

SEQUENCES AND REPERTOIRE OF HUMAN T CELL
RECEPTOR α CHAIN VARIABLE REGION GENES IN
MATURE T LYMPHOCYTES

BY YASUNOBU YOSHIKAI, NOBUHIRO KIMURA, BARRY TOYONAGA, AND
TAK W. MAK

*From The Ontario Cancer Institute; and the Department of Medical Biophysics, University of
Toronto, Toronto, Ontario, Canada M4X 1K9*

The T cell antigen receptor (TcR),¹ which recognizes antigen and the MHC gene product, seems to be a cell surface protein heterodimer consisting of an acidic (α) and a basic (β) chain (1–3). The molecular cloning of the TcR β chain (4, 5), and subsequently the α chain (6–8), established that these genes are distinct from Ig genes. Based on sequence analysis of cDNAs and germline sequences, it appears that functional TcR genes are formed by somatic recombinations of variable (V), diversity (D), joining (J), and constant (C) gene segments (4–8, 9). Chromosomal mapping of these genes indicate that they are found at locations different from those of Ig genes, indicating that these genes are different from those used in the rearrangement of Ig genes (10–13). The germline organizations of these TcR and the Ig genes share a basic structure, but definite differences are revealed upon closer examination (14–19). Thus, TcR genes have their own set of germline genes as their basis for functional diversity.

Estimates of the repertoire of TcR V_α gene segments in mouse have been reported (20, 21). The studies suggest that there may be fewer germline V_α gene segments than the number of Ig H and κ chain variable chain segments, but more than the estimated number of TcR V_β gene segments in mice (22, 23). Similar sequence analyses to estimate the repertoire of the human TcR α or β chain V gene segments are not yet available. Since preliminary studies (18) indicate that somatic mutation does not play an important role in the generation of diversity of these genes, the generation of diversity most likely rests on the extent of recombinational joinings, and thus the number of V and J gene segments is of particular significance.

In this study, we have sequenced and analyzed 24 different α chain cDNA clones derived from human peripheral blood T lymphocytes and T cell lines. The familial organization of the V_α segments and the variability within the human V_α genes have been determined.

This work was supported by the Medical Research Council of Canada, the National Sciences and Engineering Research Council of Canada, and a special research fund from the University of Toronto. Y. Yoshikai and B. Toyonaga are recipients of awards from the Medical Research Council of Canada. Address correspondence to Dr. T. W. Mak.

¹ *Abbreviation used in this paper:* TcR, T cell antigen receptor.

Materials and Methods

Constructure of cDNA Libraries. Double-stranded (ds) cDNA was synthesized from poly(A)⁺ RNA derived from PHA-stimulated peripheral human T cells. After treatment with Eco RI methylase and size selection, the ds cDNA was cloned into the Eco RI site of λ gt10 using Eco RI linkers as described before (13).

Isolation of Human α Chain cDNA Clones. The peripheral human T cell library was plated on *E. coli* C600/HFL. Screening of duplicate filters was carried out according to the standard procedure (24). Hybridizations were done for 18 h at 65°C in 5 × SSC, 5 × Denhardt's, 100 μ g/ml denatured Salmon sperm DNA, and 0.5 μ g ³²P-labelled nick-translated PY14 α cDNA probe previously described (13). Filters were washed in 2 × SSC, 0.1% SDS at room temperature several times, followed by washing in 0.2 × SSC at 65°C.

DNA Sequencing. The cDNA inserts were subcloned into M13 mp9 sites of the bacteriophage vector, and the sequences were determined using the specific-primer-directed dideoxynucleotide sequencing technique in conjunction with the dideoxy method (25).

Southern Blot Analysis. DNA was extracted from bone marrow cells and digested with Eco RI and Bam HI. DNA (10 μ g) was electrophoresed through 0.8% agarose and transferred to nitrocellulose filters as described by Southern (26). Hybridization was for 24 h at 65°C in 5 × SSC, 5 × Denhardt's, 100 μ g/ml denatured salmon sperm DNA, 10% dextran sulfate, and 0.5 μ g ³²P-labelled nick-translated cDNA probe. Filters were washed at 65°C with 3 × SSC containing 0.1% SDS.

Results

Sequence of Human α Chain cDNA Clones. To examine the repertoire of the human TcR α chain genes, we have cloned α chain-homologous cDNAs from a library of human PHA-stimulated peripheral blood T lymphocytes. The library was screened using a constant region probe from the human TcR α chain, PY14 (9), and 24 cDNAs clones were randomly chosen. The inserts were subcloned into M13 mp9, and the nucleotide sequences of the cDNAs were determined (Fig. 1). The deduced protein sequence of these clones is presented in Fig. 2. The nucleotide sequence of cDNA PY14 (9) has been included for comparison. Examination of this cDNA sequences showed great variation in the N-terminal half, which correspond to the variable region of the TcR α chain gene. These variable genes can be divided into at least two gene segments corresponding to the V and J gene segments. The exact junctions between these sequences were determined by comparison of the cDNA sequences to those previously reported for human germline V _{α} and J _{α} genes (16). As can be seen in Fig. 1, some of the sequences of the V gene segments are identical to other V gene segments. For example, V _{α} gene segments of clone HAP10 and clone HAP60 contain identical V gene segments. Similarly, identical V sequences can be found between clones HAP26 and HAP71; HAP05 and HAP44; HAP41, HAP17, and HAP49; and HAP02, HAP28, HAP29, and HAP32. A high degree of sequence homology can also be found between some cDNA clones, suggesting that they belong to the same V gene family. For example, clones HAP(10,60) and PY14; HAP21 and HAP12, HAP(41,17,49,50) and HAP50 are related to each other at above 75% homology at the nucleotide level. Lower degrees of homology exist between members of the different families, with regions of conserved sequences that code for structurally important amino acids. These conserved nucleotides and deduced amino acids for which they code are also indicated in Fig. 1. On the basis of

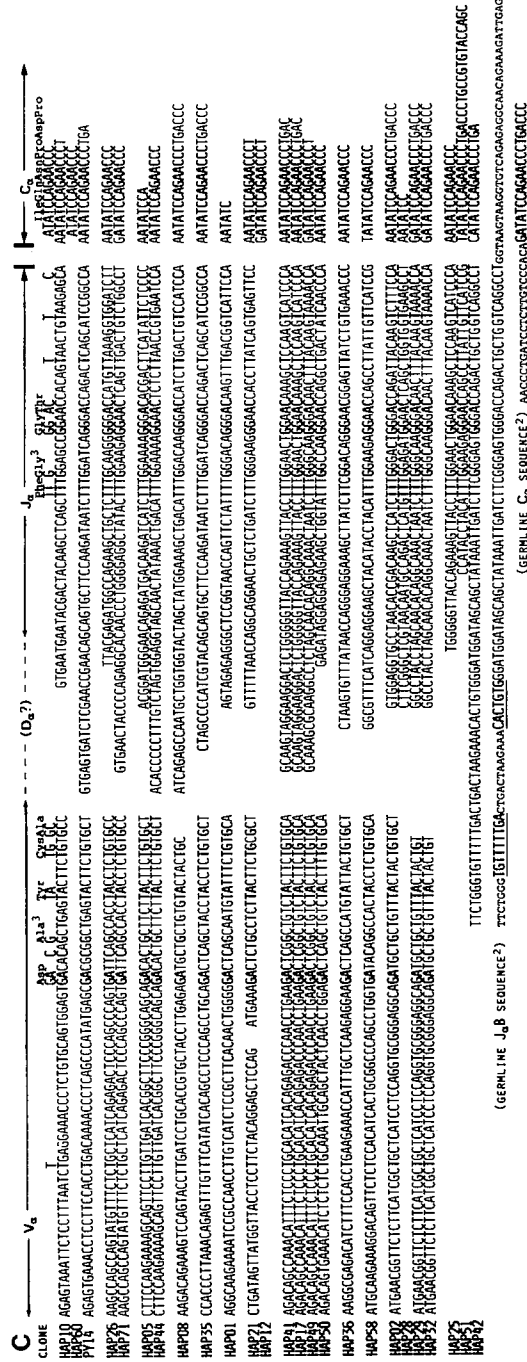


FIGURE 1. Sequences of 25 human T cell receptor α chain messages obtained from mature human T lymphocytes. 24 cDNAs from a human T cell lymphocyte library and one from human T cell line Jurkat (9) were obtained, and their sequences were determined. The sequences were aligned to obtain maximum similarity and grouped on the basis of homology to each other. Conserved nucleotides and deduced amino acids are in bold letters on top of the sequences. (A) Sequence obtained from PY14 (9). (B) Sequences of germline J α B gene segment and of C α obtained from Yoshikai et al. (16). (C) Deduced amino acid from all but one of the listed DNA sequences. V α , J α , D α , and C α are variable, diversity, joining, segment, and constant region, respectively, of human T cell receptor α chain.

these sequence analysis, 14 of the 22 V_α gene segments isolated are unique. Thus 14 is the lower limit for the number of different V_α segments used in mature T cells.

The deduced protein sequences of the V_α gene segments have been aligned for maximum homology to each other. The deduced sequence from the cDNA clone PGA is included for comparison (8). Both inter- and intrafamilial similarities between V_α genes are even more pronounced at the protein level. Two examples of this are indicated (+) in Fig. 2.

Examination of the J gene segment sequences indicated that, although there are some segments with similar or identical sequences, a large number of distinct sequences can be found. The deduced amino acid sequences of these V and J segments is summarized in Figs. 2 and 3. These consensus sequences illustrate roughly the hypervariable and framework regions of V and J segments. Comparison of the J_α nucleotide sequences determined in this study (Fig. 1) and elsewhere (16, 28) are illustrated in Fig. 3a, while protein sequence comparison can be seen in Fig. 3c. Germline J_α gene segments from Yoshikai et al. (16) are included in Fig. 3b for comparison. An examination of V_α and J_α used in different clones (Fig. 1), and their respective familial origins (Fig. 3) suggest that there are no constraints on the association between V_α and J_α segments. An interesting observation is that the J_α gene segment located closest to the C_α in the germline appears to be used four times. The assignment of J_α families is arbitrary and extends the collection sequenced from genomic germline DNA by Yoshikai et al. (16). The combined number of different cDNAs and germline J_α sequences indicated that there are more than 21 independent J_α segments that can be used in the human T cell receptor.

At this time the exact source of sequence diversity at the V_α - J_α boundary is not known. The 3–20 nucleotide junctional sequences may have arisen from insertion of nucleotides, or merely by the use of as yet unknown germline V_α , D_α , or J_α sequences. The 3' variability of the germline J_α sequences introduces further variability at the J_α - C_α junction, presumably by splicing of the germline J_α sequence into the C_α gene.

Southern Analysis of V Gene Segments in Human Germline DNA. To determine the extent of variability of V_α gene segments within germline DNA, Southern blot analyses of Bam HI- or Eco RI-digested human germline DNA was performed using the cDNAs from Fig. 1 as probes. Representative results are presented in Fig. 4. In most cases, multiple bands hybridizing to the cDNA probes can be observed at reasonably high stringency. The fragments corresponding to the constant region are denoted. The number of V gene segments appear to range from one to seven. These results support the hypothesis that the V_α gene families have more V_α gene members than V_β gene families in mouse (22, 23). On the basis of the Southern gel results, the number and size of V_α gene families can be estimated (Table I) to contain ~40 members (12 families).

Homologies Within the Variable Regions of the Human TcR α Chain Genes. Alignment of DNA and protein sequences of the 22 cDNA V_α regions reveals regions of high and low homology reminiscent of the Ig hypervariable regions proposed by Wu and Kabat (29). A variability plot of the protein sequences in their optimized alignments (from Fig. 2) is given in Fig. 5. In this

a

CLONE	alpha FAMILY	deduced amino acids: PheGly GlyThr Leu5	
HAP49	J _α 6	GCAAAAGCGCAAGGCCCTTAGCAACACAGCCGGAACCTAATC	GATATCCAGAACCCCT
HAP79	J _α 6	GGCTTACTAGCAACACAGCCGCAAACTAATC	GATATCCAGAACCCCTGACCC
HAP36	J _α 6	CTAAGTGTTTATAACCCAGCCGGAAGCTTATC	AAATCCAGAACCC
HAP02	J _α 6	GTGGAGTGCCTAACCACCCAGCAAGCTCATC	AAATCCAGAACCCCTGACCC
HAP08	J _α 6	ATCAGAGCCAAATGCTGGTACTAGCAACTGAAAGCTGACA	AAATCCAGAACCCCTGACCC
HAP44	J _α 6	GACACTGCTTACTTCTCTAGTGGAGGATAGCAACTATAAATCTGACA	AAATCCAGAACCC
HAP42	J _α 6	ATGGATAGCAGCTATATAAATTTGATC	CATATCCAGAACCCCTGA
SUPT1A.2	J _α 6	TTACAGATGGCCAGAAAGCTGTCTC	AAATCCAGAACCCCTGACCC
HAP26	J _α L	GAGATAGGAGGAGAGAGCTGGTA	AAATCCAGAACCC
HAP50	J _α M	GTGAATGAATPACGACTACAAAGCTCAGC	AAATCCAGAACCCCT
HAP10	J _α N	GCAAGTAGGAAGGACTCTGGGGTTACCAGAAAGTTACC	AAATCCAGAACCCCTGAC
HAP41	J _α O	GAAATCTGGGGTTACCAGAAAGTTACC	AAATCCAGAACCC
HAP23	J _α O	CTGGACAGCAGTCTTCCAAAGATAATC	AAATCCAGAACCCCTGACCC
PY14	J _α O	CTAGCCCCATCGTACAGCAGTCTTCCAAAGATAATC	AAATCCAGAACCCCTGACCC
PGA	J _α A	ACGGATGGGAACAGAGATGACAAAGATCATC	AAATCCAGAACCCCTGACCC
HAP35	J _α A	GTCGACTACCTACTCTGTGCT	AAATCCAGAACCC
SUPT1B.2	J _α B	GTGAAGAGGAACTGACTG	GATATCCAGAACCC
HAP05	J _α B	CTTCGGGCTGTAACTGCCAGACTCATG	AAATCC
HAP71	J _α K	GTATTCAGCCACTACCTCTGTGCC	AAATCCAGAACCCCTG
HAP28	J _α S	GATCAGCCACTACCTCTGTGCC	AAATCCAGAACCC
HAP21	J _α S	GACTTCGCCCTTACTTCTGTGCC	AAATCCAGAACCCCTG
HAP58	J _α I	GATACAGCCACTACCTCTGTGCC	TATATCCAGAACCC
HAP51	J _α I	GACTCAGCAATGTATTTCTGTGCC	TATATCCAGAACCCCTGACCC
HAP01	J _α I		AAATATC

b

α_g ←

← β_g

← (D_B?)

← V_g

b

	Jalpha FAMILY		
germline ¹	J _α A	GYSSASKIIFGSGT	IRLSIRP
germline ¹	J _α B	MDSSYKLIIFGSGT	IRLLVVP
germline ¹	J _α C	SSGSARQLTIFGSGT	IQLTVLP
germline ¹	J _α D	TTDSWGKFEIFGSGT	IQVVVTP
germline ¹	J _α E	EGQGFSPFIIFGSGT	IRLLVKP
germline ¹	J _α F	NSGNTPLVIFGSGT	IRLSVIA

FG GT

c

CLONE	Jalpha FAMILY	← V _α → (D _α ?) ← J _α → ← C _α →	
HAP49	J _α G	DsAvYfCA AKRKASNTGKLIIFGSGT	LoVvKp D I Q N P
HAP29	J _α G	DAAvYfCA GLPSNTGKLIIFGSGT	LoVvKp D I Q N P D P
HAP36	J _α H	DsAmYfCA LSVYNQGGKLIIFGSGT	ELSVKp N I Q N P
HAP02	J _α I	DAAvYfCA VEVPTDKLIIFGSGT	IRLoVfP N I Q N P D P
HAP08	J _α I	DAAvYfCA IRANAGGTSYKLIIFGSGT	ILTVhP N I Q N P D
HAP44	J _α K	DtAsYfCA TPPLSSGGSNYKLIIFGSGT	ILLTVhP N I Q N P
HAP42	J _α B	MDSSYKLIIFGSGT	IRLLVVP H I Q N P
SUPT1A ²	J _α B	MDSSYKLIIFGSGT	IRLLVVA
HAP26	J _α L	DsAtYlCA LRDGQKLIIFARGT	MlKvDL N I Q N P D
HAP50	J _α M	DsAvYfCA EIGGEKLVFGSGT	RlTINP N I Q N
HAP10	J _α N	DtAeYfCA VNEYDYKLSFGAGT	TvtVRA N I Q N P
HAP41	J _α O	DsAvYfCA ASRKDSGGYKVTFGTGK	LoVvIP N I Q N P D
HAP25	J _α O	GGYKVTFGTGK	LoVvIP N I Q N
PY14 ³	J _α A	DAAEYfCA VSDLEPNSSASKIIFGSGT	IRLSIRP N I Q N P D P
PGA ⁴	J _α A	DsAvYfCA LDSSASKIIFGSGT	IRLSIRP N I Q N P D P
HAP35	J _α A	DsAtYlCA LAPSYSASKIIFGSGT	IRLSIRP N I Q N P D
SUPT1B ²	J _α A	YSSASKIIFGSGT	IRLSIRP
HAP05	J _α P	DtAsYfCA TDGNRDDKIIFGSGT	RlHLIP N I
HAP71	J _α Q	DsAtYlCA VNYPRGTTLGRLYFGSGT	IQLTVhP D I Q N
HAP28	J _α R	LRARNNARLMFGSGT	IQLVVKP N I
HAP21	J _α S	DsAsYfCA VFNQAGTALIFGSGT	TlLvSs N I Q N P
HAP58	J _α T	DtGHYlCA GVSSGGSYIPTFGSGT	ISLIVhP Y I Q N
HAP51	J _α T	IPTFGSGT	ISLIVhP Y I Q N P D P
HAP01	J _α U	DsAmYfCA SREGSGNQFYFGSGT	ISLTVvIP N I

KL FG GT L V P
50% consensus sequence

FIGURE 3. Nucleotide and deduced protein sequences from J_α gene segments of the human T cell receptor (a) nucleotide sequences of cDNAs, (b) germline J segment protein sequences, (c) deduced protein sequences of messages ¹Yoshikai et al. (16); ²C. T. Denny et al. (28) SUPT1B V segment sequences are from an IgH V family; ³Yanagi et al. (9); ⁴Sim et al. (8); ⁵deduced amino acid from all but one sequence, HAP10.

plot, three regions of high variability can be seen which correspond to amino acid positions 20–35, 55–75, and the region of V-D-J joining, amino acid 100–110. This pattern of variability is similar to that found upon analysis of 12 N-terminally blocked human Ig V_H sequences (30), with the notable exception of the additional variability at the J_αC_α junction, which is not found in Ig V_H sequences.

Discussion

In this paper, we have presented the sequences and analyses of the variable regions of 24 different human α chain TcR cDNAs. All 18 of the 24 cDNAs that contain V segment sequences seem to be messages resulting from productive

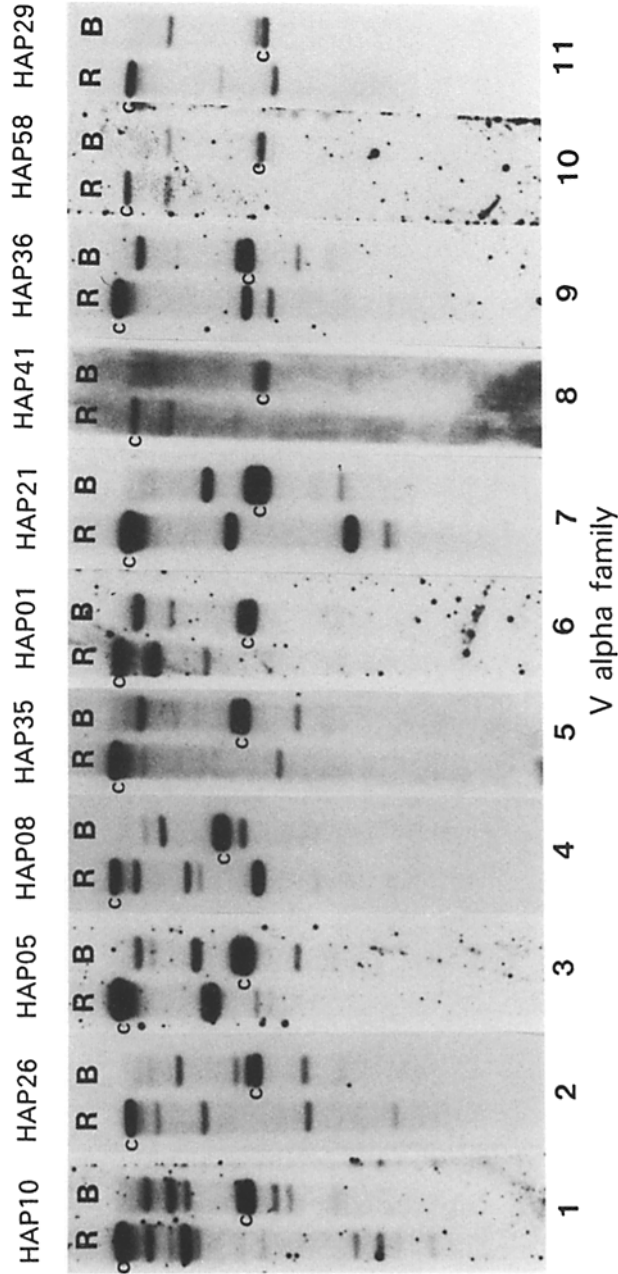


FIGURE 4. DNA was extracted from human bone marrow cells of a donor used and the assigned V_α gene families are designated. (c) Constant region and digested with restriction enzyme Eco RI (R) or Bam HI (B). Southern bands of ~30 kb in Eco RI-digested DNA and 5-7 kb in the Bam HI-digested DNA. Individual clones from Fig. 1 (26, 27).

TABLE I
Human T Cell Receptor α Chain Variable Segment Gene Families

Family	Clones	Approximate family size
V $_{\alpha}$ 1.1	HAP10, HAP60	7
V $_{\alpha}$ 1.2	PY14.1	
V $_{\alpha}$ 1.3	PY14.2	
V $_{\alpha}$ 2.1	HAP26, HAP71	5
V $_{\alpha}$ 3.1	HAP05	4
V $_{\alpha}$ 4.1	HAP08	4
V $_{\alpha}$ 5.1	HAP35	4
V $_{\alpha}$ 6.1	HAP01	3
V $_{\alpha}$ 7.1	HAP21	3
V $_{\alpha}$ 7.2	HAP12	
V $_{\alpha}$ 8.1	HAP41, HAP17, HAP49	3
V $_{\alpha}$ 8.2	HAP50	
V $_{\alpha}$ 9.1	HAP36	2
V $_{\alpha}$ 10.1	HAP58	1
V $_{\alpha}$ 11.1	HAP02, HAP28, HAP29, HAP32	1
V $_{\alpha}$ 12.1	PGA	1
Estimated total		38

Human T cell receptor α chain variable segments (Figs. 1 and 2); PY14.1 (ref. 9), PY14.2 (ref. 16), and PGA (ref. 8) were grouped on the basis of crosshybridization (Fig. 4).

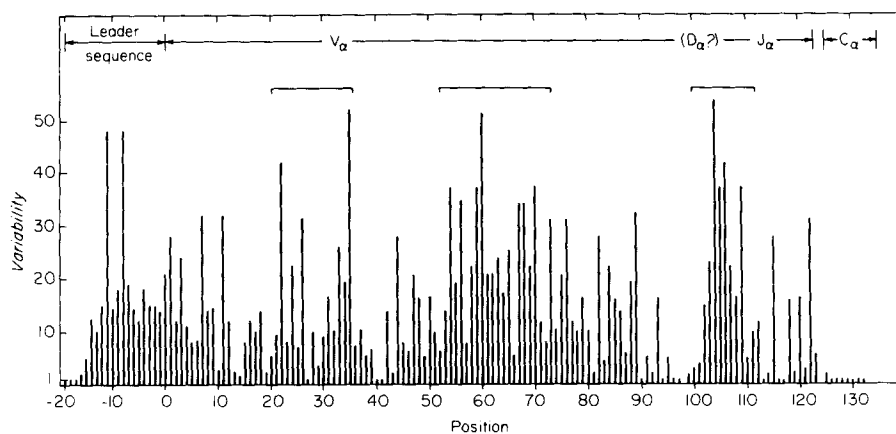


FIGURE 5. Kabat-Wu variability plot based on data presented in Fig. 2. Position: amino acid residues starting from the N terminus.

α chain TcR gene rearrangements, which are capable of encoding functional proteins since they show continuous open reading frames through variable, joining, and constant regions.

Examination of the V_α gene segments by DNA sequencing and Southern blot analysis of germline genomic DNA shows that there are at least 12 V_α families comprised of 40 or more V_α gene segments. It is unlikely that there are many more families used than the 12 described here, as data from our laboratory indicates that, of 10 additional α chain messages from another individual belong to these same 12 V_α families described here (Kimura, N., unpublished data). Furthermore, the number of fragments detected is similar in DNA from different individuals. Thus, although it is possible that this report may not describe all the human α chain V gene segments, it is fairly representative of the several individuals we have surveyed. The number of V regions of the human TcR α chain is considerably higher than those of the λ light chain Ig genes and the TcR β chain genes in the mouse (22, 23). However, it may be lower than that predicted by the number of heavy (31) and κ light (32) Ig V gene segments. The number of members in each family varies considerably among the Ig and TcR genes. For example, while there are 10–50 members in each V gene family of the heavy and κ light Ig chain genes (31, 32), there are very few V_β gene segments, often one per family in the mouse (22, 23). The human V_β gene families, however, are larger.² The murine V_α gene families are composed of one to eight members (20, 21), and our results indicate similar sizes for the human V_α families.

The human J_α gene segments differ from the other immunorecognition genes in number, lack of clustering, and in length. Our previous analysis of the germline genomic J_α organization suggested that there may be numerous J_α segments present spread over a very large distance (16). The data from the present study is consistent with this observation. In fact, the number of the J_α gene segments presented here are unique. Although the exact number of J_α in the human TcR α chain locus cannot be determined at this time, it must be considerably more than the 21 unique sequences isolated to date. A statistical estimation assuming a random assortment predicted ~55 J_α gene segments (D. Tritchler, personal communication). The J_α segments are several codons longer than those of the TcR β chain or the Ig chains. These extra codons may be accounted for by either *N*-terminal sequence diversity upon V_α - J_α joining, the incorporation of putative D_α segments, or by longer germline V_α gene segments. It is not known whether the extra codons could affect the three-dimensional structure and folding of the α and β T cell receptor heterodimer. Nonetheless, the large number and extra length of the J_α gene segments are consistent with a high level of diversity within this region of the human T cell receptor α chain gene, and may be responsible for the high levels of boundary diversity in the TcR α chain.

There are many fine differences in both function and structure between Ig and T cell receptor molecules. The former are expressed exclusively on the surface of B cells and serves as a receptor that can recognize free antigen while

² N. Kimura, B. Toyonaga, Y. Yoshikai, R. P. Du, and T. W. Mak. Sequence and repertoire of the human T cell receptor β chain genes. Manuscript submitted for publication.

the latter are found solely on T cell surfaces and can recognize antigen only in the context of major histocompatibility products (30). Subtle differences, such as in the lengths of the V regions among the Ig, TcR α and β genes also exist.

In spite of these distinctions, the gross overall structures of these genes are probably quite similar, based on previous DNA and deduced protein sequence analysis. From the results reported here, this prediction can be extended, since the variable region TcR α chain gene was found to consist of three hypervariable regions, which correspond roughly to the CDR1, CDR2, and CDR3 hypervariable regions of the Ig (H or L) gene. A similar parallel between hypervariable regions is found in the murine system (20, 21). Should the T cell receptor α and β heterodimer possess no more than the same three hypervariable regions as Ig, and should the basic three-dimensional structures of these T and B cell recognition proteins be similar, then the mechanism for T cell receptor recognition of antigen only in the context of the MHC products (33) becomes even more mysterious.

Summary

24 human T cell receptor α chain messages have been examined by cDNA sequence analysis and Southern blot. The data indicate that there are ~40 α chain T cell receptor variable gene segments, which can be divided into 12 families. Comparison of the J gene segments from the cDNAs to previously determined germline J_α sequences places the number of J_α gene segments over 21, and indicates their number to be ~55. Identical nucleotide sequences in independent isolates of V_α and J_α gene segments indicate that hypermutation may not be a common mechanism for the expansion of diversity in these genes, and suggest that the major source of diversity within the α chain repertoire is a result of recombinational joinings between germline V_α and J_α sequences, combined with imprecise junctional joining. Analysis of the V regions of these α chain messages reveals the presence of three domains of hypervariability roughly analogous to the CDR1, CDR2, and CDR3 regions of immunoglobulin.

We thank Beth Chin and Maurizio Laudisa for technical assistance, and Nicolette Caccia for comments on the manuscript.

Received for publication 5 March 1986.

References

1. McIntyre, B. W., and J. P. Allison. 1983. The mouse T-cell receptor: structural heterogeneity of molecules of normal T cells defined by xenoantiserum. *Cell*. 34:739.
2. Haskins, K., R. Dubo, J. White, M. Pigeon, J. Kappler, and P. Marrack. 1983. The major histocompatibility complex-restricted antigen receptor on T cells. I. Isolation with a monoclonal antibody. *J. Exp. Med.* 157:1149.
3. Meuer, S. C., K. A. Fitzgerald, R. E. Hussey, J. C. Hodgdon, S. F. Schlossman, and E. L. Reinherz. 1983. Clonotypic structures involved in antigen-specific human T-cell function. Relationship to the T3 molecular complex. *J. Exp. Med.* 157:705.
4. Yanagi, Y., Y. Yoshikai, K. Leggett, S. P. Clark, I. Aleksander, and T. W. Mak. 1984. A human T cell-specific cDNA clone encodes a protein having extensive homology to immunoglobulin chains. *Nature (Lond.)*. 308:145.

5. Hedrick, S. M., D. I. Cohen, E. A. Nielsen, and M. M. Davis. 1984. Isolation of cDNA clones encoding T cell-specific membrane-associated proteins. *Nature (Lond.)* 308:149.
6. Chien, Y., D. Becker, T. Lindsten, M. Okamura, D. Cohen, M. Davis. 1984. A third type of murine T-cell receptor gene. *Nature (Lond.)* 312:31.
7. Saito, H., D. Kranz, Y. Takagai, A. Hayday, H. Eisen, and S. Tonegawa. 1984. A third rearranged and expressed gene in a clone of cytotoxic T lymphocytes. *Nature (Lond.)* 312:36.
8. Sim, G. K., J. Yague, J. Nelson, P. Marrack, E. Palmer, A. Augustin, and J. Kappler. 1984. Primary structure of human T-cell receptor α -chain. *Nature (Lond.)* 312:771.
9. Yanagi, Y., A. Chan, B. Chin, M. Minden, and T. W. Mak. 1985. Analysis of cDNA clones specific for human T cells and the α and β chains of the T-cell receptor heterodimer from a human T-cell line. *Proc. Natl. Acad. Sci. USA* 82:3430.
10. Caccia, N., M. Kronenberg, D. Saxe, R. Haars, G. Bruns, J. Goverman, M. Malissen, H. Willard, Y. Yoshikai, M. Simon, L. Hood, and T. Mak. 1984. The T-cell receptor β chain genes are located on chromosome 6 in mice and chromosome 7 in humans. *Cell* 37:1091.
11. Caccia, N., G. A. P. Bruns, I. R. Kirsch, G. F. Hollis, V. Bertness, and T. W. Mak. 1985. T-cell receptor α chain genes are located on chromosome 14 at 14q11-14q12 in humans. *J. Exp. Med.* 161:1255.
12. Lebeau, M. M., M. O. Diaz, J. D. Rowley, and T. W. Mak. 1985. Chromosomal localization of the human T-cell receptor β -chain genes. *Cell* 41:335.
13. Kranz, D. M., H. Saito, C. M. Distèche, K. Swisshelm, D. Pravtcheva, F. H. Ruddle, H. N. Eisen, and S. Tonegawa. 1985. Chromosomal locations of the murine T-cell receptor alpha-chain gene and the T-cell gamma gene. *Science (Wash. DC)* 227:941.
14. Sin, G., S. Clark, Y. Yoshikai, M. Malissen, Y. Yanagi, E. Strauss, T. Mak, and L. Hood. 1984. The human T-cell antigen receptor is encoded by variable, diversity and joining gene segments that rearrange to generate a complete V gene. *Cell* 37:393.
15. Gascoigne, N. R. J., Y.-H. Chien, D. M. Becker, J. Kavaler, and M. M. Davis. 1984. Genomic organization and sequence of T-cell receptor β -chain constant- and joining-region genes. *Nature (Lond.)* 310:387.
16. Yoshikai, Y., S. P. Clark, S. Taylor, U. Sohn, B. Wilson, M. Minden, and T. W. Mak. 1985. Organization and sequences of the variable, joining and constant region genes of the human T-cell receptor α chain. *Nature (Lond.)* 316:837.
17. Winoto, A., S. Mjolsness, and L. Hood. 1985. Genomic organization of the genes encoding mouse T-cell receptor α chain. *Nature (Lond.)* 316:832.
18. Hayday, A., D. Diamond, G. Tanigawa, J. Heilig, V. Folsom, H. Saito, and S. Tonegawa. 1985. Unusual features of the organization and diversity of T-cell receptor α chain genes. *Nature (Lond.)* 316:828.
19. Toyonaga, Y., Y. Yoshikai, V. Vadasz, B. Chin, and T. W. Mak. 1985. Organization and sequences of the diversity, joining and constant region genes of the human T cell receptor β chain. *Proc. Natl. Acad. Sci. USA* 82:8624.
20. Arden, B., J. Klotz, G. Siu, and L. Hood. 1985. Diversity and structure of genes of the α family of mouse T-cell antigen receptor. *Nature (Lond.)* 316:783.
21. Becker, D., P. Patten, Y.-H. Chien, T. Yokota, Z. Eshhar, M. Giedlin, N. R. J. Gascoigne, C. Goodenow, R. Wolf, K.-I. Arai, and M. M. Davis. 1985. Variability and repertoire size in T-cell receptor V_{α} gene segments. *Nature (Lond.)* 317:430.
22. Barth, R., B. Kim, N. Lan, T. Hunkapiller, N. Sobieck, A. Winoto, H. Gershenfeld, C. Okada, D. Hansburg, I. Weissman, and L. Hood. 1985. The murine T-cell receptor employs a limited repertoire of expressed V_{α} gene segments. *Nature (Lond.)* 316:517.

23. Behlke, M. A., D. G. Spinella, H. Chou, W. Sha, D. L. Hartl, and D. Y. Loh. 1985. T-cell receptor β chain expression: Dependence on relatively few variable region genes. *Science (Wash. DC)*. 229:566.
24. Maniatis, T., E. F. Frisch, and J. Sambrook. 1982. Molecular cloning: a laboratory manual. Cold Spring Harbor Press, New York.
25. Sanger, F., S. Nicklen, and A. R. Coulson. 1977. DNA sequencing with chain terminating inhibitors. *Proc. Natl. Acad. Sci. USA*. 74:5465.
26. Southern, E. M. 1975. Detection of specific sequences among DNA fragments separated by gel electrophoresis. *J. Mol. Biol.* 98:503.
27. Toyonaga, B., Y. Yanagi, N. Suci-Foca, M. Minden, and T. W. Mak. 1984. Rearrangements of T cell receptor genes YT35 in human DNA from thymic leukemia T cell lines and functional T cell clones. *Nature (Lond.)*. 311:85.
28. Denny, C. T., Y. Yoshikai, T. W. Mak, S. D. Smith, G. F. Hollis, and I. R. Kirsh. 1985. A chromosome 14 inversion in a T cell lymphoma is caused by site-specific recombination between immunoglobulin and T cell receptor loci. *Nature (Lond.)*. In press.
29. Wu, T., and E. Kabat. 1970. Analysis of the sequences of Bence-Jones proteins and myeloma light chains and their implications of antibody complementarity. *J. Exp. Med.* 132:211.
30. Kabat, E. A., T. T. Wu, H. Bilofsky, M. Reid-Miller, and H. Perry. 1983. Sequences of Immunological Interest. U.S. Dept. of Health and Human Services, Washington, D.C.
31. Brodeur, P., and R. Riblet. 1984. The immunoglobulin heavy chain variable region (Igh-V) locus in mouse. I. One hundred Igh-V genes comprise seven families of homologous genes. *Eur. J. Immunol.* 14:922.
32. Cory, S., B. Tyler, and J. Adams. 1981. Sets of immunoglobulin V_{κ} genes homologous to 10 clones V_{κ} sequences: implications for the number of germline V_{κ} genes. *J. Mol. Appl. Genet.* 1:103.
33. Zinkernagel, R. M., and P. C. Doherty. 1979. MHC restricted cytotoxic cells: Studies on the biological role of polymorphic major transplantation antigens determining T cells restriction specificity function and responsiveness. *Adv. Immunol.* 27:51.