MOLECULAR GENETIC ANALYSIS OF THE V_Ser GROUP
ASSOCIATED WITH TWO MOUSE LIGHT CHAIN GENETIC
MARKERS

Complementary DNA Cloning and Southern Hybridization Analysis

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The extensive amino acid sequence diversity of Ig variable (V) regions is known to be derived from both evolutionary and somatic processes (1-3). Comparison of amino acid sequences of mouse myeloma and hybridoma κ light (L) chains, for example, indicates that these sequences can be arranged into groups such that members of a group are more similar to each other than to members of other groups (4-6). In the case of mouse κ L chains, multiple V region genes have been observed (7, 8) for most groups of V regions tested. Thus, the multiple germ line V genes provide a portion of the V region diversity observed at the protein level. Additional diversity is introduced by permitting each V gene to join with any one of four different active joining (J) segments, by introducing junctional diversity during the joining event, and by somatic mutation (for review, see refs. 3 and 9).

Several mouse V_Ser genetic markers have been described which involve characteristic V_Ser regions that are expressed by some inbred strains of mice, but not by others. These genetic markers have been detected by peptide mapping (10, 11) and isoelectric focusing (12, 13) of L chains from normal mouse serum Ig, by analysis of expression of various idiotypes (14, 15), and by isoelectric focusing of L chains of antiphosphorylcholine antibodies that bear the H8 idiotype (16). All of these genetic polymorphisms are determined by genes closely linked to the Lyt-2 and Lyt-3 loci on chromosome 6 (17, 18), the same chromosome that bears the κ L chain structural genes (19). A system for nomenclature of genes that determine these V_Ser polymorphisms has been proposed (20).

One of these V_Ser polymorphisms, called the I_Ser-peptide marker, was detected by tryptic peptide mapping of reduced and[^14C]iodoacetic acid-alkylated L chains from normal serum Ig of unimmunized mice (10, 11). This analysis detected a heterogeneous group of V_Ser regions that accounts for <5% of the total L chains expressed by I_Ser-positive strains. To obtain myelomas producing homogeneous
examples of \( I_s \)-positive L chains, it was necessary to cross the genetic marker onto the BALB/c genetic background, since none of the myeloma-inducible strains expresses the marker (21). Of \( \sim 200 \) myelomas induced in the C.C58 and C.AKR strains, several were found to correspond to both the \( I_s \)-peptide marker and the EF1\(^a \) marker described by Gibson et al. (12). Amino acid sequence analysis demonstrated that these L chains belonged to a group of \( V_s \) regions apparently not expressed by either BALB/c or NZB, and which we referred to as the \( V_s \)Ser group, because all such proteins observed had an unusual amino-terminal serine residue (21). A major question that remains to be answered is whether strains that do not express \( V_s \)Ser-like L chains lack \( V_s \)Ser genes altogether, or whether they contain the genes, but fail to express them due to regulatory controls.

To further characterize the \( V_s \)Ser group, full-length complementary DNA (cDNA) clones have been produced from mRNA coding for the \( I_s \)-positive L chain of the C.C58 M75 myeloma. The entire sequence of one cDNA clone has been determined and compared with the known collection of BALB/c and NZB \( \kappa \) chain sequences. Results suggest that the nucleotide sequence of the M75 \( V \) region is different from all known \( V \) regions throughout most of its length. Use of a the 5' region of this clone as a probe for \( V_s \)Ser-specific sequences in Bam HI, Hind III, and Eco RI digests of liver DNA of a large number of inbred, recombinant, and recombinant inbred strains has revealed at least one strongly hybridizing sequence in each strain tested. Thus, strains that do not express \( V_s \)Ser-associated phenotypic markers do not lack \( V_s \)Ser-related DNA sequences. However, strains could be divided into two groups based on the sizes of the strongly-hybridizing fragments. Complete correlation was observed between expression of \( V_s \)Ser-associated phenotypic markers and the presence of strongly hybridizing Bam HI, Hind III, and Eco RI fragments of 3.2 kilobases (kb), 2.8 kb, and 2.1 kb, respectively.

### Materials and Methods

**Mice, Myelomas, and DNA.** The C.C58 and C.AKR inbred strains of mice, which bear the \( Lyt-2^+ \) and \( Lyt-3^- \) alleles and \( V \), genetic polymorphisms of the C58/J and AKR/J strains, respectively, on the BALB/cAn genetic background (22), and the B6/\( Lyt-2^+ \), \( Lyt-3^- \) strain, which contains the corresponding genes of the RF strain on the C57BL/6 background (23), were bred in our laboratory. The C.C58 and C.AKR strains were inbred after 19 backcross generations. Mice of the congenic partner strain, BALB/cAn, were the gift of Dr. H. N. Eisen, Massachusetts Institute of Technology, Cambridge. Mice of the B6.PL(85NS) strain (24) and DNA from mice of the NAK strain (25) were the gifts of Dr. D. Gibson, University of Sherbrooke, Quebec, Canada. All other mice were purchased from the Jackson Laboratory, Bar Harbor, ME.

The C.C58 M75 myeloma was induced in an earlier inbreeding (N9) by three bimonthly intraperitoneal injections of pristane (tetramethylpentadecane), as described by Potter (26). The tumor had been adapted to subcutaneous growth, and small nonnecrotic tumors, \( \sim 1.5 \) cm in diameter, were quick-frozen in liquid nitrogen for mRNA isolation. DNA from the C.C58 M75 myeloma and from livers of various strains was isolated from tissue frozen in the same manner. DNA from A/J mice and from AKXL recombinant inbred strains (27) was purchased from The Jackson Laboratory, Bar Harbor, ME.

**Bacterial Strains and Vectors.** The primer and linker vectors (28) in *E. coli* K12 HB101 were the kind gifts of Dr. H. Okayama and Dr. P. Berg, Stanford University School of Medicine. The plasmid pUC18 (29) and *E. coli* K12 GM33 (30) were obtained from Dr.
R. Meyer, University of Texas, Austin. The M13mp8 and M13mp9 phage, and E. coli K12 J103 (31) were obtained from Dr. J. Walker, University of Texas, Austin. The RR1 strain of E. coli K12 and the pBR322 clone, which contained the 3.1 kb Hind III/Bam HI BALB/c genomic C (constant) fragment (32, 33) were the gifts of Dr. P. Tucker, University of Texas Health Sciences Center, Dallas.

Enzymes. Restriction enzymes were purchased from Bethesda Research Laboratories, Inc. (Gaithersburg, MD), Boehringer-Mannheim Biochemicals (Indianapolis, IN), and New England Biolabs (Beverly, MA). Avian myoblastosis virus reverse transcriptase was purchased from Life Sciences, Inc., St. Petersburg, FL. E. coli DNA polymerase I (Klenow fragment), T4 DNA polymerase, and a kit for radiolabeling DNA by strand-replacement synthesis with T4 DNA polymerase were purchased from Bethesda Research Laboratories, Inc. E. coli DNA ligase was purchased from P-L Biochemicals, Piscataway, NJ. A kit (409 Sequencing Pack) for nucleotide sequence analysis using the dideoxynucleotide procedure was obtained from New England Biolabs, Beverly, MA.

Isolation of mRNA. PolyA+ RNA was isolated from the C.C58 M75 myeloma by the guanidine thiocyanate method of Chirgwin et al. (34), followed by two passages over oligo(dT)-cellulose (Sigma Chemical Co., St. Louis, MO). Electrophoresis in formaldehyde gels, and Northern blot analyses were performed as described by Rave et al. (35), and hybridization in 50% (vol/vol) formamide was as described by Thomas (36).

Probe for Screening cDNA Library. A pBR322 subclone was obtained from Dr. P. Tucker. It contained a 3.1 kb Hind III/Bam HI fragment containing the BALB/c mouse C, region, and a portion of 5' and 3' flanking regions (32, 33). The 3.1 kb fragment was excised and isolated by two cycles of agarose gel electrophoresis, and radiolabeled with α-[32P]dATP (New England Nuclear, Boston, MA, 3,200 Ci/mmol) by nick-translation, as described by Maniatis et al. (37). Specific radioactivity of the resulting DNA was ~5 × 10⁶ cpm/µg.

Procedure for cDNA Cloning. Complementary DNA cloning of polyA+ RNA from the C.C58 M75 myeloma was performed essentially as described by Okayama and Berg (28). After second-strand synthesis and ligation, the resulting DNA was used to transform both E. coli K12 strain HB101 (Rec A-) and RR1 (Rec A+) as described and plated on L-broth agar that contained 250 µg/ml Carbenicillin (Geopen) (Pfizer, Inc., New York). Colonies were picked onto nitrocellulose filters (Millipore Corp., Bedford, MA) and subjected to colony hybridization as described by Davis et al. (38), using the nick-translated Hind III/Bam HI genomic C, fragment as probe. Colonies that gave positive hybridization signals were grown in L broth containing 250 µg/ml carbenicillin, and plasmid DNA was isolated by a cleared lysate procedure, essentially as described by Katz et al. (39).

Restriction Mapping. For restriction mapping of cloned DNA, restriction enzymes were generally used under the conditions specified by their suppliers. Fragments were analyzed by electrophoresis on agarose gels (0.8–1.5%) in the presence of ethidium bromide.

Southern Hybridization of Genomic DNA. Genomic DNA was isolated from myeloma and liver tissue as described by Blattner et al. (40) and Maniatis et al. (37). DNA samples (10 µg each) were digested with the appropriate restriction nuclease and subjected to electrophoresis on 0.6% agarose gels. The DNA was transferred to nitrocellulose filters (BA85; Schleicher and Schuell, Keene, NH), prehybridized, then hybridized with radioactive probe (see below) in 50% formamide at 41°C, essentially as described by Davis et al. (38). Filters were washed three times (10 min each) at 55°C in 2 x SSC (standard sodium citrate), 0.1% SDS followed by two washes (15 min each) at 55°C in 0.1 x SSC, 0.1% SDS. Autoradiography was performed at ~70°C with Dupont Lightning Plus intensifying screens.

The source of probe for Southern hybridization was a 200 base pairs (bp) Pst I/Kpn I DNA fragment that contained the 5’ end of the putative full-length κ L chain cDNA clone of interest, p9(35) (see below). This fragment was subcloned into the plasmid, pUC18(29), and the resulting plasmid was cleaved at one end of the insert with Pst I and radiolabeled with α-[32P]dATP (sp act 3,000 Ci/mmol) by strand-replacement synthesis with T4 DNA polymerase as described by O’Farrell (41). Specific radioactivity of the resulting probe was approximately ~10⁸ cpm/µg DNA.
**DNA Sequence Analysis.** DNA sequencing was performed by the dideoxynucleotide chain termination method of Sanger and coworkers (42) using cloning vectors M13mp8 and M13mp9 and the sequencing strategy designed by Messing and coworkers (31, 43, 44). Replicative form of M13 clones was prepared by the rapid boiling procedure described by Maniatis et al. (37) for characterization of inserts. Single-stranded form of M13 clones was prepared by a modification of the procedure of Schreier and Cortese (45) as described by New England Biolabs (sequencing kit 409; Beverly, MA). Sequencing reactions uses *E. coli* DNA polymerase I, Klenow fragment, M13 primer (pentadecamer) fragment, and mixtures of each of the four dideoxynucleotides with normal nucleotide precursors (New England Biolabs), as well as α-[32P]dATP (800 Ci/mmol; New England Nuclear) as a source of label. Gel electrophoresis was on thin polyacrylamide gels, essentially as described by Sanger and Coulson (46).

**Results**

**Production of cDNA Clones.** Total poly(A)⁺ RNA was isolated from the C.C58 M75 myeloma and subjected to formaldehyde gel electrophoresis. Hybridization with the 32P-labeled, nick-translated 3.1 kb C, probe (see Materials and Methods) demonstrated a single hybridizing 1 kb species, approximately the size expected for a kappa L chain mRNA. Complementary DNA clones of the total poly(A)⁺ mRNA were made by the method of Okayama and Berg (28). Transformants were screened by colony hybridization with the 3.1-kb C, probe, and 11 strongly hybridizing colonies were identified, all in the RR1 strain. Three of these were shown by restriction enzyme mapping to contain inserts of ~1,050 bp, large enough to encode the entire M75 L chain and 360 bp of flanking sequences.

The restriction map of the mouse DNA insert in plasmid p9(35) and the strategy employed in determining its nucleotide sequence are illustrated in Fig. 1. The presence of a Bcl I site was suspected from work of Max et al. (47), and to use it for cloning into M13mp6 and M13mp9, plasmid p9(35) was isolated after transformation of *E. coli* K12 GM33 that lacks the dam methylase system (30). To analyze the sequence at the 3' end of the insert, a fragment of p9(35) was cleaved with Pvu II and treated with the enzyme Bal-31 for various periods, as described by Poncz et al. (48). Samples at each time point were cleaved with Bcl I, and the fragments corresponding to the 3' end of the cDNA were cloned.

![Figure 1](https://example.com/figure1.png)

**Figure 1.** The strategy employed in determining the nucleotide sequence of the cDNA insert of plasmid p9(35) is indicated by the arrows beneath the figure. Sequence from right to left (3' to 5' of the mRNA) was determined from M13mp8 clones, and from left to right (5' to 3' of the mRNA) was determined from M13mp9 clones. Coding segments are indicated as follows: L, δ, V, δ, J, δ, C, δ. The 5' and 3' untranslated regions appear as a solid line (---), and vector is indicated by a dashed line (-----). The nucleotide sequence of the 3' untranslated region and poly(dAdT) segment from position 938 to approximately position 1,004 was not determined (see text).
into the Bgl I and Hinc II sites of M13mp8 for sequence analysis. The nucleotide sequence of 938 bp of the L chain cDNA insert of p9(35) is presented in Fig. 2. The sequence of ~66 bp at the extreme 3' end of the 3' untranslated region and the poly(dAdT) region, estimated at 50–60 bp, was not determined.

Southern Hybridization of Genomic DNA Fragments. High molecular weight DNA from the C.C58 M75 myeloma and from livers of the C.C58, C58/J, and BALB/cAn strains of mice was digested with Bam HI, Hind III, or Eco RI and subjected to electrophoresis on 0.6% agarose gels. The DNA was transferred to nitrocellulose and hybridized to a 32P-labeled probe consisting of a 200 bp Pst I-Kpn I fragment that contained the 5' untranslated region (5'UT), leader, first framework (Fr1), and first complementarity determining region (CDR1) of the M75 k L chain. This fragment had been cloned into the plasmid pUC18 (29) and radiolabeled as described in Materials and Methods.

Comparison of the Bam HI and Hind III fragments labeled in C.C58 M75 myeloma DNA with those in C.C58 liver DNA reveals in both digests a unique hybridizing fragment in the M75 DNA (Fig. 3a). Further studies not reported here (M. Goldrick, P. Ponath, and P. Gottlieb, unpublished results) indicated that these fragments (7.4 and 4.0 kb in the Bam HI and Hind III digests, respectively) corresponded to the rearranged L chain gene expressed by this myeloma. The fragment shared by the M75 myeloma and C.C58 liver DNA (3.2 and 2.8 kb in Bam HI and Hind III digests, respectively) is likely to correspond to an unrearranged germ line gene homologous or identical to that expressed by the M75 myeloma. As expected, liver DNA from the C58/J strain, the source of the L chain genes of the C.C58 strain (22), contains similar common fragments. Of major interest is the finding that the Bam HI and Hind III digests of liver DNA from BALB/cAn, the strain that provided the genetic background of C.C58, and which does not express the genetic markers shown to be due to M75-like L chains (21, 22), contain strongly hybridizing fragments of 7.8 and 8.4 kb, respectively. VkSer-related fragments of different size were also observed in Eco RI digests of C.C58 and BALB/c DNA (2.1 and 2.8 kb, respectively) (Fig. 3b).

Liver DNA from a variety of inbred, recombinant-inbred, and recombinant strains was then digested with Bam HI, Hind III, or Eco RI, and tested in Southern hybridizations with the VkSer-specific probe. As summarized in Table I, all strains that express the L+peptide marker and the Ef1* polymorphism contain strongly-hybridizing fragments of the size present in the C.C58 and C58/J strains (Fig. 3, a and b). Strains that do not express these markers contain hybridizing fragments identical in size to those of the nonexpressing strain, BALB/cAn.

Discussion

The nucleotide sequence of the 5'UT, leader, and V segments of the C.C58 M75 k chain cDNA clone p9(35) is aligned in Fig. 2 with the sequences determined for the BALB/c myeloma kappa chains MOPC21 (49) and MPC11 (50). These are two of the BALB/c myeloma k chains to which the M75 L chain is most homologous (6). To maximize homology, the 36-bp insertion in the V segment of the MPC11 sequence (50) has been omitted from the sequence (see Fig. 2 legend). The percentage differences observed when nucleotide sequences
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of Fr and CDR of the M75, MOPC21, and MPC11 L chains are compared pairwise are shown in Table II. The Fr1, Fr2, CDR1, CDR2, and leader plus 5'UT regions of M75 differ from the corresponding regions of MOPC21 and MPC11 by comparable amounts, ranging from 16 to 28%. In contrast, Fr3 of M75 is more closely related, differing at 13 and 5% of its nucleotides from the corresponding region of MOPC21 and MPC11, respectively. Comparison of the MOPC21 and MPC11 sequences indicate comparable differences in most segments.

The translated amino acid sequence of the C.C58 M7B L chain is compared in Fig. 4 with the amino acid sequences of BALB/c L chains, which appear to be most closely related to M75 (6). It is immediately apparent that both MOPC21 and MPC11 contain leader sequences that are nine amino acids longer than that of the M75 L chain. As summarized in Table III, large differences (39-40%) are observed between the leader and Fr1 segments of the M75 L chain and those of MOPC21 and MPC11 at the positions over which they can be compared. In contrast, the Fr2 region of M75 is nearly identical to those of MOPC21 and MPC11, differing at only 7 and 0% of the amino acids, respectively. The amino acid sequence of Fr2 of M75 is more similar to the corresponding region of MOPC21 and MPC11 than would be expected from differences at the nucleotide level (16% and 20%, respectively). This is also evident when the Fr2 regions of MOPC21 and MPC11 are compared. One interpretation of this finding is that selection at the protein level, perhaps for ability of the L chain to fold properly or to associate with H chain, may be acting on the Fr2 region. In contrast to Fr2, differences in amino acid sequence between M75 and the other proteins in Fr3 are what might be expected from their nucleotide sequences.

The J segment of the C.C58 M75 κ chain is nearly identical in nucleotide sequence to that of Jκ1, the J segment farthest upstream of the BALB/c Cκ gene (33, 54). The differences from BALB/c Jκ1 at positions 381 and 382 (Fig. 2) may reflect junctional diversity introduced at position 96 of the L chain by joining V...
FIGURE 3. Southern hybridization analysis of genomic DNA from the C.C58 M75 myeloma and from liver of the C.C58, C58/J, and BALB/cAn strains was performed as described in Materials and Methods. (a) Digestion was performed with Bam HI (1-4) and Hind III (5-8) on the following DNA samples: C58/J liver DNA (1 and 5); C.C58 liver DNA (2 and 6); C.C58 M75 myeloma DNA (3 and 7); and BALB/cAn liver DNA (4 and 8). The sizes of molecular weight standards are given in kb; (b) Digestion was performed with Eco RI on BALB/cAn, C.C58, and C58/J liver DNA (1, 2, and 3, respectively).

and J gene segments. The difference at nucleotide 416, which results in substitution of an asparagine at position 107 in M75 for a lysine in BALB/c could reflect a difference in the germ line J sequences of BALB/c and C.C58 strains, or somatic variation in the expressed M75 L chain gene. The basis of these differences will become clear from nucleotide sequence analysis of the C.C58 germ line J genes.

Comparison of the nucleotide sequence of the C, region of the C.C58 M75 L chain with that of the unrearranged BALB/c C, gene (47) revealed a single silent substitution in the codon for isoleucine 205 of the M75 L chain (Fig. 2). The 3’ untranslated region of the M75 L chain cDNA differs in sequence from the
TABLE I
Correlation of Expression of lα-peptide and EF1α Phenotypes with Size of Restriction Fragments Containing V, Ser-related Genes

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<th>Hind III</th>
<th>Eco R1</th>
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<td></td>
<td></td>
<td></td>
<td>3.2*</td>
<td>7.8</td>
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</tr>
<tr>
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<td>+</td>
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<td>-</td>
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</tr>
<tr>
<td>C58/J</td>
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<td>+</td>
<td>+</td>
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</tr>
<tr>
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<td>+</td>
<td>-</td>
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</tr>
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Most of the lα-peptide and EF1α phenotypes have been reported previously (10, 18). The EF1 phenotypes of B6.PL(85NS) and NAK mice were determined by Gibson et al. (24, 25).

* Restriction fragment lengths in kb.
* NT, not tested.

The AKXL 29 strain was originally typed as EF1α-positive (18). The strain then underwent a breeding crisis, and was outcrossed to the C57L/J strain. Progeny were backcrossed four times to AKXL 29, and inbreeding of the resulting mice resulted in fixation of the AKXL 29 strain for the EF1β allele (B. A. Taylor, The Jackson Laboratory, personal communication).

region 3' to the embryonic BALB/c Cα gene only at nucleotide 758 (Fig. 2). If the C.C58 Cα gene is derived from the C58/J strain, then the nearly complete conservation of this region suggests that it may determine some important function.
MOLECULAR GENETICS OF MOUSE V POLYMORPHISM

TABLE II
Comparison of Nucleotide Sequences of 5' Untranslated Region and Leader, Framework, and Complementarity-determining Regions of M75, MOPC21, and MPC11 L Chains

<table>
<thead>
<tr>
<th>Nucleotide differences between:*</th>
<th>M75 and MOPC21</th>
<th>M75 and MPC11</th>
<th>MOPC21 and MPC11</th>
</tr>
</thead>
<tbody>
<tr>
<td>%</td>
<td>22</td>
<td>28</td>
<td>22</td>
</tr>
<tr>
<td>Fr1</td>
<td>22</td>
<td>21†</td>
<td>15‡</td>
</tr>
<tr>
<td>CDR1</td>
<td>21</td>
<td>20</td>
<td>25</td>
</tr>
<tr>
<td>Fr2</td>
<td>16</td>
<td>20</td>
<td>14</td>
</tr>
<tr>
<td>CDR2</td>
<td>25</td>
<td>25</td>
<td>20</td>
</tr>
<tr>
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<td>5</td>
<td>12</td>
</tr>
<tr>
<td>CDR3</td>
<td>50</td>
<td>15</td>
<td>55</td>
</tr>
</tbody>
</table>

Segments compared are as defined by Kabat et al. (6): 5'UT and leader, 9-95; Fr1, 96-164; CDR1, 165-197; Fr2, 198-242; CDR2, 243-263; Fr3, 264-359; CDR3, 360-380.

* Whenever N appears in the nucleotide sequences of MOPC21 and MPC11 in Fig. 2, these comparisons assume that the nucleotide at that position is same as in M75.

† The 36-bp insertion that follows nucleotide 113 in the Fr1 region of the MPC11 L chain mRNA sequence (50) has been omitted in these comparisons.

Figure 4. Comparison of the translated amino acid sequences of the leader and V regions of the C.C58 M75 L chain, and the most closely related known BALB/c \( \kappa \) L chains, as obtained from Kabat et al. (6). Amino acid residues are represented by a one-letter code (51). 12 additional amino acid residues, which precede position 1 of the MPC11 L chain, the result of a 36-bp insertion (50), have been omitted to allow comparison with the other sequences. Positions of the leader, FR, and CDR are as defined by Kabat et al. (6). The beginning of the J segment is indicated by an arrow (\( \uparrow \)). Positions at which the sequence is identical to M75 are indicated by a dash (—).

Finally, Southern hybridization experiments have demonstrated that a V,Ser-specific probe corresponding to the 5'UT region, leader, Fr1, and CDR1 of the M75 \( \kappa \) chain hybridizes strongly to restriction fragments of liver DNA from all inbred, recombinant, and recombinant inbred strains tested. Under stringent hybridization conditions, one strongly hybridizing DNA fragment is observed in Bam HI, Hind III, and Eco RI digests (Fig. 3, a and b), and based on the size of the fragments, strains could be divided into two groups. The presence of strongly
TABLE III
Comparison of Amino Acid Sequences of Leader, Fr, and CDR of M75, MOPC21, and MPC11 L Chains

<table>
<thead>
<tr>
<th>Amino acid differences between:</th>
<th>M75 and MOPC21</th>
<th>M75 and MPC11</th>
<th>MOPC21 and MPC11</th>
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</thead>
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<tr>
<td>Leader</td>
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<tr>
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<td>39</td>
<td>39*</td>
<td>30*</td>
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<td>55</td>
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<td>46</td>
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<td>6</td>
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</tr>
<tr>
<td>CDR3</td>
<td>56</td>
<td>22</td>
<td>44</td>
</tr>
</tbody>
</table>

Segments compared are defined with respect to Fig. 4 as follows: leader, -20 to -1; Fr1, 1 to 23; CDR1, 24 to 34; Fr2, 35 to 49; CDR2, 50 to 56; Fr3, 57 to 88; CDR3, 89 to 97.

* The 12-amino acid segment that precedes residue 1 of the MPC11 L chain and results from a 36-bp insertion (50) has been omitted in these comparisons.

hybridizing Bam HI, Hind III, and Eco R1 fragments of 3.2, 2.8, and 2.1 kb, respectively, was found to correlate completely with expression by the strain of the Iβ-peptide and Ef1α markers (Table I). All nonexpressor strains had strongly hybridizing Bam HI, Hind III, and Eco R1 fragments of 7.8, 8.4, and 2.8 kb, respectively. In addition, in some Southern hybridizations (e.g. Fig. 3b) more weakly hybridizing bands are observed with DNA from strains of both groups, and preliminary results suggest that the size distribution of these bands may also be characteristic of each group. Whether or not these bands contain genes belonging to the same V gene family as the strongly-hybridizing fragment is not yet known. Finally, it is not known whether differences in flanking regions that give rise to the restriction polymorphisms observed also determine expression of V, Ser L chains by one group of strains and not by the other. Analysis of the DNA surrounding the V, Ser-like genes in strains of both groups should shed light on this question, and may provide clues to the genetic events that resulted in divergence of the two classes of strains in this chromosomal region.

Until this study, one possible explanation for expression of L chain phenotypic markers associated with the V, Ser group was that strains that do not express these markers lack V, Ser-like genes altogether. Siekevitz et al. (55) have shown that strains that do not express the major crossreactive idiotype of antiarsenate antibodies of A/J mice lack the single strongly hybridizing Vn gene present in idiotype-positive strains. This is not the case for strains that do not express V, Ser-associated markers, as shown by our Southern hybridization experiments, which show strongly hybridizing sequences in all strains tested. A second possible explanation is that the V, Ser-like genes present in strains that do not express the Iβ-peptide and Ef1α markers contain differences in the coding regions that alter the structure of the products so that they are undetectable in the assays for the phenotypic markers. If this were so, their products might nevertheless be expected to occur at random in the large BALB/c myeloma collection (6). As
shown here, even the most closely related BALB/c myeloma or hybridoma $\kappa$ chains observed differ markedly from the M75 L chain (Figs. 2 and 4). The frequency of expression of the BALB/cAn $V_Ser$-like $L$ chain genes would appear to be very low. In contrast, $V_Ser$-like $L$ chains were observed with an incidence of at least 7 out of a total of ~200 C.C58 and C.AKR myelomas induced (21). Results of studies in progress (J. Bednarczyk and P. Gottlieb, unpublished results) using the $V_Ser$-specific probe to analyze BALB/c hybridomas by the lysate hybridization method of Manser and Gefter (56) should provide information on the expression of $V_Ser$-like genes in this strain.

It is possible that $V_Ser$-like genes of strains that do not express $V_Ser$-associated markers contain in-frame termination codons in coding regions or mutations in promoter, splicing, recombination, or other signals required for their expression. Nucleotide sequence analysis of cloned unrearranged $V_Ser$-like genes from liver DNA of both BALB/cAn and C.C58 strains should show whether or not $V_Ser$-like genes of BALB/cAn are defective in coding or regulatory sequences, or conversely, whether C.C58 $V_Ser$-like genes contain unusual flanking sequences that may affect their expression. These studies are in progress. Only one strongly hybridizing fragment and one $V_Ser$-like gene has been identified to date in each strain (M. Goldrick, T. Boyd, P. Ponath, and P. Gottlieb, unpublished results). However, multiple clones must be analyzed, as shown by results of Siekevitz et al. (57), who isolated three different $V_n$ genes related to the $V_n$ gene that determines the major crossreacting anti-Ars idiotype of A/J mice from a single hybridizing 6.4 kb band of genomic DNA.

Our studies on the strain-specific nature of $V_Ser$ gene expression may be compared with studies by Bothwell et al. (58) and Loh et al. (59) on the strain-specific expression of certain $V_n$ regions in the response of C57BL/6 mice to the (4-hydroxyl-3-nitrophenyl)acetetyl (NP) hapten. Whereas only one strongly hybridizing $V_Ser$-related fragment is detected in DNA of strains that do and do not express the $I_k$-peptide and $E_{F1}^\kappa$ markers, those workers detected multiple intensely-hybridizing fragments in strains that do and do not express the NP$^b$ idiotype. Loh and coworkers showed that in C57BL/6 mice, only one of these $V_n$ genes was used in the response to NP, and that none of the related genes in BALB/c were used, three being pseudogenes, and two containing CDR differences that make them unlikely to be useful for anti-NP antibodies. BALB/c mice use different $V_n$ genes to produce anti-NP antibodies (59). Since the antigen-binding specificity of C.C58 antibodies containing $V_Ser$ $L$ chains is not known, we are unable to use immunization to help determine whether failure to express $V_Ser$-associated phenotypic markers reflects use by nonexpressor strains of a different $\kappa$ chain group. However, studies of germline $V_Ser$-like genes should reveal whether it is at least possible for phenotypically-negative strains to express the $I_k$-peptide and $E_{F1}^\kappa$ markers.

Summary

Previous studies (21) have shown that two mouse $\kappa$ light ($L$) chain variable ($V$) region polymorphisms, the $I_k$-peptide and $E_{F1}^\kappa$ markers, reflect expression of a characteristic group of $V_n$ regions, called $V_Ser$, by some inbred strains and not others. Expression of $V_Ser$ is controlled by a locus on chromosome 6, the
chromosome that contains the κ locus. To further characterize this Vκ group and begin to analyze the basis for its strain-specific expression, full-length complementary DNA (cDNA) copies were produced of L chain mRNA from the M75 myeloma that had been induced in the C58 strain of mice, and which produces a Vκ Ser L chain. The C58 strain is congenic with BALB/cAn, differing in the region of chromosome 6 that controls expression of the Vκ polymorphisms and the Lyt-2 and Lyt-3 T cell alloantigens. The complete nucleotide sequence of this cloned cDNA was determined and compared with the nucleotide sequences the most closely related BALB/c myeloma L chains known. Results indicated significant differences throughout the variable region, but particularly toward the 5′ portion of the sequence. A probe corresponding to 200 bp of the 5′ end of the cloned Vκ Ser cDNA was used in Southern hybridizations of restriction digests of liver DNA from a number of inbred, recombinant, and recombinant inbred strains. Under stringent hybridization conditions, one strongly-hybridizing fragment was observed in BamHI, HindIII, and EcoRI digests, and based on the size of the fragments, strains could be organized into two groups. The presence of strongly hybridizing BamHI, HindIII, and EcoRI fragments of 3.2, 2.8, and 2.1 kb, respectively, was found to correlate completely with expression by the strain of the Iκ-peptide and Efla markers. All nonexpressor strains yielded hybridizing fragments of 7.8, 8.4, and 2.8 kb, respectively. Possible explanations for strain-specific expression of Vκ Ser-associated phenotypic markers are discussed.

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References


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