NUCLEIC ACID AND PROTEIN SEQUENCES OF PHOSPHOCHOLINE-BINDING LIGHT CHAINS*

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Recent studies on the control of the immune response have revealed the importance of idiotypes and their recognition by both B and T cells. Most of these studies have focused on a few well-studied idiotypes, one of which is T15. This is the major idiotype elicited when BALB/c mice are immunized with the hapten phosphocholine (PC), either in its natural form as part of bacterial or parasite cell walls or artificially attached to protein and other carriers (1). Other strains of mice produce lesser amounts of T15 idiotype. The heavy-chain variable region of the T15 myeloma, an IgA κ protein that is the prototype for these antibodies, has been completely sequenced (2, 3). The amino acid sequence of the variable region of the S107 heavy chain, which is also an IgA κ myeloma, is identical to T15 (2, 4). The heavy chain of HOPC8, a third PC-binding IgA κ myeloma bearing the T15 idiotype, has also been completely sequenced and differs by only one amino acid in its third hypervariable region from T15 and S107 (2, 4). Only partial sequences through residues 30-40 of the light chains of these proteins have been reported, and the peptide containing the third hypervariable region has been especially difficult to purify, precluding the immediate completion of the protein sequences (2). It has become necessary to determine the sequence of the third hypervariable region and J segment of the S107 light chain to study hybridomas producing PC-binding antibodies and somatic variants of S107 with changes in antigen binding (5). We have therefore cloned and sequenced the rearranged light-chain variable region gene that codes for the secreted S107 light chain. Here we report the base sequence that codes for amino acid residues 1 through 108 and compare it to the amino acid sequence of the T15 light chain, which has been determined through amino acid residue 88.

Materials and Methods

Cloning of the Light-Chain Gene. The S107 cell line was obtained from the Salk cell bank (The Salk Institute, La Jolla, Calif.). S107 DNA was isolated from cultured cells and the genomic DNA was digested with Eco R1 restriction enzyme. Fragments containing the recombined κ gene DNA were identified by Southern blot analysis of S107 compared with embryo DNA with a κ-chain constant-region probe (6). Fragments were then further enriched by preparative agarose gel electrophoresis as described (7). Two distinct fragments of ~18 kilobase (kb) contained rearranged κ-chain DNA. Both were analyzed, but only one, named S107A, is

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When DNA from the S107 cell line was digested with Eco RI and analyzed for rearranged \( \kappa \)-chain constant-region genes, two bands of \( \sim 18 \) kb were identified and cloned in Charon 4A. A total of 120,000 recombinant phages were analyzed, 10 of which contained \( \kappa \) C-region sequences. On the basis of restriction endonuclease analysis and heteroduplex mapping (not shown), these clones represent two distinct genes. Both genes have been sequenced. One, which we have named S107B, has an unusual V-J recombination and shares only 50% of its coding sequence with the light chain secreted by S107. This will be described in detail elsewhere.\(^2\) A second recombined gene, which we have named S107A, is the subject of the investigations.

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\(^1\) Rudikoff, S., Y. Satow, E. Padlan, P. Davies, and M. Potter. 1981. Kappa chain structure from a captallized murine Fab': role of joining segment in hapten binding. Manuscript submitted.

\(^2\) Kwan, S.-P., E. Max, J. G. Seidman, P. Leder, and M. D. Scharff. Manuscript in preparation.
Fig. 2. Nucleotide sequence of the active S107A light chain gene and the light chain for which it codes. The numbers indicate the amino acid residue using the Kabat numbering system. The nucleotide sequence was determined as described in the text. The amino acids represent the amino acid sequence deduced from the nucleotide sequence. The solid line represents the identity of amino acid sequence of T15 determined as described in the text. The S107 light chain is of particular interest in that this chain, as well as the idiotype of the native molecule, is highly conserved in all inbred mouse strains (13), which suggests a strong selective value for these gene products. The genetic rearrangement producing the active \( \kappa \)-chain gene involves recombination of the V gene with the J1 gene segment, which is the first J found 5' from the \( \kappa \) C-region gene (14). It is intriguing that all \( \kappa \) chains analyzed to date from PC-binding proteins employ the J1 sequence, although a number of these light chains (i.e., M603 and M167) differ considerably in amino acid sequence (2, 12). The 3-dimensional X-ray analysis of the PC-binding myeloma protein M603 has demonstrated that Leu 96, the first amino acid of the J segment, is a hapten-containing residue (15). Thus J1, the only J segment encoding Leu at position 96 (15), may be required for PC binding, or these V genes may, due to genetic restrictions, only pair with J1. The nucleotide structure of the S107 \( \kappa \) chain has thus provided important information on the third hypervariable region and J segment from this molecule as well as demonstrating that the T15

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ATG TAT ATA TGT TGG TCT ATT TCT TAT TGT AGG TGC CTC GTG CAC GAC ATT GTG ATG
ASP ILE VAL MET

ACT CAG TCT GCA ACT TCT CTT GCT GTG ACA GCA AGT AAG AAG GTG ACC ACC ATT AGT TGC ACT
THR GLN SER PRO THR PHE LEU ALA VAL THR ALA SER LYS LYS VAL THR ILE SER CYS THR

GCC CTT TAT CCT GGT GCA CAA AAA CAC AAG GTG CAC TAC TGG GCT TGG TAC CAG AAG
ALA SER GLU SER LEU TYR SER SER LYS HIS LYS VAL HIS TYR LEU ALA TRP TYR GLN LYS

AAA CCA GAG GAA TCT CCA ACT ATA TAC GGG GCA ACC ACA TAC ATT GGG GTC
LYS PRO GLU GLN SER PRO LYS LEU LEU ILE TYR GLY ALA SER ASN ARG TYR ILE GLY VAL

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CAG GTT GAA GAG CTC ACA CAT TAT TAC TGT GCA CAG TTT TAC AGC TAT CCT CTC ACG TTC
GLN VAL GLU ASP LEU THR HIS TYR TYR CYS ALA GLN PHE TYR SER TYR PRO LEU THR PHE

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GOT GCT GGG ACC AAG CTG GAG CTT CAA AGT AAG TAC ACT TTT CTC ATC TTCT
GLY ALA GLY THR LYS LEU GLU LEU LYS ARG

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Reported in the present paper. This clone codes for the light chain polypeptide employed in the secreted PC-binding S107 protein. Through the restriction analysis illustrated in Fig. 1, a 1.2-kb Xba-Xba fragment containing all of the V region was obtained and its base sequence was determined. Bases 49-171 code for an amino acid sequence that is identical to that reported for the N-terminal 35 amino acids of the light chain secreted by both the T15 and S107 tumors (2). The sequence of an additional 50 amino acids of the T15 light chain has been determined. As indicated by the continuous line in Fig. 2, this sequence is also identical with that determined from the DNA sequence.

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and S107 κ chains are identical for at least their N-terminal 88 amino acids. It is therefore probable that these κ chains are identical throughout this entire V region, as has been demonstrated for the heavy-chain V regions.

Summary
An 18-kilobase DNA fragment containing the sequence coding for both the variable and constant regions of the S107 mouse immunoglobulin light chain was cloned from total cellular DNA. The complete nucleotide sequence of the κ-chain variable-region gene is reported. Determination of the amino acid sequence encoded by the DNA is found to be identical to the protein sequence of the T15 light chain through residue 88. Direct sequence analysis confirmed that the J1 joining segment is used in the recombination event producing the active κ light chain gene.

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