

## Predominant Expansion of V $\gamma$ 9/V $\delta$ 2 T Cells in a Tularemia Patient

TAKAYUKI SUMIDA,<sup>1\*</sup> TOSHIRO MAEDA,<sup>1</sup> HIDENORI TAKAHASHI,<sup>2</sup> SHOUJI YOSHIDA,<sup>2</sup>  
FUMIKO YONAHARA,<sup>1</sup> AKEMI SAKAMOTO,<sup>1</sup> HISAO TOMIOKA,<sup>3</sup> TAKAO KOIKE,<sup>1</sup> AND SHO YOSHIDA<sup>1</sup>

*Second Department of Internal Medicine, School of Medicine, Chiba University, 1-8-1, Inohana, Chiba City, Chiba 280,<sup>1</sup> and Department of Internal Medicine, Asahi General Hospital,<sup>2</sup> and Department of Internal Medicine, School of Medicine, Toho University,<sup>3</sup> Chiba, Japan*

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**We describe a 58-year-old man with tularemia and expanding  $\gamma\delta$  T cells in his peripheral blood lymphocytes (PBL) (32.7% of total PBL). In the present work, we analyzed the T-cell receptor V $\gamma$ /V $\delta$  repertoire of these cells by making use of the polymerase chain reaction and flow cytometry and found that they were mostly CD4<sup>-</sup> CD8<sup>-</sup> CD3<sup>+</sup> V $\gamma$ 9/V $\delta$ 2<sup>+</sup>. The sequence analysis of 16 cDNA clones encoding the V $\gamma$ 9-J region revealed that the V $\gamma$ 9-J $\mu$  combination was strikingly overrepresented but that the junctional (N) region was heterogeneous. This suggested that the  $\gamma\delta$  T cells in PBL from a patient with tularemia were polyclonally expanded.**

The majority of peripheral T cells express an  $\alpha\beta$  T-cell receptor (TCR) which recognizes antigen and the major histocompatibility complex expressed on antigen-presenting cells and either the CD4 or CD8 molecule (2). An additional small subset of T cells expresses a second type of TCR,  $\gamma\delta$  (8).  $\gamma\delta$  T cells do not express CD4 or CD8 molecules (6, 7, 9), and the recognition specificity of the  $\gamma\delta$  TCR is not clear. Some  $\gamma\delta$  T cells recognize mycobacterial antigens and can proliferate to mycobacterial heat shock protein or purified protein derivative (4, 15, 16, 19, 27, 29).  $\gamma\delta$  T cells also accumulate in human leprosy skin lesions and American cutaneous leishmaniasis, rheumatoid arthritis synovial fluid, and peripheral blood lymphocytes (PBL) in patients with sarcoidosis (5, 16, 27, 36). Tularemia is an infection produced by the gram-negative organism *Francisella (Pasteurella) tularensis*. The organism is acquired by humans from infected animals and insect bites and invades the lymphoid tissue. The incubation period is 2 to 7 days. Histopathological findings revealed involvement of macrophages, and there is some analogy to findings in tuberculosis (35). Tularemia results in the development of CD4<sup>+</sup> T cells, which may play a protective role in development of the disease (34, 35). Here, we report that TCR V $\gamma$ 9/V $\delta$ 2-positive T cells predominantly expanded in peripheral blood lymphocytes (PBL) from a man with tularemia. The sequence analysis showed that the V $\gamma$ 9-J $\mu$  combination was strikingly overrepresented but that the junctional (N) region was heterogeneous. The possible role of these cells in the pathogenesis of tularemia is discussed.

A 58-year-old Japanese man presented with fever and was admitted to the hospital in January 1990. His body temperature reached 38°C 10 days after contact with a dead rabbit. Lymph nodes in his bilateral axillae and arms were enlarged. These lymph nodes were 1 to 3 cm in diameter. Anemia, icterus, and eruption were absent. The serum level of glutamic oxalacetic transaminase was 103 mU/ml; glutamic pyruvic transaminase was 195 mU/ml; lactic dehydrogenase was 477 IU/liter; and C-reactive protein was 3.4 mg/dl. A skin reaction against tularemia antigen was strongly positive (30 by 30 mm), and the aggregation reaction test against tularemia antigen was also positive (1:1,240). A diagnosis of tularemia was made on day 10 of hospitalization, and then

100 mg of Minomycin (Takeda Chemical Industries, Ltd., Osaka, Japan) (minocycline hydrochloride) and an additional 1 g of streptomycin sulfate were given orally daily. On day 7 after treatment, the patient became afebrile and his serum transaminase level reverted to normal. Swelling in the lymph nodes disappeared by April.

The  $\gamma\delta$  T cells in PBL from this patient with tularemia were analyzed before and after treatment by using flow cytometry with phycoerythrin-coupled anti-CD3 (Leu4) monoclonal antibody (MAb) and fluorescein isothiocyanate (FITC)-conjugated anti-TCR  $\gamma\delta$  MAb (TCR  $\delta$ 1). PBL from the tularemia patient were isolated by Ficoll-Paque separation (Pharmacia Fine Chemicals, Piscataway, N.J.). For two-color staining, the PBL were incubated for 1 h on ice with phycoerythrin-coupled anti-CD3 (Leu4) MAb or anti-CD4 (Leu3a) plus anti-CD8 (Leu2a) MAbs (Becton Dickinson Immunocytometry Systems, Mountain View, Calif.) and FITC-conjugated MAb to  $\gamma\delta$  TCR (TCR  $\delta$ 1; T Cell Sciences, Inc., Cambridge, Mass.). After incubation, the cells were washed and resuspended at a concentration of 10<sup>6</sup> cells per ml and then analyzed by FACScan (Becton Dickinson). Figure 1a shows that CD3<sup>+</sup>  $\gamma\delta$  T cells composed 32.7% of the PBL from this patient before treatment. The normal amount of  $\gamma\delta$  T cells in PBL from 10 healthy subjects in our clinics was 2.62  $\pm$  1.57% (mean  $\pm$  standard deviation). The number of  $\gamma\delta$  T cells in this tularemia patient decreased from 32.7 to 9.6% after treatment with minocycline hydrochloride for 1 month, and a level 10 to 15% higher than that in healthy individuals was retained for several months (Fig. 1b). To examine the expression of CD4 and CD8 molecules, we stained PBL obtained from the patient 1 month after treatment with phycoerythrin-coupled anti-CD4 (Leu3a) and anti-CD8 (Leu2a) MAbs plus FITC-conjugated anti-TCR  $\gamma\delta$  MAb. Most of the CD3<sup>+</sup>  $\gamma\delta$  T cells did not stain with MAbs against CD4 and CD8 (Fig. 1b), thereby indicating that the phenotype of the  $\gamma\delta$  T cells expanded in tularemia was CD3<sup>+</sup> CD4<sup>-</sup> CD8<sup>-</sup>.

To analyze V $\gamma$  gene usage on the  $\gamma\delta$  T cells increased in tularemia, we examined the TCR V $\gamma$  repertoire by polymerase chain reaction (PCR) with primers specific for eight different V $\gamma$  genes and the primer for the C $\gamma$  gene. PBL (10<sup>7</sup>) were collected from 20 ml of blood from this patient after treatment. Total RNAs (10  $\mu$ g) were prepared from PBL by using RNAzol solution (Biotecx Laboratories, Inc., East Houston, Tex.). cDNAs were synthesized from 5  $\mu$ g of total

\* Corresponding author.

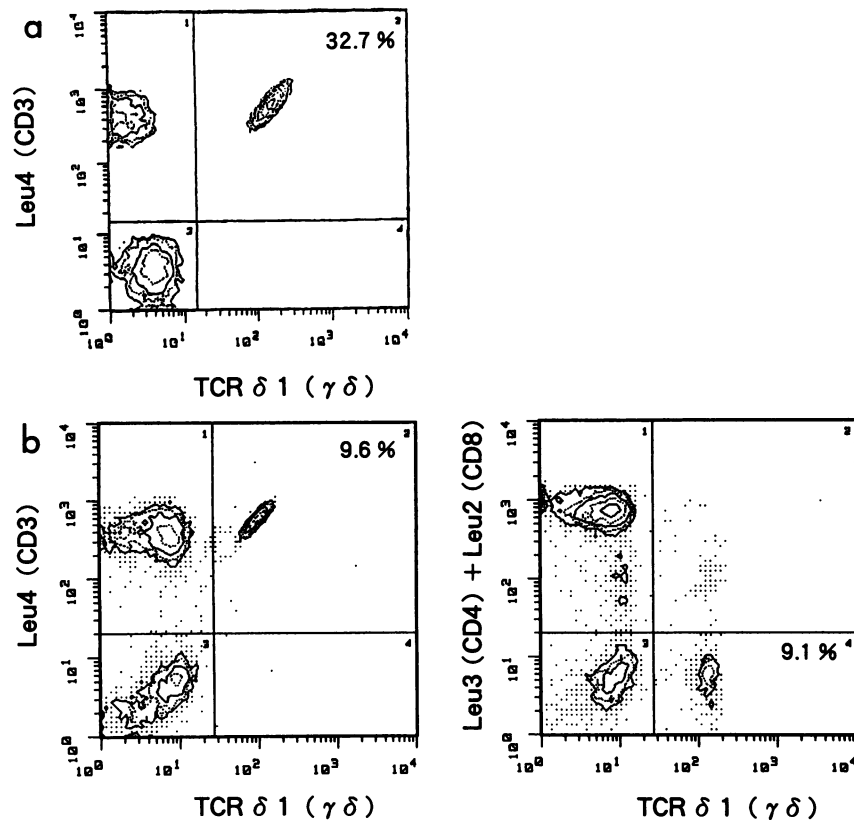


FIG. 1.  $\gamma\delta$  T cells on PBL from a tularemia patient. PBL from a patient before (a) and after (b) treatment were stained with phycoerythrin-coupled anti-CD3 (left panel) or anti-CD4 plus anti-CD8 (right panel) and FITC-conjugated anti-TCR  $\gamma\delta$  MAbs.

RNA in a 20- $\mu$ l reaction mixture containing oligo(dT) primer by using avian myeloblastosis virus reverse transcriptase. Amplification was performed with *Taq* polymerase in 50  $\mu$ l of standard buffer with 0.2  $\mu$ l of cDNA (corresponding to 50 ng of total RNA). Eight different V $\gamma$  primers (V $\gamma$ 2, 5'-GCAAGCACAAGGAACAATTG-3'; V $\gamma$ 3, 5'-ACACCCA GGAGGTGGAGCTGG-3'; V $\gamma$ 4, 5'-TATGACTCCTACAC CTCCAGC-3'; V $\gamma$ 5, 5'-ACACCGAGGAGGTGGAGCTGG-3'; V $\gamma$ 8, 5'-AGCACAGGGAAGAGCCTTAAA-3'; V $\gamma$ 9, 5'-TTGAGGTGGATAGGATACCTG-3'; V $\gamma$ 10, 5'-ACTCTCA CTTCAATCCTTACC-3'; V $\gamma$ 11, 5'-TGCTCAGGTGGGAA GACTAAG-3') and C $\gamma$  (5'-AGTGGCCTGGGGAAACA TC-3') or 5'-C $\gamma$  (5'-ATAAACAACCTTGATGCAGATG-3') and 3'-C $\gamma$  (5'-CATGTATGTGTCGTTAGTCTT-3') primers were selected from previously published data (13, 17, 23, 24). Oligonucleotides were synthesized by a DNA synthesizer (Applied Biosystems Co., Ltd., Foster City, Calif.). The denaturing step was done at 94°C for 1.5 min, the annealing step was done at 60°C for 1 min, and the extension step was done at 72°C for 1 min for 30 cycles on a DNA Thermal Cycler (Zymoreactor V2; Atto Co., Ltd., Tokyo, Japan). One-fifth of each sample was loaded on a 2% agarose gel and hybridized with the <sup>32</sup>P-labeled 165-bp C $\gamma$ -region cDNA probe. This probe was synthesized by PCR with 5'-C $\gamma$  and 3'-C $\gamma$  primers and purified by electroelution. Southern blot analysis of the PCR products showed a strong radioactive band encoding V $\gamma$ 9-JC $\gamma$  gene segments (Fig. 2a). The other seven V $\gamma$  genes were not evident, even with a longer exposure. To investigate usage of the V $\delta$  gene on the expanded  $\gamma\delta$  T cells, PBL obtained from the patient after

treatment were stained with MAb against the V $\delta$ 2 molecule (BB3) (11) and analyzed by fluorescence-activated cell sorting. As shown in Fig. 2b, most of the TCR  $\delta$ 1-positive T cells (11%) were V $\delta$ 2<sup>+</sup> T cells (10.7%); hence, the increased T cells in PBL from the patient with tularemia were V $\gamma$ 9/V $\delta$ 2 positive.

To analyze the clonality of expanded V $\gamma$ 9/V $\delta$ 2 T cells, the cDNAs encoding the V $\gamma$ 9 gene were amplified by using PCR, cloned, and sequenced. cDNA (0.2  $\mu$ l) prepared from PBL from the patient after treatment were used for PCR together with the following primers: for V $\gamma$ 9, a V $\gamma$ 9 primer with an *Eco*RI cutting site (5'-TCTAGAATTCTTGAGGTGGAT AGGATACCT-3'), and a C $\gamma$  primer with an *Eco*RI cutting site (5'-TCTAGAATTCAGACAAAGGTATGTTCCAGC-3'). The reaction was performed under the same conditions as mentioned above. PCR products were purified by phenol extraction and precipitated with ethanol and then restriction enzyme digested in excess amounts of *Eco*RI. Fragments of the expected sizes for the cDNAs were enriched by preparative low-melting-point agarose gel electrophoresis. The recovered DNA fragments were ligated to M13mp19 plasmids obtained by *Eco*RI digestion. Bacteriophages were grown on *Escherichia coli* TG-1 cells. After hybridization with the C $\gamma$  probe, single phages were picked and cultivated and recombinant phage DNA was purified for DNA sequence determinations. Sequencing reactions were done manually by using the Sequenase sequencing system (United States Biochemical Corporation, Cleveland, Ohio). The GenBank libraries were used to search for homologies (12). As shown in Table 1, 14 (88%) of 16 V $\gamma$ 9 clones sequenced

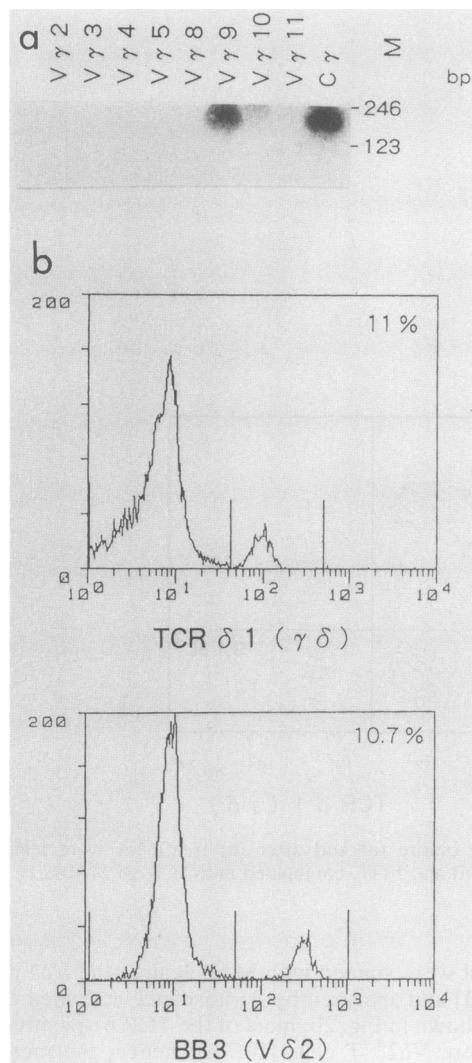


FIG. 2. (a) Analysis of  $V\gamma$  usage on  $\gamma\delta$  T cells in PBL from a patient with tularemia after treatment, using PCR. Amplified PCR products yielded a band of about 200 bp. (b)  $V\delta 2$ -positive T cells on PBL from a patient with tularemia after treatment. PBL were stained with FITC-conjugated anti-TCR  $\gamma\delta$  (TCR  $\delta 1$ ) (upper panel) or anti- $V\delta 2$  (BB3) (lower panel) MAb.

were productively rearranged. Two sets (clones 8 and 9, clones 15 and 18) of 14 productively rearranged clones had the same rearrangement and proved to be the same clone. The sequences of the other 10 clones differed. We conclude that the  $V\gamma 9$  cDNA clones had different V-J junction sequences, that  $V\gamma 9$ - $J\gamma$  diversified extensively in the junctional regions, and that the  $V\gamma 9$ -positive T cells were polyclonally expanded. In addition, 11 productively rearranged clones were combined with the  $J\gamma$  segment and the other 3 were combined with the  $J1$  segment. Thus, the  $V\gamma 9$ - $J\gamma$  combination was strikingly overrepresented in our patient with tularemia.

We have described herein the first evidence that  $\gamma\delta$  T cells are present in large numbers in PBL from tularemia patients. Several investigators have established  $\gamma\delta$  T-cell clones or T-cell hybridomas and have noted that some T-cell clones responded specifically to mycobacterial antigens, purified protein derivative, heat shock protein, tetanus toxoid, and

staphylococcal enterotoxin A (15, 16, 22, 29, 32). It was also clarified that  $\gamma\delta$  T cells accumulated in the granulomatous region of humans with leprosy (27) and American cutaneous leishmaniasis (16), synovial fluid of rheumatoid arthritis patients (5), and PBL of sarcoidosis patients (36). These findings suggested that TCR  $\gamma\delta$  cells or their secreted products play a role in development of the lesions.

Although human  $\alpha\beta$  T cells carry a broad diversity of antigen recognition by a large number of genetic elements (V, D, J), the human TCR  $\gamma\delta$  repertoire is limited since there are only eight functional  $V\gamma$  and five  $J\gamma$  gene segments (9, 30). In healthy individuals, more than 60% of TCR  $\gamma\delta$  cells utilize the  $V\gamma 9$  segment (37). In addition, analyses of  $V\gamma 9$  T-cell clones showed that the  $V\gamma 9$  gene is mostly combined to  $J\gamma p$  and  $C\gamma 1$  and paired with  $V\delta 2$  elements (38). The specificity of  $\gamma\delta$  T cells depends on extensive junctional sequence diversity generated by the addition of N-region nucleotides to the junctional ones (31).

Tamura et al. (36) found that junctional sequences associated with  $V\gamma 9$  gene segments in PBL from sarcoidosis patients were limited. They also mentioned that the limitation of junctional region diversity observed in sarcoidosis might imply a response to a small number of epitopes by the oligoclonal population of  $\gamma\delta$  T cells. In contrast, Sioud et al. (33) reported that  $V\delta 1$ -expressing T cells in patients with rheumatoid synovitis were polyclonal, as determined by junctional sequence analysis. We found, using flow cytometry and PCR, that most of the expanded  $\gamma\delta$  T cells in a tularemia patient were  $CD4^+ CD8^- V\gamma 9/V\delta 2^+$  T cells. However, sequences of  $V\gamma 9$  cDNA clones demonstrated that these expanded T cells had different V-J junctional sequences, hence the broad diversity of  $V\gamma 9$ -positive T cells in subjects with this pathology.

A collection of superantigen, which binds to class II major histocompatibility complex and engages T cells bearing particular  $V\beta$  chains, regardless of the sequences of other variable components of the TCR, has been found in mice (18, 26). Two groups of superantigens have been described so far. One of the superantigens is minor lymphocyte stimulation (Mls) antigen (14, 21, 25) and may consist of molecules encoding mammary tumor virus (1, 10), and the other is a bacterial product such as staphylococcal enterotoxins (39). In humans, the enterotoxins of *Staphylococcus aureus* bind to class II molecules and stimulate  $V\beta 2$ -positive T cells (20). It is tempting to postulate that heat shock protein and bacterial products activate  $\gamma\delta$  T cells with a particular TCR as well as  $\alpha\beta$  T cells. Therefore, the predominant expansion of  $V\gamma 9/V\delta 2$  T cells bearing the different V-J junctions in patients with tularemia may support the notion that unique epitopes on *F. tularensis* act as a superantigen and induce the expansion of a limited  $\gamma\delta$  T-cell population, without preference for junctional region sequences.

Sjostedt et al. (34, 35) reported that a 17-kDa protein of *F. tularensis* was the major T-cell-reactive membrane protein. Further, gene mapping experiments showed that peripheral  $CD4^+$  T cells recognized several epitopes of the 17-kDa protein (35). Peptides from the 17-kDa protein of *F. tularensis* induced  $CD4^+$  T-cell proliferation and the production of interleukin-2 and gamma interferon, thereby suggesting that  $CD4^+$  T cells are relevant to the host defense against *F. tularensis*, since gamma interferon enhanced antimicrobial activity in an intracellular bacterial infection (3, 28). Although the recognition specificity and the functional role of the  $CD4^+ CD8^- \gamma\delta$  T cells in tularemia are not known, these cells might play an important role in the primitive

TABLE 1. Junctional sequences of cDNA encoding the V $\gamma$ 9 gene<sup>a</sup>

Clone	V $\gamma$ 9	N	J	J $\gamma$ region	In frame <sup>b</sup>
1	GCCTTGTGGGA	T	CAAGAGTTGGGC	Jp	+
2	GCCTTGTGGGAG	TA	GCAAGAGTTGGGC	Jp	+
3	GCCTTGTGGGAGG	AGGG	TTATAAGAAA	J1	+
5	GCCTTGTGGGAGGTG	CG	AAGAGTTGGGC	Jp	-
6	GCCTTGTGGGAG		CAAGAGTTGGGC	Jp	+
7	GCCTTGTGGGAGGTG	GG	AGAGTTGGGC	Jp	+
8 <sup>c</sup>	GCCTTGTGGGAGGTG		CAAGAGTTGGGC	Jp	+
9 <sup>c</sup>	GCCTTGTGGGAGGTG		CAAGAGTTGGGC	Jp	+
10	GCCTTGTGGGAGG		AAGAGTTGGGC	Jp	+
11	GCCTTGTGGGAG	CAGGG	AGAGTTGGGC	Jp	+
12	GCCTTGTGGGAGG	AGG	AGTTGGGC	Jp	+
13	GCCTTGTGGGAG	TGCAAGGTAACGG	AAGAGTTGGGC	Jp	+
15 <sup>d</sup>	GCCTTGTGGGAGG	AGGG	TTATAAGAAA	J1	+
16	GCCT	GGTGTGGACCCGAGG	CTCTTTGGC <sup>e</sup>	J1	-
18 <sup>d</sup>	GCCTTGTGGGAGG	AGGG	TTATAAGAAA	J1	+
22	GCCTTGTGGGAGG	C	GCAAGAGTTGGGC	Jp	+

<sup>a</sup> Sequences shown include the 3' region of the V $\gamma$ 9 element (V $\gamma$ 9), the N region, the 5' region of the J $\gamma$  element (J), and the specific J $\gamma$  element (J $\gamma$ ).

<sup>b</sup> +, productive transcript; -, nonproductive transcript.

<sup>c</sup> Clones 8 and 9 were identical.

<sup>d</sup> Clones 15 and 18 had the same sequence.

<sup>e</sup> 5' portion of J $\gamma$ 1 gene segment was deleted.

immune defense against *F. tularensis* in collaboration with CD4<sup>+</sup> T cells.

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