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ORIGINAL REPORT

Second Malignant Neoplasms After Treatment of Childhood Acute Lymphoblastic Leukemia

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A B S T R A C T

Purpose
Second malignant neoplasms (SMNs) after diagnosis of childhood acute lymphoblastic leukemia (ALL) are rare events.

Patients and Methods
We analyzed data on risk factors and outcomes of 642 children with SMNs occurring after treatment for ALL from 18 collaborative study groups between 1980 and 2007.

Results
Acute myeloid leukemia (AML; n = 186), myelodysplastic syndrome (MDS; n = 69), and nonmeningioma brain tumor (n = 116) were the most common types of SMNs and had the poorest outcome (5-year survival rate, 18.1% ± 2.9%, 31.1% ± 6.2%, and 18.3% ± 3.8%, respectively). Five-year survival estimates for AML were 11.2% ± 2.9% for 125 patients diagnosed before 2000 and 34.1% ± 6.3% for 61 patients diagnosed after 2000 ($P < .001$); 5-year survival estimates for MDS were 17.1% ± 6.4% (n = 36) and 48.2% ± 10.6% (n = 33; $P = .005$). Allogeneic stem-cell transplantation failed to improve outcome of secondary myeloid malignancies after adjusting for waiting time to transplantation. Five-year survival rates were above 90% for patients with meningioma, Hodgkin lymphoma, thyroid carcinoma, basal cell carcinoma, and parotid gland tumor, and 68.5% ± 6.4% for those with non-Hodgkin lymphoma. Eighty-nine percent of patients with brain tumors had received cranial irradiation. Solid tumors were associated with cyclophosphamide exposure, and myeloid malignancy was associated with topoisomerase II inhibitors and starting doses of methotrexate of at least 25 mg/m^2 per week and mercaptopurine of at least 75 mg/m^2 per day. Myeloid malignancies with monosomy 7/5q− were associated with high hyperdiploid ALL karyotypes, whereas 11q23/*MLL*-rearranged AML or MDS was associated with ALL harboring translocations of t(9;22), t(4;11), t(1;19), and t(12;21) ($P = .03$).

Conclusion
SMNs, except for brain tumors, AML, and MDS, have outcomes similar to their primary counterparts.

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As many as one third of all deaths in childhood acute lymphoblastic leukemia (ALL) are caused by toxicities or second malignant neoplasms (SMNs).[1-4] Previously reported cumulative incidences of SMNs have varied from less than 1% to 10% or more because of differences in antileukemic therapy and in duration, accuracy, and completeness of follow-up.[1,2,5-18] Partly because of their rarity, little is known about the etiology of SMNs or about the treatment options that offer the best chances of cure.[1]

With the goal of improving overall survival in childhood ALL and providing guidelines for treatment, the international Ponte di Legno consortium of ALL study groups has studied uncommon subgroups of childhood ALL.[19-23] This is the largest study of SMNs after therapy for childhood ALL reported to date, and it presents new potential risk factors and provides survival rates for distinct subsets.

Review of Patient Data

In the February 2010 issue of *Leukemia*, 16 cooperative study groups from Europe, North America, and Asia reported clinical outcomes, including the occurrence of

SMNs, of 54,068 children and adolescents up to 21 years of age with newly diagnosed ALL enrolled onto controlled clinical trials between 1980 and 2007.[5-17,24-26] From these 16 groups as well as from FRALLE (French Acute Lymphoblastic Leukaemia Study Group) and the childhood leukemia branch of the European Organisation for Research and Treatment of Cancer (EORTC), we collected data on individuals with SMNs to form a common database with predefined variables comprising clinical and biologic data (including cytogenetic characteristics for myeloid neoplasias) as well as outcomes (Appendix Table A1, online only). Furthermore, we recorded clinical and biologic characteristics of their primary ALL as well as treatment given and status at latest follow-up. The data available for this study were retrieved from the groups' central ALL databases. If patient data on drug doses were unavailable, the patients were assigned the drugs and doses listed in the ALL protocols onto which they were enrolled. Accrual of data for patients with ALL who did not develop SMNs was not part of the study. The study was approved according to regional institutional review board requirements. All data were compiled at Rigshospitalet (Copenhagen, Denmark), and the database was approved by the Danish Data Protection Authorities.

Statistical Analysis

Differences in distribution of individual parameters among subsets were analyzed by using nonparametric tests.[27] Since accrual of data for patients with ALL who did not develop SMNs was not part of this study, odds ratios for SMNs in relation to specific exposures are not included. Instead, we analyzed patterns of ALL characteristics and therapy by subsets of SMNs to determine whether certain ALL subtypes or drug exposures were more prevalent within specific subsets of SMNs. Survival after an SMN was defined as time from diagnosis of the SMN to death as a result of any cause or to last follow-up. The Kaplan-Meier method was used to estimate survival rates with SEs calculated according to Greenwood.[28] Differences in survival rates were compared with the log-rank test.[29] The Cox proportional hazard model was used for selected analysis of survival after SMNs.[30] Two-sided P values below .05 were regarded as significant.

In all, 659 patients diagnosed with ALL between 1980 and 2007 were registered with a malignant neoplasm or a CNS tumor as the first event after diagnosis of ALL. Seventeen SMNs reported as ALL (n = 12), acute undifferentiated leukemia (n = 2), or myeloid malignancies with monosomy 7 (n = 1) or t(9;22)(q34;q11.2) (n = 2) at diagnosis of both ALL and the subsequent SMNs were excluded because the clonal relationship to the original leukemia could not be confidently verified, leaving a total of 642 study patients.

Table 1 reports clinical information on the 642 SMNs by subtype. The interval between diagnosis of ALL and occurrence of SMNs was significantly associated with the subtype of SMN, being shortest for hematologic malignancies and longest for carcinomas and meningiomas ($P < .001$; Fig 1 and Table 1). Thus, among the 48 SMNs diagnosed more than 15 years from the diagnosis of ALL, 35% were meningiomas (n = 15) or other CNS tumors (n = 2); 31% were non–skin carcinomas (n = 15), including six thyroid cancers; 15% were melanomas (n = 4) or other skin cancers (n = 3); and 17% were hematologic malignancies (n = 5); sarcomas (n = 2); or testicular cancer (n = 2). Eight patients with cancer-predisposing diseases are described in Appendix Table A2 (online only).

Patterns of SMNs by ALL-Presenting Features

Although distribution of sex, age, and WBC count at diagnosis of ALL varied significantly among the major categories of SMNs for the entire cohort (Table 1), this was not the case for the subset of 201 patients who were not irradiated and did not undergo hematopoietic stem-cell transplantation during first-line ALL treatment ($P > .45$ for all analyses; Appendix Table A3, online only).

Immunophenotype

Of the 186 patients with AML and 69 patients with myelodysplastic syndrome (MDS), the ALL lineage (B-cell precursor or T-cell lineage) was available for 217 patients. When analyzing only the 192 patients who did not receive irradiation and did not receive transplantation but who did have ALL immunophenotype available, the prevalence of T-cell ALL did not differ significantly among the categories of hematologic malignancies, CNS tumors, carcinomas, and other tumors (7.8%, 10.0%, and 16.7%, respectively; $P = .38$), but 26.6% of all patients with AML (42 of 158) and 8.5% of all patients with MDS (five of 59) initially had T-cell ALL. Patients with AML were overall more likely than those with other hematologic malignancies (n = 136) to have had T-cell ALL (26.6% v 13.2%; $P = .005$) with the same trend (10.0% v 5.6%; $P = .33$) in the subsets of patients who did not receive irradiation and did not receive transplantation. The interval between diagnosis of ALL and SMN was significantly shorter for the 11 patients who did not receive irradiation and did not receive transplantation but who had T-cell ALL than for the 130 patients with B-cell precursor ALL who had developed hematologic malignancies (median, 1.6 v 3.0 years; $P = .001$). Finally, 91% (10 of 11) of the patients who developed Langerhans cell histiocytosis had T-cell ALL compared with 20.4% among the other SMNs ($P < .001$).

Karyotype and Therapy-Related Myeloid Neoplasias

The time to develop AML was shorter than the time to develop MDS (median, 2.7 v 3.3 years; $P = .01$), reflecting a higher proportion of 11q23/*MLL* rearrangements with short latency (median, 2.5 years) in patients with AML (58% v 5% of patients with MDS with an aberrant karyotype; $P < .001$). By contrast, treatment-related myeloid neoplasia (t-MN; ie, AML or MDS) with monosomy 7 (median interval, 3.7 years) occurred in 22% of patients with AML and in 50% of patients with MDS with an aberrant karyotype ($P = .002$).

Among the 44 patients with t-MN with monosomy 7, 5q−, or 11q23/*MLL* rearrangements (one t-MN with both monosomy 7 and 11q23/*MLL* rearrangements was excluded) and an available karyotype for the ALL clone, the cytogenetic aberrations of their ALL and t-MN were highly correlated. Thus, among the 25 patients who developed 11q23/*MLL*-rearranged t-MN, 13 had ALL with classical recurrent translocations—t(9;22)(q34;q11.2) (n = 1), t(1;19)(q23;p13.3) (n = 2), t(12;21)(p13;q22) (n = 8), or 11q23/*MLL* rearrangements (n = 2 [different 11q23/*MLL* rearrangement in the two clones]—and six had a high hyperdiploid ALL karyotype (modal chromosome number above 50), and six had other structural and/or numeric aberrations. In contrast, among the 19 patients who developed t-MN with 5q− or monosomy 7, 10 had a high hyperdiploid ALL karyotype, three had ALL clones with one of the above-listed classical translocations, and six had other aberrations ($P = .03$ by likelihood-ratio χ^2 test).

Patterns of SMNs by ALL Therapy

The pattern of SMNs was significantly influenced by the preceding ALL therapy (Table 2). The 12 patients with CNS tumors who had not received CNS irradiation were diagnosed at significantly shorter intervals after ALL than the 97 patients with CNS tumors that occurred after CNS irradiation (median, 6.6 v 9.1 years; $P = .01$).

Table 1. Clinical Characteristics and 5-Year Overall Survival of 642 Patients With SMNs by Major Categories and Subtype

Type of SMN	Total		Males		ALL Immunophenotype* (n = 555)		Age at ALL (years)		WBC at ALL ($\times 10^9$/L)		Interval to SMN (years)		Age at SMN (years)		5-Year Survival Rate After SMN (%)
	No.	%	No.	%	BCP	%	Median	50% Range	Median	50% Range	Median	50% Range	Median	50% Range	
Total	642		346	53.9	434	78.2	5.2	3.2-10.3	11.4	4.7-45.0	4.8	2.6-8.9	12.6	7.8-17.5	40.4 ± 2.1†
Hematologic	345	53.7	198	57.4	234	79.6	5.2	3.2-11.2	9.0	4.2-37.0	2.9	2.0-4.5	9.4	6.5-15.2	35.2 ± 2.7
Acute myeloid leukemia	186		106	57.0	116	73.4	5.6	3.3-11.2	11.6	4.2-45.0	2.7	1.8-4.5	9.5	6.4-15.0	18.1 ± 2.9
Myelodysplastic syndrome	69		32	46.4	54	91.5	5.2	3.1-12.2	6.0	3.8-12.7	3.3	2.6-4.6	9.7	6.9-15.9	31.1 ± 6.2
Chronic myeloid leukemia	9		4	44.4	7	100.0	12.5	4.2-15.1	9	4.0-28.5	4.1	3.5-7.2	18.0	17.4-19.3	62.2 ± 17.8
Non–Hodgkin lymphomas	56		39	69.6	39	83.0	4.7	3.0-8.6	11.2	4.3-31.8	2.3	1.5-4.0	7.8	5.5-12.1	68.5 ± 6.4
Hodgkin disease	25		17	68.0	18	78.3	4.2	3.0-9.2	7.4	5.0-45.0	4.1	2.6-5.3	10.2	6.9-14.9	91.1 ± 6.0
CNS tumor	138	21.5	67	48.6	94	78.3	4.2	2.6-8.7	15.7	6.1-59.0	8.6	6.8-11.2	14.7	11.0-19.2	25.9 ± 4.2
Nonmeningioma CNS tumor	116		53	45.7	79	77.5	4.4	2.7-8.7	18.7	6.9-82.8	8.1	6.5-9.8	13.9	10.5-16.5	18.3 ± 3.8
Meningioma	22		14	63.6	15	83.3	3.5	2.3-8.5	9	5.1-30.0	16.2	12.3-18.3	21.7	17.8-25.4	90.9 ± 8.7
Carcinoma	78	12.1	34	43.6	62	84.9	5.8	3.3-10.6	12.3	4.0-45.6	10.1	6.7-14.5	17.5	12.4-22.2	82.2 ± 4.9
Nonthyroid carcinoma	46		19	41.3	35	81.4	8.4	3.9-13.0	12.9	3.6-38.5	10.2	6.1-15.0	18.0	12.4-25.8	67.3 ± 8.2
Thyroid carcinoma	32		15	46.9	27	90.0	5.0	3.1-6.5	12.1	4.3-58.5	10.1	7.8-13.5	15.5	12.1-18.3	100
Other	81	12.6	47	58.0	44	64.7	5.7	4.0-10.4	14.0	4.9-79.9	6.8	3.4-10.0	14.1	8.2-17.9	55.3 ± 6.1
Soft tissue sarcoma	29		14	48.3	14	60.9	6.0	4.1-10.4	19.8	7.3-66.0	5.4	3.3-9.6	13.3	8.0-17.2	43.9 ± 9.7
Bone tumor	22		13	59.1	14	77.8	5.3	2.9-8.1	7.0	3.1-30.9	7.8	5.2-11.4	14.4	11.9-17.9	61.9 ± 11.6
Melanoma	11		6	54.6	9	90.0	10.0	5.7-13.9	10.0	4.7-30.9	10.0	6.3-17.8	19.2	16.7-24.3	85.7 ± 13.2
Germ cell tumor	4		4	100.0	3	100.0	12.7	8.1-15.2	7.8	2.6-13.2	12.3	8.4-19.8	22.9	20.2-31.4	100
Histiocytosis	12		9	75.0	2	16.7	4.2	2.5-5.5	141.0	40.4-248.5	2.3	1.4-3.9	6.9	6.0-8.2	48.6 ± 14.8
Other	3		1	33.3	2	100.0	9.9	4.1-12.3	4.0	2.2-148.0	7.6	3.3-9.8	15.5	13.9-17.5	33.3 ± 27.2

Abbreviations: ALL, acute lymphoblastic leukemia; BCP, B-cell precursor; SMN, second malignant neoplasm.
*In all, 87 patients were excluded because immunophenotype was not reported (n = 75) or was not specified as either BCP or T-cell ALL (n = 12).
†Ten-year survival rate was 38.7% ± 2.2%.

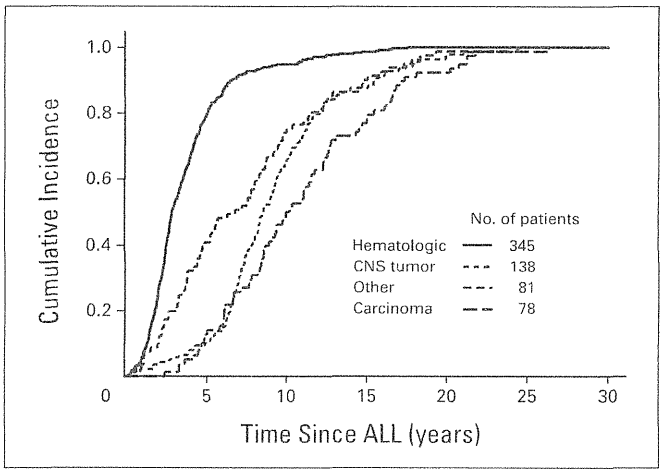

Fig 1. Kaplan-Meier estimates of the interval between diagnosis of acute lymphoblastic leukemia (ALL) and development of the four major categories of second malignant neoplasms.

Thirty-eight (76.0%) of 50 patients with t-MN with an aberrant karyotype and previous exposure to epipodophyllotoxins had 11q23/*MLL* rearrangements, whereas only four (8.0%) had monosomy 7 and none had 5q–. In contrast, among the 46 patients with t-MN (52.2%) who had not been exposed to epipodophyllotoxins, 24 developed monosomy 7 (n = 20) or 5q– (n = 4) t-MN, and only 13 (28.3%) had 11q23/*MLL* rearrangements ($P < .001$).

Among patients who did not receive irradiation, 44 (79%) of 56 patients with solid tumors had previously received cyclophosphamide compared with 82 (57%) of 143 patients with hematologic malignancies or CNS tumors ($P = .005$).

Among the patients who did not receive transplantation for whom data on maintenance therapy methotrexate (n = 431) and mercaptopurine dosage (n = 422) were available, the patients who developed t-MN received higher starting doses of methotrexate and mercaptopurine than did patients who developed other SMNs ($P < .001$ for both drugs), and this was the case for both CNS patients who received irradiation ($P < .001$ and $P = .001$, respectively) and those who did not ($P = .007$ and $P = .02$, respectively). Thus, compared with patients with other SMNs, the patients who developed t-MNs were more likely to have received methotrexate starting doses of at least 25 mg/m^2 per week (45% *v* 28%; $P < .001$) and mercaptopurine starting doses of at least 75 mg/m^2 per day (52% *v* 29%; $P < .001$).

Neither the distribution of the four major categories of SMNs ($P = .37$) nor the time interval to SMN ($P = .84$) differed significantly between patients with low (n = 13; 10 by genotype and three by phenotype) versus normal (n = 114) thiopurine methyltransferase activity. Among the 413 patients who did not undergo transplantation but who did have data on the total duration of therapy, 65 (31.3%) of the 208 patients with t-MN and 36 (17.6%) of the 205 patients with solid tumors had received ALL therapy for 2.5 years or longer ($P = .001$).

Transplantation during first remission of ALL had been performed in 29 (5.7%) of the 510 ALL patients with available information. One (1.4%) of 74 patients with CNS tumors and seven (3.6%) of 193 patients with t-MN had received transplantation compared with nine (28.1%) of 32 patients with carcinomas and eight (15.4%) of 52 with other SMNs ($P < .001$).

Survival After SMNs

The median follow-up after diagnosis of an SMN was 4.9 years for the 292 patients who were alive at their latest follow-up. In all, 350 patients died within 20.6 years from diagnosis of an SMN (median, 0.75 years; 25th to 75th percentile: 0.4 to 1.4). The overall cumulative probability of death as a result of any cause was 59.6% ± 2.1% at 5 years and 61.3% ± 2.2% at 10 years after an SMN (Table 1 and Fig 2). The 10-year cumulative incidence of death as a result of the second (n = 236) or third (n = 1) cancer was 41.1% ± 2.1%; it was 5.6% ± 1.0% for relapsed ALL (n = 31), 10.4% ± 1.3% for treatment-related toxicities among patients who received a transplantation (n = 39) and those who did not (n = 20), and 4.2% ± 0.9% for unknown causes (n = 23; Fig 3). The 10-year probability of survival was 18.9% ± 6.9% (n = 33) for patients whose SMN occurred before 1990 (n = 54), 34.8% ± 2.8% (n = 296) for patients with SMNs diagnosed between 1990 and 1999, and 40.9% ± 6.3% (n = 313) for patients diagnosed from 2000 onward ($P < .001$).

Hematologic Malignancies

Survival remained consistently lower for patients with AML compared with those who had MDS ($P < .001$). The 5-year survival estimate for AML was 11.2% ± 2.9% for 125 patients diagnosed before 2000 and 34.1% ± 6.3% for 61 patients diagnosed after 2000 ($P < .001$). For MDS, the 5-year survival was 17.1% ± 6.4% for 36 patients diagnosed before 2000 and 48.2% ± 10.6% for 33 patients diagnosed after 2000 ($P = .005$). In a Cox regression model, adjusting for sex and age at diagnosis of SMNs and the use of CNS irradiation for ALL treatment, the improved outcome after 2000 was confirmed for both AML (estimated hazard ratio [HR], 0.62; 95% CI, 0.42 to 0.90; $P = .01$) and MDS (HR, 0.30; 95% CI, 0.15 to 0.60; $P < .001$). The hazard of death after t-MN decreased by approximately 10% for every additional year of interval between ALL and AML (HR, 0.88; 95% CI, 0.80 to 0.96; $P = .004$) with a similar trend for MDS (HR, 0.92; 95% CI, 0.80 to 1.06; $P = .23$).

For 185 patients with available information on transplantation after t-MN, the 5-year survival was 30.3% ± 4.4% for the 119 patients who received a transplantation and 11.4% ± 4.0% for the 66 who did not ($P < .001$). However, with a landmark at the median waiting time to transplantation of 4.1 months from SMN diagnosis, the 5-year survival estimates for patients who had received a transplantation and those who had not did not differ (26.7% ± 4.2% and 27.2% ± 7.7%, respectively),[28,31] and this was also the case for 78 patients with t-MN diagnosed in 2000 or later (42.0% ± 7.6% *v* 46.9% ± 11.5%). Among the patients with t-MN who received a transplantation, the 10-year survival for 30 patients with 11q23/*MLL* rearrangements (24.7% ± 8.3%) did not differ significantly from that of 26 patients with monosomy 7 (28.0% ± 9.0%).

Only two of the 25 patients with Hodgkin lymphoma died, both of whom were diagnosed with Hodgkin lymphoma in the 1980s. Excluding patients who received transplantation as part of their ALL therapy, the 5-year survival was 70.5% ± 7.9% for the 34 patients with non-Hodgkin lymphoma diagnosed in the 1990s and 65.4% ± 10.8% for the 22 patients diagnosed later ($P = .64$). The 5-year survival was 76.9% ± 8.3% for the 27 patients who had developed mature B-cell non-Hodgkin lymphoma.

Table 2. Pattern of SMNs in Relation to Their First-Line ALL Treatment in Patients Who Did Not Receive Hematopoietic Stem-Cell Transplantation

					Cyclophosphamide*				6-Mercaptopurine†			
	CNS Irradiation (n = 432)		Epipodophyllotoxin (n = 446)		CNS Irradiation (n = 228)		No CNS Irradiation (n = 199)		CNS Irradiation (n = 230)		No CNS Irradiation (n = 192)	
Type of Second Cancer	Yes	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes	No
Total	230	202	185	261	186	42	126	73	53	177	94	98
Hematologic SMN	79	145	105	127	67	11	82	61	25	50	76	61
t-MN was AML or MDS	64	109	84	96	54	9	60	47	22	38	61	43
CNS tumors	97	12	48	63	76	20	7	5	24	68	5	7
Non-CNS solid tumors	54	45	32	79	43	11	37	7	4	49	13	30

Abbreviations: ALL, acute lymphoblastic leukemia; AML, acute myeloid leukemia; MDS, myelodysplastic syndrome; SMN, second malignant neoplasm; t-MN, therapy-related myeloid neoplasia.
*Only patients who did not receive transplantation who had available information on their therapy are included.
†Dose ≥ 75 mg/m^2.

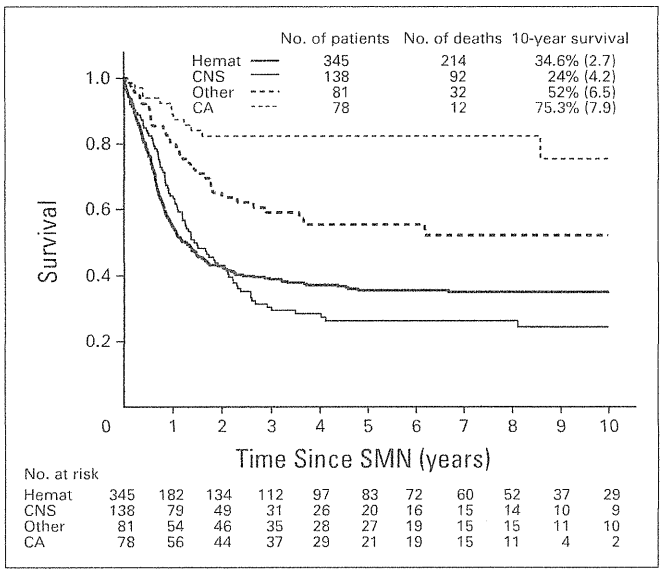

Fig 2. Survival curves according to the four major categories of second malignant neoplasms (SMNs). Hemat, hematologic; CA, carcinoma.

CNS Tumors

Although only one of 22 patients with meningioma died, the 5-year survival was very poor for the remaining 116 patients with brain tumors (18.3% ± 3.8%), including eight patients with low-grade tumors (45.0% ± 18.8%), 76 with high-grade tumors including medulloblastomas and supratentorial primitive neuroectodermal tumors (6.5% ± 3.6%), and 13 unspecified glial tumors (8.5% ± 8.2%). Overall survival after nonmeningioma brain tumor did not improve over time, with 5-year estimates of 19.6% ± 5.5% before 2000 and 16.6% ± 5.3% afterward ($P = .76$).

Nonthyroid Carcinomas

All seven patients with basal cell carcinoma and nine with parotid gland tumors survived, and the 5-year survival for the nine patients with squamous cell carcinoma was 71.4% ± 17.1%. In contrast, the overall survival for the 18 patients with other carcinomas (five, breast; four, gastrointestinal; three, liver; and one each, peritoneal, pancreas, lung, cervix uteri, urinary tract, and nasopharyngeal) was only 40.1% ± 13.7% at 5 years and 0% at 10 years ($P < .001$).

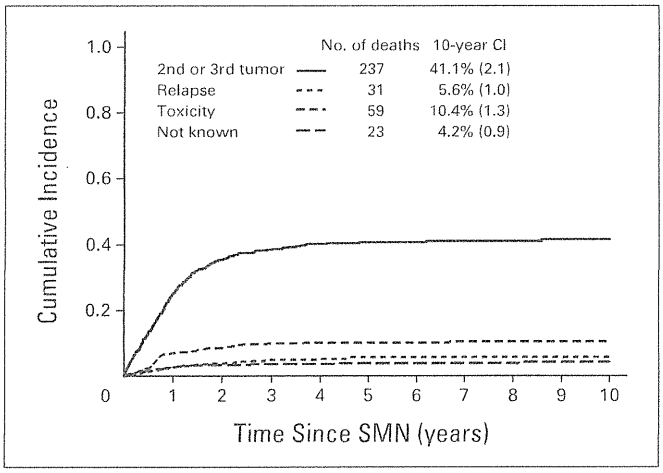

Fig 3. Cause-specific cumulative incidences (CIs) of death after development of a second malignant neoplasm (SMN).

In this study, the largest reported to date, patients with t-MN or nonmeningioma brain tumor had a poor prognosis, whereas patients with secondary meningioma, Hodgkin lymphoma, thyroid carcinoma, basal cell carcinoma, and parotid gland carcinoma had a 5-year survival exceeding 90%.

This study had some limitations since it did not allow calculations of HRs by ALL characteristics or therapy components, and it could not identify exposures that had equal influence on the risk of all major categories of SMNs. In addition, the data must be interpreted cautiously, since the completeness of recording of SMNs was influenced by the individual study groups' frequency and duration of follow-up,[1] screening strategies for thyroid carcinomas, meningiomas, or breast cancer in irradiated patients,[32-34] and linkage with population-based nationwide cancer registries.[18] The impact of such differences will be limited for secondary hematologic malignancies but will be more profound for SMNs that have long latency such as carcinomas and meningiomas. Furthermore, hematologic SMNs can be misinterpreted as relapse of ALL, and some cases of ALL and SMNs may have a common clonal origin.[35,36] Thus, an association between T-cell ALL and histiocytosis has previously been reported,[35,36] and patients with early T-cell precursor ALL have been shown to have genetic profiles similar to those of patients with myeloid malignancies,[37] which could indicate a common ancestral clone for the primary and second malignancies.

The observed association between high-hyperdiploid ALL and the development of t-MN with monosomy 7/5q– has been observed in a much smaller study,[2] although the association between ALL with specific chromosomal translocations (ie, t(9;22)(q34;q11.2), t(1;19)(q23;p13.3), t(12;21)(p13;q22)) and t-MN with 11q23/*MLL* rearrangements has hitherto not been reported. The more frequent use of topoisomerase II inhibitors such as epipodophyllotoxins in high-risk ALL cases with specific chromosomal translocation might have contributed to the development of t-MN with 11q23/*MLL* rearrangements. However, the unique gene expression profiles of ALL blast from those patients who subsequently developed SMNs, including t-MN, could also reflect inherited genetic variants[38] that could influence drug disposition (eg, glutathione S-transferases, cytochrome P-450 enzymes, quinone oxidoreductase, or the folate pathway[39,40]) or be related to cancer predisposition syndromes. International collaboration with extensive mapping of host genomic variants could be instrumental in identifying subsets of patients with ALL with genetic predispositions for whom modification of first-line ALL therapy or individualized follow-up should be offered.

This study supports previously reported associations of t-MN with higher mercaptopurine dosages during maintenance therapy and longer duration of therapy. Some study groups that offer a maintenance therapy mercaptopurine starting dose of 75 mg/m^2 have found an association between an increased risk of SMN and low-activity thiopurine methyltransferase genotypes or phenotypes.[2,41] Notably, others who used a mercaptopurine starting dose of only 50 mg/m^2 failed to find such an association.[42] The linkage between thiopurine

therapy and risk of SMN may reflect that these anticancer agents, when given at high dosage or for an extended period, may interfere with DNA repair rather than directly induce mutations.[41,43] Accordingly, the omission or interruption of maintenance therapy for patients who received a transplantation as part of their ALL therapy may explain why very few patients with brain tumor or t-MN in this cohort had received transplantation. Overall, the risk of relapse if mercaptopurine/methotrexate-based maintenance therapy is truncated[44] is far higher than the risk of t-MN indicated by this and previous studies. The goal for future research is thus to identify patients with a clearly excessive risk of t-MN and consider treatment modification only for such a limited patient subset.

Patients with t-MN have had significant improvements in survival over the last few decades, but the cure rates are still below those obtained by the best treatment protocols for primary AML.[45] Although the survival of patients with t-MN who did not receive transplantation was only 11.4% ± 4.0%, the study did not support that hematopoietic stem-cell transplantation would be beneficial for these patients when the data were adjusted for the waiting time to transplantation. Thus, future studies of this important issue, including the impact of t-MN cytogenetics, are needed.

It is uncertain whether the extremely poor survival rate for CNS tumors, the vast majority of which developed after CNS irradiation, reflects a more aggressive biology, difficulties in performing complete tumor resection in previously irradiated regions, limitations in irradiating previously irradiated regions, or a pessimistic attitude toward curative therapy for such patients. Because this subset is the second most common SMN among survivors of childhood ALL and is overall one of the most common SMNs after a childhood cancer,[18] a review of patients' records of these tumors is needed to explore these issues in depth.

Although the cure rates for some SMNs were as favorable as those obtained for their primary cancer counterparts, future strategies should continue to focus on prevention of SMNs. Thus, the frequency of secondary brain tumor is expected to fall dramatically during the coming decades with the reduced use of CNS irradiation in first-line ALL therapy,[46] and given the few patients on contemporary protocols who are exposed to epipodophyllotoxins, the risk of 11q23/*MLL*-rearranged t-MN is likely to be lower in future childhood ALL cohorts.

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1. Hijiya N, Hudson MM, Lensing S, et al: Cumulative incidence of secondary neoplasms as a first event after childhood acute lymphoblastic leukemia. JAMA 297:1207-1215, 2007

2. Schmiegelow K, Al-Modhwahi I, Andersen MK, et al: Methotrexate/6-mercaptopurine maintenance therapy influences the risk of a second malignant neoplasm after childhood acute lymphoblastic leukemia: Results from the NOPHO ALL-92 study. Blood 113:6077-6084, 2009

3. Prucker C, Attarbaschi A, Peters C, et al: Induction death and treatment-related mortality in first remission of children with acute lymphoblastic leukemia: A population-based analysis of the Austrian Berlin-Frankfurt-Münster study group. Leukemia 23:1264-1269, 2009

4. Lund B, Åsberg A, Heyman M, et al: Risk factors for treatment related mortality in childhood acute lymphoblastic leukaemia. Pediatr Blood Cancer 56:551-559, 2011

5. Schmiegelow K, Forestier E, Hellebostad M, et al: Long-term results of NOPHO ALL-92 and ALL-2000 studies of childhood acute lymphoblastic leukemia. Leukemia 24:345-354, 2010

6. Kamps WA, van der Pal-de Bruin KM, Veerman AJ, et al: Long-term results of Dutch Childhood Oncology Group studies for children with acute lymphoblastic leukemia from 1984 to 2004. Leukemia 24:309-319, 2010

7. Pui CH, Pei D, Sandlund JT, et al: Long-term results of St Jude Total Therapy Studies 11, 12, 13A, 13B, and 14 for childhood acute lymphoblastic leukemia. Leukemia 24:371-382, 2010

8. Tsuchida M, Ohara A, Manabe A, et al: Long-term results of Tokyo Children's Cancer Study Group trials for childhood acute lymphoblastic leukemia, 1984-1999. Leukemia 24:383-396, 2010

9. Tsurusawa M, Shimomura Y, Asami K, et al: Long-term results of the Japanese Childhood Cancer and Leukemia Study Group studies 811, 841, 874 and 911 on childhood acute lymphoblastic leukemia. Leukemia 24:335-344, 2010

10. Silverman LB, Stevenson KE, O'Brien JE, et al: Long-term results of Dana-Farber Cancer Institute ALL Consortium protocols for children with newly diagnosed acute lymphoblastic leukemia (1985-2000). Leukemia 24:320-334, 2010

11. Conter V, Aricò M, Basso G, et al: Long-term results of the Italian Association of Pediatric Hematology and Oncology (AIEOP) Studies 82, 87, 88, 91 and 95 for childhood acute lymphoblastic leukemia. Leukemia 24:255-264, 2010

12. Stary J, Jabali Y, Trka J, et al: Long-term results of treatment of childhood acute lymphoblastic leukemia in the Czech Republic. Leukemia 24: 425-428, 2010

13. Gaynon PS, Angiolillo AL, Carroll WL, et al: Long-term results of the children's cancer group studies for childhood acute lymphoblastic leukemia 1983-2002: A Children's Oncology Group Report. Leukemia 24:285-297, 2010

14. Salzer WL, Devidas M, Carroll WL, et al: Long-term results of the pediatric oncology group studies for childhood acute lymphoblastic leukemia 1984-2001: A report from the Children's Oncology Group. Leukemia 24:355-370, 2010

15. Möricke A, Zimmermann M, Reiter A, et al: Long-term results of five consecutive trials in childhood acute lymphoblastic leukemia performed by the ALL-BFM study group from 1981 to 2000. Leukemia 24:265-284, 2010

16. Escherich G, Horstmann MA, Zimmermann M, et al: Cooperative study group for childhood acute lymphoblastic leukaemia (COALL): Long-term results of trials 82, 85, 89, 92 and 97. Leukemia 24:298-308, 2010

17. Mitchell C, Richards S, Harrison CJ, et al: Long-term follow-up of the United Kingdom Medical Research Council protocols for childhood acute lymphoblastic leukaemia, 1980-2001. Leukemia 24:406-418, 2010

18. Olsen JH, Möller T, Anderson H, et al: Lifelong cancer incidence in 47,697 patients treated for childhood cancer in the Nordic countries. J Natl Cancer Inst 101:806-813, 2009

19. Aricò M, Valsecchi MG, Camitta B, et al: Outcome of treatment in children with Philadelphia chromosome-positive acute lymphoblastic leukemia. N Engl J Med 342:998-1006, 2000

20. Pui CH, Gaynon PS, Boyett JM, et al: Outcome of treatment in childhood acute lymphoblastic leukaemia with rearrangements of the 11q23 chromosomal region. Lancet 359:1909-1915, 2002

21. Nachman JB, Heerema NA, Sather H, et al: Outcome of treatment in children with hypodiploid acute lymphoblastic leukemia. Blood 110:1112-1115, 2007

22. Aricò M, Schrappe M, Hunger SP, et al: Clinical outcome of children with newly diagnosed Philadelphia chromosome-positive acute lymphoblastic

leukemia treated between 1995 and 2005. J Clin Oncol 28:4755-4761, 2010

23. Schrappe M, Hunger SP, Pui CH, et al: Outcomes after induction failure in childhood acute lymphoblastic leukemia. N Engl J Med 366:1371-1381, 2012

24. Liang DC, Yang CP, Lin DT, et al: Long-term results of Taiwan Pediatric Oncology Group studies 1997 and 2002 for childhood acute lymphoblastic leukemia. Leukemia 24:397-405, 2010

25. Stark B, Nirel R, Avrahami G, et al: Long-term results of the Israeli National Studies in childhood acute lymphoblastic leukemia: INS 84, 89 and 98. Leukemia 24:419-424, 2010

26. Schrappe M, Nachman J, Hunger S, et al: 'Educational symposium on long-term results of large prospective clinical trials for childhood acute lymphoblastic leukemia (1985-2000)'. Leukemia 24: 253-254, 2010

27. Glantz SA: Primer of Biostatistics (ed 6). New York, NY, McGraw-Hill Medical Publications, 2005

28. Marubini E, Valsecchi MG: Analysing Survival Data From Clinical Trials and Observational Studies. West Sussex, United Kingdom, John Wiley and Sons, 2004

29. Mantel N: Evaluation of survival data and two new rank order statistics arising in its consideration. Cancer Chemother Rep 50:163-170, 1966

30. Cox DR: Regression models and life tables. J R Stat Soc B 34:187-220, 1972

31. Simon R, Makuch RW: A non-parametric graphical representation of the relationship between survival and the occurrence of an event: Application to responder versus non-responder bias. Stat Med 3:35-44, 1984

32. Giovanella L, Toffalori E, Tozzoli R, et al: Multiplexed immunoassay of thyroglobulin autoantibodies in patients with differentiated thyroid carcinoma. Head Neck 34:1369-1371, 2012

33. Goshen Y, Stark B, Kornreich L, et al: High incidence of meningioma in cranial irradiated survivors of childhood acute lymphoblastic leukemia. Pediatr Blood Cancer 49:294-297, 2007

34. Nathan PC, Ness KK, Mahoney MC, et al: Screening and surveillance for second malignant neoplasms in adult survivors of childhood cancer: A report from the childhood cancer survivor study. Ann Intern Med 153:442-451, 2010

35. Trebo MM, Attarbaschi A, Mann G, et al: Histiocytosis following T-acute lymphoblastic leukemia: A BFM study. Leuk Lymphoma 46:1735-1741, 2005

36. Szczepanski T, van der Velden VH, Waanders E, et al: Late recurrence of childhood T-cell acute lymphoblastic leukemia frequently represents a second leukemia rather than a relapse: First evidence for genetic predisposition. J Clin Oncol 29:1643-1649, 2011

37. Zhang J, Ding L, Holmfeldt L, et al: The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. Nature 481:157-163, 2012

38. Hartford C, Yang W, Cheng C, et al: Genome scan implicates adhesion biological pathways in secondary leukemia. Leukemia 21:2128-2136, 2007

39. Bolufer P, Collado M, Barragan E, et al: Profile of polymorphisms of drug-metabolising enzymes and the risk of therapy-related leukaemia. Br J Haematol 136:590-596, 2007

40. Stanulla M, Dynybil C, Bartels DB, et al: The NQO1 C609T polymorphism is associated with risk of secondary malignant neoplasms after treatment for childhood acute lymphoblastic leukemia: A matched-pair analysis from the ALL-BFM study group. Haematologica 92:1581-1582, 2007

41. Relling MV, Rubnitz JE, Rivera GK, et al: High incidence of secondary brain tumours after radiotherapy and antimetabolites. Lancet 354:34-39, 1999

42. Stanulla M, Schaeffeler E, Möricke A, et al: Thiopurine methyltransferase genetics is not a major risk factor for secondary malignant neoplasms after treatment of childhood acute lymphoblastic leukemia on Berlin-Frankfurt-Münster protocols. Blood 114:1314-1318, 2009

43. Karran P, Attard N: Thiopurines in current medicalpractice:Molecularmechanismsandcontributions to therapy-related cancer. Nat Rev Cancer 8:24-36, 2008

44. Toyoda Y, Manabe A, Tsuchida M, et al: Six months of maintenance chemotherapy after intensified treatment for acute lymphoblastic leukemia of childhood. J Clin Oncol 18:1508-1516, 2000

45. Kaspers GJ, Creutzig U: Pediatric acute myeloid leukemia: International progress and future directions. Leukemia 19:2025-2029, 2005

46. Pui CH, Campana D, Pei D, et al: Treating childhood acute lymphoblastic leukemia without cranial irradiation. N Engl J Med 360:2730-2741, 2009

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Appendix

Table A1. SMNs Reported by the Seventeen Participating Collaborative Groups

Trial Group Name	Trial Group Acronym	Trial Group Location	No. of Patients	Date of Diagnosis of First SMN	Date of Diagnosis of Last SMN	Trial Registration Numbers
Associazione Italiana Ematologia Oncologia Pediatrica	AIEOP	Italy	22	January 4, 1985	December 11, 2007	ALL-BFM 90, ALL-BFM 95, ALL-BFM 2000 (NCT00430118)
Berlin-Frankfurt-Münster	BFM	Austria	14	September 1, 1992	June 26, 2009	ALL-BFM 86, ALL-BFM 90, ALL-BFM 95, ALL-BFM 2000 (NCT00430118)
Berlin-Frankfurt-Münster	BFM	Germany	107	December 12, 1984	February 1, 2009	ALL-BFM 2000 (NCT00430118), NCI Protocol ID 68529
Cooperative Study Group for Childhood Acute Lymphoblastic Leukaemia	COALL	Germany	36	May 10, 1984	July 19, 2007	COALL 07-03, EU-205104, NCT00343369
Children's Oncology Group (includes both the US Children's Cancer Group and the Pediatric Oncology Group)	COG	USA	136	April 4, 1990	February 12, 2008	Separate list of POG and CCG protocols
Dutch Childhood Oncology Group	DCOG	Holland	18	February 26, 1991	May 30, 2008	
Dana-Farber Cancer Institute	DFCI	USA	13	August 14, 1986	March 17, 2008	DFCI ALL Consortium Protocols 85-001, 87-001, 91-001, 96-001
European Organisation for Research and Treatment of Cancer	EORTC	Belgium and France	16	June 30, 1991	June 15, 2002	EORTC 58881 study
French Acute Lymphoblastic Leukaemia Study Group	FRALLE	France	52	March 12, 1991	June 15, 2010	FRALLE protocols 83, 87-89, 93, 2000
Israel National ALL Studies	INS	Israel	11	June 16, 1993	December 15, 2008	ALL INS 89 (mod BFM 86), ALL INS 93 (mod BFM 90), ALL INS 98 (mod BFM 95)
Tokyo Children's Cancer Study Group	TCCSG	Japan	49	June 23, 1987	May 6, 2010	TCCSG L84-11, L89-12, L92-13, L95-14
Japan Association of Childhood Leukemia Study	JACLS	Japan				Tokai-POG 9104, OCLSG 94, JACLS ALL-96, JACLS ALL-97
Japanese Children's Cancer and Leukemia Study Group	JCCLSG	Japan				CCLSG ALL841, ALL851, ALL874, ALL911, ALL941
Kyushu-Yamaguchi Children's Cancer Study Group	KYCCSG	Japan				KYCCSG AL841, HR88, ALL90, ALL96
Nordic Society for Paediatric Haematology and Oncology	NOPHO	Denmark, Finland, Iceland, Norway, Sweden	53	January 15, 1986	May 15, 2010	ALL-86, ALL-92, ALL-2000
St Jude Children's Research Hospital	SJCRH	USA	69	February 9, 1982	November 18, 2002	Total Therapies 4, 5, 6, 7, 8, 9, 10, 11, 12, 13A, and 13B
Taiwan Pediatric Oncology Group	TPOG	Taiwan	19	August 5, 1987	January 13, 2007	TCALL 84; TPOG-ALL 88, 93, 97, 2002
National Cancer Research Institute Children's Leukaemia Clinical Studies Group	NCRI	United Kingdom	27	January 15, 1994	September 15, 2007	UKALLXI ISRCTN 16757172, ALL97 ISRCTN 26727615
Total			642	February 9, 1982	June 15, 2010	

Table A2. Clinical Characteristics of Patients With Cancer-Predisposing Syndromes

Predisposing Syndrome	Type of Second Cancer	Sex	Age at ALL (years)	WBC at ALL ($\times 10^9$/L)	BCP or T-Cell ALL	Interval to SMN (years)	Age at SMN (years)	Status	Survival (years)
Down syndrome	AML	Male	3.2	16.8	B	4.0	7.2	Dead	0.8
Down syndrome	AML	Female	2.0	7.8	B	5.9	7.9	Dead	1.1
Down syndrome	Mature B-cell NHL	Male	6.2	38.1	B	2.6	8.8	Alive	7.0
Down syndrome	Ewing sarcoma	Female	6.6	2.1	B	8.3	14.9	Alive	5.4
Li Fraumeni syndrome	AML	Male	12.4	6.6	B	2.5	15.0	Dead	0.6
Ataxia telangiectasia	T-cell NHL	Male	9.5	86.0	T	12.5	22.0	Dead	0.6
Noonan syndrome	MDS	Female	16.0	2.0	B	2.7	18.7	N/A	
AIDS	Mature B-cell NHL	Male	13.7	1.8	B	4.0	17.7	Alive	10.2

Abbreviations: ALL, acute lymphoblastic leukemia; AML, acute myeloid leukemia; BCP, B-cell precursor; MDS, myelodysplastic syndrome; N/A, not available; NHL, non-Hodgkin lymphoma; SMN, second malignant neoplasm.

Table A3. Clinical Characteristics and Overall Survival of the Four Major Categories of SMNs in the Subset of 201 Patients Who Were Not Irradiated and Did Not Undergo Hematopoietic Stem-Cell Transplantation as Part of Their First-Line Treatment for ALL

Type of Second Cancer	Total		Males		ALL Immunophenotype* (n = 192)		Age at ALL (years)		WBC at ALL ($\times 10^9$/L)		Interval to SMN (years)		Age at SMN (years)		5-Year Survival Rate After SMN (%)
	No.	%	No.	%	BCP	%	Median	50% Range	Median	50% Range	Median	50% Range	Median	50% Range	
Total	201		107	53.2	173	90.1					3.6	2.3-6.6	9.0	6.5-15.1	44.1 ± 3.7
Hematologic†	145	72.1	79	54.5	130	92.2	4.3	3.0-6.5	6.1	4.0-15.3	2.9	2.1-4.3	8.2	6.0-12.7	41.1 ± 4.2
CNS tumor†	12	6.0	6	50.0	9	90.0	5.0	3.5-8.9	7.4	3.7-34.4	6.8	2.7-7.4	13.1	8.7-17.2	32.1 ± 15.0
Carcinoma†	19	9.5	7	36.8	15	83.3	4.7	3.0-8.7	6.6	3.3-38.5	11.8	6.1-16.1	16.2	10.7-23.4	77.4 ± 10.0
Other†	25	12.4	15	60.0	19	82.6	5.7	3.4-8.1	4.9	2.5-26.2	7.8	4.4-9.8	14.0	10.4-17.9	44.9 ± 11.3

Abbreviations: ALL, acute lymphoblastic leukemia; BCP, B-cell precursor; SMN, second malignant neoplasm.

*Nine patients were excluded because immunophenotype was not reported (n = 8) or was not specified as either BCP or T-cell ALL (n = 1).

†Seventy-one acute myeloid leukemia, 38 myelodysplastic syndrome, three chronic myeloid leukemia, 23 non-Hodgkin lymphoma, 10 Hodgkin disease, 10 nonmeningioma CNS tumors, two meningioma, 10 nonthyroid carcinoma, nine thyroid carcinoma, seven soft tissue sarcoma, 12 bone tumors, one germ cell tumor, four Langerhans cell histiocytosis, one other tumor.

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IKZF1 and *CRLF2* Gene Alterations Correlate With Poor Prognosis in Japanese *BCR-ABL1*-Negative High-Risk B-Cell Precursor Acute Lymphoblastic Leukemia

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Background: Genome-wide analysis studies have demonstrated that *IKZF1*, *CRLF2*, and *JAK2* gene alterations correlate with poor prognosis in pediatric B-cell precursor acute lymphoblastic leukemia (BCP-ALL). However, the prognostic significance for these gene alterations has not been clarified in Japanese patients. ***Procedure:*** A total of 194 patients with BCP-ALL enrolled in the Japanese Children's Cancer & Leukemia Study Group ALL 2004 clinical trial were assessed for the presence of three different gene alterations: *IKZF1* deletions, *CRLF2* expression and *JAK2* mutation. ***Results:*** *IKZF1* deletions and *CRLF2*-high expression were identified in 22 of 177 (12%) patients and in 15 of 141 (11%) patients, respectively. However, *JAK2* R683 mutation was detected only one of 177 patients. The 4-year event-free survival (4y-EFS) was different when comparing patients with or without *IKZF1* deletions (68.2% vs. 85.2%; $P = 0.04$) and was also different when comparing patients with different *CRLF2* expression levels (high, 66.7% vs. low, 88.1%; $P = 0.03$). The differences in 4y-EFS were statistically significant in patients with ALL in the National Cancer Institute (NCI)-high risk group (HR-ALL) (*IKZF1* deletions: yes, 58.3% vs. no, 87.0%, $P = 0.02$; *CRLF2* expression: high, 55.6% vs. low, 85.3%, $P = 0.04$) but not in patients with ALL in the NCI-standard risk group (SR-ALL; *IKZF1* deletions: yes, 80.0% vs. no, 84.4%, $P = 0.75$; *CRLF2* expression: high, 83.3% vs. low, 89.2%, $P = 0.77$). Coexistence of *IKZF1* deletions and *CRLF2*-high expression associated with poor outcomes. ***Conclusions:*** *IKZF1* deletions and *CRLF2*-high expression predicted poor outcomes in patients with HR-ALL but not in patients with SR-ALL in our Japanese cohort. Pediatr Blood Cancer 2013;60:1587–1592. © 2013 Wiley Periodicals, Inc.

Key words: acute lymphoblastic leukemia; *CRLF2*; *IKZF1*; *JAK2*

INTRODUCTION

Improvements in overall survival in patients with pediatric B-cell precursor acute lymphoblastic leukemia (BCP-ALL) have been achieved via the institution of risk-adapted multi-agent chemotherapy [1]. However, about 20% of patients still show persistent disease or experience relapse. This observation underscores the need for a better understanding of the pathophysiology of the disease as well as the identification of factors that predict outcomes or predict the response to specific therapies.

Findings from genome-wide analysis have demonstrated that alterations in *IKZF1*, which encodes the lymphoid transcription factor, IKAROS, are prevalent in patients with *BCR-ABL1*-positive ALL [2,3]. *IKZF1* alterations have also been demonstrated in patients with high-risk *BCR-ABL1*-negative ALL and are associated with poor prognosis [4–10]. Further, Mullighan et al. [11] identified Janus kinases (*JAK*s) mutations in approximately 10% of the *BCR-ABL1*-negative subgroup and reported that these mutations were associated with *IKZF1* alterations. Recent studies have also revealed that increased expression of *CRLF2*, which is predominantly caused by fusion of *P2RY8-CRLF2* or *IGH-CRLF2*, was found in approximately 5–10% of patients with high-risk ALL and in 50–60% of patients with Down syndrome-associated ALL [12–14]. Alterations in *CRLF2* often coexist with alterations in *IKZF1* and/or *JAK2*, and these gene alterations are associated with poor outcomes [15–17]. However, the prognostic significance for these gene alterations has not been clarified in Japanese patients. Therefore, the incidence and clinical significance of *IKZF1* deletions, *CRLF2* expression and *JAK2* mutations were assessed in Japanese pediatric patients with *BCR-ABL1*-negative BCP-ALL in this study.

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MATERIALS AND METHODS

Patients and Samples

A total of 194 patients were selected from 264 pediatric *BCR-ABL1*-negative BCP-ALL patients who were enrolled in the Japanese Children's Cancer & Leukemia Study Group (JCCLSG) ALL 2004 clinical trial from 2004 to 2008. One hundred seventy-seven DNA and 141 RNA samples were available and extracted from total bone marrow (BM) or peripheral blood (PB) at the time of diagnosis. These samples contained over 50% (median, 95%; range, 53.3–100%) blasts. The analyzed cohort included 131 patients with ALL classified as NCI-SR and 63 patients classified as NCI-HR. Treatment stratification in this clinical trial

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was based on age and white blood cell (WBC) count; patients with HR-ALL were treated with a HR- or very-high-risk regimen, and patients with SR-ALL were treated with a SR-regimen, except for 10 patients who were treated with intensified chemotherapy due to positivity for minimal residual disease. There were no statistical differences in the clinical characteristics (e.g., age, initial WBC, gender, and cytogenetic abnormalities) when comparing the analyzed cohort and original cohort (Supplementary Table I). The median (range) follow-up period from diagnosis was 6.0 (0.1–8.2) years. DNA samples from three healthy donors and from seven patients with solid tumor that were free from BM invasion were used as controls. This study was approved by the institutional review board at Nagoya Medical Center. Informed consent to participate in this study was obtained from patients and their guardians.

Genetic Analysis

The multiplex ligation-dependent probe amplification (MLPA) method (IKZF1 P-335, MRC-Holland, Amsterdam, NL) was used to detect *IKZF1* deletion, according to the manufacturer's instructions [18]. A total of 60 ng of DNA was used per reaction. Fragment analysis was performed using GeneScan v.3.5 (ABI310, Applied Biosystems, Foster City, CA). A probe ratio below 1.3 was considered indicative of deletion, as per the manufacturer's instructions [19]. For detection of *Ik6* and *Ik10* of *IKZF1* and the *P2RY8-CRLF2* fusion gene transcript, cDNA synthesis was performed using SuperScript II (Invitrogen Corporation, Carlsbad, CA) with 1 μg of RNA per 20 μl reaction with random primer (Invitrogen), and reverse transcription polymerase chain reaction (RT-PCR) was performed with following primers; *IKZF1* fwd, 5'-CTCCGAGGTTGCTCTT; *IKZF1* rev.: 5'-AGGTAGTT-GATGGCGTTGTTGATG; *P2RY8-CRLF2* primers were as previously reported [12]. To measure *CRLF2* mRNA levels, real-time quantitative (RQ)-PCR was performed using the TaqMan Gene Expression Assay (*CRLF2*, Hs00845692_m1; *GAPDH*, #4310884E, Applied Biosystems). RQ-PCR was performed in duplicate, using 1 μl of cDNA per reaction. The comparative C_t method was used to quantify relative mRNA levels using the endogenous control gene, *GAPDH*. To detect *JAK2* mutations, exon 12, 16, 20, and 21 were amplified and directly sequenced by Sanger sequencing with the ABI310 sequencing system, as previously reported [20].

Statistical Analysis

Descriptive statistical analyses to assess baseline characteristics of patients diagnosed with *BCR-ABL1*-negative BCP-ALL were performed. Event-free survival (EFS) and relapse-free interval (RFI) were analyzed by the Kaplan–Meier method [21], and log-rank tests [22] were used for group comparisons. EFS was defined as the time from the diagnosis to induction failure, relapse, or death from any cause, whichever occurred first. RFI was estimated for patients who achieved complete remission (CR). Cox proportional hazards regression models [23] were used to investigate factors associated with survival in univariate and multivariate analysis. A two-sided *P*-value of more than 0.05 should be interpreted with care. All data analysis was performed using SAS statistical software (version 9.1.3; SAS Institute, Inc., Cary, NC).

Results

Frequencies of *IKZF1*, *CRLF2*, and *JAK2* Alterations in BCP-ALL

IKZF1 deletions were detected in 22 (12%) of 177 DNA samples, and various deletion patterns were detected by MLPA (Supplementary Table II). Homozygous deletion was not detected. To confirm the results of MLPA, RT-PCR was performed for six patients whose RNA was available. The isoform type in the cases with the deletion of *IKZF1* exon 4–7 and 2–7 was confirmed to be the *Ik6* and *Ik10* isoform variants, respectively (Supplementary Fig. S1). *IKZF1* deletions were significantly associated with older age ($P<0.01$) and NCI-HR ($P=0.02$; Supplementary Table SIII). However, no association was determined between *IKZF1* deletions and any known chromosomal abnormalities.

CRLF2 expression was measured by RQ-PCR in 141 RNA samples. The median expression value was 13.8 copies (range: 0.07–35,100). Fifteen (10%) samples showed *CRLF2* expression that was ≥10-fold of the median value (Fig. 1A). The clinical features of patients with high *CRLF2* expression are shown in Supplementary Table SIII. High *CRLF2* expression was more prevalent in patients with HR-ALL (9/43, 21%) than in patients with SR-ALL (6/98, 6%; $P<0.01$). *P2RY8-CRLF2* fusion was detected in five of 141 patients. Two of these five patients had high *CRLF2* expression, while the other three patients had low *CRLF2* expression (Fig. 1B). Sequencing of predominant fusion transcripts demonstrated that the non-coding exon 1 of *P2RY8* bound to the start of *CRLF2* exon 1 in all five patients (Fig. 1C) [15]. In addition, transcript variants were demonstrated in three patients. One of the clones of unique patient number (UPN) 035, 099, and 219 showed *P2RY8* exon 1 fused to *CRLF2* exon 2. Sequencing of another clone of UPN219 demonstrated that *P2RY8* exon 1 bound to the 34 bp upstream sequence of *CRLF2* exon 1 (Fig. 1C).

In contrast, a *JAK2* R683 mutation was demonstrated in only one of the 177 patients. In this case, *P2RY8-CRLF2* fusion transcript, high *CRLF2* expression and *IKZF1* deletion were also recognized. Furthermore, the patient failed to achieve remission after induction therapy. We further analyzed *JAK2* exons 12, 20, and 21 in 15 patients with high *CRLF2* expression, but no mutation was detected except for a single nucleotide polymorphism (rs10974955) in two patients.

IKZF1 and *CRLF2* Alterations Are Associated With Poor Outcomes in Patients With HR-ALL

In survival analysis, the 4-year EFS was significantly lower for patients with *IKZF1* deletions than for patients without *IKZF1* deletions (68.2 ± 9.9% vs. 85.2 ± 2.9%; $P=0.04$; Fig. 2A). Interestingly, the difference in this parameter was statistically significant in patients with HR-ALL (58.3 ± 14.2% vs. 87.0 ± 5.0%; $P=0.02$) and not in patients with SR-ALL (80.0 ± 12.7% vs. 84.4 ± 3.5%; $P=0.75$; Fig. 2B). Similarly, 4-year EFS for the patients with high *CRLF2* expression was also significantly worse than that for those with low *CRLF2* expression (62.7 ± 12.1% vs. 88.1 ± 2.9%; $P=0.03$, Fig. 2C), and a statistical difference between these groups was recognized only in patients with HR-ALL (55.6 ± 16.6% vs. 85.3 ± 6.1%; $P=0.04$ for HR; 83.3 ± 15.2% vs. 89.2 ± 3.3%; $P=0.77$ for SR, Fig. 2D). Similar findings for *IKZF1* and *CRLF2* were noted in the analysis for relapse-free interval (RFI).

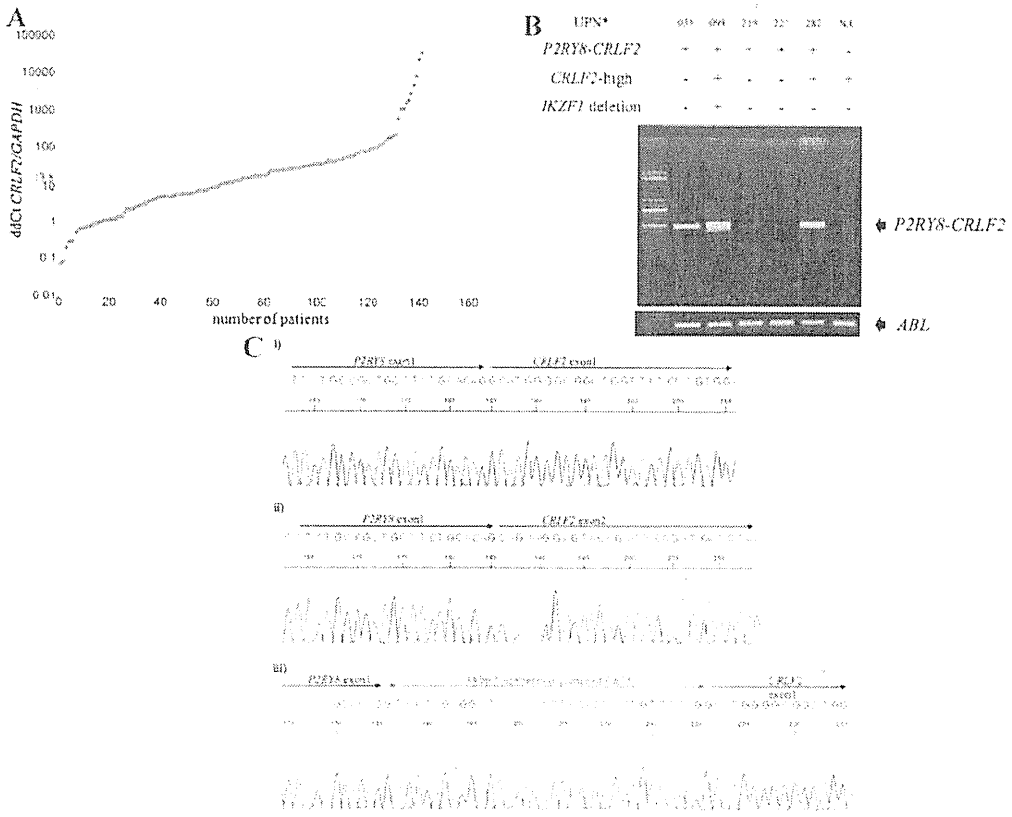

Fig. 1. Assessment of *CRLF2* expression and alterations in *CRLF2*. A: Measurement of *CRLF2* expression by RQ-PCR. The median *CRLF2* expression value (normalized to *GAPDH* expression) was 13.8. Red diamonds represent high *CRLF2* expression, defined as *CRLF2* expression that was ≥10-fold higher than the median *CRLF2* expression. Blue diamonds represent low *CRLF2* expression. B: *P2RY8-CRLF2* rearrangement detected by RT-PCR. The level of *ABL* transcription served as control. NC indicates negative control. Samples from five patients showed *P2RY8-CRLF2* fusion by RT-PCR. Two of the five samples also showed high *CRLF2* expression, and the remaining three samples showed low *CRLF2* expression. Interestingly, only one patient showed *P2RY8-CRLF2* fusion, *CRLF2* high expression and *IKZF1* deletion. C: Sequence results of *P2RY8-CRLF2* fusion. Representative sequences are shown. (i) The major sequence of all samples shows that the 3' end of non-coding *P2RY8* exon 1 bound to the 5' end of *CRLF2* exon 1. Sequence of No. 035 is shown as a representative patient. (ii) One of the No. 035 clones showed that the 3' end of non-coding *P2RY8* exon 1 bound to the 5' end of *CRLF2* exon 2 (skipped *CRLF2* exon 1). This variant was also found in No. 099 and No. 219. (iii) Thirty-four base pair upstream sequence of *CRLF2* exon 1 fused to *P2RY8* exon 1. This fusion was found in No. 219. *UPN indicated unique patient number.

Among the 124 patients whose samples were analyzed for both the *IKZF1* and *CRLF2* genes, five patients had ALL with *IKZF1* deletions and high *CRLF2* expression, simultaneously. All five patients were classified as NCI-HR, and four of the five patients experienced induction failure or relapse. In Kaplan–Meier analysis, EFS was the lowest among patients with ALL and coexisting *IKZF1* deletions and high *CRLF2* expression when compared with other categories of patients (Supplementary Fig. S3).

In comparison with other known prognostic factors in the full cohort and in the NCI-HR cohort, *IKZF1* deletions and high *CRLF2* expression were significant predictors of outcomes in univariate analysis (Table I). However, no variables retained independent prognostic significance in multivariate analysis.

DISCUSSION

Despite recent improvement in outcomes for patients with pediatric BCP-ALL, the genetic pathophysiology of the failure to respond to therapy or the occurrence of relapse remains unclear. *IKZF1*, *CRLF2*, and *JAK2* gene alterations are prognostic factors in patients with pediatric BCP-ALL [4–10,15–17,25]; therefore, we assessed for the presence of these genetic alterations in Japanese patients with *BCR-ABL1*-negative BCP-ALL.

IKZF1 deletions were found in 12% of our cohort (8% of NCI-SR, and 21% of NCI-HR), which is consistent with observations from previous reports (approximately 10–20%) [6–10,15]. Previous studies have reported that *IKZF1* deletions significantly correlated with poor relapse-free survival (RFS). Chen et al. reported that *IKZF1* deletions/mutations retained independent prognostic significance in multivariate analysis in their full cohort and were associated with poor RFS only in NCI-HR patients [9]. In our study, *IKZF1* deletions were significantly associated with outcome in univariate analysis, but not in multivariate analysis within either our full cohort or the NCI-HR cohort. Mi et al. [10] reported that the *Ik6* variant correlated with poor prognosis. In our study, *Ik6* variant was detected in only one-third of *IKZF1*-deletion patients

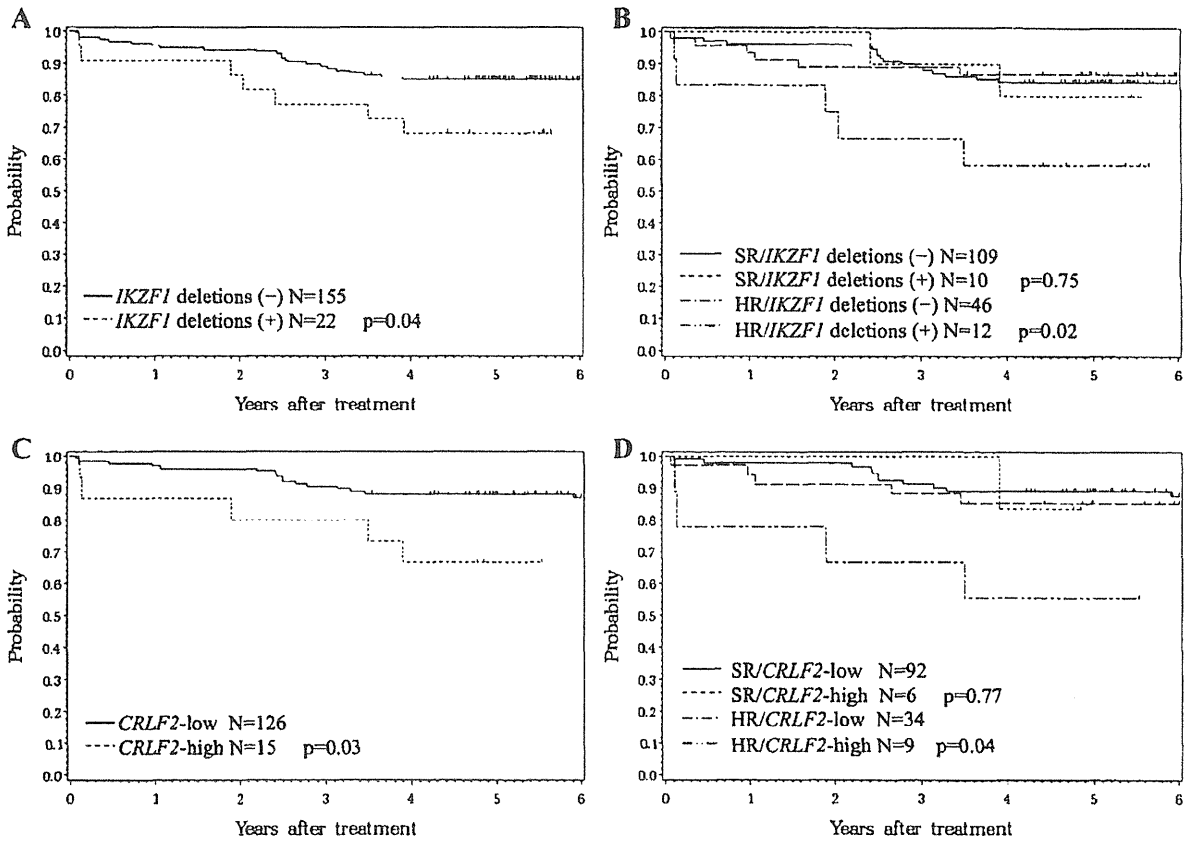

Fig. 2. Probability of EFS according to *IKZF1* deletions, *CRLF2* expression and NCI risk classification. A: Probability of EFS for patients with or without *IKZF1* deletions. B: Probability of EFS for patients with or without *IKZF1* deletions according to NCI-risk classification. C: Probability of EFS for patients with high *CRLF2* expression or low *CRLF2* expression. D: Probability of EFS for patients with high *CRLF2* expression or low *CRLF2* expression according to NCI-risk classification.

(Supplementary Table SI), and none of these patients experienced relapsed. The relationship between *Ik6* variant status and patient outcomes remains to be determined.

High *CRLF2* expression was detected in 10% of the patient in this study (6% of SR-ALL, and 21% of HR-ALL), which is consistent with observations from previous reports (5–20% of BCP-ALL) [10–16,24]. Hervey et al. [15] reported that *P2RY8-CRLF2* or *IgH-CRLF2* was highly associated with high *CRLF2* expression. On the other hand, Chen et al. [9] reported that approximately a half of patients with high *CRLF2* expression had these *CRLF2* gene alterations and that these gene alterations were detected only in the patients with high *CRLF2* expression. Palmi et al. [25] reported that *P2RY8-CRLF2* fusion was detected in 45% of patients with high *CRLF2* expression and that it was found in patients with high *CRLF2* expression as well as in patients with low *CRLF2* expression. They also demonstrated that the *P2RY8-CRLF2* fusion was associated with a high incidence of relapse (5-year cumulative incidence of relapse with or without the *P2RY8-CRLF2* fusion: 42.8% vs. 14.5%; $P = 0.001$). In the present study, the *P2RY8-CRLF2* fusion was found in 13% (2 of 15 patients) of ALL samples with high *CRLF2* expression. In addition, the *P2RY8-CRLF2* fusion was also found in 2% (3 of 126 patients) of ALL samples with low *CRLF2* expression, suggesting that a minor population clone had this fusion transcript. Furthermore, five patients with ALL positive for the *P2RY8-CRLF2* fusion are alive in first remission, except for one patient with ALL who had both the *IKZF1* deletion and high *CRLF2* expression. The prognostic impact of the *P2RY8-CRLF2* fusion remains to be clarified in a large-scale study.

Chen et al. [9] also reported that high *CRLF2* expression was associated with poor RFS in a multivariate analysis in HR-ALL patients but not in SR-ALL patients. The present study demonstrated that high *CRLF2* expression was significantly associated with poor outcomes, according to Kaplan–Meier analysis. However, high *CRLF2* expression was associated with only marginal significance for poor EFS, according to univariate and multivariate analysis in the Cox regression model. This discrepancy may be due to the relatively small number of patients analyzed in this study. Some investigators have proposed that ALL patients with high *CRLF2* expression were assigned to the intermediate-risk group because high *CRLF2* expression had no prognostic significance within multivariate analyses [10,17]. The relationship between outcomes and *CRLF2* expression may also be dependent on the specific regimen employed for treatment.

TABLE I. Prognostic Impact of *IKZF1* Deletions and High *CRLF2* Expression in Univariate and Multivariate Analyses

	Full cohort				NCI-HR			
	Univariate analysis		Multivariate analysis		Univariate analysis		Multivariate analysis	
Factors	HR[a] (95% CI[b])	*P*-value	HR (95% CI)	*P*-value	HR (95% CI)	*P*-value	HR (95% CI)	*P*-value
Age, years								
≥10 versus 10	1.74 (0.81–3.75)	0.16			2.13 (0.58–7.89)	0.26		
Gender								
Male versus female	1.31 (0.66–2.59)	0.44			1.33 (0.43–4.13)	0.62		
WBC[c], $\times 10^9$/L								
≥10 versus 10	0.95 (0.37–2.47)	0.92			0.71 (0.23–2.23)	0.56		
NCI risk classification								
HR[d] versus SR[e]	1.27 (0.62–2.58)	0.51	1.39 (0.50–3.82)	0.53	—	—	—	—
PSL[f] response								
PPR[g] versus PGR[h]	2.63 (0.80–8.60)	0.11	1.56 (0.20–12.08)	0.67	2.70 (0.59–12.34)	0.20	2.03 (0.24–17.49)	0.52
Cytogenetic abnormalities								
Hyperdiploid versus normal	1.48 (0.58–3.76)	0.41			0.49 (0.06–4.23)	0.52		
Other versus normal	1.39 (0.62–3.09)	0.42			0.80 (0.23–2.75)	0.72		
N.D.[i] versus normal	0.83 (0.19–3.69)	0.80			0.74 (0.09–6.29)	0.78		
Fusion genes								
ETV6-RUNX1 versus none	0.74 (0.24–2.34)	0.61			1.71 (0.29–10.21)	0.56		
E2A-PBX1 versus none	1.44 (0.50–4.14)	0.50			1.22 (0.20–7.28)	0.83		
N.D. versus none	1.38 (0.62–3.09)	0.43			2.04 (0.49–8.55)	0.33		
IKZF1 deletions								
Yes versus no	2.38 (1.02–5.55)	0.04	2.78 (0.94–8.27)	0.07	3.61 (1.10–11.84)	0.03	3.93 (0.75–20.75)	0.11
CRLF2 expression								
High versus low	2.97 (1.09–8.11)	0.04	2.24 (0.72–6.95)	0.16	3.56 (0.95–13.27)	0.06	1.97 (0.37–10.37)	0.43

HR[a], hazard ratio; CI[b], confidential interval; WBC[c], white blood cell count; NCI risk classification HR[d], 1–9y. and WBC $<50 \times 10^9$/L; SR[e], ≥10y. or WBC $\geq 50 \times 10^9$/L; PSL[f], prednisolone; PGR[g], prednisolone good responder; PPR[h], prednisolone poor responder; N.D.[i], not determined.

Some studies have reported that high *CRLF2* expression was highly associated with *JAK2* mutation and *IKZF1* deletions [15,16]. In the report by Chen et al. [9], *JAK* mutations were found in 21.8% of patients with high *CRLF2* expression and in 4.4% of their full cohort. Mullighan et al. reported that *JAK* mutations were detected in 20 of 187 patients with high-risk childhood BCP-ALL. A total of 16 cases had *JAK2* mutations, with 13 located in exon 16, and three located within exon 20 or 21. Another four cases had *JAK1* or *JAK3* mutations [11]. In our study, *JAK2* mutation in exon 16 was detected in only 1 of 177 cases. In addition, no mutations in *JAK2* exons 12, 20, and 21 were found in any cases of ALL with high *CRLF2* expression. These results suggest that *JAK2* mutations might be rare in Japanese patients. Further analysis of screening mutations of *JAK1* and *JAK3* as well as other sites of *JAK2* should be performed to confirm this finding.

In the Kaplan–Meier analysis from the present study, the coexistence of *IKZF1* deletions and high *CRLF2* expression, which was found only in patients with HR-ALL and not in patients with SR-ALL, was related to poor outcomes. One of the five patients with ALL and coexisting of *IKZF1* deletions and high *CRLF2* expression was positive for *JAK2* mutation, but the others were not. Therefore, they might have additional genetic alterations similar to those seen in patients with Ph-like ALL [26].

In conclusion, the present study suggests that *IKZF1* deletions and high *CRLF2* expression (and particularly, the combination of these two variables) predicted poor outcome in patients with HR-ALL but not in patients with SR-ALL in our Japanese cohort. However, the small sample size might have limited the statistical power of this study. A large-scale nationwide cohort study is planned to clarify the prognostic significance of these genetic abnormalities in Japan.

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REFERENCES

1. Jeha S, Pui CH. Risk-adapted treatment of pediatric acute lymphoblastic leukemia. Hematol Oncol Clin North Am 2009;23:973–990.
2. Mullighan CG, Miller CB, Radtke I, et al. BCR-ABL1 lymphoblastic leukemia is characterized by the deletion of Ikaros. Nature 2008;453:110–114.
3. Iacobucci I, Lonetti A, Messa F, et al. Expression of spliced oncogenic Ikaros isoforms in Philadelphia-positive acute lymphoblastic leukemia patients treated with tyrosine kinase inhibitors: Implications for a new mechanism of resistance. Blood 2008;112:3847–3855.
4. Den Boer ML, van Slegtenhorst M, De Menezes RX, et al. A subtype of childhood lymphoblastic leukemia with poor treatment outcome: A genome-wide classification study. Lancet Oncol 2009;10:125–134.
5. Mullighan CG, Goorha S, Radtke I, et al. Genome-wide analysis of genetic alterations in acute lymphoblastic leukemia. Nature 2007;446:758–764.
6. Mullighan CG, Su X, Zhang J, et al. Deletion of *IKZF1* and Prognosis in Acute Lymphoblastic Leukemia. N Engl J Med 2009;306:470–480.
7. Kuiper RP, Waanders E, van der Velden VH, et al. IKZF1 deletions predict relapse in uniformly treated pediatric precursor B-ALL. Leukemia 2010;24:1258–1264.
8. Yang YL, Hung CC, Chen JS, et al. *IKZF1* deletions predict a poor prognosis in children with B-cell progenitor acute lymphoblastic leukemia: A multicenter analysis in Taiwan. Cancer Sci 2011;102:1874–1881.
9. Chen IM, Harvey RC, Mullighan CG, et al. Outcome modeling with CRLF2, IKZF1, JAK, and minimal residual disease in pediatric acute lymphoblastic leukemia: A Children's Oncology Group Study. Blood 2012;119:3512–3522.
10. Mi JQ, Wang X, Yao Y, et al. Newly diagnosed acute lymphoblastic leukemia in China (II): Prognosis related to genetic abnormalities in a series of 1091 patients. Leukemia 2012;26:1507–1516.

11. Mullighan CG, Zhang J, Harvey RC, et al. JAK mutations in high-risk childhood acute lymphoblastic leukemia. Proc Natl Acad Sci U S A 2009;106:9414–9418.
12. Mullighan CG, Collins-Underwood JR, Phillips LA, et al. Rearrangement of *CRLF2* in B-progenitor and down syndrome associated acute lymphoblastic leukemia. Nat Genet 2009;41:1243–1246.
13. Russell LJ, Capasso M, Vater I, et al. Deregulated expression of cytokine receptor gene, CRLF2, is involved in lymphoid transformation in B-cell precursor acute lymphoblastic leukemia. Blood 2009;114:2688–2698.
14. Hertzberg L, Vendramini E, Ganmore I, et al. Down syndrome acute lymphoblastic leukemia, a highly heterogeneous disease in which aberrant expression of CRLF2 is associated with mutated JAK2: A report from the international BFM Study Group. Blood 2010;115:1006–1017.
15. Harvey RC, Mullighan CG, Chen IM, et al. Rearrangement of CRLF2 is associated with mutation of JAK kinases, alteration of IKZF1, Hispanic/Latino ethnicity, and a poor outcome in pediatric B-progenitor acute lymphoblastic leukemia. Blood 2010;115:5312–5321.
16. Cario G, Zimmermann M, Romey R, et al. Presence of the *P2RY8-CRLF2* rearrangement is associated with a poor prognosis in non-high-risk precursor B-cell acute lymphoblastic leukemia in children treated according to the ALL-BFM 2000 protocol. Blood 2010;115:5393–5397.
17. Ensor HM, Schwab C, Russell LJ, et al. Demographic, clinical and outcome features of children with acute lymphoblastic leukemia and CRLF2 deregulation: Results from the MRC ALL97 clinical trial. Blood 2010;117:2129–2136.
18. Schwab CJ, Jones LR, Morrison SL, et al. Evaluation of multiplex ligation-dependent probe amplification as a method for the detection of copy number abnormalities in B-cell precursor acute lymphoblastic leukemia. Genes Chromosomes Cancer 2010;49:1104–1113.
19. MLPA procedure, Result interpretation. MRC Holland Home Page. [Interpretation of MLPA results] http://www.mlpa.com/WebForms/WebFormMain.aspx?Tag=wl2zCjivCGANQgZPuTixrMkcAVlTx-SUI1uxaJsuta9GGaLIE8p67Q&Description version 02; 11-02-2010.
20. Bercovich D, Ganmore I, Scott LM, et al. Mutations of *JAK2* in acute lymphoblastic Leukemia associated with Down's syndrome. Lancet 2008;372:1484–1492.
21. Kaplan EL, Meier P. Nonparametric estimation from incomplete observations. J Am Stat Assoc 1958;53:457–481.
22. Mantel N. Evaluation of survival data and two new rank order statistics arising in its consideration. Cancer Chemother Rep 1966;50:163–170.
23. Cox DR. Regression models, life tables. J R Stat Soc 1972;B34:187–220.
24. Collins-Underwood JR, Mullighan CG. Genomic profiling of high-risk acute lymphoblastic leukemia. Leukemia 2010;24:1676–1685.
25. Palmi C, Vendramini E, Silvestri D, et al. Poor prognosis for P2RY8-CRLF2 fusion but not for CRLF2over-expression in children with intermediate risk B-cell precursor acute lymphoblastic leukemia. Leukemia 2012;26:2245–2253.
26. Roberts KG, Morin RD, Zhang J, et al. Genetic alterations activating kinase and cytokine receptor signaling in high-risk acute lymphoblastic leukemia. Cancer Cell 2012;22:153–166.

SUPPORTING INFORMATION

Additional supporting information may be found in the online version of this article at the publisher's web-site.

Fig. S1. Detection of Ik6/Ik10 Isoform by RT-PCR. Five patients had the deletion of *IKZF1* exon 4–7 (Ik6), while patient No. 182 showed deletion of exon 2–7 (Ik10) by MLPA. The 358-bp band (open arrow head) indicates Ik6 isoform, and the 184-bp band (closed arrow head) indicates the Ik10 isoform. The sample (WT) without *IKZF1* deletion was used as a negative control.

Fig. S2. Probability of RFI according to *IKZF1* deletion, *CRLF2* expression and NCI risk classification. A: Probability of RFI for patients with or without *IKZF1* deletion (4-year RFI: 76.2 ± 10.9% vs. 91.7 ± 2.5%; $P = 0.047$). B: Probability of RFI for patients with or without *IKZF1* deletion according to NCI-risk classification (4-year RFI: 53.3 ± 23.4% vs. 93.2 ± 3.8%; $P = 0.03$ for NCI HR; 90.0 ± 9.5% vs. 91.0 ± 3.1%; $P = 0.82$ for NCISR). C: Probability of RFI for patients with high *CRLF2* expression or low *CRLF2* expression (4-year RFI: 71.8 ± 14.0% vs. 92.4 ± 2.4%; $P = 0.06$). D: Probability of RFI for patients with high *CRLF2* expression or low *CRLF2* expression according to NCI-risk classification (4-year RFI: 68.6 ± 18.6% vs. 90.6 ± 5.2%; $P = 0.18$ for NCI HR; 75.0 ± 21.7% vs. 93.1 ± 2.7%; $P = 0.35$ for NCI SR).

Fig. S3. Probability of EFS according to *IKZF1* deletions and *CRLF2* expression. The probability of EFS was much lower for the patients with *IKZF1* deletions and high *CRLF2* expression (4y-EFS: 20.0 ± 17.9%) when compared with patients with other *IKZF1*/*CRLF2* statuses (4y-EFS: 88.0 ± 3.2% for del.(−)/low, 90.0 ± 9.5% for del.(−)/high, 88.9 ± 10.5% for del.(+)/low, 77.8 ± 6.2% for del.(−)/missing, 75.0 ± 15.3% for del.(+)/missing, 88.2 ± 7.8% for missing/low).

Table SI. Patient Characteristics of the BCP-ALL Patients Enrolled in the CCLSG ALL 2004 Clinical Study Versus the Analyzed Cohort

Table SII. *IKZF1* Deletion Patterns Detected by MLPA

Table SIII. Clinical Features of the Patients With *IKZF1* Deletions and High *CRLF2* Expression

ORIGINAL RESEARCH

IKZF1 deletion is associated with a poor outcome in pediatric B-cell precursor acute lymphoblastic leukemia in Japan

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Keywords
Acute lymphoblastic leukemia, *CRLF2*, *IKZF1* deletion, pediatric

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Abstract

Genetic alterations of *Ikaros family zinc finger protein 1* (*IKZF1*), point mutations in *Janus kinase 2* (*JAK2*), and overexpression of *cytokine receptor-like factor 2* (*CRLF2*) were recently reported to be associated with poor outcomes in pediatric B-cell precursor (BCP)-ALL. Herein, we conducted genetic analyses of *IKZF1* deletion, point mutation of *JAK2* exon 16, 17, and 21, *CRLF2* expression, the presence of *P2RY8-CRLF2* fusion and F232C mutation in *CRLF2* in 202 pediatric BCP-ALL patients newly diagnosed and registered in Japan Childhood Leukemia Study ALL02 protocol to find out if alterations in these genes are determinants of poor outcome. All patients showed good response to initial prednisolone (PSL) treatment. Ph^+, infantile, and Down syndrome–associated ALL were excluded. Deletion of *IKZF1* occurred in 19/202 patients (9.4%) and *CRLF2* overexpression occurred in 16/107 (15.0%), which are similar to previous reports. Patients with *IKZF1* deletion had reduced event-free survival (EFS) and overall survival (OS) compared to those in patients without *IKZF1* deletion (5-year EFS, 62.7% vs. 88.8%, 5-year OS, 71.8% vs. 90.2%). Our data also showed significantly inferior 5-year EFS (48.6% vs. 84.7%, log rank $P = 0.0003$) and 5-year OS (62.3% vs. 85.4%, log rank $P = 0.009$) in NCI-HR patients ($n = 97$). *JAK2* mutations and *P2RY8-CRLF2* fusion were rarely detected. *IKZF1* deletion was identified as adverse prognostic factor even in pediatric BCP-ALL in NCI-HR showing good response to PSL.

Introduction

Acute lymphoblastic leukemia (ALL) is the most common pediatric malignancy and is an important cause of morbidity and mortality in children [1, 2]. Despite progress in therapy, approximately 20% of pediatric patients with B-cell precursor (BCP)-ALL with no adverse prognostic factors still experience relapse [3–5]. Recent genome-wide profiling studies of pediatric ALL identified a number of novel genetic alterations that

target key cellular pathways for lymphoid growth and differentiation and that are associated with treatment outcome [6]. Using high-resolution single-nucleotide polymorphism (SNP) arrays and genomic DNA sequencing, Mullighan et al. [7–10] and other groups revealed that alterations in genes encoding transcriptional regulators of B-lymphocyte development and differentiation, including *PAX5*, *EBF1*, and *IKZF1*, were observed in approximately 40% of patients with BCP-ALL. They also found that deletion of *IKZF1* was very frequent in *BCR-ABL*–positive ALL and in the lymphoid blast crisis of chronic myeloid leukemia [11]. Importantly, they also revealed that *IKZF1* deletion or mutation was associated with a very poor outcome, even in *BCR-ABL*–negative BCP-ALL [12–14]. The prognostic impact of *IKZF1* deletion was also confirmed by several other groups studying pediatric BCP-ALL [15–17]. Thus, *IKZF1* deletion has recently been considered as a prognostic marker for pediatric BCP-ALL and might be useful for risk stratification [16]. In addition, activating point mutations of *JAK2* coexisted with *IKZF1* deletion in pediatric BCP-ALL with a BCR-ABL-like gene expression signature and a very poor outcome [18]. Other studies reveal that overexpression of *cytokine receptor–like factor 2* (*CRLF2*) due to *IgH@-CRLF2* fusion resulting from immunoglobulin heavy-chain locus (*IgH@*) translocation or *P2RY8-CRLF2* fusion resulting from the interstitial deletion of the pseudoautosomal region 1 (PAR1) of either of the sex chromosomes (Xp22/Yp11) was significantly associated with *JAK2* mutations, *IKZF1* alterations, and a poor outcome in BCP-ALL [19–25]. Furthermore, Hertzberg et al. [21] demonstrated that patients with Down syndrome–associated ALL harbored *JAK2* mutations in association with altered *CRLF2* overexpression, which in some patients was caused by an activating somatic mutation, F232C, in the *CRLF2* gene. In this study, we sought to test whether deletion of *IKZF1*, dysregulation of *CRLF2*, *JAK2* mutations, or deletions in *PAX5 or EBF1* are prognostic determinants in Japanese pediatric BCP-ALL patients.

Materials and Methods

Patient cohort and samples

From April 2002 to May 2008, 1139 patients aged 1–18 years with newly diagnosed BCP-ALL (standard risk, SR = 457, high risk, HR = 543, and extremely high risk, ER = 139) (risk factors for classification are described in Table S1) were enrolled in the JACLS ALL study and assigned to three risk-stratified ALL02 protocols [26, 27]. The diagnosis of BCP-ALL was based on morphological findings on bone marrow aspirates and immunophenotype analyses of leukemic cells by flow cytometry. Conventional cytogenetic analyses using G-banding method were done as part of the routine workup. Molecular studies using quantitative RT-PCR for the detection of *BCR-ABL*, *ETV6-RUNX1*, *MLL-AF4*, *MLL-ENL*, *MLL-AF9*, and *TCF3(E2A)-PBX1* were performed as part of the routine workup. None of the cases of *BCR-ABL*-positive ALL and infant ALL was included. Down syndrome–associated ALL was excluded from the genetic analysis. Thus, 542 patients were included in this study. As the study was multi-institutional and the registry of patients was drawn from 93 hospitals, appropriate DNA/RNA specimens at diagnosis could be obtained from only 202 of the 542 patients in this group. A comparison of the clinical characteristics of patients with and without DNA/RNA specimens is shown in Table 1. There was no difference between these two cohorts in age at diagnosis, gender, NCI risk [28], and other variables except for initial WBC count. Informed consent was obtained from the patients' guardians according to the Declaration of Helsinki and the protocols of treatment, and the genetic study were approved by the institutional review boards of the participating institutes.

Table 1. Comparison of characteristics in 543 high-risk BCP-ALL patients depending on whether they were included in the genetic analyses.

Number of patients	202	340	*P*-value
	Analyzed	Nonanalyzed	
Gender (male/female)	106/96	186/154	0.66
Age (yrs) at diagnosis, median (range)	5 (1–18)	6 (1–17)	0.24
WBC count (cells/μL), median (range)	21,350 (1300–400,800)	12,635 (430–26,500)	<0.01
NCI risk group, SR/HR	108/94	189/151	0.63
ETV6-RUNX1/ hyperdiploid			0.85
Yes	69	113	
No	133	227	
SCT in 1st CR (*n*)	0	9	0.03
Observation period, median (range)	5.4 (0.5–8.9)	5.1 (0.1–9.0)	0.47

WBC, white blood cell; NCI, National Cancer Institute; SR, standard risk; HR, high risk; SCT, stem cell transplantation; CR, complete remission.

Determination of abnormalities in *IKZF1* and other genes by multiplex ligation-dependent probe amplification

Genomic DNA was isolated from diagnostic bone marrow or peripheral blood samples using the Qiagen DNeasy Blood and Tissue kit according to the manufacturer's

instructions (Qiagen, Venio, the Netherlands). DNA was analyzed using the SALSA multiplex ligation-dependent probe amplification (MLPA) kit P335-A4 according to the manufacturer's instructions (MRC Holland, Amsterdam, the Netherlands). This kit includes probes for *IKZF1*, *CDKN2A*, *CDKN2B*, *PAX5*, *ETV6*, *RB1*, *BTG1*, *EBF1*, and the PAR1 region, which includes *CRLF2*, *CSF2RA*, and *IL3RA*. PCR fragments generated with the MLPA kit were separated by capillary electrophoresis on an ABI Prism 3130 Genetic Analyzer (Applied Biosystems, Foster City, CA). Peak area was measured using GeneMapper software (Applied Biosystems). The relative copy number, obtained after normalization against controls, was used to determine genomic copy number of each gene as follows: 0 (<0.6, i.e., biallelic loss), 1 (0.6–1.47, i.e., monoallelic loss), 2 (1.47–2.6, i.e., normal copy number), or 3 or more (>2.6, i.e., gain) [29].

Detection of *CRLF2* overexpression by real-time RT-PCR

Total RNA was extracted from diagnostic bone marrow or peripheral blood samples using the RNeasy Mini Kit (Qiagen) according to manufacturer's instructions. cDNA was synthesized using the SuperScript First-Strand Synthesis System (Invitrogen, Carlsbad, CA) according to manufacturer's instructions. Real-time RT-PCR was conducted using the 7300 Real-Time PCR System (Applied Biosystems) with SYBR Green II (Takara Bio, Tokyo, Japan). Relative expression of target mRNA was determined using the comparative threshold (ΔC_T) method, in which the C_T value of the glyceraldehyde-3-phosphate dehydrogenase (GAPDH) internal control mRNA is subtracted from that of the target mRNA. Data are expressed as the ratio of target mRNA to GAPDH mRNA (calculated as $2^{\Delta(CT)}$). The primer pairs used in this study are listed in Table S2. Overexpression of *CRLF2* was defined as expression tenfold or greater than the median expression value based on a previous report [23]. A total of 107 specimens were available for the *CRLF2* study.

Detection of *P2RY8-CRLF2* fusion by RT-PCR

The *P2RY8-CRLF2* fusion was detected by RT-PCR or MLPA kit P335-A4 in 202 patients. The primers used are listed in Table S2.

CRLF2 mutation analysis

Using cDNA samples with altered *CRLF2* expression, the presence of the *CRLF2* F232C point mutation was detected by direct sequencing. The primers used are listed in Table S2. Appropriate RNA samples were available from all the 16 patients who overexpressed *CRLF2*.

JAK2 mutations analysis

Genomic DNA was extracted from diagnostic bone marrow or peripheral blood samples of patients harboring an *IKZF1* deletion. Primers were used to amplify exons 16, 20, and 21 of *JAK2* (accession number NM 004972). The PCR product was analyzed by direct sequencing using a BigDye Terminator sequencing kit (Applied Biosystems). The primers used are listed in Table S2. Appropriate DNA samples from all patients with the *IKZF1* deletion were available for the *JAK2* mutations study.

Statistical analysis

Estimation of event-free survival (EFS) and overall survival (OS) was performed using the Kaplan–Meier method and the differences were compared using the log rank test. A *P*-value <0.05 (two sided) was considered significant. EFS and OS were defined as the times from diagnosis to event (any death, relapse, secondary malignancy, or failure of therapy) and from diagnosis to death from any cause or to the last follow-up. Patients without an event of interest were censored at the date of last contact. The median follow-up times for EFS and OS were 5.22 and 5.34 years, respectively. Hazard ratios for probability of relapse between subgroups were calculated using univariate Cox models. Multivariate analysis was performed using a Cox regression model, which was adjusted for other risk factors: age at diagnosis and initial WBC count. Other comparisons were performed using the chi-square test or Fisher exact test, as appropriate.

Results

Frequency of *IKZF1* deletion, *CRLF2* overexpression, and *JAK2* mutations in patients in the JACLS ALL02 HR cohort

Deletion of the *IKZF1* gene was identified in 19/202 patients (9.4%) and *CRLF2* overexpression was noted in 16/107 patients (15.0%). The *P2RY8-CRLF2* fusion and *CRLF2* F232C mutation were very rare (1/202 and 0/16 patients, respectively). A recent study demonstrated that gain of *CRLF2* copy number was observed in BCP-ALL with overexpression of *CRLF2* [24]. In consistent with this report, 8 (50.0%) of 16 patients with altered *CRLF2* expression harbored gain of *CRLF2* copy number in our cohort (8/16 vs. 2/91, $P < 0.01$). In addition, no *JAK2* mutations (exons 16, 20, 21) were detected.