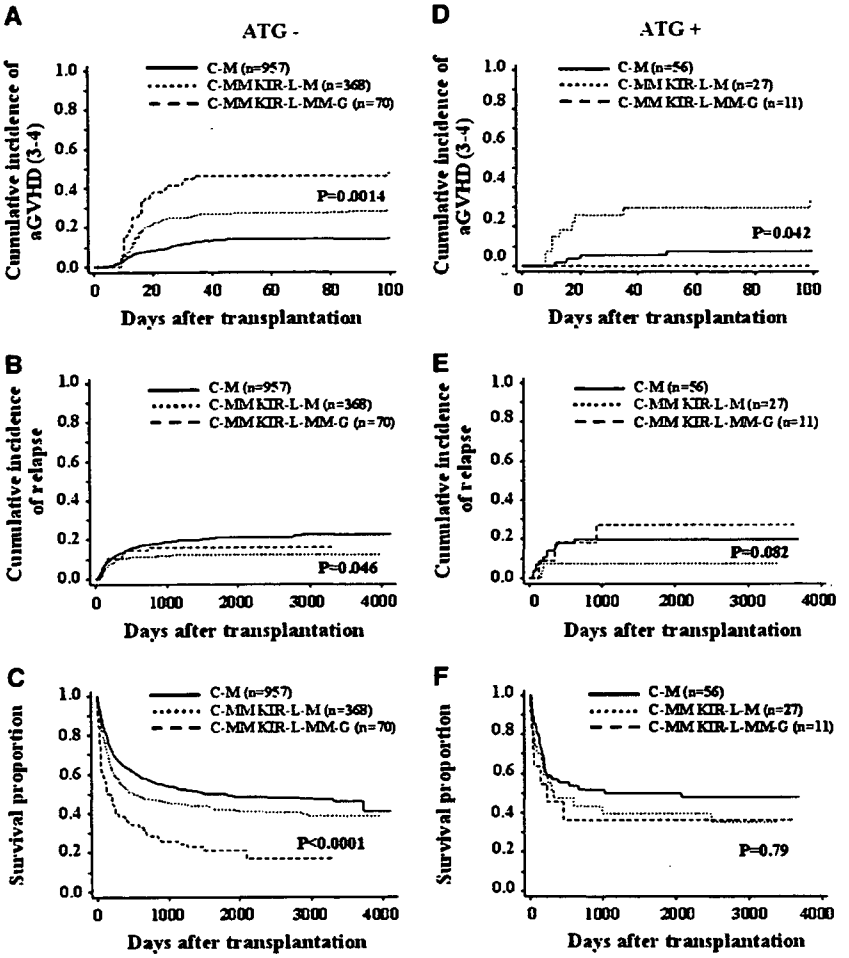

Figure 3. Effects of ATG preadministration in KIR ligand mismatch on transplantation outcome: Cumulative incidence of aGVHD, relapse, and overall survival of patients not receiving ATG (A-C) and those receiving ATG (D-F). The solid line represents HLA-C match (C-M), the thick dotted line represents HLA-C mismatch KIR ligand match in the GVHD direction (C-MM KIR-L-M), and the thin dotted line represents HLA-C mismatch KIR ligand mismatch in the GVH direction (C-MM KIR-L-MM-G). The log-rank test was applied between CMM KIR-L-MM-G and CMM KIR-L-M.

GVHD: HR = 0.56; P = .047; grade II-IV GVHD: HR = 0.63, P = .019), whereas no significant effects on relapse or OS could be seen.

The cumulative incidence of aGVHD was assessed separately in the non–ATG-administered and ATG-administered groups (Figures 3A and 3D, respectively). In the non–ATG-administered group, the incidence of grade III-IV GVHD was significantly higher in KIR-L-MM-G than in KIR-L-M (47.7% [95% CI = 35.2%-59.2%] vs 29.4% [95% CI=24.8%-34.1%]; P = .0014), as found in our previous study [5]. In contrast, no grade III-IV aGVHD was observed in KIR-L-MM-G cases in the ATG-administered group (2 cases of grade 2, 2 cases of grade 1, and 7 cases of grade 0), and the preventive effects of KIR-L-MM-G on severe aGVHD were significant (P = .042) although only a small number were analyzed (n = 38). We analyzed the effects of *2DS2* in the non–ATG-administered cases. In KIR-L-MM-G, the incidence of grade III-IV aGVHD was significantly higher in the donor *2DS2*-positive cases (n = 15) than in the donor *2DS2*-negative cases (n = 54) (76.4% [95% CI = 43.5-91.7%] vs 40.1% [95% CI = 26.5%-53.2%]; P = .048), suggesting that the adverse effects of donor *2DS2* are independent of ATG administration. In ATG-administered cases, no grade III-IV aGVHD was observed in donor *2DS2*-negative KIR-L-MM-G (n = 15); in 1 donor *2DS2*-positive KIR-L-MM-G case, the patient failed engraftment but showed no aGVHD, and died on day 35. Therefore, we could not statistically evaluate the effect of ATG on the *2DS2*-positive cases.

As shown in Figure 3B, in non–ATG-administered cases, the cumulative incidence of relapse was higher in KIR-L-MM-G than in KIR-L-M (16.1% [95% CI = 8.6%-25.8%] vs 11.9% [95% CI = 8.9%-15.3%];

P = .046), which was seen mainly in ALL (data not shown), as was found in our previous study [5]. In contrast, no significant increase in relapse was obtained in ATG-administered cases (P = .082) (Figure 3E). As in our previous study [5], in non–ATG-administered cases, overall survival rate was significantly lower in KIR-L-MM-G than in KIR-L-M (21.0% [95% CI = 12.2%-31.3%] vs 42.0% [95% CI =36.8%-47.0%]; P < .0001) (Figure 3C). On the other hand, in ATG-administered cases, no significant difference was observed between KIR-L-MM-G and KIR-L-M (36.4% [95% CI = 11.2%-62.7%] vs 39.5% [95% CI = 21.2%-57.3%]; P = .79) (Figure 3F), suggesting that ATG preadministration in the conditioning regimen abolished the adverse effect of KIR-L-MM-G on survival.

DISCUSSION

In the present study, we identified donor *KIR* genotype–patient KIR ligand combination and no ATG preadministration as critical factors for the adverse effects of KIR-L-MM-G on transplantation outcomes in the JMDP. The cases analyzed in this study were all HLA-A, -B, and -DR serologically matched; thus, we were able to evaluate the HLA-C ligand compatibility effects, because the HLA-Bw4 and HLA-A3 and -A11 KIR ligands were all matched. Other groups included mostly Bw4 ligand mismatch cases in KIR-L-MM-G analysis [2,6,7,10-12,14,21,42]. The Bw4 (patient) *-3DL1* (or *-3DS1*) (donor) combinatory effect also may affect transplantation outcome.

In the KIR-L-MM-G combination, the patient lacks the donor's KIR ligand. In this situation, donor NK cells may react with the patient cells according to the "missing self" model [43]. Previous KIR ligand compatibility data, together with the present data, confirm that the KIR-L-MM-G has potent adverse effects on UR-HSCT. In most KIR-L-MM-G cases in the JMDP, the donor and patient ligand types are C1C2 and C1C1, respectively, suggesting that C1C2 donor NK cells (and/or some T cells) respond to C1C1 patient cells. In this case, donor NK cells lack the inhibitory KIR for C1 (2DL2 and 2DL3) in terms of genotype or phenotype, or both. As shown in the present results, almost all JMDP donors examined posessed an inhibitory *KIR* gene for C1 (*2DL3*). The subpopulation of donor NK cells thus appears to lack cell surface expression of the C1-inhibitory KIR molecule, despite the presence of the genes. This is explained by the "at least one inhibitory receptor expression" model [44], in which each NK cell must express 1 inhibitory receptor for the self–major histocompatibility complex (MHC) class I to avoid autoreactivity, but expression of other receptors is "stochastic." Consequently, NK cell subpopulations lacking the C1-inhibitory *KIR* (*2DL2* and *2DL3*) but having the C2-inhibitory *KIR* (*2DL1*) would react with C1C1 (C2-lacking) patient cells. Therefore, the donor inhibitory KIR repertoire at the expression level, not at the genomic level, appears to influence outcome in the JMDP. The importance of the inhibitory KIR expression repertoire and functional analysis of donor NK cells has been discussed previously [3,45].

With a lack of inhibitory KIR signals, NK cells respond to target cells through activation signals from activating receptors. 2DS1 and 2DS2 are assigned to recognize C2 and C1, respectively, but other activating KIR ligand specificities (2DS3-5 and 3DS1) are unidentified [35]. Therefore, we were able to evaluate only these 2 KIRs for combinatory effects with their ligands. As described in Results, a higher incidence of severe aGVHD was observed in the *2DS2*-positive donors in the KIR-L-MM-G cases, but not in the KIR-L-M cases. This suggests that *2DS2*-positive lymphocytes (NK cells and/or some T cells) react with cognate ligand (C1)-positive cells and exacerbate aGVHD. Recently, La Nasa et al.[27] reported that the patient KIR ligand homozygosity, but not donor KIR genotype, is predictive for the outcome of HLA-matched UR-HCT in patients with beta-thalassemia. Their cases were all KIR ligand-matched transplantation and the donor-activating *KIR*–patient cognate ligand combination had no significant effect on the outcomes. Their results are consistent with our findings indicating that the donor *2DS2*–patient C1 combination of ligand-matched pairs has no effect on any outcomes (Figure 2E-H). This is in accordance with the notion that an activating *KIR* works only when the patient has the cognate ligand and that the donor inhibitory KIR does not function (Fig. 4). Chewning et al [36] reported that *KIR 2DS1*-positive NK cells recognized C2-expressing target cells and showed alloreactivity in vitro supporting the concept of this model.

Although adverse impacts of donor *2DS2* on transplantation outcome have been documented previously [15,18,23], the present study is the first report on the adverse effects of the *2DS2*–cognate ligand C1 combination on aGVHD incidence. Because we had an a priori hypothesis, we did not apply adjustment of P-value in our analysis; however, our results must be interpreted with caution. KIR-L-MM-G is infrequent in the JMDP (only 81 of 1489 cases in the present study), and the frequency of *2DS2* is low in Japan [32,33], and confirmation in other independent cohorts from different populations will support our findings. Combinatory effects of *2DS2* and cognate ligand C1 also have been reported in disease susceptibility studies, including studies of type I diabetes mellitus [46], ulcerative colitis [47], rheumatoid vasculitis [48], and tuberculosis [49]. Furthermore, extensive genetic analysis of *KIR* and HLA genotypes of various ethnic populations have demonstrated a strong negative correlation of activating *KIR* and its putative ligand

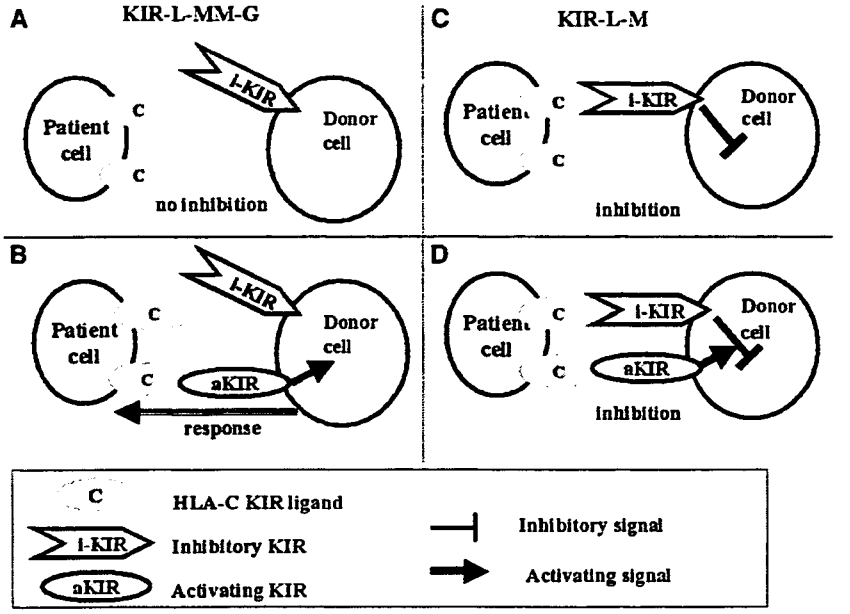

Figure 4. Model of interaction between activating KIR and cognate KIR ligand. Donor-activating KIR transduces an activating signal on recognition of the cognate KIR ligand of the patient cell in KIR-L-MM-G case (B). The activating signal is canceled by an inhibitory signal from inhibitory KIR, which recognizes the KIR ligand of the patient cell in KIR-L-M case (D).

combination including *2DS2*–C1, suggesting coevolution of the activating receptor–ligand loci [50]. Taken together with our data, these clinical and population genetic studies suggest a direct receptor–ligand interaction between 2DS2 and C1; however, binding studies using soluble 2DS2 molecules have shown no or a very weak binding to C1 molecules or C1-transfected cells, challenging the notion of C1 as a 2DS2 ligand [51-53]. Recombinant 2DS1 also showed very low or no affinity to C2 [54]. This disparity may be linked to differences in the nature of ligand binding between inhibiting and activating receptors. One possible factor is class I-binding peptides. The peptide-dependent binding with class I-binding receptors is recognized in most of the inhibitory receptors [53,55-58] and also has been suggested in activating KIR [53,58,59]. The peptide repertoire that allows strong KIR binding might be more restricted in activating KIR cases than in inhibitory ones. Alternatively, activating KIR–ligand binding may be somehow strengthened under stress conditions, such as transplantation or viral infection. Epstein Barr virus–transformed C1-positive cells were found to be stained slightly by recombinant 2DS2 tetramers [53]. A mutation study found that only 1 amino acid substitution in 2DS2 increased its level of binding to C1 to that of inhibitory 2DL2, suggesting that a very fine conformational microstructure change controls KIR binding specificity [60].

Inhibitory *2DL2* also showed a significant association with the incidence of severe aGVHD. This may be secondary to the *2DS2*–C1 association [50]; alternatively, donor 2DL2-positive NK cells might have a different effect than 2DL3-positive NK cells on acute GVHD incidence, because the binding affinity to C1 is higher in 2DL2 than in 2DL3 [60]. Other groups have analyzed activating *KIR* gene number and outcome and have reported both beneficial and adverse associations [10,16,26,37]. We did not find such quantitative *KIR* loci effects in this JMDP cohort (data not shown); *KIR* genotype variation among various ethnic groups may be responsible for these differences.

Preadministration of ATG to a patient is also a critical factor in attenuating the adverse effects of KIR-L-MM-G on transplantation outcome. Our findings demonstrate that KIR-L-MM-G had potent adverse effects (higher aGVHD incidence and lower OS) without ATG administration, and that ATG administration in the conditioning regimen ameliorated most of these adverse effects. Although the average patient age in the ATG-administered group was about 10 years younger than that in the non–ATG-administered group in this study, multivariate analysis including age as a confounder also identified the ATG effect as an independent factor for incidence of aGVHD (see Table 2). To the best of our knowledge, this is the first direct comparison UR-HSCT study on the effects of ATG preadministration under the same transplantation regimen with similar genetic backgrounds. Because far fewer ATG-administrated cases than

non–ATG-administered cases are included in the JMDP (an imbalance that could bias statistical results), further evaluation of large numbers of ATG-preadministered cases in different ethnic populations are needed.

Administration of ATG extensively depletes patient and donor T cells, thus strongly inhibiting the responses of alloreactive T cells. Because the JMDP cases are all unmanipulated T cell–replete marrow, donor alloreactive T cell response may be very strong, which would obscure some of the NK cell beneficial effects [61]. In KIR-L-MM-G without ATG preadministration, alloreactive NK cells were activated by 2DS2–C1 interaction without inhibitory KIR signals and may have augmented alloreactive donor T cell responses, resulting in increased aGVHD incidence and mortality. Alternatively, KIR-positive T cells may have been responsible for inducing aGVHD. In contrast, with ATG preadministration, donor T cells are largely depleted, and the beneficial effects of NK cell alloreactivity on aGVHD incidence may become prominent. Too few ATG-treated cases were analyzed (n = 11) to allow confirmation of the preventive effects of KIR-L-MM-G on acute GVHD, but the results are consistent with those for the HLA haplo-mismatched, ATG-preadministered R-HSCT [2]. In mouse GVHD models, alloreactive NK cells prevented donor alloreactive T cell stimulation and suppressed aGHVD by lysing donor antigen-presenting cells [2]. These mechanisms might explain the preventive effects of KIR-L-MM-G on the incidence of aGVHD. NK cell reconstitution after transplantation might be influenced by ATG treatment as well as by KIR ligand and KIR genotype variability [39,62,63]. Our data suggest that the KIR-L-MM-G combination must be avoided in JMDP transplantation unless ATG is used in the conditioning regimen.

Another possible factor is mismatch combination dissimilarity resulting from genetic variability in *HLA* and *KIR* in populations with different ethnic backgrounds. There are allele frequency differences in *HLA-C* among human populations in terms of the *HLA-C* KIR ligand [50]. Because the C1 ligand type is dominant in the Japanese population (allele frequency 0.92), KIR-L-MM-G is relatively rare (5%) compared with the incidence in White populations. Furthermore, in the KIR-L-MM-G, the C1C1 (patient)–C1C2 (donor) combination is common (95%) [5]. Therefore, we could focus on the KIR ligand incompatibility and the *2DS2* effects on the C1-homozygous patients in this study. In contrast, the White population more frequently exhibits the C2 type [50]. Consequently, the KIR-L-MM-G frequency is higher in Caucasian than Japanese and might include C2C2 (patient)–C1C2 (donor), C2C2–C1C1, and C1C1–C2C2 combinations, in addition to the C1C1–C1C2 combination. Therefore, not only the C1C1 (patient)–2DS2 (donor) combination, but also the C2C2 (patient)–2DS1 (donor) combination, might contribute considerably to the effects of KIR-L-MM-G in White [36]. The inhibitory capacity of C1 is reportedly weaker than that of C2 [64], and the binding strength of inhibitory KIR to the ligand HLA-C is different as well (2DL1 > 2DL2 > 2DL3) [60]. There may be more variability in inhibitory pathways in White populations; indeed, several groups have reported that the transplantation outcomes vary between C1-homozyous and C2-homozygous patients [15,19,38,39]. *KIR* genotype also shows ethnic variability [33,50]; Japanese have a markedly high frequency of the A haplotype and a very low frequency of *2DS2* (16% in the JMDP, compared with a frequency of > 40% in most Caucasian and African populations). One potential factor not examined in the present study is *KIR* allelic polymorphism. Yawata et al. [34] have shown that allelic polymorphism modulates the level and frequency of KIR3D expression, as well as its inhibitory capacity. These allelic differences might influence outcomes even though HLA-A- and B-KIR ligand specificities were the same in donors and recipients in the present study.

Here we found that the combination of donor-activating *KIR* genotype–patient cognate KIR ligand type and ATG administration in the conditioning regimen were critical factors in the adverse effects of KIR-L-MM-G on transplantation outcome. Alloreactivity of NK cells may be either beneficial or adverse depending on the above factors. However, other important parameters also may contribute to transplantation outcome. Further large-scale international collaborative studies, including a variety of ethnic populations and statistical comparisons under uniform regimens, are needed to gain further insight into the effects of NK cell alloreactivity on transplantation and to guide the development of cell therapy using alloreactive NK cells for leukemia and other diseases.

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Identification of human minor histocompatibility antigens based on genetic association with highly parallel genotyping of pooled DNA

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Minor histocompatibility (H) antigens are the molecular targets of allo-immunity responsible both for the development of antitumor effects and for graft-versus-host disease (GVHD) in allogeneic hematopoietic stem cell transplantation (allo-HSCT). However, despite their potential clinical use, our knowledge of human minor H antigens is largely limited by the lack of efficient methods of their characterization. Here we report a robust and efficient method of minor H gene discovery that combines whole genome association scans (WGASs) with cytotoxic T-lymphocyte (CTL) assays, in which the genetic loci of minor H genes recognized by the CTL clones are precisely identified using pooled-DNA analysis of immortalized lymphoblastoid cell lines with/without susceptibility to those CTLs. Using this method, we have successfully mapped 2 loci: one previously characterized (*HMSD* encoding ACC-6), and one novel. The novel minor H antigen encoded by *BCL2A1* was identified within a 26 kb linkage disequilibrium block on chromosome 15q25, which had been directly mapped by WGAS. The pool size required to identify these regions was no more than 100 individuals. Thus, once CTL clones are generated, this method should substantially facilitate discovery of minor H antigens applicable to targeted allo-immune therapies and also contribute to our understanding of human allo-immunity. (Blood. 2008;111: 3286-3294)

Introduction

Currently, allogeneic hematopoietic stem cell transplantation (allo-HSCT) has been established as one of the most effective therapeutic options for hematopoietic malignancies[1] and is also implicated as a promising approach for some solid cancers.[2] Its major therapeutic benefits are obtained from allo-immunity directed against patients' tumor cells (graft-versus-tumor [GVT] effects). However, the same kind of allo-immune reactions can also be directed against normal host tissues resulting in graft-versus-host disease (GVHD). In HLA-matched transplants, both GVT and GVHD are initiated by the recognition of HLA-bound polymorphic peptides, or minor histocompatibility (H) antigens, by donor T cells. Minor H antigens are typically encoded by dichotomous single nucleotide polymorphism (SNP) alleles, and may potentially be targeted by allo-immune reactions if the donor and recipient are mismatched at the minor H loci. Identification and characterization of minor H antigens that are specifically expressed in hematopoietic tissues, but not in other normal tissues, could contribute to the development of selective antileukemic therapies while minimizing unfavorable GVHD reactions, one of the most serious complications of allo-HSCT.[3,4] Unfortunately, the total number of such useful minor H antigens that are currently molecularly characterized is still disappointingly small, including HA-1,[5] HA-2,[6] ACC-1[Y] and ACC-2,[7] DRN-7,[8] ACC-6,[9] LB-ADIR-1F,[10] HB-1,[11] LRH-1,[12] and 7A7-PANE1,[13] limiting the number of patients eligible for such GVT-oriented immunotherapy.

Several techniques have been developed to identify novel minor H antigens targeted by CTLs generated from patients who have undergone transplantation. Among these, linkage analysis based on the cytotoxicity of the CTL clones against panels of lymphoblastoid cell lines (B-LCLs) from large pedigrees was proposed as a novel genetic approach,[14] and has been successfully applied to identify novel minor H epitopes encoded by the *BCL2A1* and *P2RX5* genes.[7,12] Nevertheless, the technology is still largely limited by its resolution, especially when large segregating families are not available. Linkage analysis using B-LCL panels from the Centre d'Etude du Polymorphisme Humain (CEPH) could only localize minor H loci within a range of 1.64 Mb to 5.5 Mb, which still contained 11 to 46 genes,[7,12,14] thus requiring additional selection procedures to identify the actual minor H genes.

On the other hand, clinically relevant minor H antigens might be associated with common polymorphisms within the human

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population, and therefore could be ideal targets of genetic association studies, considering recent advances of large-scale genotyping technologies and the assets of the International HapMap Project.[15,16] In this alternative genetic approach using the extensive linkage disequilibrium (LD) found within the human genome, target loci can be more efficiently localized within relatively small haplotype blocks without depending on limited numbers of recombination events, given the large number of genotyped genetic markers.[17] Moreover, since the presence of a target minor H allele in individual target cells can be determined by ordinary immunologic assays using minor H antigen-specific CTLs, the characterization of minor H antigens should be significantly more straightforward than identifying alleles associated with typical common complex diseases, for which typically weak-to-moderate genetic effects have been assumed.[18]

In this report, we describe a high-performance, cost-effective method for the identification of minor H antigens, in which whole genome association scans (WGASs) are performed based on SNP array analysis of pooled DNA samples constructed from cytotoxicity-positive (CTX^+) and cytotoxicity-negative (CTX^-) B-LCLs as determined by their susceptibility to CTL clones. Based on this method, termed WGA/CTL, we were able to map the previously characterized ACC-6 minor H locus to a 115-kb block containing only 4 genes, including *HMSD*.[9] Moreover, using the same approach, a novel minor H antigen encoded by the *BCL2A1* gene was identified within a 26-kb block containing only *BCL2A1* on chromosome 15q25. Surprisingly, the pool size required to identify these regions was no more than 100 individuals. Thus, this WGA/CTL method has significant potential to accelerate the discovery of minor H antigens that could be used in more selective, and thus more effective, allo-immune therapies in the near future.

Methods

Cell isolation and cell cultures

This study was approved by the institutional review board of the Aichi Cancer Center and the University of Tokyo. All blood or tissue samples were collected after written informed consent was obtained in accordance with the Declaration of Helsinki. B-LCLs were derived from allo-HSCT donors, recipients, and healthy volunteers. B-LCLs were maintained in RPMI 1640 medium supplemented with 10% fetal calf serum, 2 mM L-glutamine, 1 mM sodium pyruvate.

Generation of CTL lines and clones

CTL lines were generated from peripheral blood mononuclear cells (PBMCs) obtained after transplantation by stimulation with irradiated (33 Gy) recipient PBMCs harvested before HSCT, thereafter stimulated weekly in RPMI 1640 supplemented with 10% pooled human serum and 2 mM L-glutamine. IL-2 was added on days 1 and 5 after the second and third stimulations. CTL clones were isolated by standard limiting dilution and expanded as previously described.[7] CTL-1B9 was isolated from PBMCs harvested on day 30 after transplantation from a patient receiving a marrow graft from his HLA-identical sibling (HLA A11, A24, B39, B51, Cw7, Cw14), and CTL-2A12 has been described recently.[9]

Chromium release assay

Target cells were labeled with 0.1 mCi (3.7 MBq) of ^{51}Cr for 2 hours, and 10^3 target cells/well were mixed with CTL at the effector-to-target (E/T) ratio indicated in a standard 4-hour cytotoxicity. All assays were performed at least in duplicate. Percent specific lysis was calculated as follows: ((Experimental cpm − Spontaneous cpm) / (Maximum cpm − Spontaneous cpm)) × 100.

Immunophenotyping by enzyme-linked immunosorbent assay

B-LCL cells (20 000 per well, which had been retrovirally transduced with restriction HLA cDNA for individual CTLs, if necessary) were plated in each well of 96-well round-bottomed plates, and corresponding CTL clones (10 000 per well) were added to each well. After overnight incubation at 37°C, 50 μL supernatant was collected and released IFN-γ was measured by standard enzyme-linked immunosorbent assay (ELISA).

Construction of pooled DNA and microarray experiments

Genomic DNA was individually extracted from immunophenotyped B-LCLs. After DNA concentrations were measured and adjusted to 50 μg/mL using the PicoGreen dsDNA Quantitation Reagent (Molecular Probes, Eugene, OR), the DNA specimens from CTX^+ and CTX^- B-LCLs were separately combined to generate individual pools. DNA pools were analyzed in pairs using Affymetrix GeneChip SNP-genotyping microarrays (Affymetrix, Tokyo, Japan) according to the manufacturer's protocol,[19,20] where 2 independent experiments were performed for each array type (for more detailed statistical analysis for generated microarray data, see Document S1, available on the *Blood* website; see the Supplemental Materials link at the top of the online article).

Estimation of LD blocks

LD structures of the candidate loci were evaluated based on empirical data from the International Hap Map Project (http://www.hapmap.org/).[15] LD data for the relevant HapMap panels were downloaded from the HapMap web site and further analyzed using Haploview software (http://www.broad.mit.edu/mpg/haploview/).[21]

Transfection of 293T cells and ELISA

Twenty thousand 293T cells retrovirally transduced with HLA-A*2402 were plated in each well of 96-well flat-bottomed plates, cultured overnight at 37°C, then transfected with 0.12 μg of plasmid containing full-length *BCL2A1* cDNA generated from either the patient or his donor using Trans IT-293 (Mirus, Madison, WI). B-LCLs of the recipient and his donor were used as positive and negative controls, respectively. Ten thousand CTL-1B9 cells were added to each well 20 hours after transfection. After overnight incubation at 37°C, 50 μL of supernatant was collected and IFN-γ was measured by ELISA.

SNP identification by direct sequencing

Complementary DNA prepared from B-LCLs was polymerase chain reaction (PCR) amplified for the coding region of *BCL2A1* using the following primers: sense: 5′-AGAAGATGACAGACTGTGAATTTGG-3′; antisense: 5′-TCAACAGTATTGCTTCAGGAGAG-3′.

PCR products were purified and directly sequenced with the same primer and BigDye Terminator kit (version 3.1) by using ABI PRISM 3100 (Applied Biosystems, Foster City, CA).

Confirmatory SNP genotyping

Genotyping was carried out using fluorogenic 3′-minor groove binding (MGB) probes in a PCR assay. PCR was conducted in 10-μL reactions containing both allelic probes, 500 nM each of the primers, 1 × TaqMan Universal PCR Master Mix (Applied Biosystems), and 1 μL (100 ng) DNA. PCR cycling conditions were as follows: predenature, 50°C for 2 minutes, 95°C for 10 minutes, followed by 35 cycles of 92°C for 15 seconds and 60°C for 1 minute in a GeneAmp PCR System 9700 (Applied Biosystems). The PCR products were analyzed on an ABI 7900HT with the aid of SDS 2.2 software (Applied Biosystems).

Epitope reconstitution assay

The candidate *BCL2A1*-encoded minor H epitope and its allelic counterpart (DYLQYVLQI) peptides were synthesized by standard Fmoc chemistry. ^{51}Cr-labeled CTX^- donor B-LCLs were incubated with graded concentrations of the peptides and then used as targets in standard cytotoxicity assays.

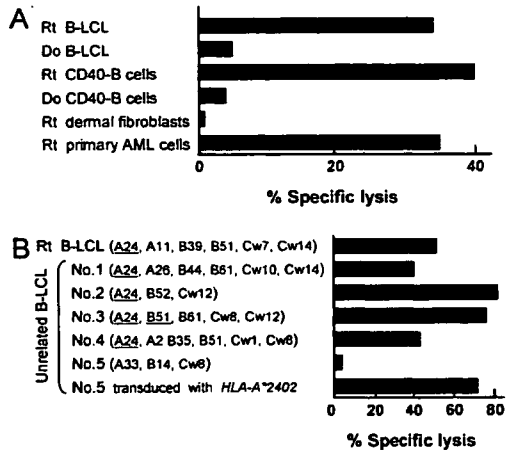

Figure 1. Specificity of CTL-1B9 against hematopoietic cells and its restriction HLA. (A) The cytolytic activity of CTL-1B9 was evaluated in a standard 4-hour ^{51}Cr release assay (E/T ratio, 20:1). Targets used were B-LCL, CD40-activated (CD40-B) B cells, dermal fibroblasts, and primary acute myeloid leukemia cells from the recipient (Rt), and B-LCL and CD40-B cells from his donor (Do). Rt dermal fibroblasts were pretreated with 500 U/mL IFN-γ and 10 ng/mL TNF-α for 48 hours before ^{51}Cr labeling. (B) Cytolytic activity of CTL-1B9 against a panel of B-LCLs derived from unrelated individuals, each of whom shared 1 or 2 class I MHC allele(s) with the recipient from whom the CTL-1B9 was generated. The shared HLA allele(s) with the recipient are underlined. B-LCLs (no. 5) which did not share any HLA alleles with the recipient, were retrovirally transduced with HLA-A*2402 cDNA and included to confirm HLA-A*2402 restriction by CTL-1B9. Results are typical of 2 experiments and data are the mean plus or minus the standard deviation (SD) of triplicates.

Results

CTL-based typing and SNP array analysis of pooled DNA

CTL-2A12 and CTL-1B9 are CTL clones established from the peripheral blood of 2 patients with leukemia who had received HLA-identical sibling HSCTs. Each clone demonstrated specific lysis against the B-LCLs of the recipient but not against donor B-LCLs, indicating recognition of minor H antigen (Figure 1A and Kawase et al[9]). The minor H antigen for CTL-2A12 had been previously identified by expression cloning[9]; on the other hand, the target minor H antigen for the HLA-A24–restricted CTL-1B9 clone, which was apparently hematopoietic lineage–specific (Figure 1A) and present in approximately 80% of the Japanese population (data not shown), had not yet been determined. Using these CTL clones, a panel of B-LCLs expressing the restriction HLA (HLA-B44 for CTL-2A12 and HLA-A24 for CTL-1B9) endogenously or retrovirally transduced, were subjected to "immunophenotyping" for the presence or absence of the minor H antigen by ELISA and, if necessary, by standard chromium release assay (CRA). Based on the assay results, for CTL-2A12 we initially collected 44 cytotoxicity-positive (CTX^+) and 44 cytotoxicity-negative (CTX^-) B-LCLs after screening 132 B-LCLs, while 57 CTX^+ and 38 CTX^- B-LCLs were obtained from 121 B-LCLs for CTL-1B9. From these sets of B-LCL panels, pools of DNA were generated and subjected to analysis on Affymetrix GeneChip 100 K and 500 K microarrays in duplicate.[19,20]

Detection of association between minor H phenotypes and marker SNPs

Genetic mapping of the minor H locus was performed by identifying marker SNPs that showed statistically significant deviations in allele-frequencies between CTX^+ and CTX^- pools based on the observed allele-specific signals in the microarray experiments. For this purpose, we evaluated the deviations of observed allele ratios between CTX^+ and CTX^- pools for each SNP on a given array (Document S1). An SNP was considered as positive for association if its test statistic exceeded an empirically determined threshold that provided a "genome-wide" P value of .05 in duplicate experiments (Document S1, Figures S1,S2, and Table S1). Threshold values for different pool sizes are also provided in Table S2 for further experiments. The positive SNPs eventually obtained for both CTLs are summarized in Table 1, where the 10 SNPs showing the highest test statistics are listed for individual experiments.

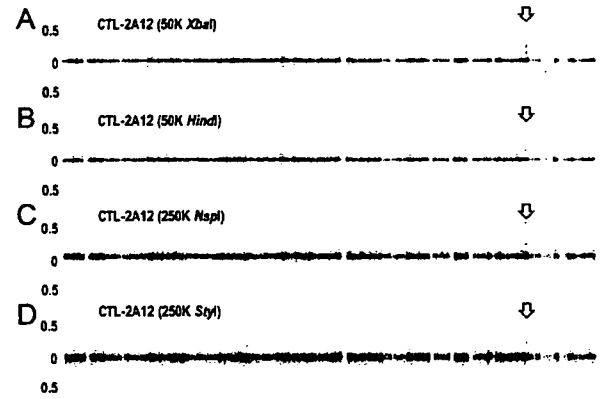

Figure 2. Whole genome association scans performed with pooled DNA generated based on immunophenotyping with CTL-2A12. Pooled DNAs generated from 44 CTX^+ and 44 CTX^- B-LCLs were analyzed with 50 K *Xba*I (A), 50 K *Hind*III (B), 250 K *Nsp*I (C), and 250 K *Sty*I (D) arrays. Test statistics were calculated for all SNPs and plotted in the chromosomal order. In all SNP array types, a common association peak is observed at 18q21, to which the minor H antigen for CTL-2A12, encoded by the *HMSD* gene, had been mapped based on expression cloning[9] (arrows).

Mapping of the minor H loci by WGASs

All the SNPs significantly associated with susceptibility to CTL-2A12 were correctly mapped within a single 115 kb LD block at chromosome 18q21 containing the *HMSD* gene (Figures 2 and 3A), which had been previously shown to encode the ACC-6 minor H antigen recognized by CTL-2A12.[9] According to the above criteria, no false-positive SNPs were reported in any array types (Table 1). Confirmation genotyping of individual B-LCLs from both panels revealed none of the 44 that had been immunophenotyped as CTX^- were misjudged, while 8 of the 44 CTX^+ B-LCLs were found to actually carry no minor H-positive allele for ACC-6, which was likely due to the inclusion of individual B-LCLs showing borderline cytotoxicity (data not shown).

On the other hand, positive association of the target minor H antigen with CTL-1B9 was detected in 2 independent loci: SNP rs1879894 at 15q25.1 in 250 K *Nsp*I (Table 1, Figure 4A-B, and Figure S5) and SNP rs1842353 at 8q12.3 in 50 K *Hind*III (Table 1 and Figure S3A). We eventually focused on rs1879894, as it showed a much more significant genome-wide P value than SNP rs1842353 (Table 1). In contrast to the CTL-2A12 case, where many mutually correlated SNPs around the most significant one created a broad peak in the statistic plots (Figure 2 arrows and Figure S3), the adjacent SNPs (rs6495463 and rs2562756; Figure 3B solid arrows) around rs187894 (Figure 3B open arrow) did not show large test statistic values, reflecting the fact that no marker SNPs on 100 K and 500 K arrays exist in high LD (Figure 3B dashed red lines encompassing 26 kb) with this SNP according to the HapMap data. To further confirm the association, we generated additional B-LCL pools consisting of 75 CTX^+ and 34 CTX^-

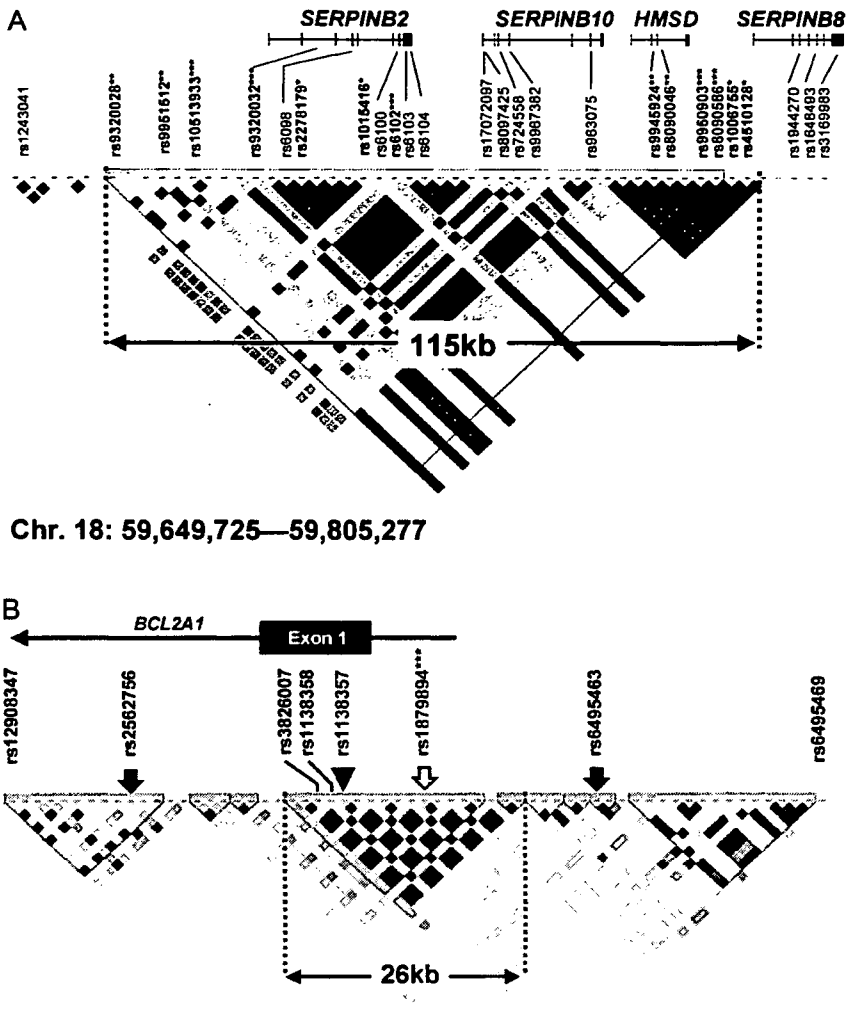

Figure 3. Linkage disequilibrium (LD) block mapped by CTL-2A12 and CTL-1B9. (A) An LD block map identified by pairwise r^2 plot from HapMap CEU data are overlayed with SNPs available from Affymetrix GeneChip SNP-genotyping microarrays (arrows) and 4 genes in the 115 kb block. SNPs that emerged repeatedly in the 2 independent experiments are indicated in blue. The genomewide *P* values for positive SNPs are shown as follows: $*P < .05$; $**P < .01$; $***P < .001$. The intronic SNP (rs9945924) controlling the alternative splicing of *HMSD* transcripts and expression of encoded ACC-6 minor H antigen is indicated in red. (B) LD blocks identified by pairwise r^2 plot from HapMap JPT data are overlayed with SNPs available from Affymetrix GeneChip SNP-genotyping microarrays (arrows) and exon 1 of the *BCL2A1* gene. The only SNP showing a high association with CTL-1B9 immunophenotypes (rs1879894) is shown as an open arrow. The nonsynonymous SNP (rs1138357) controlling the expression of the minor H antigen recognized by CTL-1B9 is indicated by a red arrowhead. ***SNP with genomewide $P < .001$. The 2 SNPs adjacent to the 26 kb LD block (rs2562756 and rs6495463) never gave a significant genomewide *P* value.

B-LCLs from another set of 128 B-LCLs, and performed a WGAS. As expected, the WGAS of the second pools also identified the identical SNP with the highest test statistic value in duplicate experiments, unequivocally indicating that this SNP is truly associated with the minor H locus of interest (Figure 4C,D and Table S3). The association was also detected when the references in the first and second pools were swapped (data not shown).

Identification of the minor H epitope recognized by CTL-1B9

The LD block containing SNP rs1879894 that was singled out from more than 500 000 SNP markers with 2 sets of DNA pools only encodes exon 1 of *BCL2A1* (Figure 3B). To our surprise, this was the region to which we had previously mapped an HLA-A24–restricted minor H antigen, ACC-1^Y.[7] We first confirmed that full-length *BCL2A1* cDNA cloned only from the recipient but not his donor could stimulate interferon-γ secretion from CTL-1B9 when transduced into donor B-LCL (Figure 5A), indicating that *BCL2A1* is a bona fide gene encoding minor H antigen recognized by CTL-1B9. We next genotyped 3 nonsynonymous SNPs in the *BCL2A1* exon 1 sequence (Figure 3B) and comparison was made between the genotypes and the susceptibility to CTL-1B9 of 9 HLA-A*2402$^+$ B-LCLs, including ones generated from the recipient (from whom CTL-1B9 was established) and his donor. Susceptibility to CTL-1B9 correlated completely with the presence of guanine at SNP rs1138357 (nucleotide position 238, according to the mRNA sequence for NM_004049.2) and thymine at SNP rs1138358 (nucleotide position 299) (Table 2), suggesting that the expression of the minor H epitope recognized by CTL-1B9 is controlled by either of these SNPs. We searched for nonameric amino acid sequences spanning the 2 SNPs using BIMAS software,[22] since most reported HLA-A*2402 binding peptides contain 9 amino acid residues.[23] Among these, a nonameric peptide, DYLQCVLQI (the polymorphic residue being underlined), has a predicted binding score of 75 and was considered as a candidate minor H epitope. As shown in Figure 5B, the DYLQCVLQI was strongly recognized by CTL-1B9, whereas its allelic counterpart,

Table 1. Positive SNPs from pooled DNA analysis

CTL-2A12, Exp 1				CTL-2A12, Exp 2				CTL-1B9, Exp 1				CTL-1B9, Exp 2			
rsID	Chr	Position	$\Delta R_{A\Delta R_B}$	rsID	Chr	Position	$\Delta R_{A\Delta R_B}$	rsID	Chr	Position	$\Delta R_{A\Delta R_B}$	rsID	Chr	Position	$\Delta R_{A\Delta R_B}$
50K X bal															
rs10513933	18	59699669	0.366*	rs10513933	18	59699669	0.511†	rs1363258	5	103297593	0.239	rs10499174	6	131209689	0.352*
rs9320028	18	59668150	0.255‡	rs9320028	18	59668150	0.360*	rs726083	3	67093729	0.203	rs30058	5	122325602	0.240
rs6102	18	59721450	0.221	rs10485873	7	3503743	0.157	rs639243	5	31392931	0.198	rs150724	16	61960443	0.213
rs724533	23	116440574	0.137	rs219323	14	59510440	0.150	rs1936461	10	56519024	0.186	rs1993129	8	63618836	0.208
rs1341112	6	104919391	0.136	rs10506892	12	82478539	0.147	rs763876	12	94922502	0.186	rs356946	13	69066751	0.201
rs470490	18	61182216	0.136	rs10492269	12	97786333	0.144	rs958404	7	133054441	0.179	rs2869268	4	86421898	0.184
rs2826718	21	21471423	0.134	rs10483466	14	35986827	0.139	rs10486727	7	41672315	0.178	rs287002	12	40312537	0.183
rs10506697	12	73241741	0.128	rs5910124	23	116408616	0.137	rs2833488	21	32010112	0.176	rs1146808	13	67688608	0.182
rs10506891	12	82393029	0.127	rs10512545	17	66337079	0.134	rs379212	5	60977687	0.172	rs10501287	11	42446011	0.180
rs308995	14	59657919	0.125	rs295678	5	58186928	0.131	rs1954004	14	58627872	0.170	rs564993	5	31393476	0.177
50K *Hind*III															
rs9320032	18	59712191	0.486†	rs9320032	18	59712191	0.506†	rs1842353	8	63617543	0.244*	rs9300692	13	101216476	0.225‡
rs8090046	18	59773066	0.207‡	rs8090046	18	59773066	0.245*	rs10521202	17	12755289	0.201‡	rs1842353	8	63617543	0.210‡
rs1474220	2	108525317	0.193‡	rs10498752	6	41876488	0.210‡	rs7899961	10	59696431	0.198‡	rs10520983	5	31314700	0.195‡
rs10498752	6	41876488	0.178	rs1941538	18	37994337	0.176	rs9320974	6	124421441	0.197‡	rs1334375	13	80897038	0.173
rs2298578	21	21632551	0.167	rs7682770	4	152748018	0.174	rs10520983	5	31314700	0.179	rs10519164	15	75412758	0.163
rs7516032	1	91618962	0.165	rs1445862	5	3675257	0.169	rs1862446	5	147460749	0.170	rs9322063	6	146852196	0.152
rs5030938	10	70645922	0.164	rs4696976	4	21058616	0.167	rs1358778	20	13266796	0.169	rs8067384	17	37926265	0.150
rs1883041	21	44921845	0.158	rs5030938	10	70645922	0.165	rs1873790	4	83422480	0.166	rs10521202	17	12755289	0.147
rs3902916	4	189045176	0.155	rs3902916	4	189045176	0.165	rs1220724	4	70888705	0.162	rs7914904	10	62749969	0.141
rs1000551	20	58709208	0.154	rs1883041	21	44921845	0.164	rs9300692	13	101216476	0.157	rs1220724	4	70888705	0.141
250K *Nsp*I															
rs9950903	18	59781783	0.534†	rs9950903	18	59781783	1.036†	rs1879894	15	78055874	0.846†	rs1879894	15	78055874	1.072†
rs1463835	3	23539615	0.532†	rs8090586	18	59781864	0.518†	rs9646294	16	6110019	0.484†	rs6771859	3	190642054	0.387†
rs16975459	18	37802275	0.383*	rs6473170	8	80664840	0.338*	rs17734332	5	134945240	0.365†	rs10512261	9	98804394	0.299*
rs8090586	18	59781864	0.367*	rs4510128	18	59782312	0.310‡	rs566619	7	41381538	0.345*	rs12122772	1	60384564	0.287*
rs16872621	4	22081055	0.312‡	rs1006755	18	59782026	0.300‡	rs17737566	6	50345280	0.310*	rs2153155	4	26034162	0.248‡
rs870582	6	125097114	0.301‡	rs7039378	9	118735938	0.258	rs3849955	9	28350374	0.285*	rs17126896	14	53320494	0.246‡
rs1015416	18	59720363	0.270‡	rs1860563	16	6418899	0.258	rs4616156	13	86581518	0.273*	rs1328652	13	35607527	0.240
rs2155907	11	97599883	0.227	rs4699126	4	105709109	0.212	rs2484698	1	217474460	0.263*	rs7021551	9	27446645	0.237
rs2112948	5	50994294	0.222	rs10275055	7	156212079	0.204	rs17139603	11	79638632	0.262*	rs252817	5	106752487	0.237
rs2919747	2	129681506	0.217	rs1526411	7	124658309	0.201	rs2156737	4	100642529	0.246‡	rs10772587	12	12681356	0.235
250K *Sty*I															
rs6102	18	59721450	0.597†	rs6102	18	59721450	0.495†	rs9383925	6	151975774	0.819†	rs201204	6	104842863	0.688†
rs9951512	18	59690885	0.374*	rs9945924	18	59771746	0.407*	rs6497397	16	19646258	0.311‡	rs12556155	23	108836419	0.442†
rs6496897	15	90493249	0.320‡	rs9951512	18	59690885	0.317‡	rs917252	7	22219990	0.289‡	rs4791422	17	10605304	0.435†
rs9945924	18	59771746	0.315‡	rs1983205	3	157782892	0.314‡	rs1019403	3	7823997	0.260‡	rs7749012	6	106459559	0.336*
rs12707805	8	107404746	0.303‡	rs950865	5	2720684	0.307‡	rs17053134	5	155373544	0.259‡	rs509951	5	31385483	0.308‡
rs10971778	9	33893184	0.296‡	rs2278179	18	59715512	0.292‡	rs11710880	3	72214965	0.246	rs16879024	8	32225711	0.256‡
rs6565076	16	81487818	0.294‡	rs10427722	22	36417752	0.289‡	rs17167866	7	13919264	0.237	rs2100054	15	75293482	0.252
rs2278179	18	59715512	0.291‡	rs17156659	7	82046820	0.271	rs10867062	9	137935241	0.237	rs11811023	1	143805934	0.240
rs7806238	7	29906442	0.290‡	rs4502324	18	4811261	0.262	rs5925800	23	23278707	0.235	rs17382798	15	75256074	0.231
rs965888	18	38062658	0.283‡	rs1348428	2	225927288	0.260	rs2255831	4	146614313	0.234	rs2030302	17	12526591	0.231

Significant SNPs that appeared on both experiments are underlined.
*Genomewide $P < .01$.
†Genomewide $P < .001$.
‡Genomewide $P < .05$.

DYLQ*Y*VLQI, was not. Decameric peptide, QDYLQ*C*VLQI, on the other hand, appeared to be weakly recognized; however, it is likely that the nonameric form was actually being presented after N-terminal glutamine cleavage by aminopeptidase in the culture medium. Because it was possible that the cystine might be cysteinylated, recognition of synthetic peptides DYLQCVLQI and cysteinylated DYLQC*VLQI were assayed using CTL-1B9. Half-maximal lysis for the former was obtained at a concentration of 200 pM, whereas recognition of the latter was several-fold weaker (Figure 5C). Thus, we concluded that DYLQCVLQI defines the cognate HLA-A*2402–restricted CTL-1B9 epitope, now designated ACC-1^C. This incidentally provides a second example of products from both dichotomous SNP alleles being recognized as HLA-A*2402–restricted minor H antigens, the first example being the HB-1 minor H antigen.[24] Finally, real-time quantitative PCR revealed that T cells carrying the complementarity-determining region 3 sequence identical to CTL-1B9 became detectable in the patient's blood at the frequencies of 0.22%, 0.91%, 1.07% and 0.01% among $TCR\alpha\beta^+$ T cells at days 30, 102, 196, and 395 after transplantation, respectively, suggesting that ACC-1^C minor H antigen is indeed immunogenic (Figure 5D).

Discussion

Recent reports have unequivocally demonstrated that WGASs can be successfully used to identify common variants involved in a wide variety of human diseases.[25-27] Our report represents a novel

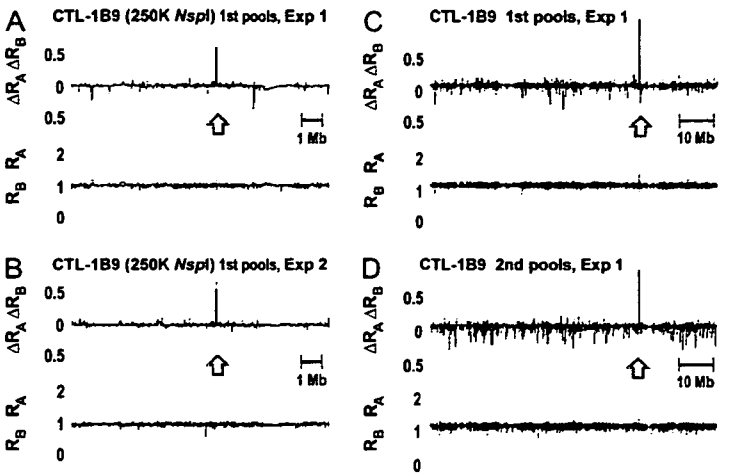

Figure 4. Reproducible detection of association with the immunophenotypes determined by CTL-1B9 at the *BCL2A1* locus. The maximum test statistic value was observed at a single SNP (rs1879894) within 15q25.1 in duplicate experiments for the first pools consisting of 57 CTX$^+$ and 38 CTX$^-$ B-LCLs (A-C). The peak association at the same SNP was reproduced in the experiments with the second pools consisting of 75 CTX$^+$ and 34 CTX$^-$ LCLs (D). Test statistic values ($\Delta R_A \Delta R_B$) are plotted by blue lines together with their R_A (red) and R_B (green) values. The expected $\Delta R_A \Delta R_B$ values multiplied by r^2 correlation coefficients for the adjacent SNPs within 500 kb from the SNP rs1879894 are overlaid by red lines (A,B).

application of WGASs to transplantation immunology, which provides a simple but robust method to fine-map the genetic loci of minor H antigens whose expression is readily determined by standard immunophenotyping with CTL clones established from patients who have undergone transplantation.

The current WGA/CTL method has several desirable features that should contribute to the acceleration of minor H locus mapping. In comparing the method to those of linkage analysis and other nongenetic approaches, including direct peptide sequencing of chemically purified minor H antigens[5,6,10,13] and conventional

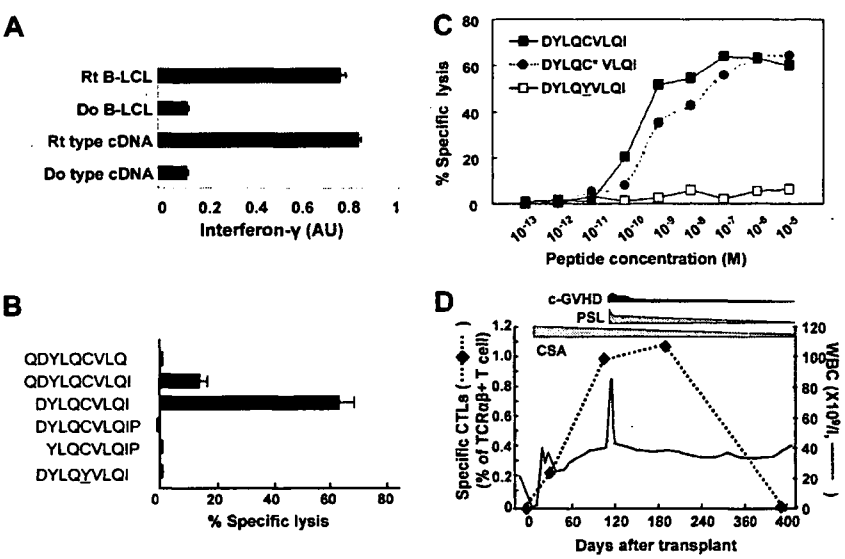

Figure 5. Identification of the CTL-1B9 minimal minor H epitope. (A) Interferon-γ production from CTL-1B9 against HLA-A*2402–transduced 293T cells transfected with plasmid encoding full-length *BCL2A1* cDNA cloned from either the recipient (Rt) from whom CTL-1B9 was isolated or his donor (Do). Rt B-LCL and Do B-LCL were used as positive and negative controls, respectively. Secreted interferon-γ was measured by ELISA and is expressed in arbitrary units (AUs) corresponding to optical density at 630 nm. Results are typical of 2 experiments and data are the mean plus or minus SD of triplicates. (B) A peptide reconstitution assay was conducted to determine the minimal epitope for CTL-1B9. Nonameric peptide (DYLQCVLQI), 2 nonameric peptides shifted by one amino acid to N- or C-terminus, N- and C-terminal extended decameric peptides, and its allelic counterpart (DYLQYVLQI) were synthesized and tested by adding to antigen-negative donor B-LCL at 10 nM in a standard ^{51}Cr release assay. Results are typical of 2 experiments and data are the mean plus or minus SD of triplicates. (C) Titration of the candidate minor H peptide by epitope reconstitution assay. Chromium-labeled donor B-LCLs were distributed to wells of 96-well round-bottomed plates, pulsed with serial dilutions of the indicated peptides for 30 minutes at room temperature, and then used as targets for CTL-1B9 in a standard ^{51}Cr release assay. A cysteinylated peptide (indicated by an asterisk) was included as an alternative form of the potential epitope. Results are typical of 2 experiments. (D) Tracking of ACC-1^C–specific T cells in the recipient's peripheral blood. In order to longitudinally analyze the kinetics of the ACC-1^C–specific CTLs in peripheral blood from the patient from whom CTL-1B9 was established, a real-time quantitative PCR was conducted. Complementary DNAs of peripheral blood mononuclear cells from the donor and patient before and after HSCT were prepared from the patient. Real-time PCR analysis was performed using a TaqMan assay as described previously.[9] The primers and fluorogenic probe sequences spanning the CTL-1B9 complementarity-determining region 3 (CDR3) were used to detect T cells carrying the CDR3 sequences identical to that of CTL-1B9. The primers and fluorogenic probe sequences spanning constant region of TCR beta chain (TCRBC) mRNA were used as internal control. Samples were quantified with the comparative CT method. The delta CT value was determined by subtracting the average CT value for TCRBC from the average CTL-1B9 CDR3 CT value. The standard curve for the proportion of CTL-1B9 among TCR$\alpha\beta^+$ T cells was composed by plotting mean delta CT values for each ratio, and the percentages of T cells carrying the CDR3 sequence identical to CTL-1B9 were calculated by using this standard curve. During this period, quiescent chronic GVHD, which required steroid treatment, developed; however, involvement of immune reaction to ACC-1^C minor H antigen was unlikely since its frequency increased even after resolution of most chronic GVHD symptoms. c-GVHD, chronic GVHD; CSA, cyclosporine A; PSL, prednisolone; WBC, white blood cell count.

Table 2. Correlation of *BCL2A1* sequence polymorphisms with susceptibility to CTL-1B9

	HLA-A*2402–positive B-LCLs								
	Rt	Do	UR1	UR2	UR3	UR4	UR5	UR6	UR7
Cytolysis by CTL-1B9	+	−	+	+	+	+	+	−	−
Detected SNP, position*									
rs1138357, 238	G/A	A	G	G	G/A	G/A	G/A	A	A
rs1138358, 299	T/G	G	T	T	T/G	T/G	T/G	G	G
rs3826007, 427	G	G/A	G	G	G	G	G/A	G/A	G

Rt indicates recipient; Do, donor; UR, unrelated; +, yes; and −, no.

*Nucleotide positions are shown according to the NM_004092.2 mRNA sequence, available at http://www.ncbi.nlm.nih.gov/ as GEO accession GSE10044.

expression cloning,[8,9,11] there are differences in terms of power, sensitivity, and specificity. Direct sequencing of minor H antigen peptide guarantees that the purified peptide is surely present on the cell surface as antigen, but it requires highly specialized equipment and personnel. Expression screening of cDNA libraries is also widely used and has become feasible with commercially available systems. However, it depends highly on the quality of the cDNA library and expression levels of the target genes. In addition, it often suffers from false-positive results due to the forced expression of cDNA clones under a strong promoter. The current method of WGA/CTL genetically determines the relevant minor H antigen locus, not relying on highly technical protein chemistry using specialized equipment, or repetitive cell cloning procedures. It is also not affected by the expression levels of the target antigens.

As a genetic approach, the current method based on genetic association has several advantages over conventional linkage analysis: the mapping resolution has been greatly improved from several Mb in the conventional linkage analysis to the average haplotype block size of less than 100 kb,[17,25-27] usually containing a handful of candidate genes, compared with the dozens as typically found in linkage analysis. This means that the effort needed for the subsequent epitope mapping will be substantially reduced. In fact, the 115 kb region identified for CTL-2A12 contains 4 genes compared with 38 genes as revealed by the previous linkage study (data not shown), and the candidate gene was uniquely identified within the 26 kb region for CTL-1B9, for which linkage analysis had failed due to very rare segregating pedigrees among the CEPH panels with this trait (now ACC-1^C; data not shown).[15,16] In addition, before moving on to epitope mapping, it would be possible to evaluate the clinical relevance of the minor H antigens by examining the tissue distribution of their expression, based on widely available gene expression databases such as Genomic Institute of the Novartis Research Foundation (GNF, http://symatlas.gnf.org/SymAtlas/).[28]

Second, the required sample size is generally small, and should be typically no more than 100 B-LCLs for common minor H alleles. This is in marked contrast to the association studies for common diseases, in which frequently thousands of samples are required.[17,25-27] In the current approach, sufficiently high test statistic values could be obtained for the relevant loci with a relatively small sample size, since the minor H allele is correctly segregated between the CTX^+ and CTX^- pools by the highly specific immunologic assay. Combined with high accuracy in allelic measurements, this feature allows for the use of pooled DNAs in WGAS, which substantially saves cost and time, compared with the genotyping of individual samples. Unexpectedly, our method allows for a considerable degree of error in the immunophenotyping, indicating the robustness of the current method; in fact, the minor H locus for CTL-2A12 was successfully identified in spite of the presence of 8 (~10%) immunophenotyping errors. When the minor H allele has an extreme allele frequency (eg, $< 5\%$ or $> 95\%$), which could be predicted by preliminary immunophenotyping, WGAS/CTL may not be an efficient method of mapping, due to the impractically large numbers of B-LCLs that would need to be screened to obtain enough CTX^+ or CTX^- B-LCLs. However, such minor H antigens would likely have limited clinical impact or applicability.

Sensitivity of the microarray analysis seems to be very high when the target SNP has good proxy SNPs on the array, because we were able to correctly identify the single SNP correlated with the target of CTL-1B9 from more than 500 000 SNP markers. On the other hand, genome coverage of the microarray is definitely important. In our experiments on CTL-2A12, the association was successfully identified by the marker SNPs showing r^2 values of approximately 0.74 with the target locus of ACC-6. Since the GeneChip 500 K array set captures approximately 65% of all the HapMap phase II SNPs with more than 0.74 of r^2[29] and higher coverage will be obtained with the SNP 6.0 arrays having more than 1 000 K SNP markers, these arrays can be satisfactorily used as platforms for the WGA/CTL method.

As shown in the current study, the intrinsic sensitivity and specificity of the WGA/CTL method in detecting associated SNPs were excellent. In other words, as long as target SNPs are captured in high r^2 values with one or more marker SNPs within the Affymetrix 500 K SNP set, there is a high likelihood of capturing the SNP with the current approach. To evaluate the probability of a given minor H antigen being captured in high r^2 with marker SNPs, we checked the maximum r^2 values of known minor H antigen SNPs with the Affymetrix 500 K SNPs, according to empirical data from the HapMap project (www.hapmap.org). Among 13 known minor H antigens, 7 have their entries (designated minor H SNP) in the HapMap phase II SNP set (HA-3,[30] HA-8,[31] HB-1,[11] ACC-1 and ACC-2,[7] LB-ADIR-1F,[10] and 7A7-PANE1[13]), and were used for this purpose (note that absence of their entries in the HapMap data set does not necessarily mean that they could not be captured by a particular marker SNP set). As shown in Table S4, all 7 minor H SNPs are captured by at least one flanking SNP that is included in the Affymetrix 500 K SNP set with r^2 values of more than 0.74 in at least one HapMap panel. The situation should be more favorable in the recently available SNP 6.0 array set with 1 000 K SNPs, indicating the genome coverage with currently available SNP arrays would be sufficient to capture typical minor H antigens with our approach.

Most patients who have received allo-HSCT could be a source of minor H antigen-specific CTL clones to be used for this assay, since the donor T cells are in vivo primed and many CTL clones could be established using currently available methods. In fact, substantial numbers of CTL clones have been established worldwide and could serve as the probes to identify novel minor H antigens.[32,33] Once constructed, a panel of B-LCLs, including those transduced with HLA cDNAs, could be commonly applied to immunophenotyping with different CTL clones, especially when

CTLs are obtained from the same ethnic group. In addition, by adopting other immunophenotyping readouts such as production of IL-2 from $CD4^+$ T cells, this method could be applied to identification of MHC class II–restricted minor H antigens which have crucial roles in controlling CTL functions upstream. This may open a new field in the study of allo-HSCT since MHC class II–restricted mHags have been technically difficult to identify by conventional methods.

Finally, the discovery of ACC-1^C as a novel minor H antigen indicates that all the mismatched transplants at this locus could be eligible for allo-immune therapies, since we have previously demonstrated that the counter allele also encodes a minor H antigen, ACC-1^Y, which is preferentially expressed and presented on blood components including leukemic cells and may serve as a target of allo-immunity.[7,34] Indeed, CTLs specific for ACC-2, an HLA-B44–restricted minor H antigen restricted by the third exonic SNP on *BCL2A1*,[7] was independently isolated from the peripheral blood of a patient with recurrent leukemia re-entering complete remission after donor lymphocyte infusion.[32] The number of eligible allo-HSCT recipients has now been effectively doubled, accounting for 50% of transplants with HLA-A24 or 20% of all transplantations performed in the Asian population. In conclusion, we have described a simple but powerful method for minor H mapping to efficiently accelerate the discovery of novel minor H antigens that will be needed to contribute to our understanding of the molecular mechanism of human allo-immunity.

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Authorship

Contribution: T.K. performed most immunologic experiments and preparation of pooled DNA and quantative PCR, analyzed data, and wrote the manuscript; Y.N. performed the majority of genetic analyses and analyzed the data; H.T. performed T-cell receptor analysis and designed q-PCR primers and probes; G.Y. contributed to the organization of software for linkage analysis and simulation; S.M. prepared the pooled DNA; M.O., K.M., Y.K, and Y.M. collected clinical data and specimens; T.T. and K.K. contributed to data analysis and interpretation, and to the writing of the article; S.O. and Y.A. supervised the entire project, designed and coordinated most of the experiments in this study, contributed to manuscript preparation, and are senior coauthors.

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