

Autoaggressive Myocytotoxic T Lymphocytes Expressing an Unusual γ/δ T Cell Receptor

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Summary

Polymyositis mediated by γ/δ T cells is a unique disease in which autoaggressive T lymphocytes surround, invade, and destroy muscle fibers. Histochemically, the vast majority of muscle-infiltrating T cells in a patient with polymyositis were reactive with a pan- γ/δ T cell receptor (TCR)-specific monoclonal antibody (TCR- $\delta 1^+$), but unlike >90% of peripheral blood γ/δ T cells, these lymphocytes did not react with V $\delta 1$ - or V $\gamma 9$ -specific antibodies (A13⁻ and Ti γ A⁻, respectively). Differential reactivity with two different V $\delta 2$ -specific monoclonal antibodies (BB3⁻/TiV- $\delta 2^+$) indicated that the infiltrating T cells express a V $\delta 2$ -containing TCR with unusual additional structural features. Using conventional and anchored polymerase chain reaction for the analysis of TCR transcripts, we found a striking predominance of one unusual V $\delta 2$ -J $\delta 3$ recombination and one V $\gamma 3$ -J $\gamma 1$ recombination. Both the unusual phenotype (TCR- $\delta 1^+$ /A13⁻/Ti γ A⁻/BB3⁻/TiV- $\delta 2^+$) and the dominance of distinct TCR transcripts are compatible with the assumption that one T cell clone, which expresses a V $\gamma 3$ -J $\gamma 1$ -C $\gamma 1$ /V $\delta 2$ -J $\delta 3$ -C δ disulfide-linked TCR, dominates among the infiltrating T cells of the polymyositis muscle specimen analyzed.

Although γ/δ T cells are suspected to be involved in autoimmunity, there is little direct evidence to support this hypothesis in human autoimmune disease. One notable exception is a recently described inflammatory muscle disease that represents a variant of polymyositis (1). In this disease autoaggressive γ/δ T cells can be demonstrated to surround, invade, and destroy muscle fibers (1). Our analysis of TCR transcripts of the myocytotoxic T cells provides the first complete structural description of a TCR used by autoaggressive human γ/δ T cells.

Materials and Methods

Clinical Material. A biopsy specimen of the left triceps muscle of a patient previously described (1) was taken before treatment and was divided for immunocytochemical studies and for RNA extraction.

Immunohistology. 4- μ m cryostat sections of muscle were used for single and paired immunofluorescence studies. The following antibodies were used: anti-CD3 (5 μ g/ml; Dako Corp., Carpinteria, CA); anti-TCR- $\delta 1$ (5 μ g/ml; T Cell Sciences, Cambridge, MA); Ti γ A (5 μ g/ml; T. Hercend, Institute Gustave Roussy, Villejuif, France); TiV- $\delta 2$ (2 μ g/ml; T. Hercend); A13 and BB3 (6 μ g/ml; L. Moretta, Istituto Nazionale Per La Ricerca Sul

Cancro, Genova, Italy). All antibodies were mouse mAbs except anti-CD3, which was an affinity-purified rabbit polyclonal antibody. The primary mouse mAbs were detected using a biotin-labeled second antibody followed by treatment either with rhodamine-avidin or with FITC-avidin. The rabbit anti-CD3 primary antibody was detected using rhodamine-labeled goat anti-rabbit IgG. Isotype-matched IgG at identical concentrations was substituted for primary antibodies for negative controls. Smears of PBMC and thymocytes were used as positive controls for antibodies specific for subsets of γ/δ T cells. Tissue samples used as controls included sections from patients with different inflammatory myopathies and from normal control subjects with no evidence of muscle disease.

Analysis of TCR Transcripts. Total RNA was prepared from a sample (25 mg) of the muscle biopsy specimen by the acid guanidinium thiocyanate phenol-chloroform method (2) and its integrity verified by running a portion of the material on an agarose gel. First-strand cDNA was prepared from total RNA using a poly(dT) primer and AMV reverse transcriptase (Boehringer, Mannheim, Germany) (3). PCR was carried out as described previously (3, 4) with 0.5 μ M of oligonucleotide primers and 1 U of Taq polymerase (Bethesda Research Laboratories, Gaithersburg, MD) using incubation times of 30 s at 93°C, 1 min at 50°C, and 1 min at 72°C in a reaction volume of 100 μ l. DNA bands of the expected size were isolated from 1% agarose gels and blunt-end cloned into the SmaI site of Bluescript KS (Stratagene, La Jolla, CA) (3). Double-

stranded plasmid DNAs were sequenced directly with the Sequenase kit (U.S. Biochemical Co., Cleveland, OH).

PCR amplification of δ chain cDNA was accomplished by use of a C δ antisense primer (GACAAGCGACATTTGTTCCA) in combination with either a V δ 2 sense primer (CAAAGAACCTGGCTGTAC) or a set of V δ sense primers (V δ 1: TACTCTGGATCAAGTGTGGC; V δ 2: GCAGGAGTCATGTCAGCCAT; V δ 3: GGCACGCTGTGTGACAAAGT). In one experiment the relative abundance of V δ 2-J δ 1 and V δ 2-J δ 3 rearrangements in cDNA derived from the muscle biopsy, and from Ficoll-purified PBMC of a healthy donor, were compared. Here amplifications were done using a V δ 2 sense primer (GCAGGAGTCATGTCAGCCAT) either in combination with a J δ 1 (GGTCCACAGTCACACGGGT) or with a J δ 3 (GGCTCCACGAAGAGTTTGAT) antisense primer.

For the analysis of the junctional regions of γ chain transcripts, cDNA derived from the muscle biopsy was amplified using single-stranded PCR carried out by a modification (4) of a published method (5). cDNA was size fractionated by Bio-Gel A-5m (Bio-Rad Laboratories, Richmond, CA) column chromatography and an oligo(dG)-tail was added to the 3' end of cDNAs of appropriate size using terminal deoxynucleotide transferase (Bethesda Research Laboratories) (4). Two successive amplifications of the oligo(dG)-tailed cDNA were accomplished with an oligo(dC) primer (dC₁₆) in combination with one of two different C γ (exon 1) antisense primers (GGTATGTTCCAGCCTTCTGG or the nested C γ primer AAGGAAGAAAATAGTGGGC). Analysis of γ chain transcripts by conventional PCR was done with C γ (exon 1) antisense primers (AAGGAAGAAAATAGTGGGC) in combination with a set of V γ sense primers (V γ subgroup I: TGCTTCTAGCTTTCCTG; V γ 9: ATCAACGCTGGCAGTCC; V γ 10: TCCTCCTGGGCTCCTGA; V γ 11: TTCTTCTCCCTCTGGGT) or with C γ (exon 3) antisense primers (TGAGGAGCAGGAGGAGGTAC) in combination with a V γ subgroup I sense primer (TGCAGCCAGTCA-GAAATCTT). Since the different V γ gene segments of subgroup I are highly homologous (6), it was possible to design universal primers for the amplification of rearrangements with all members of this subgroup.

Results and Discussion

For the analysis of the structure and heterogeneity of TCR transcripts from muscle-infiltrating γ/δ T cells, RNA was

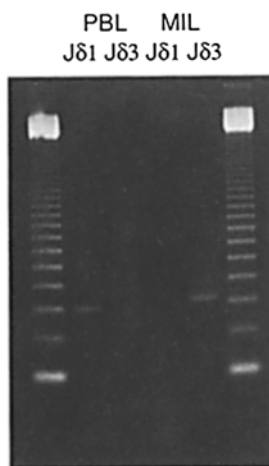


Figure 2. V δ 2-J δ 1 and V δ 2-J δ 3 TCR gene rearrangements expressed in muscle-infiltrating lymphocytes (MIL) and PBL. Agarose gel analysis of ethidium bromide-stained PCR amplification products. cDNA obtained from the muscle biopsy or from Ficoll-purified mononuclear cells from a healthy donor was amplified with a V δ 2 sense primer in combination with either a J δ 1 or a J δ 3 antisense primer.

isolated from a polymyositis biopsy specimen that had previously been characterized by immunohistology (1). RNA was transcribed into cDNA, and TCR-specific cDNA was amplified either by conventional or by anchored PCR. PCR products of expected size were cloned and the sequences of independently isolated clones analyzed. A set of sense primers for the most commonly used V δ gene segments, V δ 1, V δ 2, and V δ 3 (7), was used in combination with a C δ antisense primer for the amplification of cDNA derived from TCR δ chain transcripts. Only V δ 2 PCR products were obtained and only one unique rearrangement was found when randomly chosen clones were analyzed (Fig. 1A). One D δ gene segment and nongermline-encoded nucleotides at the V-D and the D-J junctions contributed to the junctional region of this dominant transcript. While both ends of the D δ gene segment were shortened, the entire coding sequences of the V δ and the J δ gene segments were conserved in this rearrangement. To rule out the possibility that the dominance of this sequence was the result of an accidental preferential amplification of one particular cDNA, we performed a second independent amplification using a different V δ 2-specific sense

V δ 2	P/N	D δ 3	P/N	J δ 3	Frequency
A					
TGT GCC TGT GAC ACC	GT	CTGGGGGA	CCTCAAAGAG	C TCC TGG GAC	9/10
TGT GCC TGT GAC ACC	GT	CTGGGGGA	CCTCTAAGAG	C TCC TGG GAC	1/10
B					
TGT GCC TGT GAC ACC	GT	CTGGGGGA	CCTCAAAGAG	C TCC TGG GAC	4/6
TGT GCC TGT GAC ACC	GT	TTGGGGGA	CCTCAAAGAG	C TCC TGG GAC	1/6
TGT GCC TGT GAC ACC	GT	CAGGGGGA	CCTCAAAGAG	C TCC TGG GAC	1/6
germline					
V δ 2	TGT GCC TGT GAC ACC caccttg				
D δ 3	cactgtg ACTGGGGGATACG cacagtg				
J δ 3	taatgtg C TCC TGG GAC				

Figure 1. Junctional regions of δ chain cDNA sequences from muscle-infiltrating γ/δ T cells. The 3' and the 5' ends of the V, D, and J regions were determined from genomic clones (8, 9). PCR amplification of the δ chain cDNA was accomplished by use of a C δ antisense primer in combination with a set of sense primers for V δ 1, V δ 2, and V δ 3 (A), or a second different V δ 2 sense primer (B).

	V γ 3	P/N	J γ 1	Frequency
A	TGT GCC ACC TGG GAC	GGTT	AT TAT TAT AAG AAA	14/14
B	TGT GCC ACC TGG GAC	GGTT	AT TAT TAT AAG AAA	5/5
C	TGT GCC ACC TGG GAC	GGTT	AT TAT TAT AAG AAA	10/13
	TGT GCC ACC TGG GAC	GGTT	AT TAT TAT AAG AAG	1/13
	TGT GCC ACC TGG GAC A	CAGAAG	AT TAT AAG AAA	2/13

germline TGT GCC ACC TGG GAC AGGcaccagtg cactgtgg AAT TAT TAT AAG AAA

Figure 3. Junctional regions of γ chain cDNA sequences from muscle-infiltrating γ/δ T cells. The 3' and the 5' ends of the V and J regions, respectively, were determined from genomic clones (6, 14). Five J γ segments have been identified, with J γ 1 being identical in amino acid sequence to J γ 2. J γ 1 is located upstream of C γ 1, whereas J γ 2 is located between C γ 1 and C γ 2 (14, 15). cDNA was amplified by single-sided PCR (A), by conventional PCR using a C γ (exon 1) antisense primers in combination with a set of sense primers for the different V γ families (B), or by conventional PCR using a C γ (exon 3) antisense primers in combination with a V γ subgroup I sense primer (C).

primer. All clones derived from this second amplification product were identical to the rearrangement observed in the first experiment (Fig. 1 B). A few of the analyzed junctional sequences differed from the others by a single nucleotide exchange. Since the fidelity of the *Thermus aquaticus* (Taq) DNA polymerase in DNA amplification is relatively low, such polymerase-induced point mutations tend to accumulate during PCR amplification (10).

A high proportion of γ/δ T cells in peripheral blood express a limited receptor repertoire: V δ 2-J δ 1-C δ usually pairs with V γ 9-J γ P-C γ 1 (11, 12). V δ 2-J δ 3 rearrangements such as the one observed here have previously been described in γ/δ T cell clones (13), but are rare in peripheral blood T cells. To further verify the dominance of V δ 2-J δ 3 transcripts in the muscle biopsy, PCR was performed with a V δ 2 sense primer in combination with either a J δ 3 or a J δ 1 antisense primer. Whereas only a V δ 2-J δ 3-PCR band was observed when cDNA from the muscle biopsy was used as a template, a V δ 2-J δ 1-band was dominant in reactions with cDNA derived from PBL (Fig. 2). This demonstrates that the majority of γ/δ T cells in the biopsy represent a unique subpopulation rather than a polyclonal infiltrate of peripheral T cells. This conclusion is further supported by the observation that >90% of the γ/δ T cells present in the blood at the time of biopsy had a different phenotype (BB3⁺, T γ A⁺) than the infiltrating γ/δ T cells (BB3⁻, T γ A⁻) (1).

For the analysis of TCR γ chain transcripts a modification of the single-sided PCR amplification method (4, 5) was used that requires sequence information only from the 3' end of

the target receptor cDNA (constant gene segment) and therefore allows V segment sequence-independent amplification. PCR products in the predicted size range were cloned and the sequences of a set of randomly chosen isolates were determined. All 14 sequences analyzed were identical, representing a V γ 3-J γ 1 recombination with addition of four nongermline-encoded nucleotides and shortening of both the V and the J coding region by imprecise joining (Fig. 3 A). The same sequence was obtained when an independent second amplification was performed by conventional PCR with a set of sense primers for all eight functional human V γ gene segments (Fig. 3 B).

Of the 14 V γ gene segments that have been identified in the human genome, six are considered to be pseudogenes. The functional genes fall into four distinct subgroups (15). Whereas five functional genes (V γ 2, V γ 4, V γ 5, and V γ 8, in addition to the V γ 3 gene segment found in the transcripts analyzed here) belong to subgroup I, subgroups II, III, and IV each consist of a single gene (V γ 9, V γ 10, V γ 11, respectively). The degree of variation of the γ chains is increased by the existence of polymorphic γ constant region gene segments (C γ). The C γ 1 gene segment consists of three exons (ex1, ex2, ex3), whereas C γ 2 contains in some cases two and in others three copies of exon 2 (15, 16). Exons 1 and 3 of both gene segments are virtually identical. The C γ 1 gene products possess a cysteine residue in the second exon that is responsible for disulfide bond formation with the δ chain, while the corresponding exon 2 of C γ 2 lacks the cysteine. It is not known whether these structural differences between

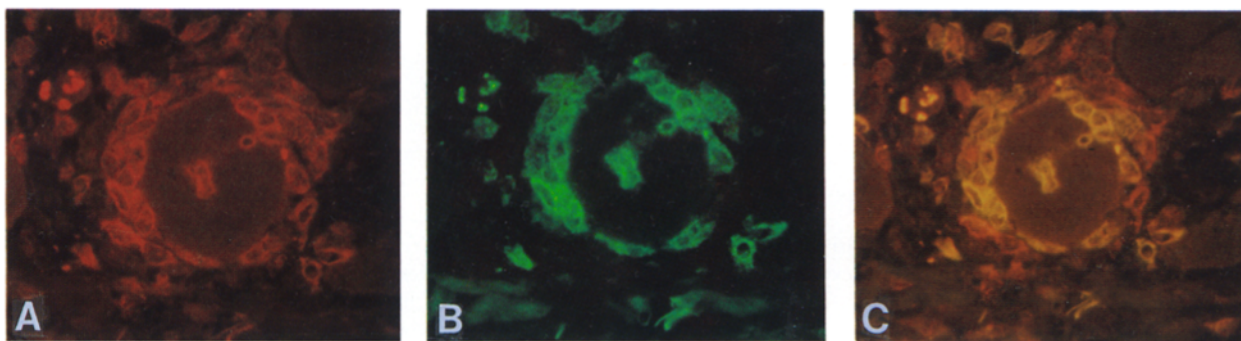


Figure 4. Localization of CD3 antigen with red rhodamine fluorescence (A) and of the T_HV- δ 2 antigen with green FITC fluorescence. (A) CD3⁺ T cells focally surround and invade a muscle fiber. (B) Demonstration that most of these cells are T_HV- δ 2⁺ cells. (C) Double exposure of A and B, revealing CD3⁺ T_HV- δ 2⁺ cells in yellow. A and B, \times 410; C, \times 365.

the C γ gene segments affect the functional properties of the TCR. It is known, however, that the V γ and the J γ segments associated with C γ 1 and C γ 2 differ at least in peripheral blood γ/δ T cells, where C γ 1 is preferentially rearranged with V γ 9/J γ P and C γ 2 with V γ 2/J γ 1 (17). To analyze the C γ gene usage in the muscle-invading T cells, we performed PCR with a V γ subgroup 1 sense primer in combination with a C γ exon 3 antisense primer, and sequenced the bracketed DNA. This analysis revealed an association of the dominant V γ 3-J γ 1 rearrangement with C γ 1. In addition, we observed one additional unique V γ 3 rearrangement (Fig. 3 C) associated with a C γ 2 gene segment that contained three copies of exon 2. The fact that the very same sequences were found in the products of several independent amplifications using different amplification techniques and primers rules out the possibility that the dominance of the V δ 2-J δ 3 and V γ 3-J γ 1 rearrangements are merely PCR artifacts. Furthermore, a preliminary PCR analysis of TCR transcripts from another small portion of the biopsy had also yielded the dominant V δ 2-J δ 3 and V γ 3-J γ 1 rearrangements. Here V δ 2-J δ 1 and V γ 9-J γ P rearrangements that are commonly found in peripheral γ/δ T cells and thus presumably derived from contaminating PBMC were obtained in addition.

Taken together, the above results suggest that one T cell clone expressing a V δ 2-J δ 3-C δ /V γ 3-J γ 1-C γ 1 disulfide-linked TCR dominates the population of infiltrating T cells of the analyzed muscle specimen. The phenotype of the vast majority of γ/δ T cells in this specimen was previously established as CD2⁺, CD3⁺, CD4⁻, CD8⁻, TCR- δ 1⁺, T γ A⁻, A13⁻, BB3⁻ (1). While TCR- δ 1 stains all γ/δ T cells, the mAbs T γ A and A13 are specific for subsets V γ 9 or V δ 1, respectively. While the observed TCR- δ 1⁺, T γ A⁻, A13⁻

staining pattern was expected for a V γ 3/V δ 2-expressing T cell population, the BB3⁻ phenotype seems to be incompatible with the genetic data, since BB3 is considered specific for V δ 2 (18). One possible explanation for the discrepancy was that the rare V δ 2-J δ 3 rearrangement and/or combination with V γ 3 eliminates the epitope recognized by mAb BB3. To address this problem, we used another V δ 2-specific mAb, T γ V- δ 2 (19), for additional immunohistochemical studies. All the T cells surrounding and invading muscle fibers reacted with T γ V- δ 2 (Fig. 4), indicating that these cells express V δ 2, although in a form that is not recognized by antibody BB3. Hence, both sequence analyses and antibody reactivities are consistent with the assumption that the autoaggressive lymphocytes express a V γ 3-J γ 1-C γ 1/V δ 2-J δ 3-C δ TCR that is unusual both with respect to its V δ -J δ recombination and its specific V γ /V δ combination.

In conclusion, our results provide the first complete description of a human γ/δ TCR expressed by autoaggressive T cells. A striking predominance of one clone of T cells was observed in the inflammatory muscle infiltrate. This clone uses an unusual combination of TCR V and J segments and is associated with a TCR phenotype that has not previously been described among the major populations of human γ/δ T cells. It should be noted that *Mycobacteria*- and heat shock protein-responsive γ/δ T cells, which have been postulated to participate in autoimmune processes (20), express dominantly V γ 9-J γ P/V δ 2-J δ 1 TCR variable regions (21-23). We anticipate that the molecular characterization of the V γ 3-J γ 1-C γ 1/V δ 2-J δ 3-C δ TCR associated with the myocytotoxic T cells, which share only the V δ 2 segment with the known heat shock protein-reactive T cells, may eventually help to identify the unknown autoantigen in this disease.

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