Heterogeneous Epstein-Barr Virus Infection Patterns in Peripheral T-Cell Lymphoma of Angioimmunoblastic Lymphadenopathy Type

By Ioannis Anagnostopoulos, Michael Hummel, Teresa Finn, Markus Tiemann, Petra Korbjunn, Christiane Dimmler, Kevin Gatter, Friederike Dallenbach, Mohammed R. Parwaresh, and Harald Stein

In this study, 32 cases of T-cell lymphoma of angioimmunoblastic lymphadenopathy type (AILD-TCL) were investigated for their association with Epstein-Barr virus (EBV). For this purpose, three different approaches were applied: polymerase chain reaction (PCR) for the presence of EBV-DNA, in situ hybridization (ISH) for EBV-encoded small nuclear RNAs (EBER), and immunohistochemistry for EBV-encoded latent membrane protein (LMP). PCR and EBER-ISH produced almost identical results, showing that all but one case of AILD-TCL contained EBV genomes. Three distinctive patterns of EBV were identified: (1) in 26% of the cases, B and T cells were infected, the majority of which were B cells of immunoblastic morphology located in the remnants of lymphoid follicles; (2) in 42% of the cases, the vast majority of infected cells were neoplastic T cells diffusely distributed in the lymph nodes, but infected B cells were also present; and (3) in 32% of the cases, there were only a few infected small lymphoid cells. Detectable LMP was frequent in cases exhibiting patterns 1 and 2. These findings suggest that in AILD-TCL patients, B cells and especially T cells are highly susceptible to a persistent EBV infection, which often leads to a growth advantage of the infected cells. Thus EBV, in conjunction with genetic abnormalities and selective defects of the immune system, might be involved in the pathogenesis of AILD-TCL.

© 1992 by The American Society of Hematology.
EBV IN ANGIOIMMUNOBLASTIC TYPE T-CELL LYMPHOMA

The diagnosis of AILD-TCL was established on the basis of the silver impregnation. Immunohistological analysis involved the use of monoclonal antibodies (MoAbs) for the detection of T- and direct association with the proliferated HEV.

<table>
<thead>
<tr>
<th>Antibody Designation</th>
<th>Cluster of Differentiation</th>
<th>Specificity</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>βF1</td>
<td>T-cell receptor β chain</td>
<td>T-Cell Sciences</td>
<td></td>
</tr>
<tr>
<td>UCHL1</td>
<td>CD45RO</td>
<td>Pan-T cell</td>
<td>Dako</td>
</tr>
<tr>
<td>DF-T1</td>
<td>CD43</td>
<td>Pan-T cell</td>
<td>Dako</td>
</tr>
<tr>
<td>UCHT1</td>
<td>CD3</td>
<td>Pan-T cell</td>
<td>Dako</td>
</tr>
<tr>
<td>MT310</td>
<td>CD4</td>
<td>T-helper cell</td>
<td>Dako</td>
</tr>
<tr>
<td>DK25</td>
<td>CD8</td>
<td>T-suppressor cell</td>
<td>Dako</td>
</tr>
<tr>
<td>L26</td>
<td>CD20</td>
<td>Pan-B cell</td>
<td>Dako</td>
</tr>
<tr>
<td>Ki-B3</td>
<td>CD45RB</td>
<td>B-cell subset</td>
<td>Lab. Parwaresch</td>
</tr>
<tr>
<td>4KB5</td>
<td>CD45RA</td>
<td>Most B cells</td>
<td>Dako</td>
</tr>
<tr>
<td>1F8</td>
<td>CD21</td>
<td>Follicular dendritic cells (FDC), B-cell subset*</td>
<td>Dako</td>
</tr>
<tr>
<td>Ki-M4p</td>
<td>CD30</td>
<td>FDC</td>
<td>Lab. Parwaresch</td>
</tr>
<tr>
<td>Ben-H2</td>
<td>CD30</td>
<td>Activated T and B blasts, plasma cell subset</td>
<td>Dako</td>
</tr>
<tr>
<td>PG-M1</td>
<td>CD68</td>
<td>Macrophages</td>
<td>Dako</td>
</tr>
<tr>
<td>KP1</td>
<td>CD68</td>
<td>Granulopoetic cells, macrophages</td>
<td>Dako</td>
</tr>
<tr>
<td>Ki-M1p</td>
<td>CD68</td>
<td>Macrophages</td>
<td>Lab. Parwaresch</td>
</tr>
<tr>
<td>CS 1-4</td>
<td>CD68</td>
<td>EBV-encoded latent membrane protein (LMP)</td>
<td>Lab. Rowe; Dako</td>
</tr>
</tbody>
</table>

Manufacturer locations: T-Cell Sciences: Cambridge, MA; Dako: Glostrup, Denmark; Lab. Research: Kiel, Germany; Lab Rowe: Birmingham, UK.

*Predominant reactivity with FDC in paraffin sections.

and eosin (H&E), Giemsa, periodic acid–Schiff (PAS), and Gomori silver impregnation. Immunohistological analysis involved the use of monoclonal antibodies (MoAbs) for the detection of T- and B-cell antigens, immunoglobulin light chains, CD21 antigen, etc. (see Table 1 for clone designation of most frequently used MoAbs). The diagnosis of AILD-TCL was established on the basis of the following criteria: (1) diffuse effacement of nodal architecture replaced by a mixture of small, medium, and large T cells, B lymphocytes, B immunoblasts, plasma cells, macrophages, epithelioid cells, and occasional neutrophils and eosinophils; (2) marked proliferation of high endothelial venules (HEV) with arborizing pattern and PAS-positive hyalinized distention of basement membranes; and (3) “burned out” germinal centers with ill-defined, stretched meshworks of follicular dendritic cells (FDC), usually in direct association with the proliferated HEV.

**Immunohistology**

The bound antibodies were made visible by using the alkaline phosphatase-anti-alkaline phosphatase (APAAP) method according to Cordell et al.22 and/or a modified streptavidin-biotin-complex (ABC) method according to Hsu et al.28

**PCR**

Ten-micrometer thick paraffin sections were cut from each specimen under conditions preventing DNA cross-contamination. Sections were dewaxed in xylol, precipitated with ethanol, and digested overnight with proteinase K (1 µg/µL) at 37°C. One tenth of the digested material was used for amplification after boiling for 15 minutes. PCR was performed in a thermocycler (BioMed 60, BioMed, Theres, Germany) using AmpliTaq (Perkin Elmer-Cetus, Norwalk, CT) for 40 cycles as previously described.29 For reamplification, 1% of the volume of the first round of amplification was submitted to another 40 rounds of PCR using a set of nested primers (see Table 2 for list of primers used). The optimal concentration of MgCl₂ for each pair of primers was empirically determined. Ten to twenty microliters of the PCR product was examined with a 2% ethidium-bromide-stained agarose gel for the presence of appropriate bands, blotted on nylon membranes30 (Hybond N, Amersham, Germany), and hybridized with a 32p terminal-transferase–labeled internal oligonucleotide. The positive controls used for each stage of experimentation were the Namalwa cell line harboring one to two copies of EBV,31 as well as an EBV-positive case of Hodgkin’s disease (HD). The negative controls were the EBV-negative cell line HUT102 (Dako) for each stage of experimentation were the EBV-negative cell line HUT102 and DNA-negative samples (data not shown). The amplification of a section of the β-globin gene served to determine the amplifiability of extracted DNA (Table 2). The sensitivity of the PCR approach was determined by using serial dilutions of Namalwa cell-line DNA, in which only a single copy viral genome could be detected (not shown).

**In Situ Hybridization**

**Plasmids and probes.** Plasmids pJJJ1 and pJJJ2 containing EBER1 and EBER2, kindly donated by Dr J. Arrand, Manchester, UK,32 were linearized before in vitro transcription with a combination of T3 or T7 RNA polymerases33 (Bethesda Research Laboratories, Gaithersburg, MD) and 32P-UTP or digoxigenin (DIG)-UTP.

**Hybridization protocol.** Hybridization was performed according to established protocols35 on paraffin-embedded tissue sections with either radioactive (32P) or nonisotopic (DIG) labeled in vitro transcribed sense and antisense EBER probes. To increase the sensitivity of in situ hybridization (ISH), a mixture of EBER1 and EBER2 antisense probes was applied. A cocktail of the sense

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence</th>
<th>Use</th>
<th>Position</th>
</tr>
</thead>
<tbody>
<tr>
<td>EBV up</td>
<td>5'-GCAGTAAGGTAATCTCTGG-3'</td>
<td>1st PCR</td>
<td>20124-20145</td>
</tr>
<tr>
<td>EBV low (R)</td>
<td>5'-ACTTTAGAGGCAATGGGCG-3'</td>
<td>2nd PCR</td>
<td>20210-20230</td>
</tr>
<tr>
<td>EBV low</td>
<td>5'-ACCAAAATACTGCAAGACC-3'</td>
<td>1st PCR</td>
<td>20524-20504</td>
</tr>
<tr>
<td>EBV low (R)</td>
<td>5'-TGGTGCTGTCTGGTACG-3'</td>
<td>2nd PCR</td>
<td>20459-20439</td>
</tr>
<tr>
<td>β-globin up</td>
<td>5'-ATGGTGCAACTGACTCTGG-3'</td>
<td>1st PCR</td>
<td>2205-2226</td>
</tr>
<tr>
<td>β-globin up (R)</td>
<td>5'-ATAACAGCATCGAGAGTG-3'</td>
<td>2nd PCR</td>
<td>2229-2247</td>
</tr>
<tr>
<td>β-globin low</td>
<td>5'-GCCATCACTAAAGGCACCACG-3'</td>
<td>1st PCR</td>
<td>2259-2538</td>
</tr>
<tr>
<td>β-globin low (R)</td>
<td>5'-AACGCTGCCGTTACCTGCC-3'</td>
<td>2nd PCR</td>
<td>2501-2483</td>
</tr>
<tr>
<td>EBV probe</td>
<td>5'-TATCTTTAAAGGGAAAGGAAATAAG-3'</td>
<td>Detection</td>
<td>20314-20341</td>
</tr>
</tbody>
</table>

Abbreviation: (R), reamplification.

---

From www.bloodjournal.org by guest on September 24, 2017. For personal use only.
Table 3. EBV-DNA, Distribution, Number, and Morphology of EBER- and LMP-Positive Cells in 32 Cases of AILD-TLC

<table>
<thead>
<tr>
<th>Case No.</th>
<th>EBV-DNA by PCR</th>
<th>Distribution and No. of EBV* Cells</th>
<th>Morphology of EBER+ Cells (ISH)</th>
<th>Morphology of LMP+ Cells (immunostaining)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>First Group</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>Positive</td>
<td>Nodular, many cells</td>
<td>B-IB, RS-cell-like &amp; B-lymphocytes</td>
<td>B-IB, RS cell-like</td>
</tr>
<tr>
<td>2</td>
<td>No β-globin amplification</td>
<td>Nodular, many &amp; diffuse, single cells</td>
<td>Small B and T lymphocytes</td>
<td>No positive cells</td>
</tr>
<tr>
<td>3</td>
<td>Positive</td>
<td>Nodular, many &amp; diffuse, single cells</td>
<td>Small B lymphocytes &amp; medium sized pleom T cells (tumor cells)</td>
<td>No positive cells</td>
</tr>
<tr>
<td>4</td>
<td>Positive</td>
<td>Nodular, many &amp; diffuse, single cells</td>
<td>B-IB, RS cell-like &amp; small T lymphocytes</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>No β-globin amplification</td>
<td>Nodular, many &amp; diffuse, single cells</td>
<td>B-IB &amp; small T lymphocytes</td>
<td>B-IB</td>
</tr>
<tr>
<td>6</td>
<td>No β-globin amplification</td>
<td>Nodular, many &amp; diffuse, single cells</td>
<td>B-IB &amp; medium sized pleom T cells (tumor cells)</td>
<td>No positive cells</td>
</tr>
<tr>
<td>7</td>
<td>Positive</td>
<td>Nodular, many &amp; diffuse, single cells</td>
<td>Small B &amp; T lymphocytes</td>
<td>Small B &amp; T lymphocytes &amp; medium sized pleom T cells (tumor cells)</td>
</tr>
<tr>
<td><strong>Second Group</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>Positive</td>
<td>Nodular, many cells</td>
<td>B-IB, HD-cell-like</td>
<td>B-IB, HD-cell-like</td>
</tr>
<tr>
<td>9</td>
<td>Positive</td>
<td>Diffuse, many cells</td>
<td>20% of tumor cells &amp; B-IB &amp; few small B lymphocytes</td>
<td>B-IB &amp; tumor cells</td>
</tr>
<tr>
<td>10</td>
<td>Positive</td>
<td>Diffuse, many cells</td>
<td>15%-20% of tumor cells</td>
<td>Single tumor cells</td>
</tr>
<tr>
<td>11</td>
<td>Positive</td>
<td>Diffuse, many cells</td>
<td>5%-10% of tumor cells &amp; B-IB</td>
<td>B-IB &amp; small T lymphocytes</td>
</tr>
<tr>
<td>12</td>
<td>Positive</td>
<td>Diffuse, single cells</td>
<td>5% of tumor cells</td>
<td>No positive cells</td>
</tr>
<tr>
<td>13</td>
<td>No β-globin amplification</td>
<td>Diffuse, many cells</td>
<td>5% of tumor cells &amp; B-IB</td>
<td>Single tumor cells &amp; B-IB</td>
</tr>
<tr>
<td>14</td>
<td>Positive</td>
<td>Diffuse, many cells</td>
<td>20% of tumor cells &amp; B-IB</td>
<td>No positive cells</td>
</tr>
<tr>
<td>15</td>
<td>No β-globin amplification</td>
<td>Diffuse, few cells</td>
<td>5% of tumor cells &amp; single B-IB</td>
<td>B-IB &amp; small T lymphocytes</td>
</tr>
<tr>
<td>16</td>
<td>Positive</td>
<td>Diffuse, few cells</td>
<td>1%-5% of tumor cells &amp; small B lymphocytes</td>
<td>No positive cells</td>
</tr>
<tr>
<td>17</td>
<td>No β-globin amplification</td>
<td>Diffuse, few cells</td>
<td>2% of tumor cells &amp; small B lymphocytes</td>
<td>Small T- &amp; B-lymphocytes</td>
</tr>
<tr>
<td>18</td>
<td>No β-globin amplification</td>
<td>Diffuse, few cells</td>
<td>2% of tumor cells</td>
<td>No positive cells</td>
</tr>
<tr>
<td>19</td>
<td>No β-globin amplification</td>
<td>Diffuse, many cells</td>
<td>15% of tumor cells</td>
<td>Single tumor cells</td>
</tr>
<tr>
<td>20</td>
<td>Positive</td>
<td>Follicular, many cells</td>
<td>20% of tumor cells &amp; B-IB</td>
<td>B-IB, HD cell-like</td>
</tr>
<tr>
<td>21</td>
<td>No β-globin amplification</td>
<td>Diffuse, few cells</td>
<td>2% of tumor cells in cutaneous infiltrate</td>
<td>No positive cells</td>
</tr>
<tr>
<td><strong>Third group</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>No β-globin amplification</td>
<td>Diffuse, few cells</td>
<td>Small T &amp; B lymphocytes</td>
<td>No positive cells</td>
</tr>
<tr>
<td>23</td>
<td>Positive</td>
<td>Single cells</td>
<td>Small T lymphocytes</td>
<td>No positive cells</td>
</tr>
<tr>
<td>24</td>
<td>Positive</td>
<td>Single cells</td>
<td>Small T &amp; B lymphocytes</td>
<td>Small T &amp; B lymphocytes</td>
</tr>
<tr>
<td>25</td>
<td>No β-globin amplification</td>
<td>Single cells</td>
<td>Small T lymphocytes</td>
<td>No positive cells</td>
</tr>
<tr>
<td>26</td>
<td>Positive</td>
<td>Single cells</td>
<td>Medium sized pleom T cells</td>
<td>Medium sized pleom T cells</td>
</tr>
<tr>
<td>27</td>
<td>Positive</td>
<td>Single cells</td>
<td>Small T lymphocytes</td>
<td>No positive cells</td>
</tr>
<tr>
<td>28</td>
<td>Positive</td>
<td>Diffuse, few cells</td>
<td>Small B lymphocytes</td>
<td>No positive cells</td>
</tr>
<tr>
<td>29</td>
<td>Positive</td>
<td>Single cells</td>
<td>Small T lymphocytes</td>
<td>No positive cells</td>
</tr>
<tr>
<td>30</td>
<td>Negative</td>
<td>Single cells</td>
<td>Small T lymphocytes</td>
<td>No positive cells</td>
</tr>
<tr>
<td>31</td>
<td>Positive</td>
<td>Single cells</td>
<td>Small B &amp; T lymphocytes</td>
<td>Small B lymphocytes</td>
</tr>
<tr>
<td>32</td>
<td>No β-globin amplification</td>
<td>No labeled cells</td>
<td>—</td>
<td>—</td>
</tr>
</tbody>
</table>

Abbreviations: B-IB, B immunoblasts; RS cell-like, similar to Reed-Sternberg cells; pleom, pleomorphic; HD cell-like, similar to Hodgkin cells.
control probes was also used. After dewaxing with xylene and
digestion with proteinase K (500 μg/mL), the slides were incu-
bated for 12 hours at 37°C with a hybridization solution containing
either 1.2 × 10^6 cpm/mL of 35S-labeled or 1 ng of DIG-labeled
EBER cocktail per section. After washing in 50% formamid and
RNase A treatment, immobilized radioactive probes were de-
tected by dipping the slides into a 1:2 solution of Ilford G5 (Ilford,
Mobberly, UK) emulsion, followed by exposure for 3 to 10 days at
4°C. The slides were then developed and counterstained. An
immunologic detection was performed in the case of DIG-labeling.
Briefly, the washed slides were incubated with a DIG-specific
phosphatase-conjugated Fab fragment and developed with Naphtol-
as-biphosphate and New Fuchsin (Merck, Darmstadt, Germany).26
All steps comprising pretreatment of the slides and hybridization
were performed under conditions avoiding RNase contamination.
To demonstrate the RNA origin of our targets, an RNase
predigestion step was introduced for several cases, resulting in
complete disappearance of the signal. Additional ISH with a
cocktail of labeled unrelated oligonucleotides on several cases did
not lead to any cross-reactivity. Furthermore, no hybridization
signal was detected using the EBER sense probes. Sense and
antisense probes were checked for their suitability on several
EBER-positive and -negative cell lines. The case that was negative
for EBER-ISH (case 32) was hybridized with an oligo(dT) primer
to ascertain the presence of tissue RNA.

Double labeling: For double labeling, the immunohistologic
demonstration of T-cell–specific or characteristic (B-FI and
CD45RO), B-cell–specific (CD20) and FDC-characteristic (CD21)
antigens was performed before ISH under RNase-free conditions.
In specific, the APAAP technique was used to visualize the
detection of the antigens before the application of 35S-labeled
EBER probes, whereas the ABC system was applied in the case of
DIG-labeled EBER probes.

RESULTS

EBV-DNA Detection by PCR

In 12 of the 32 cases of AILD-TCL and 2 of the 12 normal
lymphoid tissue samples, the extracted DNA was not
amplifiable as shown by the nonappearance of a β-globin–
specific band after amplification and reamplification with
appropriate primers. In 19 of the remaining 20 AILD-TCL
cases, PCR analysis showed EBV-specific sequences (Table
3; Fig 1). In contrast, EBV-specific DNA was demonstrable
with the same technique in only 2 of the remaining 10
normal lymphoid tissue samples.

Detection of EBER by ISH

Both radioactive and nonradioactive antisense probes
specific for EBER were applied and gave identical results:
EBV-infected cells were demonstrable in all but 1 of the 32
AILD-TCL cases (see Table 3), as well as in 3 of the 12
normal lymphoid tissue samples.

The comparison of these data with the PCR results
showed that the latter data were congruent with the
findings of EBER-ISH in all but one instance. In this one
exception (case no. 30), EBER-ISH detected only 16
labeled cells in the whole section.

Both the radioactive and nonradioactive EBER-specific
probes were suitable for the determination of the overall
frequency and distribution of EBV-infected cells. The
nonradioactive probes proved to be superior for the morpho-
logic evaluation of the EBV-infected cells. With the latter
reagents, it could be clearly shown that only lymphoid cells
were EBER-positive. All other cell types, including granulo-
cytes, macrophages, endothelial cells, fibrocytes, and plasma
cells, were EBER-negative.

To identify the lineage allocation of the EBV-infected
lymphoid cells, the EBER-ISH labeling was compared with the
immunohistological staining reactions obtained on
serial sections using the MoAbs listed in Table 1. Three
patterns of EBV-infection were distinguished: (1) A nodu-
lar distribution of EBER-positive lymphoid cells predomi-
nantly located in the remnants of lymphoid follicles in 8 of
31 cases (Fig 2A). The majority of these cells exhibited the
morphology of immunoblasts with large oval, round, or
slightly lobated nuclei and usually a centrally located,
prominent nucleolus (Fig 2C). In several specimens, some
EBER-positive cells displayed one or two large nuclei,
similar to small-sized variants of HD and Reed-Sternberg
(RS) cells (Fig 2C, insert). In addition, EBER signals were
observed in medium-sized cellular elements showing the
morphology of proliferating (neoplastic) T cells. (2) A
diffuse distribution of many small, medium, and large
EBER-positive lymphoid cells in 13 of 31 cases (Fig 3A).
They were identical in size and cytology to (neoplastic) cells
expressing T-cell antigens. In addition, there were EBER-
positive cells with the morphology of immunoblasts. In
several instances, EBER-positive cells were in mitosis. (3)
An occasional occurrence of EBER-positive cells in 10 of 31

![Fig 1. PCR amplification products of EBV-specific DNA sequences](https://example.com/fig1.png)

Fig 1. PCR amplification products of EBV-specific DNA sequences in extracted tissue DNA from lymph nodes of five different AILD-TCL cases. Products are visible in ethidium-bromide-stained agarose gel as bands of 249 base pairs (bp) in various quantities due to different amounts of amplifiable DNA (upper part). Hybridization of corresponding Southern blot with 32P-labeled internal oligonucleotide disclosed bands of appropriate size in all cases after 12 hours exposure (lower part).
cases (Fig 4). These cells were small and possessed a round or slightly irregularly shaped nucleus, resembling the occasional EBER-positive lymphoid cells occurring in 3 of 12 normal lymphoid tissue samples (Fig 5).

**Double Labeling for EBER and Lineage Markers**

All AILD-TCL cases were analyzed using a combination of labeling with nonisotopic EBER probes and immunohistochemistry. Radioactively labeled EBER probes were applied in six cases, two of which were of EBV infection pattern 1 and four of EBV infection pattern 2. Both approaches produced congruent results. The majority of EBER-positive, immunoblast-like cells of the cases showing infection pattern 1 reacted with L26, confirming the B-cell nature of most of these cells (Fig 2B). The majority of the EBER-positive small, medium, and large cells, as well as many of those in mitosis present in the cases showing infection pattern 2, were reactive with the MoAbs βF1 and/or UCHL1, hence verifying their T-cell nature (Fig 3B). In addition, several of the immunoblast-like EBER-positive cells observed in this group of cases reacted with L26. The single EBER-positive lymphocytes present in the cases showing infection pattern 3 were reactive with either MoAbs βF1 and/or UCHL1 or with L26, indicating their T- or B-cell nature (Fig 4, insert).

Double labeling for EBER and CD21 did not lead to a colocalization of the labeling in any of the cases studied, which means that all of the CD21-positive cells, including all FDC, were not infected by EBV.

**Detection of EBV-Encoded LMP**

The cocktail of four MoAbs directed against different epitopes on the LMP led to the staining of lymphoid cells in 17 of the 32 AILD-TCL. The number of LMP-positive cells was, in all instances, less than the number of EBER-positive cells. LMP was demonstrated on the cell membrane, usually in a patchy distribution, and, in addition, in the cytoplasm. The intensity of the LMP staining varied considerably both within the same case and between cases. The comparison of the LMP staining with the three EBV infection patterns seen with the EBER-ISH led to the following findings: Of the eight AILD-TCL cases displaying infection pattern 1, five contained LMP-positive cells. In four cases, the nodular distribution of the LMP-positive cells was similar to that of the EBER-positive cells, which had the morphology of B immunoblasts and, occasionally, that of binucleated RS cells (Fig 2D). In the fifth case, the
EBV IN ANGIOIMMUNOBLASTIC TYPE T-CELL LYMPHOMA

1809

Fig 3. Diffuse EBV infection pattern in AILD-TCL. (A) ISH by using DIG-labeled EBER1- and EBER2-specific probes. Detection of many positive cells diffusely distributed in the lymph node, which is referred to as “EBV infection pattern 2.” Positive nuclei vary in size from small, to medium, to large. Note the labeled mitotic figures (arrow). (Original magnification × 400.) (B) Double labeling for CD45RO (MoAb UCHL-1; APAAP technique) and EBER (ISH with EBER-specific 32P-labeled probes; exposure time, 5 days). Many EBER-positive cells are labeled with MoAb UCHL-1 (arrows). (Original magnification × 400.)

LMP positivity was associated with medium-sized lymphoid cells, which—as shown in adjacent sections—were reactive with anti-T-cell antibodies. In the second group of 13 cases showing infection pattern 2, nine were LMP-positive. The LMP-positive cells were diffusely scattered throughout the diseased tissue. Most of the LMP-positive cells resembled small, medium, and large pleomorphic T cells. In several cases, some of the LMP-positive cells were similar to immunoblasts, HD cells, or RS cells. In the group of 10 cases with infection pattern 3, only three cases contained occasional LMP-positive cells, most of which were the size of small lymphoid cells.

There were no LMP-positive cells detectable in the 12 normal lymphoid tissue samples, including those that contained EBER-positive cells.

DISCUSSION

The data presented here indicate a strong association of AILD-TCL with EBV (97% of cases studied). This evaluation was accomplished by the application of two different and independent nucleic acid detection methods: the PCR technique for the demonstration of EBV-specific DNA sequences and ISH for the detection of EBER. Both methods produced almost identical results, showing that EBER-ISH was no less sensitive than PCR. The high sensitivity of the EBER-ISH is not surprising when the high copy number of EBER (up to 10^6 per infected cell) in the nuclei of the infected cells is considered. EBER-ISH proved to be superior to PCR as demonstrated by the fact that the DNA of 11 cases was not amplifiable (as shown by nonappearance of a β-globin band), whereas the application of EBER-ISH produced clearly specific signals in these cases.

When compared with normal lymphoid tissue, it became evident that EBV is more frequently present in AILD-TCL (97%) than in nondiseased lymphoid tissue (25%), which suggests a strong involvement of EBV in the pathogenesis of AILD-TCL. To assess the possible role of EBV in AILD-TCL, the number and identity of EBV-infected cells

Fig 4. Occasional EBV infection in AILD-TCL. ISH by using 32P-labeled EBER1- and EBER2-specific probes (exposure time, 3 days). Only a single cell is labeled and is therefore referred to as “EBV-infection pattern 3.” (Original magnification × 160.) Additional double labeling for EBER using DIG-labeled specific probes and MoAb βF1 for the β-chain of the T-cell receptor (insert). Note that the EBER-positive cell (with red nucleus) is colabeled with the MoAb βF1 demonstrated by ABC reaction (brown label). (Original magnification × 1,000.)

Fig 5. EBV infection pattern in normal lymph nodes. ISH for EBER in normal lymphoid tissue by using DIG-labeled EBER1- and EBER2-specific probes. Note that the single EBER-positive cell (insert) resembles the other small B lymphocytes in morphology and size. (Original magnification × 160; insert × 1,000.)
were investigated. In these experiments, the nonradioactive EBER-specific probes proved to be ideal for the morphologic evaluation of the infected cells, whereas ISH with radioactive EBER-specific probes could be well combined with immunohistologic labeling for the determination of the antigenic profile of the infected cells. Through the correlation of the ISH results with morphology and immunohistology, three patterns of EBV-infection were observed: (1) predominant EBV infection of large immunoblast-like B cells nodularly distributed in the area of residual lymphoid follicle and minor infection of neoplastic T cells (8/31 cases); (2) predominant EBV infection of many small, medium, and large neoplastic T cells, including those in division, and minor infection of B cells (13/31 cases); and (3) EBV infection of occasional small lymphoid cells (10/31 cases).

LMP was detectable in all three infection pattern groups, with a predominance in the cases of groups 1 and 2. This indicates the transcriptional and translational activity of EBV genes in AILD-TCL in contrast to normal lymphoid tissue, in which the EBV-positive cells were consistently LMP-negative. LMP expression of the EBV-infected cells in AILD-TCL appears to be relevant, as it has already been demonstrated that, in vitro, LMP has transforming potential and can prolong cell survival (probably by blockage of programmed cell death through induction of bcl-2 expression).

The predominant infection of B cells in the nodularly EBV-positive cases and the predominant infection of T cells in the diffusely EBV-positive cases was confirmed by double labeling for EBER and lineage markers performed on all AILD-TCL cases. The pathway of B- and T-cell infection by EBV in AILD-TCL is unclear, as cells harboring EBV expressed no detectable levels of the EBV-receptor antigen molecule CD21.41-44 Interestingly, the proliferated FDC also did not contain any detectable EBV, although the EBV-receptor molecule CD21 was expressed—as in normal and other lesions—in all instances at a high density.

The EBV infection of two cell lineages would appear to be unique to AILD-TCL, as this has not yet been reported for other malignancies. This may reflect the differences in the chromosomal aberrations and the configuration of antigen receptor genes between AILD-TCL and other malignant lymphomas. In AILD-TCL, simultaneous rearrangements of T-cell receptor and immunoglobulin genes can be found in a number of instances.16 Over the course of time, rearrangements disappeared and were occasionally replaced by new ones.15 The frequent presence of karyotypically unrelated abnormal clones and/or cells with nonclonal chromosomal abnormalities and a large proportion of normal mitotic cells, as well as a high incidence of trisomy 3 and 5, have been reported.8,9 Sequential studies have found different patterns of cytogenetic abnormalities, with some clones emerging and predominating over time, and others disappearing completely.8,10 With regard to these findings, it is tempting to speculate that AILD-TCL develops from a persistent EBV-infection during which EBV infects different cell lineages and possibly different cell clones within a cell lineage. Dependent on growth advantage due to genetic alterations and the T-cell reaction against the EBV-infected cells, certain EBV-positive or EBV-negative clones expand or diminish, the result of which is the heterogeneity in the EBV infection patterns described above. Hence, it would appear possible that the disease begins with a deregulated response to antigenic stimulation as a consequence of damage or loss of regulatory cell populations that might otherwise confine EBV infection and limit lymphocyte expansion during immunologic challenge.

A challenge for future research is to elucidate the precise role of EBV in the pathogenesis of AILD-TCL. One possible step in this direction would be the correlation of the EBV detection at the single-cell level with the clinical presentation, appearance, and disappearance of antigen receptor rearrangements and chromosomal abnormalities, mutated oncogenes, and suppressor genes, as well as the course of the disease. Given the rarity of this lymphoma entity, such investigations could only be achieved by a multiinstitutional study.

ACKNOWLEDGMENT

We wish to thank L. Oehring for his photographical assistance, and H.-H. Müller for his technical assistance. Our special thanks go to J.-A. Sutton for her excellent editorial contributions.

REFERENCES

lymphadenopathy with dysproteinemia-type features. Blood 72: 413, 1988


41. Fingeroth JD, Weis JJ, Tedder TF, Strominger JL, Biro PA, Faeron DT: Epstein-Barr virus receptor on human B lymphocytes is the C3d receptor CR2. Proc Natl Acad Sci USA 81:4510, 1984

42. Frade R, Barel M, Ehlin-Henrikson, Klein G: GP140, the C3d receptor on human B lymphocytes, is also the Epstein-Barr virus receptor. Proc Natl Acad Sci USA 82:1490, 1985


Heterogeneous Epstein-Barr virus infection patterns in peripheral T-cell lymphoma of angioimmunoblastic lymphadenopathy type

I Anagnostopoulos, M Hummel, T Finn, M Tiemann, P Korbjuhn, C Dimmler, K Gatter, F Dallenbach, MR Parwaresch and H Stein