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**Molecular cloning of a human immunoglobulin  $\lambda$  chain variable sequence**

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**ABSTRACT**

We have cloned a human  $V\lambda$  cDNA sequence from an  $Ig\lambda$ -producing human Burkitt lymphoma cell line (BL2) by taking advantage of a cloned constant region gene as a primer for cDNA synthesis instead of an oligo(dT) primer. The amino acid sequence deduced from the nucleotide sequence of  $V\lambda$  clones is highly related to that of the NEW  $V\lambda$  protein of subgroup I. Southern blot hybridization of human DNAs with the  $V\lambda_1$  probe showed at least 12 hybridizing  $V\lambda$  fragments. These fragments are amplified in K562 cells which derive from a case of chronic myelogenous leukemia and contain an amplified c-abl oncogene and amplified  $C\lambda$  sequences.

**INTRODUCTION**

Immunoglobulin chains are encoded by three unlinked gene families:  $\lambda$  light chain,  $\kappa$  light chain and heavy chain genes which are located on chromosomes 22, 2 and 14, respectively, in man (1-4). The formation of an active immunoglobulin (Ig) gene involves the somatic joining of two or three separated segments of chromosomal DNA (5).

In the case of the mouse  $\kappa$  chain locus, several hundred germ line  $V\kappa$  genes (6,7) exist as units separated from a single  $C\kappa$  gene and the translocation of one of the  $V\kappa$  genes to one of the four active  $J\kappa$  segments of the  $C\kappa$  locus results in the formation of a functional  $\kappa$  chain gene (8,9). The organization of the human  $\kappa$  locus is very similar to mouse (10). On the other hand, the gene organization of the  $\lambda$  locus seems to differ between mouse and human. Approximately 40% of human Igs contain  $\lambda$  chains (11), while only 3-5% of mouse Igs do (12,13). While inbred mouse strains contain only four  $C\lambda$  genes (15), at least six  $C\lambda$  genes are present on each human chromosome 22 in man (16). Three of the four inbred mouse  $C\lambda$  genes ( $C\lambda_1$ ,  $C\lambda_2$  and  $C\lambda_3$ ) are functional, while the fourth gene ( $C\lambda_4$ ) is a non-functional pseudogene (17). A single joining segment is associated with each  $C\lambda$  gene in mice (14,15). The feral mice show, however, considerable variation in the number of  $C\lambda$  genes (18). In inbred mouse strains the  $C\lambda_2$

segment is linked with the  $C\lambda_4$  segment, while the  $C\lambda_3$  is associated with the  $C\lambda_1$  segment (17). All inbred mouse strains which were examined have only two  $V\lambda$  genes (19-21), while feral mice have at least three  $V\lambda$  genes (22).

In order to analyze the germ line organization of human  $V\lambda$  genes, we have attempted to clone cDNA of human  $V\lambda$  sequences.

### MATERIALS AND METHODS

#### RNA Extraction

Cytoplasmic RNA of Burkitt lymphoma cell line (BL2) was prepared by the cesium chloride method (23). The poly(A)<sup>+</sup> mRNA was isolated by oligo(dT)-cellulose column chromatography.

#### cDNA Cloning

The DdeI-RsaI DNA fragment (146 bp) of  $C\lambda_2$  DNA (Fig. 1) was isolated. Two pmoles of DNA fragment was digested with exonuclease III (50 units) in 6.6 mM Tris-HCl (pH 7.5)/60 mM NaCl/6.6 mM MgCl<sub>2</sub>/5 mM sodium phosphate (pH 7.0)/6.6 mM  $\beta$ -mercaptoethanol at 23°C for 6 to 10 min (about 40 to 70 bases digested). Two pmoles of  $C\lambda$  primer was hybridized with 5  $\mu$ g of BL2 poly(A)<sup>+</sup> RNA at less stringent conditions in 50% formamide/20 mM Tris-HCl (pH 7.5)/0.1 mM EDTA/0.1% sodium dodecyl sulfate (SDS) successively at 37°, 26°, and 15°C for 60 min each. The double-stranded cDNA was synthesized by the procedures described in ref. 24. The cDNA longer than 350 bp was selected by agarose gel electrophoresis and after ligation of EcoRI molecular linker, cloned into  $\lambda$ gt 11 phage vector (25).

#### DNA Sequencing

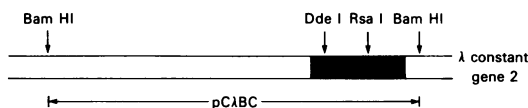
The nucleotide sequences were determined by the chemical degradation technique of Maxam and Gilbert (26).

#### Southern Blotting Analysis

Cellular DNA samples were digested with EcoRI and subjected to 0.7% agarose gel. Transfer of DNA from gel to nitrocellulose sheet was performed essentially as described by Southern (27). The filters were hybridized with <sup>32</sup>P-labeled probe DNA, as described in the figure legends, and finally washed with 2X SSC at 65°C.

### RESULTS AND DISCUSSION

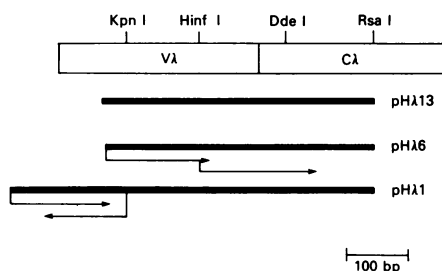
The poly(A)<sup>+</sup> mRNA was isolated from Ig  $\lambda$ -producing BL2 carrying a t(8;22) chromosome translocation. As primer for cDNA synthesis, we used a DNA segment of human  $C\lambda$  gene instead of oligo(dT) because a primer derived



**Fig. 1** Physical map of the human germ line  $\lambda$  light chain constant region #2 gene (16). The filled box represents the amino acid coding region. All restriction sites for DdeI and RsaI are not shown.

from a  $C\lambda$  gene is specific for Ig $\lambda$  chain mRNA. We chose the  $C\lambda_2$  gene (Fig. 1) as a DNA source of the primer although it was not known which  $C\lambda$  gene is utilized in BL2 cells, since the different  $C\lambda$  coding regions seem to differ by a very limited number of nucleotides (16). The DdeI-RsaI DNA fragment (146 bp) of  $C\lambda_2$  DNA (28) shown in Figure 1 was isolated and digested with exonuclease III, as described in Materials and Methods. The purpose of exonuclease III digestion was twofold: i) to obtain a single-stranded region of primer to make the hybridization between mRNA and primer more effective, and ii) to increase the probability of base-matching at the 3' end of the primer.  $C\lambda$  DNA primers were hybridized with BL2 poly(A)<sup>+</sup> RNA at low stringency conditions, as described in Materials and Methods. The double-stranded cDNA was synthesized using AMV reverse transcriptase and cloned into  $\lambda$ gt11 phage vector, as described in Materials and Methods.

By screening with <sup>32</sup>P-labeled pC $\lambda$ BC (Fig. 1), recombinant clones containing  $C\lambda$  sequence were selected. The restriction maps of three clones are shown in Figure 2.



**Fig. 2** Restriction map of cDNA clones representing human Ig  $\lambda$  light chain gene and the strategy for DNA sequencing. The regions shown by arrows were sequenced by the chemical degradation technique of Maxam and Gilbert (26). The box shown at the top indicates the amino acid coding region of Ig  $\lambda$  light chain gene. Each insert of three clones has EcoRI sites at both ends because EcoRI molecular linker was joined to double-stranded cDNA before cloning into  $\lambda$  gt11 vector (25).

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-30      -20      -10      +1      10      20      30
  .
GCT GAA GCA ,GAG CTC GGG ACA ATC TTC ATC ATG ACC TGC TCC CCT CTC CTC ACC CTT
      .
      Met Thr Cys Ser Pro Leu Leu Leu Thr Leu

          40          50          60          70          80          90
CTC ATT CAC TGC ACA GGG TCC TGG GCC CAG TCT GTG TTG ACG CAG CCG CCC TCA GTG TCT
Leu Ile His Cys Thr Gly Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser

          100          110          120          130          140          150
GGG GCC CCA GGA CAG AAG GTC ACC ATC TCC TGC TCT GGA AGC AGC TCC AAC ATT GGG AAT
Ala Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn
-----
                          Gly --- Thr -----

          160          170          180          190          200          210
GAT TAT GTA TCC TGG TAC CAA CAG GTC CCA GGA ACA GCC CCC AAA CTC CTC ATT TAT GAC
Asp Tyr Val Ser Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp
Asn ----- His Leu -----

          220          230          240          250          260          270
AAT AAT AAA CGA CCC TCA GGG ATT CCT GAC CGA TTC TCT GGC TCC AAG TCT GGC ACG TCA
Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser
Asp ----- Ile --- Ala -----

          280          290          300          310          320          330
GCC ACC CTG GGC ATC ACC GGA CTC CAG ACT GGG GAC GAG GCC GAT TAT TAC TGC GGA ACA
Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr
----- Ala ----- Arg -----

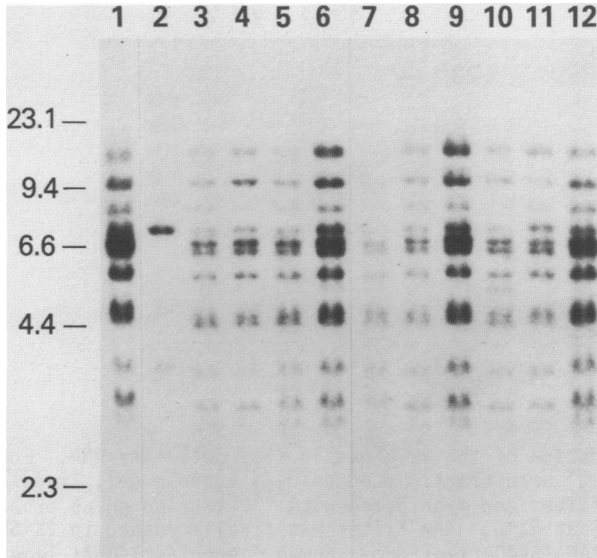
          340          350          360          370          380          390
TGG AAT AAC AGC CTG AGT GGT TGG GTG TTC GGC GGA GGA ACC AAG CTG ACC GTC CTA GGT
Trp Asn Asn Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
--- Asp Ser ----- Asn Ala Val ----- Val -----

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**Fig. 3** Nucleotide sequence of human  $\lambda$  variable region. The amino acid sequences deduced are shown below the nucleotide sequence which coincides best with the amino acid sequences of NEW subgroup I light chain (29) shown at the bottom line. A dash in NEW amino acid sequence indicates identity in that amino acid position to the sequence of cloned  $V\lambda$  DNA.

To confirm that these recombinant clones contain human  $V\lambda$  sequences, we have determined nucleotide sequences of clones 1 and 6 (Fig. 3). Human  $V\lambda$  chains have been classified into six subgroups according to their amino acid sequences. As shown in Figure 3, the amino acid sequence deduced from nucleotide sequence corresponds closely to the NEW protein (29) of  $V\lambda$  subgroup I (matching of 92 amino acid residues out of 110). Thus BL2 cells seem to produce a subgroup I  $V\lambda$  chain. Therefore we call this  $V\lambda$  gene  $V\lambda_I$ . The amino acid sequence determined from the DNA sequence of pH $\lambda$ 1 has an additional 19 amino acid residues beginning with methionine at the N terminus of the mature  $V\lambda$  sequence, which is likely to correspond to the signal peptide of precursor Ig $\lambda$  chain.

Since human  $V\lambda$  genes may comprise a large family, we have tried to determine their multiplicity in human DNA. A DNA fragment, EcoRI (+133) to



**Fig. 4** Southern blot hybridization of human DNA with  $V\lambda_I$  probe. Human DNAs were digested with *EcoRI*, fractionated on a 0.7% agarose gel and transferred to the nitrocellulose filter. The DNA on the filter was hybridized with pHV $\lambda_6$  containing only  $V\lambda$  sequence in the solution of 4X SSC/50% formamide at 37°C. The filter was finally washed with 2X SSC at 65°C. Lane 1, MC 116 ( $\lambda$ -producing Burkitt lymphoma) DNA; lane 2, BL2 ( $\lambda$ -producing Burkitt lymphoma) DNA; lane 3, U266 ( $\lambda$ -producing human myeloma) DNA; lane 4, GM1056 ( $\lambda$ -producing human lymphoblastoid cell) DNA; lane 5, SK0-007 (U266 HPRT<sup>-</sup>) DNA; lane 6, CEM (human T-cell lymphoma) DNA; lane 7, PA682 ( $\kappa$ -producing Burkitt lymphoma) DNA; lane 8, JI ( $\kappa$ -producing Burkitt lymphoma) DNA; lane 9, Daudi ( $\kappa$ -producing Burkitt lymphoma) DNA; lane 10, DS178 ( $\kappa$ -producing Burkitt lymphoma) DNA; lane 11, PAF (SV40-transformed human fibroblast cell) DNA; lane 12, Colo 320 (human colon carcinoma) DNA (31-32).

HaeIII (+310) of p $\lambda_6$ , containing only  $V\lambda$  sequence (Fig. 3), was subcloned (pHV $\lambda_6$ ) and used as a probe for the analysis of human  $V\lambda$  genes in human DNA.

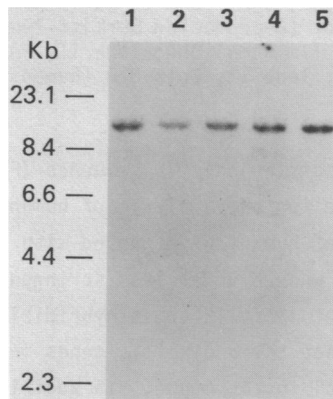
Southern blot filter of human DNA digested with *EcoRI* was hybridized with <sup>32</sup>P-labeled pHV $\lambda_6$  and washed under less stringent conditions. As shown in Figures 4 and 5, at least 12 cross-hybridizing bands were detected in human DNA, suggesting that the pool of  $V\lambda$  genes in man might be much larger than the  $V\lambda$  gene pool in the mouse. In addition, the number and DNA sequence of human  $V\lambda$  genes cross-hybridizing with  $V\lambda_I$  probe seem to be well conserved among individuals. This is in striking contrast to human  $C\lambda$  locus, remarkable polymorphism of which has been reported (16,30). Further, many of the  $\lambda$ -producing cell lines examined do not show any promi-



**Fig. 5** Amplification of the  $V\lambda$  genes in K562 cell line DNA. *EcoRI*-digested human DNAs (10  $\mu$ g) were fractionated on 0.7% agarose gel, transferred to a nitrocellulose filter and hybridized with  $^{32}$ P-labeled pHV $\lambda$ 6 probe in 50% formamide/6X SSC at 37°C. The filter was finally washed in 2X SSCS at 65°C. Lane 1, PAF (SV40-transformed human fibroblast) DNA; lane 2, K562 DNA; lanes 3, 4 and 5, human T-cell lymphoma DNA.

ment DNA rearrangement of  $V\lambda_I$  gene (Fig. 4), indicating that these producer cells utilize other  $V\lambda$  genes for chain production. Thus, man seems to have other functional  $V\lambda$  genes which are not detectable by the  $V\lambda_I$  probe.

Interestingly, we observed only two  $V\lambda$  bands hybridizing with the  $V\lambda_I$  probe in BL2 DNA (Fig. 4). The upper band corresponds to the productively



**Fig. 6** The nitrocellulose filter described in Fig. 5 was rehybridized with a human *myc* cDNA probe specific for the two coding exons of the *c-myc* gene (Ryc 7.4) (28). As shown in the figure, the intensity of the *c-myc* band in K562 cells (lane 2) was not more prominent than in the other cell DNAs, indicating that the  $V\lambda$  sequences were amplified in K562 cells (Fig. 5).

rearranged  $V\lambda$  gene on chromosome 22 of BL2 cells (28) since it cross-hybridizes with a  $C\lambda$  probe (data not shown). The lower band may represent a rearranged  $V\lambda$  gene on the 22q<sup>-</sup> chromosome of BL2 cells. In this cell line, the c-myc gene is in its germ line configuration and remains on the 8q<sup>+</sup> chromosome, while a rearranged  $C\lambda$  locus contained within a 12.0 kb EcoRI fragment is translocated to a chromosomal region 3' to the c-myc oncogene (28). The chromosomal breakpoint in this cell line is approximately 9 kb 3' to the c-myc oncogene on chromosome 8 and immediately 5' of a rearranged  $C\lambda$  locus gene on chromosome 22 of BL2 DNA (Erikson and Croce, manuscript in preparation). Thus, most of the  $V\lambda$  DNA fragments homologous to the  $V\lambda_I$  DNA probes are deleted on both chromosomes 22 of BL2 cells.

Cloning and sequencing of members of other families of human  $V\lambda$  genes will provide a better understanding of the structure and organization of the  $\lambda$  locus in man.

We have also examined the DNA of K562 human leukemic cells for the amplification of the  $V\lambda_I$  sequences, since a five to ninefold amplification of both the c-abl oncogene and of the  $C\lambda$  locus has been detected in these cells (31,32). The result of this amplification is a small marker chromosome, which is probably derived from a Philadelphia chromosome and carries co-amplified c-abl and  $C\lambda$  sequences (32). As shown in Figure 5, we detect amplification of the  $V\lambda_I$  sequences in K562 cells. The intensity of the  $V\lambda_I$  bands in the K562 lane is approximately sixfold higher than the intensity of the  $V\lambda_I$  bands in the other cell lines. Rehybridization of the same filter with a probe specific for the c-myc oncogene (Ryc 7.4) (28) indicates that no amplification of the c-myc oncogene occurred in K562 cells (Fig. 6). These results indicate that the amplification unit involving the joining of chromosomes 9 and 22 on the Philadelphia chromosome in K562 cells must be extremely large, since it contains all  $V\lambda_I$  hybridizing DNA segments, all  $C\lambda$  DNA segments (32) and the c-abl oncogene (32).

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