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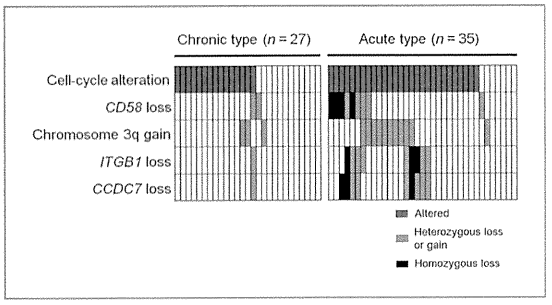


Figure 3. Distribution of genomic alterations frequently observed in acute-type ATL among ATL samples. Heatmap with rows corresponding to the indicated alterations and columns representing individual ATL cases. Gray, a heterozygous loss or gain; black, a homozygous loss. Dark gray also shows the alterations of any cell-cycle–related gene. Alterations frequently found in acute-type ATL were not mutually exclusive of the alteration of cell-cycle–related genes. Cases with losses of *ITGB1* and *CCDC7* always exhibited the alterations of cell-cycle–related genes. Most cases with loss of *CD58* or gain of 3q also exhibited the alterations of cell-cycle–related genes, but a case showing the loss of *CD58* or gain of 3q without disruption of the cell cycle existed in each type of ATL. The loss of *CD58* and gain of 3q were almost mutually exclusive, except for two cases of acute-type ATL.

*CD58*. Homozygous loss of *CD58* was observed only in acute-type ATL samples. Furthermore, expression of CD58 was reduced in acute-type ATL cases accompanied with the genomic loss (Fig. 4B). Flow cytometric analyses also suggested that genomic loss of *CD58* reduced the expression on the cell surfaces (Fig. 4C). Sequence analysis of *CD58* revealed a nonsense mutation in one acute-type ATL case. This mutation indicated that the 97th position of serine changed to a stop codon (p.S97X; c.290C>A; Fig. 4D). The nontumor cells of this patient showed no mutation, and we therefore regarded this mutation as a somatic mutation. One-nucleotide substitution registered as an SNP in the NCBI database (http://www.ncbi.nlm.nih.gov/gene/) was found in 7 cases (c.43A>G; rs17426456; Supplementary Table S2). Combined with the results of the genomic and mutation analyses, 29% of acute-type and 7% of chronic-type ATL had genetic alteration of *CD58*. These alterations were significantly specific to acute-type ATL compared with chronic-type ATL (Fig. 4E, $P = 0.05$).

In addition to the alteration of *CD58*, inactivation of *B2M* is also reported to play a pivotal role in the immune escape mechanism of DLBCLs (20). Among analyzed cases, only a chronic-type ATL case (C-2) had heterozygous loss of *B2M*, and this case also showed heterozygous loss of *CD58* (Supplementary Table S2). No somatic mutations of *B2M* were observed in ATL cases analyzed.

### Genomic alterations predicting acute transformation of chronic-type ATL

We investigated the associations of MCRs that were characteristic of acute-type ATL and that were commonly found in more than 20% of chronic- and acute-type ATL with cumulative acute transformation rates among chronic-type ATL cases (Supplementary Table S3).

Cases exhibiting gain of *RXRA* and loss of *ITGB1*, *CCDC7*, or *CD58* were significantly associated with early progression to acute-type ATL ($P = 0.01$, 0.02, 0.02, and 0.04, respectively; Fig. 5A). Chronic-type ATL cases having the alterations of cell-cycle–related genes also tended to show early progressions to acute-type ATL ($P = 0.07$; Fig. 5B), although cases having only the loss of *CDKN2A* were not significantly associated with the progression (Supplementary Table S3). A chronic-type ATL case with losses of *ITGB1* and *CCDC7* had the alterations of cell-cycle–related genes, and we therefore analyzed the chronic-type ATL cases by the presence of alterations of *CD58* and/or cell-cycle–related genes. This analysis revealed that cases with these alterations were specifically associated with earlier progression to acute-type ATL ($P = 0.03$, Fig. 5C).

## Discussion

We have studied 27 cases of chronic-type ATL and compared with 35 cases of acute-type ATL. Until now, only a few chronic-type ATL cases had been analyzed, and the molecular mechanisms of the transformation were investigated by focusing on the well-known tumor suppressor genes (*CDKN2A* and *TP53*; refs. 6–12). In contrast, our investigation comprehensively analyzed genomic profiles, and molecular aspects were analyzed using unbiased and whole-genome methods. Our study of chronic-type ATL represents the largest study to date that has analyzed the whole-genomic status of chronic-type ATL cases. We could identify characteristic molecular profile of chronic-type ATL and could demonstrate possible molecular mechanisms of acute transformation. This study suggested that alterations of cell-cycle–related genes and *CD58* are new predictive implications for chronic-type ATL (Fig. 5C).

### Common genomic alterations in chronic- and acute-type ATL

Genomic alteration profiles of chronic- and acute-type ATL were found to be almost identical (Fig. 1). The number of genomic alterations was found to be higher in acute-type ATL than in the chronic-type, and the frequently altered regions of chronic-type ATL were also observed in the acute-type. Thus, chronic-type ATL might be a pre-acute form of the disease.

The common MCRs in chronic- and acute-type ATL included genes involving T-cell receptor signaling, such as *FYN* and *SYK* (27, 28). We also identified *SYNCRIP* as a common MCR in both types of ATL. *SYNCRIP* is a gene known to be involved in maturation of mRNA (29). *RXRA*, which has been reported to be implicated in colorectal carcinogenesis (30), is also frequently altered in both types of ATL. In addition, our analysis suggested that gain of *RXRA* is involved in acute transformation of chronic-type ATL because the chronic-type ATL possessing the gain of *RXRA* showed earlier progression to the acute-type. These MCRs may play important roles in the development of ATL coordinately with HTLV-1.

### Deregulation of the cell-cycle pathway: an alteration related to acute transformation

Our analyses of genomic alterations revealed that no single genomic alteration seems to be responsible for the mechanism

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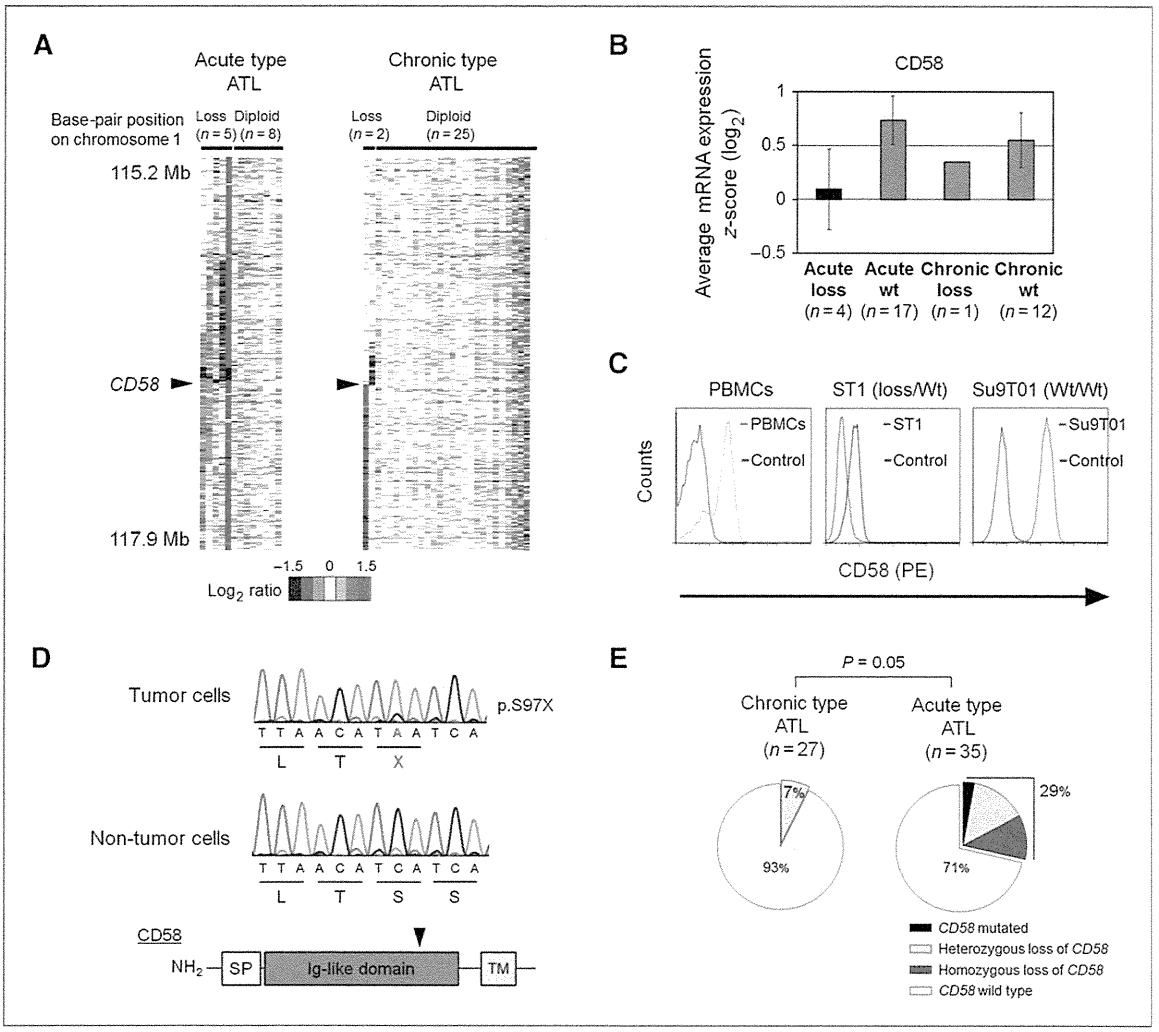


Figure 4. Alteration of *CD58* in acute transformation of chronic-type ATL. A, genomic alterations of chromosome 1p, including *CD58*. Heatmap analysis of 400K aCGH shows $\log_2$ ratios of ATL cases. White, blue, and red represent diploid, loss, and gain, respectively. Arrowhead, the *CD58* locus. B, gene expression levels of CD58. Expression was analyzed in 13 chronic-type and 21 acute-type ATL cases by GEP. Average gene expressions and SDs are shown in cases grouped as indicated. CD58 expression was reduced only in acute-type ATL cases exhibiting loss of *CD58*. Probe A_23_P138308 (CD58) was used in experiments. C, CD58 expressions on ATL cell lines and peripheral blood mononuclear cells (PBMC). Flow cytometric analysis of PBMCs from a healthy donor and two ATL cell lines for surface CD58 expression (orange line, PBMCs; blue line, ST1; red line, Su9T01). ST1 with heterozygous loss of CD58 had the low expression. The gray lines represent the cell lines with the isotype control antibody. D, DNA sequencing chromatogram of an acute-type ATL case (A-35) showing nonsense mutation in exon 2 of *CD58* (top). DNA extracted from nontumor cells (CD4-negative cells in peripheral blood of this patient) did not show the mutation (middle). Bottom, a schematic representation of the CD58 protein depicting the location of the single peptide (SP), Ig-like domain, and transmembrane domain (TM). The inverted triangle indicates the position of the mutation. E, characterization of *CD58* alteration in ATL. Seven percent of chronic-type ATL cases showed genomic loss of *CD58*, whereas 29% of acute-type ATL cases showed genomic alteration of *CD58*, with one case exhibiting mutation (Fisher exact test; $P = 0.05$).

of acute transformation, and various genomic alterations and combinations of alterations exist in this mechanism (Fig. 3). We found that deregulation of the cell cycle, including genomic loss of *CDKN2A*, might be an important event in the transformation. Genomic loss of *CDKN2A* was also reported to play a crucial role in the transformation of chronic lymphocytic leukemia known as Richter syndrome (31, 32).

Although previous studies using Southern blot analysis revealed that 11% to 17% of acute-type ATL had the homozygous loss of *CDKN2A* (7, 9), our analyses using unbiased and whole-genome methods were able to reveal the frequency of the loss in greater detail. We found that approximately 30% of acute-type ATL cases showed a homozygous loss of the *CDKN2A/CDKN2B* locus, and 50% of acute-type ATL cases

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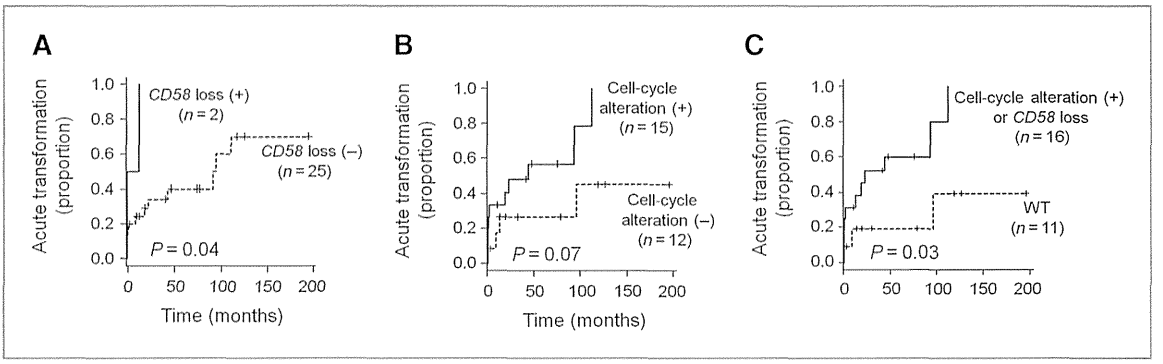


Figure 5. Genomic alterations associated with acute transformation in chronic-type ATL. A, genomic loss of *CD58* was significantly associated with earlier acute transformation ($P = 0.04$). B, chronic-type ATL cases with alterations of cell-cycle–related genes tended to exhibit earlier progression to acute-type ATL ($P = 0.07$). C, cases with either *CD58* loss or alterations of cell-cycle–related genes showed a much shorter time to acute transformation within chronic-type ATL cases ($P = 0.03$).

exhibited the homozygous or heterozygous loss of this locus. Yamagishi and colleagues used high-resolution aCGH analyses and found that this loss was frequently found in ATL samples (33). We also found that 5 of 27 chronic-type ATL cases had heterozygous loss of *CDKN2A*. Three of the 5 cases with *CDKN2A* loss progressed to the acute type, but 11 of the 22 cases without *CDKN2A* loss also showed acute transformation. Because of this finding, *CDKN2A* loss was not significantly associated with the earlier acute transformation in our study (Supplementary Table S3). Although previous studies revealed that approximately 5% of chronic-type had this loss (7, 9, 10), these previous studies did not show the cumulative acute transformation rate according to *CDKN2A* loss.

CDKN2A expression was reduced in acute-type ATL samples exhibiting genomic loss of the *CDKN2A* locus. A portion of acute-type ATL cases without the genomic loss showed a low expression level of CDKN2A, suggesting that methylation of the gene might affect the expression in these samples (11, 12). However, we consider that the genomic loss of *CDKN2A* has a greater influence on the expression of the gene than the methylation because the CDKN2A expression levels were remarkably reduced in accordance with the genomic loss (Fig. 2B and D).

Alterations of both *CDKN2A* and *TP53* were previously reported to be mutually exclusive (34), and our results showed the same trend. In addition, loss of *TP53* and gains of *MDM4/RFWD2* tended to be mutually exclusive in our acute-type ATL samples. Because these genes are involved in the TP53 pathway, our findings indicate that the TP53 pathway may also play a pivotal role in the pathophysiology of acute-type ATL. In fact, 80% of acute-type ATL had the alterations of cell-cycle–related genes, including *CDKN2A* and *TP53*. On the basis of this finding, we found that the alterations of cell-cycle–related genes might be predictive factors for acute transformation in chronic-type ATL cases (Fig. 5B).

### Disruption of the immunosurveillance system in acute transformation of chronic-type ATL

The combined analyses of aCGH and sequencing revealed that 19% of ATL cases (7% of chronic-type and 29% of acute-type ATL) exhibited the *CD58* alteration. One acute-type ATL case showed somatic mutation, and the other cases showed genomic loss of the *CD58* locus. The alteration of *B2M* was a rare event in ATL compared with DLBCL (20). CD58 is a ligand of the CD2 receptor that is expressed on CTLs and NK cells and contributes to adhesion and activation of these cells. Previous reports showed that CTLs and NK cells could not recognize and injure target cells when treated with monoclonal CD58 antibody (35, 36). It is important to note that immune escape mechanism by CD58 inactivation was proven in DLBCL by Challa-Malladi and colleagues (20). The genomic loss and nonsense mutation of CD58 were for the first time demonstrated in ATL in this study and were suggested to be a predictive marker for acute transformation in chronic-type ATL. Therefore, the immune escape mechanism by the CD58 inactivation is likely to be involved in the pathophysiology of ATL as shown in DLBCL although detailed analysis is needed in the future.

Administration of immunosuppressive drugs to HTLV-1 carriers is currently considered a risk factor for early development of ATL (37, 38). It has been also suggested that immune escape from CTLs is induced by inactivation of the Tax protein derived from HTLV-1 in ATL (39–41). In addition, a report also suggested that immune escape from NK cells played an important role in ATL development (42). These findings suggest the presence of an immune escape mechanism in the pathophysiology of ATL. The present result regarding the significance of *CD58* alteration as a predictive factor for acute transformation in chronic-type ATL should be validated in more number of cases in the future study. Further studies are also needed regarding the protein expressions of CD58, B2M, and human leukocyte antigen class I.

In conclusion, our comparison of the molecular characteristics of chronic-type and acute-type ATL revealed that deregulation of the cell cycle and escape from the immune system are likely to be involved in acute transformation of chronic-type ATL. Development of ATL is thought to involve accumulation of several genomic alterations (43). The alterations of both pathways discovered in this study might be the late events following viral infection in the pathophysiology of ATL. These alterations could serve as biomarkers for patients with

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chronic-type ATL. Furthermore, the presence of genomic alterations related to immune escape should be considered in the development of immunotherapeutic approaches for ATL.

## Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

## Authors' Contributions

**Conception and design:** N. Yoshida, A. Utsunomiya, K. Tsukasaki, A. Umino, M. Seto

**Development of methodology:** K. Karube

**Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.):** N. Yoshida, A. Utsunomiya, K. Tsukasaki, Y. Imaizumi, N. Taira, K. Arita, S. Tsuzuki, K. Ohshima

**Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis):** N. Yoshida, A. Utsunomiya, K. Arita, M. Suguro, S. Tsuzuki

**Writing, review, and/or revision of the manuscript:** N. Yoshida, K. Karube, A. Utsunomiya, K. Tsukasaki, T. Kinoshita, M. Seto

**Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases):** A. Utsunomiya, N. Uike, T. Kinoshita, M. Seto

**Study supervision:** K. Karube, M. Seto

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# Molecular Characterization of Chronic-type Adult T-cell Leukemia/Lymphoma

Noriaki Yoshida, Kennosuke Karube, Atae Utsunomiya, et al.

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bjh research paper

# Japan Clinical Oncology Group (JCOG) prognostic index and characterization of long-term survivors of aggressive adult T-cell leukaemia-lymphoma (JCOG0902A)

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## Summary

This study evaluated the clinical features of 276 patients with aggressive adult T-cell leukaemia-lymphoma (ATL) in 3 Japan Clinical Oncology Group (JCOG) trials. We assessed the long-term survivors who survived >5 years and constructed a prognostic index (PI), named the JCOG-PI, based on covariates obtained by Cox regression analysis. The median survival time (MST) of the entire cohort was 11 months. In 37 patients who survived >5 years, no disease-related deaths in 10 patients with lymphoma-type were observed in contrast to the 10 ATL-related deaths in other types. In multivariate analysis of 193 patients, the JCOG-PI based on corrected calcium levels and performance status identified moderate and high risk groups with an MST of 14 and 8 months respectively (hazard ratio, 1·926). The JCOG-PI was reproducible in an external validation. Patients with lymphoma-type who survived >5 years might have been cured. The JCOG-PI is valuable for identifying patients with extremely poor prognosis and will be useful for the design of future trials combining new drugs or investigational treatment strategies.

**Keywords:** adult T-cell leukaemia-lymphoma, Japan Clinical Oncology Group trials, long-term survivors, prognostic index.


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Adult T-cell leukaemia-lymphoma (ATL) is a distinct peripheral T-lymphocytic malignancy associated with human T-cell lymphotropic virus type I (HTLV-1) (Uchiyama *et al*, 1977; Poiesz *et al*, 1980; Hinuma *et al*, 1981; Miyoshi *et al*, 1981; Yoshida *et al*, 1982). Classification of clinical subtypes into acute, lymphoma, chronic and smouldering was proposed based on prognostic factors, clinical features and the natural history of the disease (Shimoyama, 1991). Patients with aggressive ATL (i.e., acute, lymphoma and unfavourable chronic types) have frequently been treated as a subtype of aggressive non-Hodgkin lymphoma (NHL), whereas those with indolent ATL (i.e., favourable chronic and smouldering types) have been managed as a subtype of chronic lymphoid leukaemia (Shimoyama, 1994; Tobinai & Watanabe, 2004). Aggressive ATL typically has a very poor prognosis compared with aggressive B-cell lymphomas, such as diffuse large B-cell lymphoma and peripheral T-cell lymphoma excluding ATL (The International Non-Hodgkin's Lymphoma Prognostic Factor Project's, 1993; Shimoyama, 1994; Gallamini *et al*, 2004; Watanabe *et al*, 2010). In the 1980's, patients with aggressive ATL were reported to have a median survival time (MST) of approximately 8 months, with a 2-year survival rate of <5% because of the multidrug-resistant phenotype of their malignant tumour cells, rapid proliferation of the tumour cells, a large tumour burden with multi-organ failure, hypercalcaemia, and/or frequent opportunistic infections (Lymphoma Study Group, 1991; Shimoyama, 1991, 1994; Tobinai & Watanabe, 2004).

The Japan Clinical Oncology Group (JCOG)-Lymphoma Study Group (LSG) has conducted consecutive clinical trials to improve the survival of patients with ATL. Earlier trials (JCOG7801, JCOG8101, and JCOG8701) revealed poor prognosis of ATL compared with other aggressive NHLs (Shimoyama *et al*, 1988; Tobinai *et al*, 1994). Furthermore, the disappointing results with conventional chemotherapies in the 1980s and the proposal for a subtype classification of ATL led us to conduct clinical trials with new agents that exclusively targeted aggressive ATL. The first phase II trial, JCOG9109 (1991–1993), evaluated combination chemotherapy with deoxycoformycin, an inhibitor of adenosine deaminase, which had been effective as a single agent against relapsed or refractory ATL (Tobinai *et al*, 1992). However, the results were disappointing with an MST of 7 months, similar to the findings of previous JCOG-LSG trials (Tsukasaki *et al*, 2003). The next phase II trial, JCOG9303 (1994–1996), evaluated the chemotherapy regimen VCAP-AMP-VECP (LSG15) against aggressive ATL. This dose-intensified multi-agent chemotherapy consisted of vincristine, cyclophosphamide, doxorubicin (DXR) and prednisone (PSL) for VCAP, DXR, ranimustine and PSL for AMP, and vindesine, etopside, carboplatin and PSL for VECP, supported by granulocyte colony-stimulating factor and intrathecal (IT) prophylaxis with methotrexate (MTX) and PSL. This phase II trial showed promising results, with complete remission (CR) and overall response rates of 36% and 81%, respectively, and an MST of 13 months at the expense of haematological and other toxicities (Yamada *et al*, 2001). Based on these results, we proceeded to the phase III trial JCOG9801 (1998–2003), which compared a modified VCAP-AMP-VECP regimen (shortened from 7 to 6 courses), to which cytarabine was added to the IT prophylaxis, *versus* CHOP (cyclophosphamide, DXR, vincristine and PSL)-14 supported by granulocyte

colony-stimulating factor and IT prophylaxis identical to the former regimen. The CR and 3-year overall survival (OS) were higher in the modified VCAP-AMP-VECP arm than in the CHOP-14 arm (40% vs. 25% and 24% vs. 13% respectively), suggesting that the former is a more effective regimen at the expense of greater toxicity for patients with newly diagnosed aggressive ATL (Tsukasaki *et al*, 2007).

Through these 3 JCOG trials for patients with aggressive ATL, the 5-year OS was improved, from 5% in the 1980's to 15% in the 1990s. To characterize the long-term survivors of aggressive ATL and to develop a new prognostic index (PI) for the disease, we performed a combined analysis (JCOG0902A) of all the patients enrolled in the 3 JCOG trials.

## Methods

### *Study population*

A total of 276 patients who were registered in the 3 JCOG trials described above were enrolled in this study (Yamada *et al*, 2001; Tsukasaki *et al*, 2003, 2007). Some patients did not receive anti-viral therapy using interferon-alpha and zidovudine because these drugs for ATL was not covered by the National Health Insurance in Japan. The eligibility criteria for the 3 JCOG trials were detailed in previous reports (Yamada *et al*, 2001; Tsukasaki *et al*, 2003, 2007). Briefly, patients were eligible to participate if they had aggressive ATL (i.e., acute, lymphoma, or unfavourable chronic type) with no prior chemotherapy, were aged 15–69 years and had preserved organ functions, no proven central nervous system (CNS) involvement and a performance status (PS) of 0–3 or 4 due to hypercalcaemia caused by ATL. The diagnosis of ATL was made based on seropositivity for HTLV-1 antibody and histologically and/or cytologically proven peripheral T-cell malignancy. Monoclonal integration of HTLV-1 provirus was analysed in 104 of 276 patients studied. Among these 104 patients, integration was detected in 100 patients and not detected in four patients.

The PI for the JCOG trials, which we refer to as the JCOG-PI, was constructed from the data of patients who participated in these trials (training set) and was then applied to an external validation set. The external validation set consisted of 136 patients who had not participated in prior JCOG studies but had received anthracycline-containing regimens as initial chemotherapy at three sites (Nagasaki University Hospital, Nagasaki Medical Centre, and Sasebo City General Hospital) under the remit of the JCOG-LSG. These patients were a subset of those from a previous retrospective study (Katsuya *et al*, 2012) and their OS and corrected calcium levels were reviewed.

### *Data and analysis sets*

The endpoint of this study was OS, defined as the duration between registration to each JCOG trial and death from any cause or censored at the last follow up in living patients. For the validation data set, we substituted the date of treatment initiation for the date of registration.

Candidate covariates were sex, age, Eastern Cooperative Oncology Group (ECOG) PS, B symptoms, clinical stage, liver involvement, lactate dehydrogenase, blood urea nitrogen (BUN), corrected calcium levels, serum total protein, serum albumin, white blood cell count, total (normal and abnormal) lymphocyte count, neutrophil count and platelet count. We excluded the treatment regimen from the covariates because our aim was to create an index that could stratify the patients' prognosis and be applicable to future clinical trials evaluating various promising regimens. Cut-off values were determined clinically by dividing the continuous biological and laboratory test variables into no more than three categories. The data of 193 patients with a complete set of candidate covariates were used for the training set (Fig 1).

The protocol of this study was reviewed and approved by the JCOG Protocol Review Committee.

### *Statistical analysis*

Patients who survived >5 years were categorized according to ATL subtype (acute, lymphoma or unfavourable chronic types). In addition, to evaluate the ATL-related death events for each subtype, a disease-specific mortality curve was estimated, for only those patients who survived >2 years, by means of a competing risks framework (Kalbfleisch & Prentice, 2002). The proportion of patients who survived >5 and >10 years was calculated to evaluate the association between long-term survival and CR (including CR unconfirmed) for initial treatment. The proportion of cases with

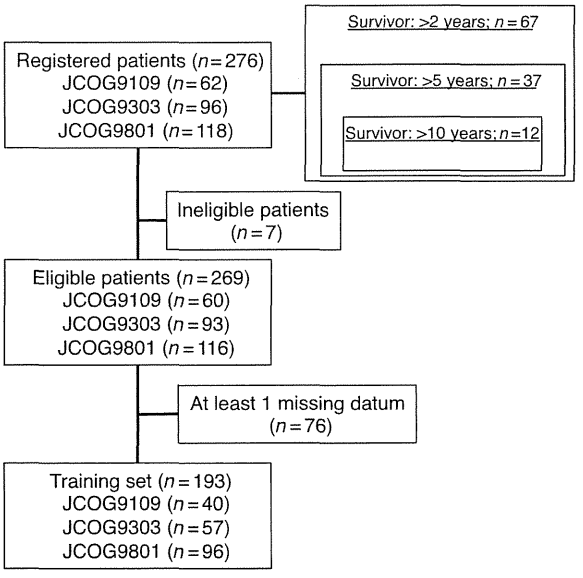


**Fig 1.** Patient disposition of the training set.

CNS involvement was compared among the JCOG trial regimens in an exploratory evaluation of the efficacy of prophylactic IT treatment. The prophylactic IT treatments against CNS involvement were: none in JCOG9109, MTX and PSL in JCOG9303, and MTX, cytarabine and PSL in both regimens in JCOG9801. Confidence intervals (CIs) for all the above proportions were computed using the Clopper–Pearson method (Clopper & Pearson, 1934).

Analyses for the development and validation of the JCOG-PI were performed according to a pre-specified analysis plan. The JCOG-PI consisted of risk groups that were developed using Cox's proportional hazards model. Before constructing the JCOG-PI, covariates with several definitions were selected for those with the smallest Akaike's Information Criteria (Akaike, 1973) on univariate analysis. Next, we verified the correlations between covariates to avoid multi-colinearity. Stepwise Cox regression analysis was then performed to identify unfavourable prognostic factors for constructing the JCOG-PI. The entry criterion was $P < 0{\cdot}20$ and the removal criterion was $P > 0{\cdot}15$.

The maximum number of risk group strata was set at three, based on the opinions of JCOG-LSG members who commented that too many strata were impractical for evaluating risk. The risk group was divided with patients equally distributed. The log-rank test was used to assess the discrepancy between the risk groups and the Kaplan–Meier method was applied to estimate OS.

All statistical analysis was performed using SAS Release 9·1 (SAS Institute, Inc, Cary, NC, USA). All reported $P$ values are two-sided and $P < 0{\cdot}05$ was considered statistically significant.

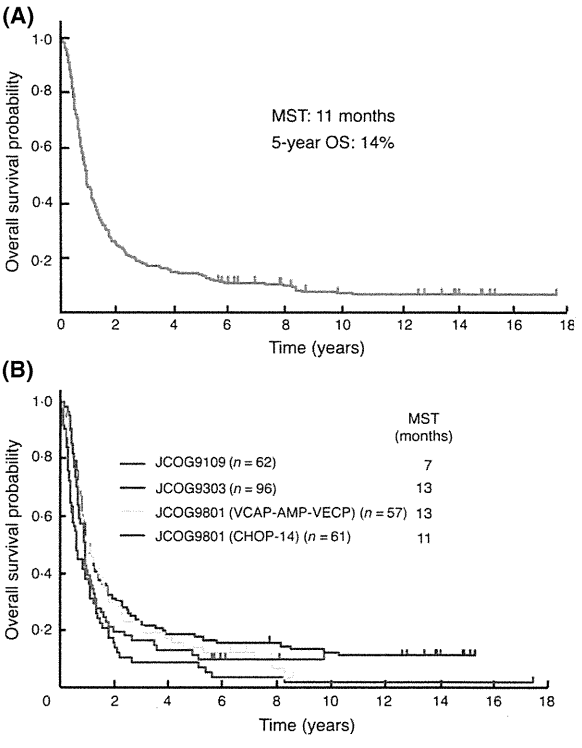


Fig 2. Overall survival (OS) of all registered patients in 3 Japan Clinical Oncology Group (JCOG) trials and according to treatment regimens. (A) OS of all 276 registered patients. Median survival time (MST) and the 5-year OS were 11 months and 14%, respectively.(B) OS according to different treatment regimens. MST was 7 months in JCOG9109, 13 months in JCOG9303, 13 months in VCAP-AMP-VECP of JCOG9801 and 11 months in CHOP-14 of JCOG9801.

## Results

### *Patient characteristics*

A total of 276 patients were registered in the 3 trials (JCOG9109, $n = 62$; JCOG9303, $n = 96$; and JCOG9801, $n = 118$) from 58 institutions in Japan. The MST and the 5-year OS of all patients were 11 months and 14% respectively (Fig 2A). The OS of each treatment regimen during the long follow up reconfirmed the findings of each original report (Fig 2B) (Yamada *et al*, 2001; Tsukasaki *et al*, 2003, 2007). Clinical characteristics are shown in Table I.

### *Long-term survivors according to subtype and initial response*

The disease-specific mortality curve of patients who survived >2 years according to subtype is presented in Fig 3. Among the 37 patients (acute, $n = 22$; lymphoma, $n = 8$; unfavourable chronic, $n = 7$) who survived >5 years, there were no ATL-related deaths in lymphoma type, which was in contrast to the 10 ATL-related deaths in the acute and unfavourable chronic types after 5 years.

Of the 276 patients, 88 (32%) achieved CR with initial treatment. Of these 88 patients, 24 (27%) patients had survived >5 years and 11 (13%) patients had survived >10 years. Of the remaining 188 patients who did not achieve CR, 13 (17%) patients who survived >5 years and only 1 (0·5%) patient survived >10 years.

### *CNS involvement by treatment regimen*

CNS involvement was 1·6% (95% CI, 0·04–8·7) in JCOG9109, 6·3% (95% CI, 2·3–13·1) in JCOG9303, and 3·5% (95% CI, 0·4–12·1) in the VCAP-AMP-VECP arm and 8·2% (95% CI, 2·7–18·1) in the CHOP-14 arm of JCOG9801. No significant differences in the proportion of CNS involvement were observed among the regimens.

### *Development of the PI*

In univariate analyses, three covariates showed significant associations with OS, namely PS, corrected calcium level and serum total protein (all $P < 0{\cdot}05$; Table II). Stepwise Cox regression analysis returned three unfavourable prognostic

Table I. Clinical characteristics of 15 covariates in all 276 registered patients.

| | | JCOG9109 ($n$ = 62) | JCOG9303 ($n$ = 96) | JCOG9801 ($n$ = 118) | Total ($n$ = 276) |
|---|---|---|---|---|---|
| Initial date of registration | | November 1991 | January 1994 | July 1998 | |
| Final date of registration | | July 1993 | December 1996 | October 2003 | |
| Number of sites | | 30 | 20 | 27 | 49 |
| Sex | Male/female | 38/24 | 54/42 | 61/57 | 153/123 |
| Age, years | ≥20, <30 | 0 | 1 | 0 | 1 |
| | ≥30, <40 | 2 | 7 | 6 | 15 |
| | ≥40, <50 | 14 | 29 | 20 | 63 |
| | ≥50,<60 | 27 | 24 | 44 | 95 |
| | ≥60, <70 | 19 | 35 | 48 | 102 |
| PS | 0/1 | 23/22 | 19/25 | 49/46 | 91/93 |
| | 2/3/4/NE | 7/9/1/0 | 17/9/8/18 | 18/4/1/0 | 42/22/10/18 |
| B symptoms | +/−/NE | 22/36/4 | 39/57/0 | 45/73/0 | 106/166/4 |
| Stage | I/II/III/IV | 1/4/8/49 | 2/6/14/74 | 0/4/8/106 | 3/14/30/229 |
| Liver invasion | +/− | 10/52 | 20/76 | 25/93 | 55/221 |
| LDH, iu/l | <−1 × ULN/> | 9/53 | 10/86 | 20/98 | 39/237 |
| BUN, mmol/l | <−1 × ULN/>/NE | 47/14/1 | 80/15/1 | 107/11/0 | 234/40/2 |
| Corrected Ca, mmol/l | <2·75/≥/NE | 49/9/4 | 75/16/5 | 93/25/0 | 217/50/9 |
| Serum protein, g/l | <60/≥/NE | 18/44/0 | 27/69/0 | 30/87/1 | 75/200/1 |
| Albumin g/l | <35/35–40/≥40/NE | 18/26/15/3 | 35/39/18/4 | 28/64/26/0 | 81/129/59/1 |
| WBC ($\times 10^9$/l) | <3/≥ | 48/14 | 77/19 | 104/14 | 229/47 |
| Lymphocytes ($\times 10^9$/l)* | <4/4–15/≥15/NE | 28/16/14/4 | 54/19/23/0 | 64/33/20/1 | 146/68/57/5 |
| Neutrophils ($\times 10^9$/l) | <8/≥/NE | 49/12/1 | 75/21/0 | 94/24/0 | 218/57/1 |
| Platelets ($\times 10^9$/l) | <150/≥ | 16/46 | 19/77 | 19/99 | 54/222 |

B symptoms: fever, night sweats, and weight loss.
JCOG, Japan Clinical Oncology Group; ECOG PS, Eastern Cooperative Oncology Group performance status; Ca, calcium level; WBC, white blood cell count; ULN, upper limit of normal; NE, not evaluated.
*total (normal + abnormal) lymphocyte count.

factors associated with OS, namely a high, corrected calcium level, high PS (2–4), and the existence of B symptoms, although the third factor was not statistically significant (Table II). Table II also presents the results of the model when the two significant factors of corrected calcium and ECOG PS were included. The hazard ratios (HRs) estimated by this model were 1·574 (95% CI, 1·088–2·277; $P$ = 0·016) for corrected calcium and 1·554 (95% CI, 1·120–2·157; $P$ = 0·008) for ECOG PS.

The four categories consisting of the two prognostic factors (corrected calcium level and PS) were combined into a dichotomous PI, named the JCOG-PI, by considering its potential for clinical use. Similarly, we constructed a dichotomous PI including B symptoms with two prognostic factors. We excluded B symptoms from further assessment because the Akaike Information Criteria of JCOG-PI (1537·8) was smaller than that of PI (1545·6).

According to the JCOG-PI, the MST and 5-year OS were 14 months and 18% in patients with both corrected calcium <2·75 mmol/l and a PS of 0 or 1 (moderate-risk group) and were 8 months and 4% in patients with corrected calcium ≥2·75 mmol/l and/or a PS of 2–4 (high-risk group) respectively (Fig 4A). The HR and 95% CI were 1·926 and 1·423–2·606 respectively ($P$ < 0·0001).

*External validation*

Nine patients in the validation set of 136 patients had missing corrected calcium or PS data, resulting in 127 evaluable patients (Fig 5). The median and longest follow-up periods were 9 months and 97 months, respectively. The HR was 2·138 (95% CI, 1·414–3·233, $P$ = 0·0003) with an MST of 18 months and 6 months in the moderate- and high-risk groups respectively and JCOG-PI showed good reproducibility (Fig 4B).

## Discussion

In this first prospective analysis of a large cohort of aggressive ATL patients from prospective clinical trials conducted after the clinical subtype classification of ATL was introduced, we constructed the JCOG-PI based on corrected calcium level and PS and validated it with external data. The ascertained discrepancy was stronger among the external validation set. In addition, OS of high-risk patients was worse in the external validation set than in the training set, probably reflecting poor organ functions and other unfavourable prognostic factors in patients not participating in clinical trials. The OS of the moderate-risk patients was better in the

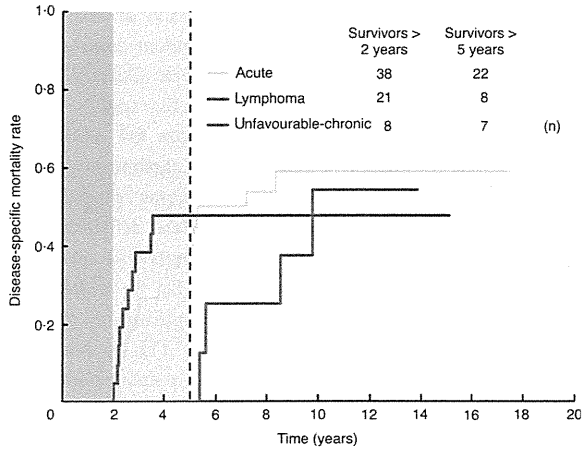


**Fig 3.** ATL-related deaths of patients who survived >2 years according to subtype. Among the 37 patients who survived >5 years, there were no ATL-related deaths in lymphoma type in contrast to the 10 ATL-related deaths in other types after 5 years.

external validation set than in the training set, possibly reflecting recent advances in treatment, including chemotherapy and allogeneic haematopoietic stem cell transplantation (allo-HSCT).

In our analysis of patients who survived >5 years, no ATL-related deaths occurred in those with lymphoma type, which is in contrast to the ATL-related deaths seen among patients with acute or unfavourable chronic type (Fig 3). This suggests that about 10% of patients with lymphoma type survived >5 years, most of whom might have been cured. Although abnormalities of comparative genomic hybridization might differ between acute and lymphoma types (Oshiro *et al*, 2006), the difference in clinical course between lymphoma type and acute or unfavourable chronic type remains unclear, and further analyses on the molecular and biological features of these types are needed.

Of the 276 patients studied, 20 received an allo-HSCT. The 5-year OS rate of these patients was 40%, compared with 12% in patients who did not undergo transplantation

**Table II.** Results of univariate and multivariate analyses in the training set ($n$ = 193).

| Factor | | Univariate analysis HR (95%CI) | *P* value | Pre-planned multivariate analysis (AIC = 1545·6) HR (95%CI) | *P* value | Model used for constructing JCOG-PI (AIC = 1537·8) HR (95%CI) | *P* value |
|---|---|---|---|---|---|---|---|
| Ca, mmol/l | <2·75 | Ref | | Ref | | Ref | |
| | ≥2·75 | 1·742 (1·214–2·498) | 0·002 | 1·688 (1·156–2·466) | 0·007 | 1·574 (1·088–2·277) | 0·016 |
| ECOG PS | 0–1 | Ref | | Ref | | Ref | |
| | 2–4 | 1·680 (1·219–2·314) | 0·001 | 1·493 (1·073–2·078) | 0·018 | 1·554 (1·120–2·157) | 0·008 |
| B symptoms | − | Ref | | Ref | | | |
| | + | 1·249 (0·926–1·685) | 0·145 | 1·288 (0·945–1·755) | 0·109 | | |
| Sex | Male | Ref | | | | | |
| | Female | 0·999 (0·743–1·342) | 0·994 | | | | |
| Age, years | <60 | Ref | | | | | |
| | ≥60 | 1·108 (0·818–1·502) | 0·504 | | | | |
| Stage | I–II | Ref | | | | | |
| | III–IV | 1·293 (0·682–2·451) | 0·429 | | | | |
| Liver invasion | − | Ref | | | | | |
| | + | 1·238 (0·867–1·768) | 0·241 | | | | |
| LDH, iu/l | ≤ULN | Ref | | | | | |
| | >1 × ULN | 1·325 (0·840–2·091) | 0·226 | | | | |
| BUN, mmol/l | ≤ULN | Ref | | | | | |
| | >1 × ULN | 1·332 (0·871–2·036) | 0·184 | | | | |
| Serum protein, g/l | <60 | Ref | | | | | |
| | ≥60 | 0·642 (0·457–0·901) | 0·010 | | | | |
| Lymphocytes, $\times 10^9$/l | <4 | Ref | | | | | |
| | 4–14·9 (vs. <4) | 1·110 (0·785–1·570) | 0·553 | | | | |
| | ≥15 (vs. <4) | 1·102 (0·747–1·626) | 0·626 | | | | |
| Neutrophils, $\times 10^9$/l | <8 | Ref | | | | | |
| | ≥8 | 1·271 (0·888–1·817) | 0·189 | | | | |
| Platelets, $\times 10^9$/l | <150 | Ref | | | | | |
| | ≥150 | 0·900 (0·626–1·294) | 0·569 | | | | |

AIC, Akaike's Information Criteria; JCOG, Japan Clinical Oncology Group; PI, Prognostic index; HR, hazard ratio; CI, confidence interval; Ref, reference; ECOG PS, Eastern Cooperative Oncology Group performance status; LDH, lactate dehydrogenase; BUN, blood urea nitrogen.

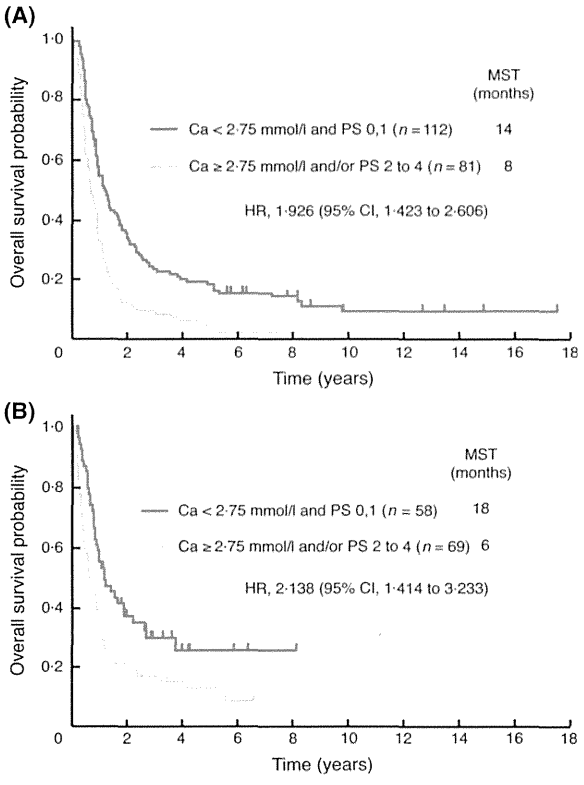


Fig 4. Overall survival of the patients in the training set and in the external validation set according to the JCOG-PI. (A) OS in the training set. The median survival time (MST) and 5-year OS were 14 months and 18% in moderate-risk group (blue line) and were 8 months and 4% in high-risk group (yellow line), respectively (B) OS in the validation set. The MST of 18 months and 6 months in the moderate- (blue line) and high-risk (yellow line) groups, respectively, and JCOG-PI showed good reproducibility.

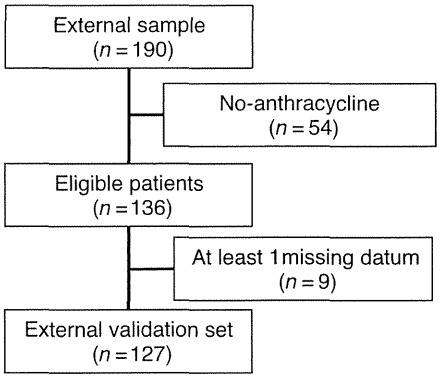


Fig 5. Patient disposition of the external validation set.

(data not shown). However, it was too difficult to evaluate the efficacy of allo-HSCT in our cohort because the disease status at transplantation and the duration from registration to transplantation were rather heterogeneous and the transition to allo-HSCT was time-dependent. To adjust this time-dependent causality, periodical data collection of, for example, indicators of treatment and time-dependent confounders, is necessary. The causal relationship between allo-HSCT and OS should be evaluated in a future prospective trial.

Several reports have revealed risk factors for ATL. In a prospective randomized trial against NHL parsimonious conducted between 1981 and 1983, Shimoyama *et al* (1988) demonstrated that poor PS and high lactate dehydrogenase levels were poor prognostic factors in patients with advanced T-cell lymphoma/leukaemia, including ATL. In a Japanese nationwide survey of 854 patients, a multivariate analysis identified major prognostic indicators of ATL as poor PS, high lactate dehydrogenase levels, age ≥40 years, >3 involved lesions and hypercalcaemia (Lymphoma Study Group, 1991). These factors were then used to construct a risk model. Additional factors reportedly associated with poor prognosis, as determined by multivariate analyses, include thrombocytopenia (Yamada *et al*, 1997), eosinophilia (Utsunomiya *et al*, 2007), bone marrow involvement (Takasaki *et al*, 2007), high interleukin (IL)5 and IL10 serum levels (Inagaki *et al*, 2006), C-C chemokine receptor 4 (CCR4) expression (Ishida *et al*, 2003), lung resistance-related protein (Ohno *et al*, 2001), *TP53* mutation (Tawara *et al*, 2006) and *CDKN2A* deletion (Yamada *et al*, 1997). Specific to chronic-type ATL, multivariate analysis has identified high lactate dehydrogenase levels, high blood urea nitrogen levels and low albumin levels as poor prognostic factors in several retrospective analyses (Shimoyama, 1994).

Recently, an ATL-PI consisting of Ann Arbour clinical stage, PS, age, serum albumin level and soluble IL2 receptor level was used to identify three risk groups for patients with acute and lymphoma types of ATL (Katsuya *et al*, 2012). However, in that study, both the ATL-PI and the risk grouping in the 1980's were constructed based on the results of questionnaires collected retrospectively; hence the treatments used were diverse and the prognostic factors might not have been evaluated homogeneously, in contrast to present study based on the three prospective trials (Lymphoma Study Group, 1991; Katsuya *et al*, 2012).

In the present study, monoclonal integration of HTLV-1 was not detected in four of 104 patients analysed. It was previously demonstrated that about 20% of patients with lymphoma-type ATL did not have monoclonal integration of HTLV-1, by Southern blot analysis, when investigating lymph node specimens (Ohshima *et al*, 1998). From this aspect, the possibility that a fraction of patients with the lymphoma type in the present study had non-ATL-peripheral T-cell lymphoma cannot be completely excluded. Further studies are required to differentiate lymphoma-type ATL from non-ATL-peripheral T-cell lymphoma by analysing monoclonal integration of the HTLV-1 provirus by Southern blot analysis or integration site-specific polymerase chain reaction.

In this study, the median age of 56 years in the training set was notably younger than that in other recent reports and that of the average population of patients with ATL. The

population investigated in the present study represents a selection of fairly young and physically fit patients with preserved organ functions. Although we expected to define a favourable prognosis group in the international PI for aggressive NHL, which consists mostly of diffuse large B-cell lymphoma, the difference in the OS between the two risk groups was small. This finding was similar to a recent retrospective nationwide survey in Japan of all patients with acute or lymphoma type at each institute (Katsuya *et al*, 2012). Therefore, the JCOG-PI could not be used to identify patients with aggressive ATL who could be treated with intensive chemotherapy alone and spared from more intensive therapy, such as allo-HSCT, as is the case with the ATL-PI (Katsuya *et al*, 2012). However, we did manage to identify patients with extremely poor prognosis despite undergoing intensive chemotherapy in clinical trials. These patients might be candidates for future trials that combine new agents or investigational strategies.

Recently, the results of several phase I and II trials using a defucosylated anti-CCR4 antibody for relapsed patients with aggressive ATL have demonstrated clinically meaningful antitumour activity and an acceptable toxicity profile (Yamamoto *et al*, 2010; Ishida *et al*, 2012a). Moreover, allo-HSCT with myeloablative and reduced intensity conditioning for patients with aggressive ATL has been reported to cure diseases associated with the graft-*versus*-ATL effect, despite the high transplant-related mortality (Hishizawa *et al*, 2010; Ishida *et al*, 2012b; Kanda *et al*, 2012). To further improve patient outcomes, two trials are ongoing in Japan: a phase II trial of VCAP-AMP-VECP followed by allo-HSCT with myeloablative conditioning for patients aged <55 years with aggressive ATL (JCOG 0907), and a randomized phase II trial of VCAP-AMP-VECP with or without anti-CCR4 antibody (Jo *et al*, 2013).

In conclusion, patients with lymphoma-type ATL who survived >5 years might have been cured, which is in contrast to long-term survivors with acute or unfavourable chronic type. The JCOG-PI, based on corrected calcium levels and PS, is a simple and valuable tool for identifying patients with aggressive ATL having extremely poor prognosis in clinical trials, and it will be useful for the design of future studies combining new drugs or investigational strategies.

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## Authorship

T.F., M.S, H.F., K. T. and K.T. designed the study and wrote the paper. T.H. designed the study. S.N. and T.S. designed the study, analysed data and wrote the paper. Y.I., Y.M., T.T., K.U., Y.K., N.F., A.U., M.T., K.N., M.H., N.U., S.Y., K.T., K.I., M.K. and M.N. collected data and reviewed the paper.

## Disclosure

The authors report no potential conflict of interest.

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