Flanking V and J Sequences of Complementary Determining Region 3 of T Cell Receptor (TCR) δ1 (CDR3δ1) Determine the Structure and Function of TCRγ4δ1*

Received for publication, March 17, 2011 Published, JBC Papers in Press, May 23, 2011, DOI 10.1074/jbc.M111.239624

Yan Jiang, Yang Guo, Xueyan Xi, Lianxian Cui, and Wei He1

From the Department of Immunology, Institute of Basic Medical Sciences, Chinese Academy of Medical Sciences and School of Basic Medicine, Peking Union Medical College, National Key Laboratory of Medical Molecular Biology, Beijing 100005, China

The γδ T cell receptor (TCR) differs from immunoglobulin and αβ TCR in its overall binding mode. In human, genes δ1, δ2, and δ3 are used for TCRδ chains. Previously, we have studied antigen binding determinants of TCRδ2 derived from dominant γδ T cells residing in peripheral blood. In this study we have investigated the critical determinants for antigen recognition and TCR function in TCRδ1 originated from gastric tumor-infiltrating γδ T lymphocytes using three independent experimental strategies including complementary determining region 3 (CDR3) of TCRδ1 (CDR3δ1)-peptide mediated binding, CDR3δ1-grafted TCR fusion protein-mediated binding, and TCRγδ1- and mutant-expressing cell-mediated binding. All three approaches consistently showed that the conserved flanking V and J sequences but not the diverse D segment in CDR3δ1 determine the antigen binding. Most importantly, we found that mutations in the V and J regions of CDR3δ1 also abolish the assembly of TCR and TCR-CD3 complexes in TCRγδ1-transduced Jurkat T3.5 cells. Together with our previous studies on CDR3δ2 binding, our finding suggests that both human TCRδ1 and TCRδ2 recognize antigen predominately via flanking V and J regions. These results indicate that TCRγδ recognizes antigens using conserved parts in their CDR3, which provides an explanation for a diverse repertoire of γδTCRs only recognizing a limited number of antigens.

T lymphocytes can be divided into two distinct subsets, αβ and γδ T cells, based on the type of T cell receptors (TCR)2 expressed. The αβ T cells mainly recognize peptide antigens bound to class I or class II major histocompatibility complex (MHC) molecules, whereas γδ T cells mount immune responses directly to nonpeptide antigens and superantigens (1). Extensive studies suggest that γδ T cells may function in many aspects of immunity including infection, tumor immunity, tissue homeostasis, and immune regulation (2–4). In humans, γδ T cells use three main Vδ (δ1, δ2, δ3) and various Vγ genes to make their functional TCRs (5, 6). Most of γδ T cells in peripheral blood express Vδ2 chain paired with Vγ9 chain, whose TCRs are dedicated to the recognition of nonpeptide phosphoantigens, alkylamines, and synthetic aminobisphosphonates (7). Whereas in other tissues γδ T cells express TCRs primarily made of predominant Vδ1 or a few Vδ3 chains paired with a diverse array of Vγ chains. Vδ1 T cells reside mainly in mucosal and epithelium tissue and recognize MHC-related molecules such as MHC class I chain-related gene A (MICA) and MICB as well as several other ligands (8, 9).

The structural basis of antigen recognition of αβ TCR is well defined. However, the parallel information for γδ TCR is largely lacking due to the fact that only a limited number of γδTCR-specific ligands have been identified so far. Although αβ TCRs often use all six complementary determining region (CDR) loops in their recognition of peptide-MHC complexes, the crystallographic structure study showed that predominantly germ line-encoded residues of the CDR3 of human TCRδ (CDR3δ) are responsible for most of the interactions between the G8 γδ TCR and MHC class Ib T22 protein in mice (10). Moreover, the residues involved in the recognition interface are derived predominantly from germ line-encoded Dδ segment. In addition, recently studies have shown that mutations in all CDR loops of human Vγ9δ2 TCR could alter the antigen binding, suggesting that the recognition of prenyl pyrophosphates by Vγ9δ2 TCR is dependent on all its CDRs (11).

CDR3δ is composed of V, N-D-N, and J gene segments. The flanking V and J sequences are conserved, whereas N-D-N region is diverse as the result of VDJ recombination and insertion of N nucleotides (12, 13). Our groups have successfully identified two self-proteins including heat shock protein 60 and human mutS homolog 2 (hMSH2) as TCRδ2 ligands using affinity chromatography analysis with a synthetic CDR3δ2 peptide as the probe and confirmed their recognition by TCRδ2-expressing cells in peripheral blood (14). Furthermore, we also demonstrated that the direct antigen recognition role of CDR3δ2 sequences in TCRγδ2 derived from ovarian epithelial carcinoma (OEC) (15). We have identified that the flanking V and J regions of human CDR3δ play a critical role in ligand

1 To whom correspondence should be addressed: Dept. of Immunology, Institute of Basic Medical Sciences, Chinese Academy of Medical Sciences, Peking Union Medical College, National Key Laboratory of Medical Molecular Biology, Beijing 100005, China

2 The abbreviations used are: TCR, T cell receptor; hMSH2, human mutS homolog 2; CDR3δ, complementary determining region 3 of human TCRδ; CDR3δ1/2, CDR3 of human TCRδ1/2; TIL, tumor infiltrating lymphocyte; OEC, ovarian epithelial carcinoma; GTM, one master sequence of CDR3δ1 representing four cases of gastric tumor γδTILs; SPR, surface plasmon resonance; MICA, MHC class I chain-related gene A.

© 2011 by The American Society for Biochemistry and Molecular Biology, Inc. Printed in the U.S.A.

Author's Choice — Final version full access.

* This work was supported by grants from the National Program for Key Basic Research Projects, Ministry of Science and Technology, China PR (2004CB518706), the National High Technology Research and Development Program, Ministry of Science and Technology, China (2006AA02A245 and 2007AA021109), and by the National Natural Science Foundation of China (20490224).
Flanking V and J Sequences of CDR3δ1 Determine TCRγδ1

EXPERIMENTAL PROCEDURES

Cell Lines and Tumor Tissues—Various tumor cell lines including BGC823, G401, GLC-82, HT29, SKOV3, Daudi, and J. RT3-T3.5 were obtained from American Type Culture Collection (ATCC). Fresh tumor tissues and tissue specimens were obtained from the Peking Union Medical College Hospital. Tumor tissues were used or processed within 2 h after surgery.

Generation of γδ T Cell-enriched Tumor-infiltrating Lymphocyte (TIL) —The tissues were rinsed with RPMI 1640 media containing cidofovir, penicillin, and streptomycin and cut into pieces. After washed twice, the tissue pieces were added to a 24-well plate coated by anti-TCR γδ antibody (Beckman Coulter) for 2 h and cultured in RPMI 1640 media containing 10% FCS supplemented with 1-glutamine and 2-mercaptoethanol and 400 units/ml IL-2 for generation of γδ T cell-enriched cells that were spontaneously released from tumor tissues and expanded again by immobilized anti-TCR γδ antibody for 2 or 3 weeks. After immunofluorescence analysis in flow cytometry (BD Biosciences), the expanded γδ T cell-enriched TILs were used for experiments.

cDNA Cloning and Mutagenesis of Human CDR3δ1 —RNA was isolated from TILs of gastric carcinoma tissues (TRizol reagent, Promega) followed by cDNA synthesis using Moloney murine leukemia virus reverse transcriptase (Promega) and oligo-dT (Promega). First, the V region of δ1 was amplified using Vδ1- and Cδ-specific primers and cloned into the pGEM-T easy vector (Promega) for sequence analysis with the ABI automatic sequencer 3770. We chose one master sequence representing four cases of gastric tumor γδ TILs (termed GTM) for mutagenesis. Synthetic peptides with engineered mutations in the V, N-D-N, and J regions are named as GTMVm, GTMDm, and GTMJm, respectively (Table 1). We then amplified dominant full-length δ1 chain with GTM as its CDR3δ1 and γδ chain in one case of gastric tumor-derived γδ TIL that paired with δ1 chain. For protein and transfectant mutagenesis, the full-length δ1 and γδ were cloned from gastric carcinoma γδ TIL first, and different mutants of CDR3δ1 were constructed by overlapping PCR. The full-length δ1 mutants, called as δ1(GTMVm), δ1(GTMDm), δ1(GTMJm), δ1(GTMVAm), δ1(GTMDAm), and δ1(GTMJAm), were constructed respectively.

CDR3δ1 Peptide Synthesis—Peptides including GTM and its mutant variants were synthesized in the peptide synthesis facility of the Academy of Military Medical Sciences, China. The CH3 sequence, one epitope sequence of another CDR3δ2 derived from OEC was synthesized for a negative peptide control (WPNNWWPHFKVK). The purity of each synthetic peptide was >90% as shown by HPLC analysis. The synthesized peptides were totally labeled with a biotin at their N terminus (16).

Chimeric Protein and MICA Protein Expression—The engineered chimeric protein and its mutants containing the extra-cellular domains of the human TCRγδ and TCR81 chains fused to the hinge region, CH2 and CH3 domains of human IgG1 heavy chain, were expressed by the Sino Biological Inc. (16). The CDR3δ1 sequence of the chimeric protein is concordant with the GTM peptide and its V/D/I mutants. Proteins γδ-Fc/δ1(GTM)-Fc, γδ-Fc/δ1(GTMVm)-Fc, γδ-Fc/δ1(GTMDm)-Fc, and γδ-Fc/δ1(GTMJm)-Fc were purified and verified by SDS-PAGE and Western blot, respectively. The pET42a-MICA1–3 containing the extracellular domains of MICA was cloned in our laboratory, and the recombinant MICA1–3α protein was expressed in Escherichia coli BL21. Purified recombinant MICA1–3α was verified by SDS-PAGE and Western blotting.

Construction of TCRγδ1-expressing Cell Line—Three lentiviral vectors, pWPXL-δ1 (GTM)-GFP, pWPXL-γδ4, and pWPXL-δ1(GTM)-IRES-γδ4, were constructed, inserting δ1 or γδ4 into pWPXL (Addgene). In pWPXL-δ1 (GTM)-GFP vector, δ1 chain was inserted immediately in the upstream of GFP. There was no termination code in the downstream primer so that a δ1-GFP gene was transcribed. pWPXL-γδ4 was constructed in the same way, but there was a termination code in the downstream primer so that only γδ4 was transcribed. To create bicistronic pWPXL-δ1(GTM)-IRES-γδ4, δ1 and γδ chain were cloned into pIRES (Clontech) separately and then inserted into pWPXL between sites PmeI and SpeI. Similarly, other mutant vectors were constructed as well. The full-length Vδ1 chain and full-length Vγ4 chain were amplified with Phusion High Fidelity DNA polymerase (Finzymes Oy). All constructs were verified by DNA sequence analysis. Lentiviral vectors were prepared by the transient transfection of 293T cells using a Lipofection-based method of cotransducing lentiviral gene transfer plasmid pWPXL, the helper plasmid psPAX2, and envelope plasmid pMD2.G (14, 24). In brief, the 293T cells were seeded in a 60-mm plate at 1 × 106 cells and incubated overnight. The cells were cotransfected with pWPXL, psPAX2, and pMD2.G plasmids in accordance with the method of Lipofection. 48 h after transfection, the viral supernatants were collected, centrifuged, and used for infecting J.RT3-T3.5 cells (24).

| TABLE 1 Amino acid sequences of GTM and its mutants in V, N-D-N, and J region of CDR3δ1 |
|-----------------|-------------|---------------|-----------|
| Peptide | V | N-D-N | J |
| GTM | CA | FLPHA | DKLIFGKG |
| GTMVm | FL | FLPHA | DKLIFGKG |
| GTMDm | YA | YRDEK | DKLIFGKG |
| GTMJm | CA | FLPHA | PASNCWTH |

binding, as targeting for OEC cells/tissues and hMSH2 protein (16).

Compared to Vδ2, Vδ1 T cells differ in Vδ gene usage, paired γ chains (17, 18), resident tissue (19, 20), and antigen specificity (8, 21–23). It remains unclear if the Vδ1 subset utilizes a distinct antigen recognition mechanism and the nature of the contribution of CDR3δ1 domain to the antigen recognition. In this study we aim to answer these questions by investigating the involvement of flanking V and J sequences of CDR3δ1 in antigen recognition using a specific Vγδ1 TCR-derived from gastric tumor infiltrating γδ T lymphocytes. Three independent but complimentary strategies, including utilizing synthetic CDR3δ1 peptides, CDR3δ1-grafted TCR fusion proteins, and cells expressing TCRγδ1, were employed in the present study to investigate the structural basis of specific CDR3δ1 binding to tumor antigens. We found that the conserved flanking V and J sequences of CDR3δ1 are critical for antigen binding as well as the assembly of functional TCRγδ1 complex.
TCRγδ1-transduced J.RT3-T3.5 cells were validated for γδ TCR expression by immunofluorescent analysis in flow cytometer and Western blot.

**Immunofluorescent Analysis by Flow Cytometry**—To determine the binding of peptides or proteins with various tumor cell lines, tested cells were incubated with biotin-conjugated GTM peptide, γ4-Fc/δ1 (GTM)-Fc protein, or their V/D/J mutants for 30 min at 4 °C. Fluorescein isothiocyanate (FITC)-conjugated streptavidin (Pierce) or FITC-conjugated goat anti-human IgG antibody was then added and incubated for 30 min at 4 °C. The cells were analyzed on a flow cytometer (BD Biosciences). Controls included CH3 peptide shown above or wild type human IgG-Fc. The expression of fusion protein δ1-GFP on J.RT3-T3.5 cells was determined by immunofluorescent analysis directly. To determine the expression of TCRγδ1 on J.RT3-T3.5 cells, cells were stained with phycoerythrin (PE)- or FITC-conjugated antibodies and the corresponding isotype controls (Beckman). Immunofluorescence was measured by Accuri C6 Flow Cytometer and analyzed by CFlow Software. Cell sorting was conducted on a FACS ARIA cell sorter. Specific anti-human antibodies including anti-TCRγδ antibody, anti-CD3, and isotype controls were purchased from Beckman Coulter. Anti-δ and anti-actin antibodies for Western blot were purchased from Santa Cruz Biotechnologies.

**Confocal Microscopy**—Cells were plated on plastic sheets overnight and fixed on slides with 4% cold paraformaldehyde. Then fixed cells were incubated with biotin-conjugated GTM peptide or the γ4-Fc/δ1(GTM)-Fc protein and their V/D/J mutants followed by incubating with FITC-conjugated streptavidin or goat anti-human IgG antibody (Pierce). Controls included CH3 peptide or human IgG-Fc as the primary antibody. Slides were examined with a confocal laser microscope (LSM 510; Carl Zeiss) (16).

**Immunohistochemistry**—Formalin-fixed paraffin-embedded sections of tumor tissues were deparaffinized and then boiled in microwave for antigen retrieval. After quenching with peroxide, the sections were blocked with 5% goat serum. Biotin-conjugated peptides or γ4-Fc/δ1(GTM)-Fc protein or their mutants were then added to the slides. The sections were incubated with HRP-conjugated streptavidin or HRP-conjugated goat anti-human IgG antibody (Pierce). Controls included CH3 peptide or human IgG-Fc as the primary antibody. The latter are termed as GTMVm, GTMDm, and GTMJm, respectively, and each condition was plated in triplicate. There were four control groups: maximal cpm release group, volume corrected group, background group, and spontaneous cpm release group. We detected the cytotoxicity assay according to a cytotok 96 nonradioactive cytotoxicity assay reagents kit (Promega) instruction (25, 26).

**RESULTS**

**Binding of CDR3δ1 Peptide to Target Tumor Cells/Tissues and TCRγδ-specific Antigen MICA Depends on Its Flanking V and J Sequences**—We recently obtained a dominant δ1 chain from gastric tumor-derived γδTILs isolated from four patients and a matching γ4 chain from one patient. We named this CDR3δ1 sequence as GTM. CDR3δ1 consists of the conserved flanking V and J segments as well as diverse N-D-N (D) sequences (Fig. 1A). To determine which segment in CDR3δ1 determines the specific antigen recognition, we synthesized GTM peptide based on the sequence of isolated γδTILs and the mutant peptides by replacing V, D, or J segments of GTM with randomly arranged amino acid sequences of the same length. The latter are termed as GTMv1, GTMv2, and GTMv3, respectively (Fig. 1A). Binding of these synthetic wild type and mutant peptides to target cells and tissues in vitro was examined by flow cytometry and microscopy, respectively. As shown in Fig. 1, B and C, in contrast to the staining with wild type GTM peptide, tumor cell lines BGC823, G401, GLC-82, HT29, and SKOV3 all showed dramatic reduction in binding to the mutant peptides GTMv1 and GTMv2, whereas their binding to mutant peptide GTMv3 with mutations in the inner N-D-N region was only slightly affected. Similar binding profiles of these peptides to primary tumor specimens were also observed (Fig. 1D). Our data suggest that the conserved flanking V and J
sequences but not the diverse D regions are critical for the binding to target tumor cells.

To further demonstrate that the peptides indeed interacted with TCRγδ1-specific antigen on those tumor cells, we next examined the interaction of GTM peptide and its mutants with known TCRγδ1 reactive self-antigen MICA protein (27, 28). As shown in Fig. 1E by SPR and in Fig. 1F by ELISA, the binding of mutant peptides GTMVm and GTMJm to the extracellular segment of MICA was significantly reduced, whereas that of GTMDm was not overtly affected. These data suggest that

![Figure 1. Binding activity of CDR3γδ1 and its mutant peptides to tumor cells/tissues or ligand MICA.](image)

A. A, shown are schema of the amino acid sequences of GTM and its V/D/J mutants. GTM, GTMVm, GTMDm, and GTMJm represent the wild type and mutant peptides in V, D, and J region of a CDR3γδ1, respectively. B, shown are flow cytometry profiles of the binding of GTM or its mutant peptides to various tumor cell lines BGC823, G401, GLC-82, HT29, and SKOV3. After incubation with biotinylated peptides, tested cells were stained with FITC-streptavidin and then analyzed by flow cytometry. Data are representative of three independent experiments. C, shown are confocal images of the binding of GTM peptide or its mutant peptides to various tumor cells. After incubation with the peptides, tested cells were stained with FITC-streptavidin and then analyzed by laser scanning confocal microscopy. Confocal images are one representative of at least three independent experiments. D, binding of GTM peptide and its mutants to primary tumor specimens was analyzed by immunohistochemistry. CH3 peptide was served as negative control. Binding was visualized using diaminobenzidine as the substrate (brown) (×100). G, gastric cancer; R, renal carcinoma; L, lung carcinoma; C, colon carcinoma; O, ovarian cancer. E, binding of GTM peptide and its mutants to MICA was analyzed by ELISA. Data shown are the mean of three independent experiments. F, binding of GTM peptide and its mutants to MICA was analyzed by SPR. The *K_{D}* values are shown in the figure.
GTM binding to the extracellular domain of MICA is specific, and the V and J segments are the primary determinants for the binding, whereas the sequence in the D region only contributes to the binding minimally. Our data also demonstrate that the differential binding of GTM or its mutant peptides to target tumor cells in Fig. 1, A and B, was likely through specific γδ TCR/antigen interaction.

Engineered Soluble CDR3δ1 Fragment Is Critically Dependent on Its V and J Sequences for the Antigen Binding—To further validate the binding of CDR3δ1 peptide GTM or its mutants to its antigen in the context of intact TCRγδ, we engineered chimeric proteins composed of the extracellular domains of γδ and δ1 containing GTM or its V, D, J mutant sequences fused to the hinge region, CH2, and CH3 domains of human IgG1 heavy...
chain. We expressed the fusion proteins (γ4-Fc/Δ1(GTM)-Fc, γ4-Fc/Δ1(GTMVm)-Fc, γ4-Fc/Δ1(GTMdm)-Fc, and γ4-Fc/Δ1(GTMjm)-Fc) in E. coli. (Fig. 1A). We examined the binding capacity of these recombiant γ4-Fc/Δ1-Fc fusion proteins to tumor cells followed by flow cytometry and confocal microscopy. As shown in Fig. 2, the binding activity of γ4-Fc/Δ1(GTMVm)-Fc or γ4-Fc/Δ1(GTMjm)-Fc but not γ4-Fc/Δ1(GTMdm)-Fc was significantly compromised compared with that of γ4-Fc/Δ1(GTM)-Fc on various tumor cell lines (Fig. 2, B and C) and primary tumor specimens (Fig. 2D), further supporting that the conserved flanking V and J domains of CDR3Δ1 play critical roles in antigen binding. Similar results were also observed from the direct binding of γ4-Fc/Δ1(GTM)-Fc or its mutant fusion proteins to antigen MICA in SPR and ELISA assays (Fig. 2, E and F).

The V and J Sequences of CDR3Δ1 Are Critical for Formation and Function of TCRγδ1 in Transduced J.RT3-T3.5 Cells—To further substantiate the roles of the V and J segments of CDR3Δ1 of γδTILs in antigen recognition at cellular level, we lentivirally transduced the wild type or mutant δ1 chains along with the full-length γ4 into J.RT3-T3.5 cells to establish stable cell lines expressing different CDR3Δ1-grafted TCR dimers on the cell surface. Flow cytometry analysis demonstrated that TCRgδ expression on J.RT3-T3.5 cells cotransduced with pWPXL-γ4 and pWPXL-δ1(GTM) (termed T-GFP/R) or pWPXL-γ4 and pWPXL-δ1(GTMdm) (termed D-GFP/R) was readily detectable (Fig. 3A). However, no γδTCR expression was found on the surface of cells transduced with pWPXL-γ4 and pWPXL-δ1(GTMvm) (termed V-GFP/R) or pWPXL-γ4 and pWPXL-δ1(GTMjm) (termed J-GFP/R) (Fig. 3B). These data suggest that mutations in the V and J regions of CDR3Δ1 are disruptive to the assembly of γδTCR on cell surface. To further confirm this finding, we randomly substituted amino acids in the V, N-D-N, and J regions of CDR3Δ1 with alanines by mutagenesis (termed VA-GFP, DA-GFP, and JA-GFP, respectively) to eliminate the impact of different amino acids. As shown in Fig. 3B, only cells transduced with DA-GFP/R but not with VA-GFP/R and JA-GFP/R, exhibited TCR expression, consistent with the results from D-GFP/R, V-GFP/R, and J-GFP/R. To further rule out a possibility of imbalanced expression of γ4 and δ1 chains by two different co-expression constructs, we engineered bicistronic pWPXL-Δ1-ires-γ4 constructs expressing both γ4 chain and wild type (termed TR) or mutant δ1 chain (termed VR, DR, JR, VAR, DAR, and JAR). Upon the lentiviral transduction, we only observed wild type or D region mutant construct-derived TCR expression on the surface of J.RT3-T3.5 cells, whereas constructs with mutations in the V or J region resulted in detectable TCR expression (Fig. 3, B and C), further indicating the importance of the V and J segments in the assembly of TCRγδ1. In conclusion, our data demonstrated that the V and J regions of CDR3 Δ1 play critical roles in antigen binding as well as TCRγδ assembly.

Although Western analysis confirmed the cellular expression of δ1 and its mutant proteins in the transduced cells (Fig. 3E), we found that J.RT3-T3.5 cells had no detectable surface expression of TCR when transduced solely with the construct pWPXL-δ1 (GTM) (T-GFP) or its mutants in the absence of γ4 chain (Fig. 3A), suggesting an absolute dependence of γ4 chain for the surface expression of δ1 chain. It is also known that the TCR-CD3 complex can only be transported to the cell surface after all required subunits of the complex are completely assembled (29). We hypothesized that the detection of CD3 surface expression on cells transduced with TR or its mutants was another surrogate measure for TCR surface expression. Indeed, cells transduced with TR or its mutants in D region (DR and DAR) showed robust CD3 expression, whereas cells expressing mutants in the V and J regions (VR, VAR, JR, and JAR) had little detectable CD3 expression (Fig. 3D). These results show the indispensable role of the V and J sequences in the assembly of functional TCR and TCR-CD3 super complex.

Finally, we tested whether mutations in the V and J regions would impact the functionality of γδ T cells. However, TCRγδ1 used in our study was obtained from primary γδTILs with yet to be determined antigen specificity. Despite the fact that Burkitt’s lymphoma cell line Daudi has been used as the target cell for measuring γδ T cell cytotoxicity (30), it has been reported that some γδ1 T cells may also exhibit reactivity toward Daudi cells (31, 32). We, therefore, examined the cytotoxic effect of J.RT3-T3.5 cells transduced with TCRγδ1 or its mutants on Daudi cells. Cells transduced with pWPXL or V-GFP/R, J-GFP/R, V-A-GFP/R, and J-A-GFP/R showed certain cytolytic effect on Daudi cells (Fig. 3F, left). However, T-GFP/R, D-GFP/R, and J-D-GFP/R-expressing J.RT3-T3.5 cells exhibited promoted cytolytic activity toward Daudi cells (Fig. 3F, left). Furthermore, the enhanced Daudi cell cytolytic activity of J.RT3-T3.5 cells were readily blocked by anti-TCRγδ antibody, suggesting that the cytolytic activity is mediated by TCRγδ (data not shown). We also found that J.RT3-T3.5 cells transduced with TR and its mutants exhibited similar Daudi cells cytotoxicity (Fig. 3F, right). Taken together, the V and J but not D regions are also critical for the cytotoxic function of γδ T cells in our assay system.

**FIGURE 3. The surface expression and cytotoxic function of TCRγδ1 and its mutants.** A, expression of TCRγδ and GFP in J.RT3-T3.5 transduced with T-GFP and its mutants was analyzed by flow cytometry. Phycoerythrin labeled anti-TCRγδ antibody, which recognizes all subtypes of γδT cells. B, shown is flow cytometry analysis of the surface expression of TCRγδ in J.RT3-T3.5 transduced with T-GFP/R or its mutants. C, shown is flow cytometry analysis of the surface expression of TCRγδ in J.RT3-T3.5 transduced with TR and its mutants. D, expression of TCRγδ and CD3 in J.RT3-T3.5 transduced with TR and its mutants was analyzed by flow cytometry. E, Western analysis of the expression of TCRγδ components in J.RT3-T3.5 cells is shown. J, transduced with pWPXL (containing a GFP gene); 2, transduced with T-GFP or T-GFP/R or TR; 3, J.RT3-T3.5 transduced with V-GFP or V-GFP/R or VR mutants in V fragment of CDR3; 4, J.RT3-T3.5 transduced with D-GFP or D-GFP/R or DR; 5, J.RT3-T3.5 transduced with J-GFP or J-GFP/R or JR; 6, J.RT3-T3.5 transduced with VA-GFP or VA-GFP/R or VAR; 7, J.RT3-T3.5 transduced with DA-GFP or DA-GFP/R or DAR; 8, J.RT3-T3.5 transduced with JA-GFP or JA-GFP/R or JAR. Anti-actin (left panel) or anti-Vδ1 (right panel) were used as the primary antibodies. F, shown is cytotoxicity analysis of J.RT3-T3.5 transduced with TCRγδ1 and its mutants on Daudi cells. Left, J.RT3-T3.5 cells transduced with pWPXL, T-GFP/R, and V/D/J mutants. Right, J.RT3-T3.5 cells transduced with pWPXL, TR, and V/D/J mutants. The cytotoxicity was determined using the LDH cytotoxicity detection kit. The ratios of effector:target cells were 1:2.5:1, 2.5:1, 5:1, and 10:1. Data are representative of three independent experiments.
DISCUSSION

γδ T cells together with αβ T cells and B cells are the only cells that use somatic rearrangement to generate a diverse antigen receptor repertoire. Compared with immunoglobulin and αβ TCRs, γδ TCRs have the most potential of CDR3 diversity generated by VDJ recombination (33). Despite the vast repertoire of TCR-γδ, only a few TCR-γδ-specific antigens have been identified by our group and others, including murine MHC class Ib molecules T10 and T22 (10), human MHC class I-like molecules MICA/B (28), an ATP synthetase F1-apolipoprotein A-I complex (23), and hMSPH2 (14). Developmentally, it is known that T cells somatically rearrange their δ locus before any other TCR chains at the CD4/CD8 double negative stage in the thymus, suggesting the critical role of TCR-γδ in lineage determination. Functionally, γδ T cells possess “innate-like” property due to their rapid antigen response and lack of MHC class I or II restriction. Therefore, understanding the structural determinants of TCR-γδ in antigen recognition is at the center of γδ T cell biology.

Previously, we have studied the ligand recognition of TCRγ982 from the major subset of γδT cells (11, 16). Here we further expanded our study to a dominant TCR-γδ1 derived from gastric tumor TILs. We explore the functional importance of the individual V, D, or J segment of CDR3δ1 on antigen recognition using a well established strategies including the use of synthetic CDR3δ1 peptides and CDR3δ1-grafted TCR fusion proteins as well as cells with forced expression of TCRγδ1. Mutations of amino acid sequences in the V and J regions but not the D region of CDR3δ1 peptide significantly abolish the recognition of antigen on tumor cells/tissue as well as in the form of pure protein (MICA). Consistent results were also obtained from using CDR3δ1-grafted TCR fusion proteins, further confirming the hypothesis that the conserved flanking V and J regions of CDR3δ1 play a critical role in antigen binding to TCRγδ1, whereas the D sequence is dispensable for antigen recognition. These results are apparently in contradiction with the findings in mice that the D segment is responsible for binding to T22 antigen for G8 γδT cells (10). This may be explained by the difference of species and/or the length of CDR3δ. Indeed, G8 sequence of mouse CDR3δ is much longer than human GTM, indicating that a different folding and recognition mode may exist.

During the course of our studies, we unexpectedly observed that the conserved V and J sequences were also required for the assembly of functional TCRγδ1 on T cell surface, which is a prerequisite for the surface expression of CD3γε and CD3ζζ in the form of CD3/TCRγδ1 multisubunit super complex necessary for differentiation, survival, and function of γδT cells (34, 35). More specifically, our results showed that only wild type δ1 chain and its mutants in the D region, but not in the V or J regions, could be paired with γδ chain to form a TCRγδ-CD3 complex that is readily detectable with anti-TCRγδ or anti-CD3. Despite their robust intracellular protein expression, it seems that mutations in the V and J segments render the δ1 chain assembly incompetent, leading to the disruption of γδTCR-CD3 surface expression. The unassembled polypeptide chains are likely to be sequestered in the endoplasmic reticulum and subsequently degraded (29). Indeed, J.RT3-T3.5 cells, a CD3 negative Jurkat cell variant, became endogenous CD3-positive upon the forced expression of δ1 and γδ chains. In fact, a similar observation has been reported in the case of TCRαβ expression (36). Our results support the notion that the V and J sequences also dictate the assembly of γδTCR-CD3 and, therefore, the differentiation, survival, and function of T cells.

In our previous study we similarly found that the flanking V and J sequences, but not the D region of CDR3δ2, were critical in the antigen recognition. Together with our current data, it seems that this is a common feature of γδ T cells. Our collective data suggest that γδ T cell repertoire may be much smaller than we originally calculated based on the diversity of D segment. This apparently answers the lingering question of why only a handful of TCRγδ-specific antigens have ever been identified 25 years after the first discovery of γδ T cells. On the other hand, the role of flanking V and J regions of TCRγδ1 in TCR assembly is unique to Vγ4δ1 T cells as no TCR assembly disruption was observed when similar mutations were introduced into the same flanking regions of TCRγ982 (16).

Various studies have shown that human Burkitt’s lymphoma cell line Daudi is sensitive to γδ T lymphocytes and could be efficiently killed by Vγ9Vδ2 T cells (20, 37, 38) and some Vγ9Vδ1 T cells (31, 32). Here we show that Vγ4Vδ1 T cells also have specificity toward Daudi cells. However, CDR3δ1 antigen MICA is not expressed by Daudi cells (data not shown), raising the question of how exactly different types of γδ T cells could recognize tumor cells in general. Of note, both γδ1 T cells used in our current study and γδ2 T cells in our previous study were isolated from TILs of different tumors. It is possible that γδ T cells use their TCR as a pattern recognition receptor to sense the stress-induced self-molecules and use other receptors to detect tumor-specific antigens given the fact that γδ T cells also express various NK cell receptors including NKG2D, NKG2A, and KIR (39). The ligation of both receptors in concert may lead to the engagement of the cytolytic effect on tumor cells. Indeed, a recent structure study reveals that both TCRδ1 and NKG2D competitively bind to MICA with different binding modes, constituting the tumor recognition and killing mechanisms (40). However, definitive answers to this very important question remain to be substantiated at the functional level.

Given our similar findings in CDR3δ2, our results suggest that both human TCRδ1 and TCRδ2 recognize antigen predominately via the flanking V and J region. Our data indicate that TCR-γδ recognizes antigens using conserved parts in their CDR3 and provide a reason for why the diverse repertoire of γδTCR only could recognize a limited number of antigens. In another word, γδ T cells might use a limited TCR repertoire to recognize antigen.

Acknowledgment—We greatly appreciate Dr. Liangzhi Xie for help with chimeric proteins expression.

REFERENCES

1. Rust, C. J., Verreck, F., Vietor, H., and Koning, F. (1990) Nature 346, 572–574
2. Zocchi, M. R., and Poggi, A. (2004) Front. Biosci. 9, 2588–2604
Flanking V and J Sequences of CDR3Δ1 Determine TCRγ4Δ1