Cytogenetic analysis and clinical significance in adult T-cell leukemia/lymphoma: a study of 50 cases from the human T-cell leukemia virus type-1 endemic area, Nagasaki

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Identification of cytogenetic abnormalities is an important clue for the elucidation of carcinogenesis. However, the cytogenetic and clinical significance of adult T-cell leukemia/lymphoma (ATLL) is still unclear. To address this point, cytogenetic findings in 50 cases of ATLL were correlated with clinical characteristics. Karyotypes showed a high degree of diversity and complexity. Aneuploidy and multiple breaks (at least 6) were observed frequently in acute and lymphoma subtypes of ATLL. Breakpoints tended to cluster at specific chromosomal regions, although characteristic cytogenetic subgroups of abnormalities were not found. Of these, aberrations of chromosomes 1p, 1q, 1q10-21, 10p, 10p13, 12q, 14q, and 14q32 correlated with one or more of the following clinical features: hepatosplenomegaly, elevated lactate dehydrogenase, hypercalcemia, and unusual immunophenotype, all indicators of clinical severity of ATLL. Multiple breaks (at least 6); abnormalities of chromosomes 1p, 1p22, 1q, 1q10-21, 2q, 3q, 3q10-12, 3q21, 14q, 14q32, and 17q; and partial loss of chromosomes 2q, 9p, 14p, 14q, and 17q regions correlated with shorter survival. These cytogenetic findings are relevant in predicting clinical outcome and provide useful information to identify chromosomal regions responsible for leukemogenesis. This study also indicates that one model of an oncogenic mechanism, activation of a proto-oncogene by translocation of a T-cell-receptor gene, may not be applicable to the main pathway of development of ATLL and that a multistep process of leukemogenesis is required for the development of ATLL.

Introduction

Adult T-cell leukemia/lymphoma (ATLL) is a distinct clinical entity characterized by a mature T-cell surface-marker profile, the association with human T-cell leukemia virus type-1 (HTLV-1), and abnormal lymphocytosis with markedly deformed pleomorphic nuclei. Identification of recurring cytogenetic abnormalities may provide important clues to the elucidation of the pathogenesis of ATLL. Cytogenetic findings and the analysis of their clinical significance are still limited in mature T-cell malignancies compared with those of B-cell malignancies. Although many cytogenetic studies have been performed, the cytogenetics of ATLL is complicated by clinical heterogeneity and a plethora of secondary abnormalities. To improve the accurate evaluation of karyotypes and to identify specific chromosomal abnormalities in ATLL, a large number of karyotypes from various laboratories were reviewed by the ATL Karyotype Review Committee 1985 in Japan. Several recurring abnormalities such as trisomy 3, 7, and 21; monosomy X in the female; loss of a Y in the male; translocations involving 14q11 or 14q32; and deletion in 1p, 3q, 5q, 6q, 7p, 9q, 10p, and 13q have been confirmed. However, correlation between these clinical features, as reported in non-Hodgkin lymphoma (NHL), has not been attempted in ATLL.

This study reports the detailed cytogenetic findings observed in 50 patients with ATLL and correlates them with clinical characteristics.

Patients, materials, and methods

Patients

A total of 50 newly diagnosed ATLL patients between 1989 and 1996 were studied. These patients were natives of Nagasaki prefecture, one of the clustering areas of ATLL incidence in Japan. Diagnosis and subclassification of ATLL were done according to previously described criteria. We classified 3 cases that were in the smoldering or chronic phase before progression to the acute phase as the acute subtype because cytogenetic analysis was performed at the time of progression, and cytogenetic findings exhibited abnormalities possibly of the acute phase. Histologic diagnosis of the lymphoma subtype was based on the findings of biopsied lymph nodes according to the updated Kiel classification. Immunophenotypic analysis of tumor cells was performed by direct and indirect immunofluorescence assays, as described previously. Based on the immunophenotype of ATLL cells, the cases were classified into 2 categories: usual phenotype showing CD4+CD8− phenotype, and unusual phenotype showing CD4−CD8+ or CD4−CD8− phenotype, because this phenotypic diversity correlates with clinical outcome. Patients with acute and lymphoma subtypes were treated by an intensive combination chemotherapy regimen (VEPA, LSG4, or LSG11). Patients with the chronic subtype were monitored without chemotherapy until they progressed to the acute or lymphoma subtype. Patients who received autologous bone marrow transplantation unsuccessfullly.

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Cytogenetic analysis

Samples for the cytogenetic studies were obtained from the peripheral blood of patients with acute and chronic subtypes, or from the biopsied lymph nodes of patients with the lymphoma subtype at the time of diagnosis before therapy.

Chromosome analysis was performed using G- and/or Q-banding techniques after culturing without mitogens. Karyotypes were described according to the International System for Human Cytogenetics Nomenclature (1995).22

To identify the specific abnormalities and avoid the secondary changes, the stemline karyotype (ie, the simplest abnormal clone) was used as the representative karyotype for almost all analyses. In patients who showed composite karyotypes (8 cases) or when stemline karyotypes could not be specified (3 cases), we created a "stemline karyotype," which contained common abnormalities in all analyzed karyotypes.

Numbers of chromosomal breaks from structural abnormalities were calculated as the sum of all breaks whose derivation by band could be identified in the stemline karyotype. Marker chromosomes were not included for analysis of numbers of chromosomal breaks. Breakpoints of isochromosomes 1q, 6p, 7q, 8q, 18q, and 21q were included in breaks on chromosomes 1p10, 6q10, 7p10, 8p10, 18p10, and 21p10, respectively. Multiple rearrangements of the same break site observed in the same patient chromosomes 1p10, 6q10, 7p10, 8p10, 18p10, and 21p10, respectively.

We also assessed recurrent gains or losses of specific chromosomal segments, termed a "chromosomal segmental representation profile (CSRP)," in stemline karyotypes of each patient according to methods described by Thompson et al.23 One patient whose stemline karyotype showed near-triploidy was not included in CSRP analysis.

Statistical analysis

All chromosomal abnormalities occurring in more than 5 cases were correlated with the clinical factors described in Table 1. Associations between clinical variables and chromosomal abnormalities were tested using the Fisher exact test as determined by expected frequencies of variables in 2 × 2 tables. P < .05 was used as the criterion for statistical significance.

Generally, survival was calculated from the date of diagnosis. In 3 patients who were in the smoldering or chronic phase before progression to the acute phase, survival was calculated from the date of acute transformation. Overall survival was calculated by the method of Kaplan and Meier.24 Differences between survival curves were assessed using the log-rank test.22 Association between the shorter survival group (less than 6 months) and chromosomal abnormalities was also tested using the Fisher exact test to find specific abnormalities for a shorter survival group.

Results

Clinical characteristics of patients

The clinical characteristics of the 50 patients analyzed are summarized in Table 1. All patients were positive for anti–HTLV-1

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Acute (n = 37)</th>
<th>Lymphoma (n = 6)</th>
<th>Chronic (n = 7)</th>
<th>Total (n = 50)</th>
<th>Acute vs Lymphoma</th>
<th>Acute vs Chronic</th>
<th>Survival ≥ 6 (n = 34)</th>
<th>&lt; 6 (n = 16) mo</th>
<th>Overall</th>
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<td>Male</td>
<td>24 (64.9%)</td>
<td>5 (83.3%)</td>
<td>3 (42.9%)</td>
<td>32 (64.0%)</td>
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<td>NS</td>
<td>NS</td>
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<td>32-81</td>
<td>32-81</td>
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<td>6 (100%)</td>
<td>1 (14.3%)</td>
<td>18 (36.0%)</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
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<td>Peripheral lymphadenopathy</td>
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<td>5 (83.3%)</td>
<td>2 (28.6%)</td>
<td>33 (66.0%)</td>
<td>P &lt; .05†</td>
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<td>NS</td>
<td>NS</td>
<td>NS</td>
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<td>Hepatosplenomegaly</td>
<td>21 (56.6%)</td>
<td>3 (50.0%)</td>
<td>2 (28.6%)</td>
<td>26 (52.0%)</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
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<td>CNS involvement</td>
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<td>1 (16.7%)</td>
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<td>6 (12.0%)</td>
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<td>Pleural effusion and/or ascites</td>
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<td>0</td>
<td>7 (14.0%)</td>
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<td>NS</td>
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<td>236-9517</td>
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<td>Hypercalcemia</td>
<td>23 (62.2%)</td>
<td>4 (66.7%)</td>
<td>0</td>
<td>27 (54.0%)</td>
<td>P &lt; .01†</td>
<td>P &lt; .05‡</td>
<td>P &lt; .01‡</td>
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<td>WBC, ×10⁹/L</td>
<td>24 (48%)</td>
<td>3 (50%)</td>
<td>0</td>
<td>27 (54.0%)</td>
<td>P &lt; .01†</td>
<td>P &lt; .05‡</td>
<td>P &lt; .01‡</td>
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<tr>
<td>Absolute abnormal lymphocyte count, ×10⁹/L</td>
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<td>0</td>
<td>2.1</td>
<td>7.2</td>
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<td></td>
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<td>0-114.2</td>
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<td></td>
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<tr>
<td>Unusual immunophenotype</td>
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<td>1 (16.7%)</td>
<td>0</td>
<td>8 (16.0%)</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
<td>P &lt; .01‡</td>
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<tr>
<td>Survival, mo</td>
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<td>14.0</td>
<td>59.0</td>
<td>10.05</td>
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</tr>
<tr>
<td>Range</td>
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<td>0.6-20.0</td>
<td>12.0-148.0</td>
<td>0.2-148.0</td>
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<td></td>
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<tr>
<td>&lt; 6</td>
<td>14 (37.8%)</td>
<td>2 (33.3%)</td>
<td>0</td>
<td>16 (32.0%)</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
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<tr>
<td>Overall</td>
<td>NS</td>
<td>P &lt; .01‡</td>
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</tbody>
</table>

CNS indicates central nervous system; LDH, lactate dehydrogenase; WBC, white blood cell count; NS, not significant.
*Statistically significant in acute and lymphoma subtypes.
†Fisher exact test.
‡Log-rank test.
§Statistically significant in the shorter-survival group (less than 6 mo).
antibodies and for monoclonal integration of the HTLV-1 provirus. Among 6 cases of lymphoma type, 5 cases were classified as pleomorphic, medium-sized and large cell type, and one as large cell, anaplastic type.

Peripheral lymphadenopathy and abnormal elevation of serum lactate dehydrogenase (LDH) and calcium levels were significantly more frequent in the combined group of acute and lymphoma subtypes than in the chronic subtype ($P < .05$, $P < .01$, respectively). Abnormal elevation of serum LDH and calcium was found significantly more frequently in the shorter-survival group (less than 6 months) than in the longer-survival group (at least 6 months) ($P < .05$ and $P < .01$, respectively). Hepatosplenomegaly, central nervous system (CNS) involvement, abnormal elevation of serum LDH and calcium, unusual immunophenotype, and clinical subtype (acute and lymphoma subtypes) were statistically significant clinical factors for overall survival ($P < .05$, $P < .01$, $P < .01$, $P < .01$, respectively, log-rank test). Patients in the combined group of acute and lymphoma subtypes showed shorter survival than patients with the chronic subtype ($P < .01$, log-rank test). These findings show that clinical factors such as peripheral lymphadenopathy, hepatosplenomegaly, CNS involvement, elevation of serum LDH and calcium, unusual immunophenotype, and clinical subtype (acute and lymphoma subtypes) correlate with clinical severity in this study.

**Cytogenetic findings**

All 50 patients showed abnormal karyotypes (the table containing the detailed cytogenetic findings can be obtained on request). Of 43 patients with acute and lymphoma subtypes, 11 showed pseudodiploid, 6 hypodiploid, 25 hyperdiploid, and one near-triploid stemline karyotype. Of 7 patients with chronic subtype, 5 showed pseudodiploid and 2 hyperdiploid karyotypes. Aneuploidy was found significantly more frequently in the combined group of acute and lymphoma subtypes than in the chronic subtype ($P < .01$, log-rank test). Of 43 other patients showed only numerical abnormalities or an extra marker chromosome. A total of 295 breaks were observed (Figures 2 and 3). The median number of breaks was highest in the acute subtype (6.0), followed by lymphoma (3.5) and chronic (1.0) subtypes. Multiple breaks (at least 6) were found significantly more frequently in the combined group of acute and lymphoma subtypes than in the chronic subtype ($P < .05$), which indicates the cytogenic complexity of the acute and lymphoma subtypes compared with the chronic subtype.

Almost all chromosomes were affected, but with variations in frequency. Chromosomes involved in more than 5 patients (at least 10%) were the short arms of chromosomes 1 (12 cases, 24%), 7, 9, 10 (8 cases, 16%, each), 3 (7 cases, 14%), 21 (6 cases, 12%), and 17 (5 cases, 10%); and the long arms of chromosomes 3 (23 cases, 46%), 6 (18 cases, 36%), 7 (14 cases, 28%), 1 and 14 (13 cases, 26%, each), 13 (11 cases, 22%), 4 and 12 (9 cases, 18%, each), 2 (8 cases, 16%), 9 and 11 (6 cases, 12%, each), and 5, 10, and 17 (5 cases, 10%, each). The types of structural abnormalities were balanced and unbalanced translocations (balanced type, 76 breaks, and unbalanced type, 39 breaks; total 115, 40%), followed by deletion (79, 26.8%), addition (51, 17.3%), duplication or triplication (18, 6.1%), inversion (12, 4.1%), dicentric chromosome (8, 2.7%), isochromosome (8, 2.7%), insertion (2, 0.7%), and translocations with a homogeneously staining region (2, 0.7%). Most abnormalities were not recurrent, with the exception of inv(3)(p25q21) (2 cases), iso(6)(p10) (2 cases), iso(18)(q10) (2 cases), and several deletion abnormalities. Chromosomal breaks tended to cluster at specific bands. The specific bands observed in more than 5 patients (at least 10%) were 3q10-12 (11 cases, 22%), followed by 14q11 (8, 16%), 1q10-21, 3q21, 6q15, 10p11 (7, 14%, each), 3q25, 7q10-11, 13q22, 13q32, 21p11 (6, 12%, each), and 1p22, 4q31, 6q21, 6q23, 7q22, 7q32, 10p13, and 14q32 (5, 10%, each). Deletion frequently affected chromosome 10 (8 cases, 16%), followed by 3q, 6q (7, 14%, each), and 13q (6, 12%).

In the sideline karyotype, isochromosome of 18q (4 cases, 8%) and rearrangement of the centromeric region on chromosome 3 (3 cases, 6%) were observed, which indicates additional changes in
the ATLL karyotype (Figure 3A). Del(2)(q), del(3)(p), dup(4)(q),
del(6)(p), del(6)(q), del(13)(q), and add(18)(p) were other abnor-
malities of sideline karyotype observed in 2 patients each.

In many cases, more than one of the structural or numerical
abnormalities occurred simultaneously. Associations of structural
abnormalities between chromosomes 1p and 3q (10 cases), 1p and
14q (7 cases), 3q and 11q (6 cases), and 7q and 9q, 7q and 13q32,
and 9p and 13q (5 cases, each) were found in more than 5 patients
and were statistically significant (\(P < .01\)).

By CSRP analysis, gains were frequently observed in chromo-
some 3p (17 cases, 34%), 3q centromeric region (14, 28%), 7q (13,
26%), 1q, 8q (7, 14%, each), 8p, 9q (6, 12%, each), and 21q (5,
10%); and losses were observed in 10p (13 cases, 26%), 6q, 14q
telomeric region, 21p (8, 16%, each), 2q telomeric region, 4q (7,
14%, each), 9q telomeric region, 9q telomeric region, 14q centro-
meric region (6, 12%, each), and 7p telomeric region and 17q
telomeric region (5, 10%, each) among 49 stemline karyotypes
(Figure 3B). Many of the del(3)(q) and unbalanced translocations
of chromosome 1q and 7q resulted in partial trisomy of 3p, 1q, and
7q, respectively.

Correlation between cytogenetic findings and clinical
characteristics

Significant correlations noted between cytogenetic findings and
clinical characteristics are summarized in Table 2. Multiple breaks
(at least 6) and aneuploidy were found to be significantly more
frequent in the combined group of acute and lymphoma subtypes
than in the chronic subtype. There were no significant differences
in cytogenetic findings between acute and lymphoma subtypes.

Multiple breaks (at least 6); abnormalities of chromosomes 1p,
1q, 1q10-21, 1p, 10p13, 12q, 14q, and 14q32; and deletion of
chromosome 10p correlated with one or more of the following
clinical factors: hepatosplenomegaly, elevated serum LDH, hyper-
calcemia, and unusual immunophenotype. The correlation between
these clinical factors and clinical severity suggests that these
abnormalities contribute to clinical severity.

Multiple chromosomal breaks (at least 6) (\(P < .01\), log-rank
test) and abnormalities of 1p, 1p22, 1q10-21, 3q, 3q10-12,
3q21, and 17q (\(P < .05\), \(P < .01\), \(P < .05\), \(P < .01\), \(P < .05\), \(P < .05\), and \(P < .01\), respectively, log-rank test) gave
statistically significant shorter overall survival (Figure 4). Abnor-
malities of chromosomes 1p, 1p22, 2q, 3q, 14q, and 14q32
(\(P < .05\), \(P < .05\), \(P < .05\), \(P < .05\), and \(P < .05\), respectively) were significantly more frequent in the shorter-survival
group (less than 6 months), indicating that these abnormalities are
specific for the aggressive clinical course of ATLL.

Based on the findings of CSRP, we also analyzed the correlation
between chromosomal imbalance region and prognosis. Loss of
chromosome 9p telomeric region (6 cases) and 17q telomeric
region (5 cases) gave significantly shorter overall survival (both
\(P < .05\), log-rank test). Loss of chromosome 2q telomeric region (7
cases), 14p11 terminal region (6 cases), and 14q telomeric region (8
cases) were significantly more frequent in the shorter-survival
(group (\(P < .01\), \(P < .05\), and \(P < .05\), respectively). Other imbal-
ance regions did not correlate with prognosis.

Discussion

Karyotypes of ATLL showed a high degree of diversity and
complexity. However, abnormalities were undoubtedly nonran-
dom, and this study demonstrated clinical significance of some of
the cytogenetic abnormalities.

Simple numerical abnormalities observed in this study were
trisomy 3, trisomy 21, monosomy X, and loss of Y, reported
previously as major numerical changes in ATLL.\(^{12,17}\) Of these,
trisomy 3, monosomy X, and loss of Y were also observed in the
sideline karyotypes. Trisomy 7 is another common numerical
abnormality reported in T-cell malignancies and ATLL.\(^{8,12,17}\) Only
one patient showed simple trisomy 7, but partial trisomy of
chromosome 7q resulting from unbalanced translocation, duplica-
tion, or isochromosome 7q was common in 12 patients. Partial
trisomy of 7q was also observed in the sideline karyotype of 2
patients. These findings indicate that trisomy 3, partial trisomy of
### Table 2. Significant correlation between clinical characteristics and cytogenetic findings

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>n</th>
<th>Age, ≥ 50 y</th>
<th>Skin lesion</th>
<th>Hepatosplenomegaly</th>
<th>Pleural effusion and/or ascites</th>
<th>LDH, ≥ 1100 IU/μL</th>
<th>Hypercalcemia</th>
<th>WBC, ≥ 30.0 × 10^9/L</th>
<th>Absolute abnormal lymphocyte count, ≥ 15.0 × 10^9/L</th>
<th>Unusual immunophenotype</th>
<th>Acute and lymphoma vs chronic</th>
<th>Survival</th>
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n indicates number of cases. See Table 1 for other abbreviations.
*Statistically significant in acute and lymphoma subtypes.
†Fisher exact test.
‡Log-rank test.
chromosome 7q, monosomy X, and loss of Y are not primary changes but may be secondary changes of ATLL. Trisomy 3 and partial trisomy of chromosome 7q did not correlate with clinical characteristics.

As reported in other hematologic malignancies,26-28 this study showed that karyotypic complexity, represented by the number of breaks, clearly correlated with poor prognosis (Figure 4A). Interestingly, multiple breaks (at least 6) were observed more frequently in the older age group (50 years or older) (Table 2). This correlation indicates that more genetic changes accumulate in tumor cells of the older age group than in those of the younger age group. This finding is compatible with the hypothesis of multistep carcinogenesis in ATLL.29

This study disclosed that abnormalities of chromosomes 1p, 1q, 2q, 3q, 9p, 10p, 12q, 14p, and 17q correlated with clinical severity. Of these abnormalities, involvement of chromosomes 1p, 10p, and 14q has been indicated to be specific for T-cell malignancy.4-6,17

Abnormalities of chromosome 1p are indicated to be significantly associated with T-cell NHL,6 but are also observed as primary and secondary abnormalities in B-cell NHL28,30,31 and other solid tumors.23,32-35 In this study, abnormality of chromosome 1p, especially 1p22, correlated with aggressive clinical features and poor prognosis (Figure 4B). The presence of loss of heterozygosity (LOH) regions on chromosome 1p, indicating the presence of tumor suppressor genes (TSGs), has been suggested in several malignancies.30,36-40

All abnormalities of chromosome 10p observed in 8 patients were del(10)(p), and the common deleted region was located around band 10p13. In lymphoid malignancies, many del(10)(p) abnormalities have been reported in ATLL cases,17 and less frequently in cutaneous T-cell lymphoma and mycosis fungoides/Sézary syndrome.41,42 Loss of an entire copy of chromosome 10 is common in solid tumors.54 There was a noticeable correlation with unusual phenotype of ATLL cells, resulting in an aggressive clinical course. Recent studies have indicated the presence of several TSGs in the chromosome 10p region.53,54 Interestingly, unbalanced translocations of chromosome 10q11 observed in 3 patients resulted in deletion of 10q11-pter.

On chromosome 14, 2 critical breakpoint-clustering regions were reported at bands q11 and q32 in ATLL. We found 14q11 abnormalities in 8 patients and 14q32 abnormalities in 5 patients. These abnormalities were not recurrent, except for del(14)(q11q13). The TCRA/D is mapped to 14q11,56 and 14q11 is involved frequently in T-cell malignancies.4,5,47,48 Abnormality of chromosome 14q11 in ATLL was first reported by Sadamori et al,11,14 and the specificity of this abnormality for ATLL has been confirmed.15-17 Within the 14q32 region, there are 2 loci often involved in B- and T-cell malignancies. One is the IGH locus and the other is the TCL1 locus, which is often involved in T-cell prolymphocytic leukemia (T-PLL).49 Chromosome 14q32 is also involved frequently in ATLL,7,10,17 but it is more commonly involved in B-cell malignancies. Recently, 2 genes (TML1 and TCL6)57 were cloned within 100 kb around the TCL1 locus. However, the involvement of these genes located at the 14q11 and 14q32 regions has not been confirmed in ATLL. Our recent molecular cytogenetic studies52,53 suggested a lower frequency of involvement of the TCRA than that expected by cytogenetic analysis. More interestingly, our study disclosed the presence of breakpoints clustering or deleted regions different from TCRA/D, TCL1, and IGH loci in the 14q11 and 14q32 regions. The presence of LOH in chromosome 14q has been reported in solid tumors.33,38,54-57 Abnormalities of chromosome 14q correlated with elevated LDH (1100 IU/L or higher), unusual phenotype, and shorter survival (less than 6 months). These findings suggest the cytogenetic and clinical importance of chromosome 14q rearrangement except for the TCL1, TCRA/D, and IGH loci.

Other abnormalities correlating with clinical severity (1q, 2q, 3q, 9p, 12q, 14p, and 17q) have been reported in various hematologic malignancies and solid tumors. Abnormalities of chromosome 1q observed in 13 patients correlated with the older age group (50 years or older), elevation of normal lymphocytes (15 × 109/L or higher), unusual phenotype, and shorter overall survival (Figure 4C). A correlation between abnormalities around chromosome 1q21-23 region and poor outcome is indicated in B-cell NHL.28,58 CSRCP also revealed a high frequency of gain of 1q. Increased copy number of chromosome 1q has been reported by cytogenetic and molecular studies in NHL and solid tumors, and a correlation between gain of 1q and disease progression has been indicated.23,35,59-61

Structural abnormalities of chromosome 3 have been commonly found in various malignancies, and we also observed these abnormalities frequently in this study. Not only deletion, but also various structural abnormalities were found in chromosome 3q, and the breakpoints were clustered at bands q10-12, q21, and q25. Abnormality of 3q (and bands 3q10-12, 3q21) was clearly correlated with clinical severity (1q, 2q, 3q, 9p, 12q, 14p, and 17q) have been reported in various hematologic malignancies and solid tumors. Abnormalities of chromosome 1q observed in 13 patients correlated with the older age group (50 years or older), elevation of normal lymphocytes (15 × 109/L or higher), unusual phenotype, and shorter overall survival (Figure 4C). A correlation between abnormalities around chromosome 1q21-23 region and poor outcome is indicated in B-cell NHL.28,58 CSRCP also revealed a high frequency of gain of 1q. Increased copy number of chromosome 1q has been reported by cytogenetic and molecular studies in NHL and solid tumors, and a correlation between gain of 1q and disease progression has been indicated.23,35,59-61

Correlation between chromosome 9p abnormalities and poor outcome has been reported in childhood acute lymphoblastic leukemia.60 Deletion of the putative TSGs MTS1/CDK4lp16INK4A (CDK2) and MTS2/CDKN2B (CDK2B), which are mapped to 9p21-22, was found to correlate with the development and poor outcome of ATLL.53,64 Abnormalities of 9p were observed in 8 patients, and 6 patients with imbalance (loss) of the 9p22-pter region showed shorter overall survival.

Abnormality of chromosome 17 has been shown to correlate
with poor prognosis.\textsuperscript{65-67} The tumor suppressor gene \textit{TP53} is mapped to chromosome 17p13, and the alteration has been described in lymphoid malignancies, including ATLL.\textsuperscript{68} LOH of 17q25 region has also been reported in solid tumors.\textsuperscript{55,69,70} In this study, abnormality of 17p did not correlate with prognosis, but abnormality of 17q (all 5 abnormalities were observed in 17q23-25 region) clearly correlated with shorter survival (Figure 4E), indicating that these abnormalities involve important genes participating in leukemogenesis of ATLL.

Abnormalities of chromosomes 6q, 7, and 13q were also observed frequently in this study and were reported to be major abnormalities in ATLL. In particular, several studies indicated the specificity of del(6)(q) abnormality in ATLL.\textsuperscript{17} However, the correlation with aggressive clinical course, hypercalcemia, and poor outcome described by Whang-Peng et al\textsuperscript{13} was not found in this study. Abnormal elevation of white blood cell count correlated with abnormalities of band 7q10-11, but did not correlate with prognosis. The \textit{TCRB} and \textit{TCRG} genes have been mapped to chromosome 7q35 and p15, respectively. However, breakpoints were not clustered at these loci in ATLL. Deletion of 13q is reported in progression of B-cell NHL,\textsuperscript{31,71} and correlation with poor prognosis is indicated.\textsuperscript{71} In this study, many of the 13q abnormalities were deletion of 13q telomeric region (q22 terminal) different from 13q14, which has been reported to be frequently involved in B-cell chronic lymphocytic leukemia and retinoblastoma.\textsuperscript{4,5} Abnormality of chromosome 13q did not correlate with clinical characteristics. In addition, abnormalities of chromosomes 6q, 7, and 13 have been frequently observed in various B-cell malignancies and solid tumors.\textsuperscript{4,5} Their clinical relevance seems to be limited in ATLL.

More than one of the abnormalities described here frequently occurred concomitantly. Interestingly, a similar concomitant correlation between 1p and 14q was observed in advanced stages of malignant meningioma and neuroblastoma by cytogenetic and molecular genetic analyses,\textsuperscript{32,33,36,38} indicating the possibility that abnormalities of 1p and 14q contribute to disease progression of ATLL.

Abnormalities resulting in chromosomal imbalance regions, such as unbalanced translocation, deletion, duplication, or triplication, were commonly observed in this study. Imbalance patterns observed in some specific chromosomes showed striking similarity to those observed in solid tumors. In addition, characteristic cytogenetic abnormalities in ATLL were not found. These cytogenetic findings are similar to those observed in many solid tumors. ATLL is classified to T-cell malignancies, and involvement of 14q11 region has been reported cytogenetically.\textsuperscript{11,14-17} The molecular involvement of \textit{TCRA/D}, located at 14q11, has been shown repeatedly in T-cell malignancies, most of which are T-cell acute lymphoblastic leukemia (T-ALL) and T-PLL.\textsuperscript{47,48} By this analogy, the similar mechanism of oncogenesis that translocation of \textit{TCRA/D} locus cause the deregulation of proto-oncogene was speculated in the development of ATLL.\textsuperscript{47,72} However, lack of recurrent balanced rearrangements, presence of many chromosomal imbalance regions, and the molecular complexity of 14q11 and 14q32 regions\textsuperscript{52,53} indicate that the above paradigm of proto-oncogene deregulation may not be applicable to molecular pathogenesis of ATLL.

Why the same T-cell malignancies show different cytogenetic and clinical characteristics between T-ALL/T-PLL and ATLL is a difficult but interesting question. T-ALL is a prethymic T-cell malignancy and involvement of the \textit{TCRA/D} by specific translocations occurs frequently in the \textit{D8-J6} region,\textsuperscript{48} and the \textit{TCRD} locus is not deleted. Many involved genes by translocations of \textit{TCR} genes in T-ALL are transcription factors, which are closely related to the early lymphocyte differentiation. T-PLL is classified as a postthymic T-cell malignancy, and abnormal T-PLL cells show mature T-cell phenotype.\textsuperscript{49} The \textit{Ja} region of the \textit{TCRA} is involved in specific translocations associated with T-PLL.\textsuperscript{73} Normally, the expression of the \textit{TCL1}, which is activated by abnormal translocations of \textit{TCR} genes in T-PLL, is observed in early T- and B-cell progenitors.\textsuperscript{49} In contrast, we previously reported the biallelic functional deletion of the \textit{TCRD} locus in all 6 analyzed patients with ATLL.\textsuperscript{74} Our recent study of 50 cases of ATLL also revealed that the involvement of the \textit{TCRA/D} locus was less frequent compared with T-ALL and T-PLL, and these rearrangements occurred within the \textit{TCRAV} region.\textsuperscript{52} Actually, HTLV-1 infects mainly CD4\textsuperscript{+}CD8\textsuperscript{-} mature T cells, which is the common phenotype of ATLL cells, and the \textit{TCRD} locus of mature T cells is functionally deleted biallelically during the T-cell maturation process.\textsuperscript{75} These findings indicate that acquired abnormal translocations of \textit{TCRA/D} locus occur at different differentiation stages of T-cell maturation between T-ALL/T-PLL and ATLL.

Cytogenetic and molecular genetic differences between T-ALL/T-PLL and ATLL may be based on modified status of chromatin and kinds of activated or inactivated genes corresponding to T-cell differentiation stage when T cells are involved in the malignant process. Lower frequency of involvement of chromosomes 7p15, 7q35, and 14q11 at \textit{TCR} gene loci in other mature T-cell malignancies may be based on a similar situation of T-cell differentiation. In other words, the mechanism of leukemogenesis speculated for T-PLL in ataxia-telangiectasia\textsuperscript{67,72} cannot be considered as the main pathway of development of ATLL and other mature T-cell malignancies.

It is now accepted that cancer is a multistep process.\textsuperscript{79} Our cytogenetic findings of ATLL are compatible with this concept. Okamoto et al\textsuperscript{80} proposed 5 steps of multiple events that are needed for leukemogenesis of ATLL. Actually, alterations of several known TSGs, such as \textit{TP53},\textsuperscript{68} \textit{Rb1},\textsuperscript{76} \textit{MTS1}/\textit{CDK4}/\textit{p16INK4A} (\textit{CDK2}), and \textit{MTS2}/\textit{p15INK4B} (\textit{CDK2B}),\textsuperscript{63,64} have been found in ATLL. Similar to the role of Epstein-Barr virus in oncogenesis of Burkitt lymphoma, HTLV-1 may not be oncogenic directly.\textsuperscript{47} Recent studies indicate that HTLV-1 induces DNA instabilities by interference with mitotic checkpoint function\textsuperscript{77} or defects in DNA repair function.\textsuperscript{78} The stepwise process and accumulation of chromosomal abnormalities may result in oncogenesis, and variation of these processes and involved genes may show marked clinical differences of ATLL. We cannot exclude the possibility that unidentified recurrent translocations cause the activation of proto-oncogenes. However, it should be noted that the possible activation of proto-oncogenes is one event in the sequential multistep process of carcinogenesis.

This study revealed that several breakpoints were clustered at regions where LOH was frequently reported in other malignancies and were of clinical relevance. Many efforts have been focused on studying LOH regions. It is still difficult work to narrow the specific regions for oncogenesis. To characterize these breakpoints observed in ATLL may be extremely helpful in identifying the responsible genes, not only for the development of ATLL but also for the oncogenesis of other malignancies.

Acknowledgments

We thank Dr Gouri Nanjungud for helpful comments on the manuscript and Amelia Panico for artwork assistance.
References


Cytogenetic analysis and clinical significance in adult T-cell leukemia/lymphoma: a study of 50 cases from the human T-cell leukemia virus type-1 endemic area, Nagasaki

Takahiro Itoyama, R. S. K. Chaganti, Yasuaki Yamada, Kunihiro Tsukasaki, Sunao Atogami, Hideo Nakamura, Masao Tomonaga, Koichi Ohshima, Masahiro Kikuchi and Naoki Sadamori