Common Clonal Origin of Chronic Lymphocytic Leukemia and High-Grade Lymphoma of Richter’s Syndrome

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Patients with B-cell chronic lymphocytic leukemia (CLL) infrequently may develop high-grade B-cell lymphoma, or Richter’s syndrome lymphoma (RS lymphoma). Such lymphomas differ from the original leukemia in both histology and clinical behavior. Studies seeking to define the clonal relationship between the cells of the two malignancies in any one patient have yielded conflicting reports. We examined the clonal relationship between the early and late neoplastic cells of a patient who underwent Richter’s transformation. In contrast to the original leukemia cells, the secondary high-grade lymphoma was CD5−. However, both the leukemia cells and the evolved RS lymphoma expressed surface IgM reactive with Lc1, a murine monoclonal antibody specific for a supratypic cross-reactive idio-}

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began monthly chemotherapy with CVP (cyclophosphamide, vincristine, and prednisone) because of bulky adenopathy. In November 1991, a peripheral blood sample was taken for the analyses we report here. Because of progressive diffuse adenopathy, he underwent diagnostic cervical and inguinal lymph node biopsies in January 1992. Despite aggressive therapy, the patient experienced a clinical course typical for that of patients with RS and died 5 months later.2,3

**Immunohistochemistry and flow cytometry.** Lc1, a murine IgG1 monoclonal antibody (MoAb), was provided by Dr J.G. Sissons (Cambridge University, Cambridge, UK)28 and conjugated with phycoerythrin (PE) in our laboratory. PE-conjugated mouse IgG1a antimouse CD3 and mouse IgG1b antihuman CD3, and fluorescein isothiocyanate (FITC)-conjugated mouse IgG1 antihuman CD20 are as described.27 Conjugates of an irrelevant mouse IgG1 (MOPC21; Caltag, South San Francisco, CA) were used to control for specificity. Immunohistochemistry and flow cytometry analyses were performed as described.27,28

**Polymerase chain reaction (PCR).** Genomic DNA preparations extracted from peripheral blood lymphocytes (PBL) or from cryostat tissue sections were used as templates. To amplify Ig VH4 regions of the rearranged Ig heavy-chain genes, we used the subgroup-specific leader sense oligonucleotide primer 5'-gtcgaattcagcttATGAAACAYCTGTGGTTCTTC-3' and JH consensus antisense primer 5'-ggcgaattcACCTGAGGAGACRGTGACC-3' (NC-IUB nomenclature25; linkers and restriction sites are in lower case), as described.28 Rearranged Ig VH genes were amplified using oligonucleotides 5'-gtggaattcagcttTTGACYCAWCGSYCTCAG-3' and 5'-ctcgaattcTTACCTAGGACGGTGAGCTTGGCT-Y, corresponding to an Ig VH first framework region (FR1) sense strand consensus sequence and a JH antisense consensus sequence, respectively. The amplified fragments were ligated, cloned, and sequenced as described.27 DNA hybridization. Amplified Ig VH4 genes were detected in 10-μL samples from the PCR reaction mixtures by agarose gel electrophoresis and subsequent Southern blot analyses, essentially as described,30 but performing final stringent washes at 65°C in 0.2X SSC (0.2X SSC is 3 mol/L NaCl, 0.3 mol/L sodium citrate, pH 7.4). A 660-bp fragment containing the entire human Ig VH4 gene was used to probe PCR fragments, as described. This probe was labeled with 32P using the Oligolabelling Kit (Pharmacia, Uppsala, Sweden). The amplified Ig VH4 genes were registered as distinct bands of DNA of expected size (410 bp) in agarose gel electrophoresis.

**Immunohistochemistry and flow cytometry.** A section from a paraffin block of a cervical lymph node biopsy stained with hematoxylin and eosin (original magnification × 250).

Fig 2. Logarithmic red fluorescence histograms of live-gated CD20+ leukemia B cells (CLL, left histogram) or CD20+ high-grade lymphoma (RS Lymphoma, right histogram) stained with either PE-conjugated Lc1 (A) or PE-conjugated IgG1 isotype control (B).
leader oligonucleotide sense primer and a JH consensus antisense primer to amplify the rearranged Ig VH genes from genomic DNA isolated from the patient’s CLL cells or RS lymphoma. Two separate PCR were performed on the genomic DNA of the CLL cells, and on the genomic DNA of the RS lymphoma obtained from each of two disparate anatomic sites, eg, cervical (ne) and inguinal (pe) lymph nodes. In all cases, such PCR generated fragments of approximately 660 bp that hybridized specifically with a 32P-labeled human Ig VH4 gene probe. These fragments were cloned for sequence analyses. Two clones from each PCR reaction were sequenced. Each contained a functionally rearranged Ig VH4 gene. All shared the same Ig VH3DJH, indicating that they were derived from a common clonal ancestor. The rearranged Ig VH segment belongs to the Ig VH4 family, and has the closest homology (96%) with a previously published germline sequence V71-4.31 The region deduced as being encoded by a JH segment is most homologous to JH6, with only one base difference from that of the reported germline JH6 sequence (Fig 4). The G → C substitution noted at position 102 also has been noted in other reported JH6 gene segments and may represent a genetic polymorphism.27,32,33 Of all the known germline D segments, the nucleic sequence between that encoded by Ig VH and JH had the highest homology with the D2 minigene,34 sharing greater than 91% sequence homology over a stretch of 23 bp. The sequences of Ig VH4 genes of the CLL and RS lymphoma share several nucleotide codons that are distinct from those of the putative germline Ig VH4 gene, V71-4. However, the Ig VH4 genes of the RS lymphoma share a set of four additional substitutions in codons 21, 71, 82A, and 82C that are not present in the Ig VH4 genes expressed by the leukemia B-cell population. Nucleotide changes in codons 82A and 82C result in amino acid substitutions (Fig 5). The sequences of Ig VH4 genes from other CLL and RS lymphoma-derived clones and from the putative germline gene. The other Ig VH gene clones share more than 99.8% homology with the consensus sequence, with only two base differences: one in codon 3 of the clone ne5, and another in codon 44 of clone pb4. The rearranged Ig VH genes were cloned in a similar way via PCR using a consensus sense primer for the FR1 of human Ig Vλ and a consensus antisense primer for Jλ. Each clone contained a functionally rearranged Ig VH gene (Fig 6). Sequence analyses of the clones derived from CLL or RS lymphoma genomic DNA showed that both malignant B-cell populations expressed the same Ig VH genes rearranged with the same JAC1 cluster. Moreover, the Ig VJX junctions are identical. Deduced amino acid sequences are shown in Fig 7.

A computer search for known germline Vλ genes in GenBank identified the cloned Ig Vλ genes to have the highest homology (86%) to V1S2, an Ig Vλ gene of the Vλ1 subgroup.35 However, the differences between the cloned Ig Vλ genes and V1S2 include an in-frame one codon deletion in the first complementarity determining region (CDR). Such deletions generally do not arise through the process of Ig somatic mutation. Also, higher homology (90%) is observed between these Ig Vλ genes and a functionally rearranged Ig

**RESULTS**

**Histology and immunophenotype.** In contrast to lymph nodes typically observed from patients with CLL, the enlarged lymph nodes of COT were effaced by a diffuse proliferation of large lymphoid cells admixed with a few small lymphocytes (Fig 1). This histology is typical for that of RS.3 In contrast, the leukemia B cells had the morphology of small well-differentiated lymphocytes (not shown). Immunohistochemical analyses showed that the original leukemia B cells and the RS lymphoma B cells expressed surface IgMλ (not shown). Flow cytometric analyses showed that both neoplastic B-cell populations react specifically with Le1, a murine MoAb specific for a supratypic cross-reactive idiotype (sCRI) encoded by Ig VH4 genes of the Ig VH4 subgroup (Fig 2). CLL cells were noted to coexpress CD5 and pan-B-cell surface antigens, such as CD20; however, the RS lymphoma cells were CD5− (Fig 3).

**Sequence analysis of the Ig V genes expressed by CLL and RS lymphoma cells.** We used an Ig VH4 subgroup-specific

![Fig 3. Two-color contour plots depicting the logarithmic fluorescence of cells stained with PE-conjugated IgG1 anti-CD3 and FITC-conjugated IgG1 anti-CD20 (top row) or PE-conjugated IgG1 anti-CD3 and FITC-conjugated IgG1 anti-CD20 (bottom row). The column marked CLL displays the FACS analyses of the PBL, of which 64% were leukemia B cells expressing CD6 and CD20, but not CD3. The column labeled RS Lymphoma displays the FACS analyses of lymphocytes obtained from the cervical lymph node, of which 91% were high-grade lymphoma cells expressing CD20, but not CD3 or CD5.](image-url)
Fig 4. Nucleotide sequences of the rearranged Ig VH4 genes cloned from CLL cells (clones pbl, pb2, pb3, and pb4), and from RS lymphoma lesions in a cervical lymph node (clones ne2 and ne5) and in an inguinal lymph node (clones pel and pe3). Also shown are previously reported germline (V71-4) and rearranged (WRD2) Ig VH4 genes with closest sequence homology, and the germline D2 and JH6 segments. Dots indicate homology with the clone pbl. Sequences corresponding to the primers used for PCR are double underlined. Amino acid residues are numbered according to Kabat et al.41 Base differences resulting in amino acid substitutions are shown in upper case; silent base changes are in lower case.

Fig 5. Deduced amino acid sequences of the cloned Ig VH4 genes. The clones are indicated as in Fig 4.
RS lymphoma of a patient who underwent Richter's transformation. We found that both CLL and RS lymphoma cells express Ig bearing the Lc1 sCRI (Fig 2). This sCRI previously was identified on human Igs encoded by a subset of genes with that of previously reported genes encoding Lc1-reactive Ig heavy chains shows high homology. The isolated Ig VH genes have the highest homology with WRD (95%), a functionally rearranged Ig VH gene isolated from an inguinal lymph node (clone pe22d). Previously reported germline (V1S2) and rearranged (1B9/F2) Ig VH genes with closest sequence homology are shown below (see also legend for Fig 4).

![Fig 6. Nucleotide sequences of the rearranged Ig V \( \alpha \) genes cloned from CLL (clones pb8x and pb7x), and from RS lymphoma lesions in a cervical lymph node (clones ne1d, ne2x, and ne4x) and in an inguinal lymph node (clone pe22d). Previously reported gene V1S2) and rearranged (1B9/F2) Ig V \( \alpha \) genes with closest sequence homology are shown below (see also legend for Fig 4).](#)

![Fig 7. Deduced amino acid sequences of the cloned Ig V \( \alpha \) genes. The clones are indicated as in Fig 6.](#)
the same Ig V\(\lambda\) gene and have identical Ig V\(\lambda\)J\(\lambda\) gene rearrangements. Formed during the process of B-cell differentiation, such Ig rearrangements generate novel CDR3 junctional sequences between the Ig V\(\mu\), D, and J\(\mu\) gene segments for the Ig heavy chain and the V and J genes for Ig light chain. Furthermore, D and J\(\mu\) gene segments of the Ig heavy chain generally undergo N-terminal nucleic acid base insertion immediately before V\(\mu\) gene rearrangement.\(^\text{37,38}\)

Because of the tremendous potential for diversity in these regions, the sequences that comprise the Ig heavy- and light-chain CDR3s generally are unique for each B-cell clone. Finding that the RS lymphoma has Ig light- and heavy-chain CDR3s that are identical to that of the original B-cell CLL population provides compelling evidence that these two neoplastic processes arose from a common clonal ancestor.

It is not likely that cross-contamination of one malignant B-cell population with that of the other accounts for our identifying identical Ig gene rearrangements for both leukemia and lymphoma B-cell populations. Flow cytometric analyses showed that greater than 95% of the CD20\(^+\) B cells in the peripheral blood expressed CD5, whereas greater than 99% of the B cells in the RS lymphoma population were CD5\(^+\) (Fig 3). These data indicate that the studied neoplastic populations were homogeneous and exclusive of one another. Additional evidence is provided by the sequence analyses of the isolated Ig V\(\gamma\) genes. Four unique nucleotide substitutions (in codons 21, 71, 82A, and 82C) are identified in each of the Ig V\(\mu\) genes cloned from the CLL lymphoma, but not in the CLL-derived Ig V\(\mu\) genes (Fig 4). Also, each of the Ig V\(\lambda\) genes isolated from the lymphoma shared the same base substitution in codon 83, distinguishing these genes from CLL-derived Ig V\(\lambda\) genes (Fig 5). Furthermore, the Ig V\(\gamma\) gene clones of the CLL were isolated from two independent PCR amplifications, and the rearranged Ig V\(\gamma\) genes of the RS lymphoma were isolated from independent PCR performed on DNA from RS lymphoma tissues obtained from two distinct anatomical sites. That all independently isolated lymphoma Ig V\(\gamma\) genes should share the same base substitutions from the CLL-derived Ig V\(\gamma\) gene consensus sequence argues strongly that these base differences cannot be secondary to mutations introduced by PCR. Rather, these base differences argue that the Ig V\(\gamma\) genes isolated from the RS lymphoma are derived from a B-cell population that is distinct from that of the clonally related B-cell CLL.

Finding that an RS lymphoma is derived from the same clone as that of the original B-cell CLL supports earlier studies indicating that the RS lymphoma and CLL cells from any one patient may have similar Ig gene rearrangements by Southern blot analyses.\(^\text{69}\) However, in other studies, different patterns of Ig rearrangements were identified in DNA from CLL compared with that of the RS lymphoma of the same individual.\(^\text{11,13-15,17}\) The latter may be secondary to somatic mutations in or around the expressed Ig genes that fortuitously permute the recognition sequence(s) of the restriction enzyme(s) used in these analyses. In addition, recent studies have shown that fully differentiated B cells may undergo reiterative Ig V\(\gamma\) gene rearrangements subsequent to successful expression of Ig heavy and light chain genes.\(^\text{23-25,39}\)

Similarly, differences in the isotype of the Ig light chains expressed by CLL versus RS lymphoma may reflect a transformation-related genetic instability in the expression of Ig genes.\(^\text{4,18}\)

In this regard it is noteworthy that the sequence diversity is much greater between the CLL Ig V\(\gamma\) genes and those of the RS lymphoma than between those of individual isolates of either population alone. Ignoring the regions that correspond to the PCR primers, the Ig V\(\gamma\) genes cloned from the RS lymphoma are virtually identical. We observed a total of three nucleotide substitutions in more than 3,000 nucleotide bases in the 12 Ig V\(\mu\) and Ig V\(\lambda\) RS lymphoma-derived clones studied. These substitutions result in only a 0.06% overall difference in nucleic acid sequence, and may be secondary to the known inaccuracy of PCR.\(^\text{40}\) However, the RS lymphoma-derived Ig V\(\mu\) genes have an average of 5.25 base differences per clone from the consensus sequence of the CLL-derived Ig V\(\mu\) genes (clone pb1, Fig 4). On the other hand, the CLL-derived Ig V\(\mu\) genes have an average of only 1.25 base changes per clone from this same consensus sequence. Similarly, Ig V\(\lambda\) genes isolated from the RS lymphoma, although virtually homologous to one another, have an average of 1.5 base differences per clone from the consensus sequence of the CLL-derived Ig V\(\lambda\) genes (pb8xs, Fig 6), whereas the CLL-derived Ig V\(\lambda\) genes have an average of only 0.5 base differences per clone from this same consensus sequence. Thus, the sequence diversity noted between Ig V\(\gamma\) genes of the CLL versus that of the RS lymphoma exceeds the diversity noted in the Ig V\(\lambda\) genes used by either population alone. As such, it appears that the nucleic acid base substitutions noted in the Ig V\(\gamma\) regions expressed by RS lymphoma may have been acquired abruptly during a period of genomic instability that may accompany Richter's transformation. Conceivably, such instability may be secondary to an abortive attempt to activate the process of Ig somatic hypermutation, resulting in Ig V\(\gamma\) gene mutations and possibly other cytogenetic changes that contribute to the development of Richter's syndrome. Further investigation of the molecular events that occur during the early stages of Richter's transformation may show mechanisms of genetic instability important in the evolution of this disease.

REFERENCES

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