

# Complete Protein Sequences of the Variable Regions of the Cloned Heavy and Light Chains of a Human Anti-Cytomegalovirus Antibody Reveal a Striking Similarity to Human Monoclonal Rheumatoid Factors of the Wa Idiotype Family

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## Abstract

The complete amino acid and nucleotide sequences of the variable regions of the heavy and light polypeptide chains of a human neutralizing IgG1 anti-cytomegalovirus (CMV) antibody reveal a striking homology to IgM rheumatoid factors (RFs) of the Wa idiotype family. The anti-CMV antibody and Wa RFs have in common V<sub>K</sub>IIIb, J<sub>K</sub>1, and V<sub>H</sub>Ia gene segments but use different D<sub>H</sub> and J<sub>H</sub> gene segments. The anti-CMV antibody does not have RF activity and does not express the Wa idiotype. The Wa RFs do not have anti-CMV activity. A subset of Wa RFs, however, and the anti-CMV antibody do share several idiotypes on the V<sub>H</sub>Ia and V<sub>K</sub>IIIb polypeptides. Since there are major differences in the antigen binding characteristics and some of the other expressed idiotypes, these data suggest that the D and J region amino acids are crucial to such specificities. Although the use of such highly homologous gene segments in different immune responses is well-documented in murine systems, these data represent the first such example in the human.

## Introduction

Although there is extensive structural data on human immunoglobulin variable regions, most sequences are derived from immunoglobulins of unknown antibody specificity or autoantibodies. While this information has been crucial to elucidating the structure of human antibodies and has formed the basis of hypotheses relating to the generation of human antibody diversity, it is likely that much of the human immunoglobulin variable region repertoire is directed at specific exogenous antigens. The study of immunoglobulins with functional antibody activity is key to establishing the biological context of variable region sequence data and confirming the applicability of principles based on sequences of myeloma proteins and autoantibodies.

During the course of continued investigations on the structure of human antibodies, we examined an MAB

(EVI-15) that neutralizes cytomegalovirus (CMV).<sup>1</sup> The complete amino acid sequences of the variable regions of this antibody revealed a striking homology to human monoclonal rheumatoid factors (RFs) of the major idiotype family. Specifically, the VK, JK, and VH gene segments of both the Wa RFs and EVI-15 are derived from the same or very closely related germ line gene segments. Consistent with their structural similarity, Wa RFs and EVI-15 share several serological determinants. The structural and serologic similarity of these molecules provides a possible link between the immune response to a ubiquitous virus and a common autoantibody.

The striking similarity of EVI-15 to a subpopulation of RFs raises interesting questions relating to the human variable region repertoire and the idiotype network theory of immunoregulation, as well as the association of viral infection and autoantibody production. While viral infections have been implicated in several forms of acute arthritis (1, 2), their role in the etiology and/or pathogenesis of RA remains unclear (3). EBV (4-8), rubella (9, 10), hepatitis B (1), vaccinia (11), and CMV (12, 13) have been associated with RA, although the role of viruses in the inflammatory process has resisted elucidation. Postulated mechanisms include (a) cross-reactivity between viral antigens and host tissue, (b) alteration of host tissue by virus rendering host tissue antigenic, and (c) chronic infection and/or destruction of host tissue directly leading to inflammation (2). The circumstantial evidence implicating viruses includes rising titers of antiviral antibodies during the course of rheumatoid disease (7), isolation of live virus from rheumatoid joint tissue (12), and extensive epidemiologic analysis (3). Nonetheless, the issue has remained controversial.

A major feature of RA is the autoimmune diathesis present in most patients. Over 75% of adult patients with rheumatoid disease produce RF (14), an anti-gamma globulin whose serum titer has been shown to correlate with disease activity (15). More significant has been the direct demonstration that RFs may be produced in vitro by synovial B cells (16). The finding that RF was virtually the only immunoglobulin synthesized locally in the rheumatoid synovium refocused attention on RF and its possible primary or secondary role in the basic disease process.

Since the RFs produced in adult RA are polyclonal in nature, although of restricted heterogeneity (17), most structural and serologic studies on RFs have taken advantage of the syndrome of mixed cryoglobulinemia. Extensive studies of these human monoclonal RFs have defined groups of RFs

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1. Abbreviations used in this paper: CDR, complementarity determining regions; CMV, cytomegalovirus; D, diversity region; Fab, antibody binding fragment; Fc, crystallizable fragment; H, heavy chain; IDDM, insulin-dependent diabetes mellitus; J, joining region; L, light chain; RF, rheumatoid factors; V, variable region.

based on the expression of cross-reactive idiotypes (18, 19). The Wa idiotype family, representing ~ 60% of monoclonal RFs, has been found to be highly restricted in the use of light and heavy chain variable region gene segments (20–28). This is analogous to the restricted use of immunoglobulin variable region gene segments in murine antigen specific systems, many of which bear cross-reactive idiotypes. The relationship between these monoclonal RFs and the RFs present in RA was demonstrated by Pernis and his colleagues, who showed that the plasma cells of patients with RA contained idiotype-positive material (29). Some of the autoantibodies produced during the course of RA thus are structurally similar to the antibodies so extensively studied in mixed cryoglobulinemia (30). Since anti-idiotypic antibodies to RF have been described in patients with monoclonal RFs (31), they may play a role in the regulation of RF production and thus may either initiate or perpetuate RF synthesis.

## Methods

**Preparation of monoclonal anti-CMV antibodies.** The antibody EVI-15 was generated by fusing human splenic B lymphocytes with the SPAZ cell line (Östberg, L., E. Pursch, and M. Scriba, manuscript in preparation). This antibody was purified from tissue culture supernatants by affinity chromatography using Staphylococcal Protein A.

**Preparation of monoclonal IgM RFs.** These antibodies were purified from the plasma (a gift from R. Wistar, Naval Medical Research Institute, Bethesda, MD) of patients BOR, KAS, and RIV with mixed cryoglobulinemia as previously described (32).

**Antigenic specificity.** EVI-15, BOR, KAS, and RIV were tested for RF activity both by latex agglutination and ELISA. For the ELISA, plates were coated with 10 µg/ml crystallizable fragment (Fc) (from human IgG1) in carbonate-bicarbonate buffer, pH 9.6, for 16 h at 4°C. Incubations were performed with the IgM RFs at concentrations of 0.02–2.0 pM, with a monoclonal IgG RF (SFL) (33) at concentrations of 20–200 pM, and with EVI-15 at concentrations of 20–500 pM. The bound MAbs were detected with peroxidase-conjugated goat anti-human kappa antisera (Cappel Laboratories, Cochranville, PA). EVI-15, BOR, KAS, and RIV were tested for anti-CMV activity by neutralization assays and by ELISA (Östberg, L., E. Pursch, and M. Scriba, manuscript in preparation).

Sera from 20 patients with classical RA or insulin-dependent diabetes mellitus (IDDM) and 40 normal controls were tested for RF activity by ELISA as above. Sera were diluted 1:50 in PBS for initial screenings. Total RF, detected by the peroxidase-conjugated goat anti-human kappa antiserum and IgM RF, detected by peroxidase-conjugated goat anti-µ (Fc specific) antiserum was measured.

**Expressed Idiotype.** BOR, KAS, RIV, EVI-15; sera from patients with RA and IDDM; and normal controls were analyzed by ELISA for reactivity to a goat antiserum that detected a private idiotype on EVI-15 (34). Briefly, plates coated with 10 µg/ml antiidiotypic antisera were incubated with 100 µl of monoclonal RFs, 200 ng EVI-15, or sera from patients or normal controls (diluted 1:100 in PBS). The bound antibodies were detected with peroxidase-conjugated goat anti-human kappa antiserum. An irrelevant, peroxidase-conjugated goat anti-mouse Ig antiserum (Cappel Laboratories) was used in parallel to control for antibodies reactive to goat immunoglobulin. The BOR, KAS, RIV, and EVI-15 MAbs were assayed for expression of the Wa idiotype and idiotopes found on human monoclonal RFs as previously described (22). Patient and normal sera (as above), the RFs, EVI-15, and other random myeloma proteins were analyzed for reactivity to the antibody binding fragment, (F[ab']<sub>2</sub>) of an absorbed rabbit serum raised to EVI-15 that was affinity purified from the RF BOR, which defines a new idiotype 1–15(B) by ELISA using the conditions as outlined for the analysis of the private EVI-15 idiotype.

**Reactivity with antisera raised to the complementarity determining regions (CDR) of a Wa RF (SIE).** The heavy and light chains of EVI-15 were separated on SDS-PAGE and immunoblotted with antisera to the peptides PSL2, PSL3, and PSH3 as previously described (35–37).

**Preparation of fragments for protein sequencing.** Fab fragments of EVI-15 were made by digesting the IgG1 with papain (HG papain, Worthington Biochemicals, Malvern, PA) according to the method of Poljak et al. (38). The Fab and Fc were separated by affinity chromatography using Protein A-Sepharose (Pierce Chemical Co., Rockford, IL).

The purified Fab fragments were chemically cleaved with an equal weight of cyanogen bromide. The cyanogen bromide digest was reduced and alkylated as previously described (39). Peptides were separated initially by reverse phase chromatography using a C4 column (Vydac, Hesperia, CA) and a linear gradient of 0.1% trifluoroacetic acid in water to 0.1% trifluoroacetic acid in 50% acetonitrile and 15% isopropanol for 90 min at a flow rate of 1.0 ml/min. The initial peaks were further resolved using reverse phase chromatography on a C18 column (Aquapore RP300; Brownlee Labs, Santa Clara, CA) developed with the gradient described above. Peptides that were ≥ 35 amino acids long were further digested with trypsin with or without prior citraconylation (39). The resultant peptides were separated by reverse phase chromatography as above.

Initial studies showed that the amino terminus of the heavy chain resisted Edman degradation. Therefore, pyroglutamic amino peptidase was used according to the method of Podell and Abraham (40) to cleave the cyclized amino-terminal amino acid.

**Protein sequencing.** Peptides were subjected to automated Edman degradation using either the gas phase sequencer (model 470; Applied Biosystems Inc., Foster City, CA) with the model 120, on-line HPLC phenylthiohydantoin amino acid identification system, or a spinning cup sequencer (model 890M; Beckman Instruments, Inc., Fullerton, CA). In the latter case, the phenylthiohydantoin amino acids were identified using a NovaPac column in an HPLC system (model 840; Waters Associates, Milford, MA). Compositional analyses of peptides were done by amino acid analysis using an amino acid analyzer (model 6300; Beckman Instruments, Inc.).

**Cloning the EVI-15 rearranged heavy and light chain genes.** The DNA fragments encoding the EVI-15 light and heavy chain variable regions were identified by Southern filter hybridization. Bam HI-digested DNA from human placenta, EVI-15, and the SPAZ cell lines were probed with a human C<sub>K</sub>-specific 2.7-kb Eco RI fragment (41) and a 7.5-kb Hind III fragment encoding the human gamma 1 exons (42). Methods for the cloning procedures were essentially as described by Heinrich et al. (43). Briefly, DNA fragments of the appropriate size were selected from Bam HI-digested EVI-15 DNA on a agarose-gel and cloned into bacteriophage lambda EMBL4. Approximately 4 × 10<sup>5</sup> phage plaques were screened with the C<sub>K</sub> probe and 5 × 10<sup>4</sup> plaques were screened with the C probe. Three phage clones for each heavy and light chain were found to hybridize specifically with the probes. Subfragments encoding the rearranged heavy chain variable region gene, identified by crosshybridization with human J<sub>H</sub> specific oligonucleotide probes (synthesized on an Applied Biosystems 380 A DNA synthesizer), were cloned into bacteriophage M13mp18 for nucleotide sequencing.

**Heavy and light chain recombination experiments.** The heavy and light chains of EVI-15, BOR, and RIV (the latter a structurally and idiotypically unrelated RF) were separated and recombined following the procedure of Jeske et al. (44). Briefly, the immunoglobulin of interest was reduced and alkylated in the presence of 5 M guanidine and 50 mM Tris-HCl, pH 8.0. Heavy and light chains were separated by gel filtration in guanidine, using a S200 column (2.5 × 100 cm) (Pharmacia Fine Chemicals, Piscataway, NJ). Fractions were analyzed by SDS-PAGE for heavy or light chain and then pooled. Heavy and light chains were mixed to form homologous or heterologous molecules and dialyzed slowly into Tris-buffered saline (50 mM Tris-HCl and 0.15 M NaCl, pH 7.4). Recombined molecules were separated

from free light and heavy chains by precipitation with 40% ammonium sulfate. The precipitated molecules migrated at 75–90 kD (depending on the heavy chain in question) in nonreducing SDS-PAGE and as a light chain (24 kD) and a heavy chain (50–65 kD) in reducing conditions. Homologous and heterologous chain recombinants were analyzed for biological activity and expression of idiotype as above.

## Results

**The light chain variable region sequence of anti-CMV antibody EVI-15.** Southern filter hybridization using the kappa specific probe demonstrated hybridization with a 10.5- and 11-kb fragment in EVI-15 and placental DNA digested with Bam HI, respectively, indicating a rearranged C<sub>K</sub> gene (data not shown). The probe did not crosshybridize with any SPAZ DNA fragment. This result confirms previous karyotypic analysis of the SPAZ cell line, which showed that it had lost all but two human chromosomes. After library screening, the 3.4-kb Eco RV fragment of the light chain variable region was cloned into the Sma I site of M13mp18. The nucleotide sequence and the derived amino acid sequence of the cloned EVI-15 light chain is presented in Fig. 1. The EVI-15 V<sub>K</sub> gene segment is joined in frame to the human J<sub>K</sub>1 gene segment (45). The leader peptide is interrupted by a 186-bp intron. The amino acid sequence determined by classical protein sequencing techniques was determined independently and was found to be identical to that deduced from the nucleotide sequence. The variable region exon can be classified as a human kappa light chain of the V<sub>K</sub>IIIb subgroup (46).

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ACCAACATCTCTGGCTCAATCTAGGTGATGGTGGAGACAGGACACAGGGGTTAAATTTCTGTGG -480
CCGCAGGGGAGAGGTCTTCACTCCAGACTGAGCCAAAGGOCCTTTCTGGCCTGATCACTGGGGCATG -413
GGCTGCTGAGAGCAAAAGGGAGGCGAGTGTCTCTCTGCACTGCAAGGOCAGCAAGGOCAGGCT -346
10-bpI
GCCTTGGCATGTTCCTCCAGGOCCTGCACTCCAGGOCCTTCACTGCAATGOCCTGGGTGAGAGCTCTG -279
      M E T P A Q L L F
GAGAGAGCTGCTCGAGGAGGACCGAGGAAACC ATG GAA ACC CCA GCG CAG CIT CTC TTC-220
L L L L W L P A
CTC CTG CTA CTC TGG CTC CCA G GTGAGGGGAACATGGGATGTTTTCATGTGTCAGTGAAG -161
ACCCCTCCTAGTCCCTGTTAACCCTGGCAGCTCTGCTCAGTCCATTAATTAATTAAGGCTCAATTAAG -94
CAATTAATTTCTGGCTCTCTGGGAGGACCAATCCCTTGTGATTTAGTACATGGGTCACATTTCTGTTTT -27
      T T G E I V L T Q S P G
TATTTCCATCTCCAG AT ACT ACC GGA GAA ATT GTG TTG ACG CAG TCT CCA GGC +27
T L S L S P G E R A T L S C R A S
ACC CTG TCT TTG TCT CCA GGA GAA AGA GGC ACC CTC TCC TGC AGG GGC AGT +78
Q S V S S N E L A W Y Q Q K P G Q
CAG AGT GTT AGC AGC AAC GAA TTA GGC TGG TAC CAG CAG AAA OCT GGC CAG +129
A P R L L I S G A S R R R A T G I P
GCT OCC AGG CTC CTC ATC TCT GGT GCA TOC AGA AGG GCC ACT GGC ATC CCA +180
D R F S G S G S G T D F T L T I S
GAC AGG TTC AGT GGG AGT GGG TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC +231
R L E P E D F A M Y Y C Q Q Y G S
AGA CTG GAG OCT GAA GAT TTT GCG ATG TAT TAC TGT CAG CAG TAT GGA AGT +282
T P R T F G Q G T K V E I K R
ACA OCT GGA AGC TTC GGC CAG GGG ACC AAG GTG GAA ATC AAA CGTGAGT +331

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Figure 1. The nucleotide sequence of the light chain Eco RV fragment of EVI-15. Amino acids are designated by the single-letter code. The CDRs are boxed.

**The heavy chain variable region sequence of anti-CMV antibody EVI-15.** Southern filter hybridization of EVI-15 and placental Bam HI-digested DNA using the C probe showed four and five crosshybridizable fragments, respectively (data not shown). After library screening, the 2.2-kb Bam HI-Hind III fragment was cloned into the Sma I site of M13mp18 for nucleotide sequence analysis. The heavy chain clone contained only the part of the variable region encoding the mature variable domain (exon 2) because of a Bam HI site within the leader intron. The amino acid sequence determined by classical protein sequencing techniques was identical to the sequence deduced from the DNA sequence in the coding region of this rearranged gene (Fig. 2). This variable region can be classified as a heavy chain belonging to the V<sub>H</sub>Ia subgroup (22). When the DNA sequence of EVI-15 was compared with another V<sub>H</sub>Ia subfamily member, the 783 rearranged gene (J. V. Ravetch and S. Korsmeyer, personal communication), 89% nucleotide identity was detected in the coding region and 87% identity in the entire cloned gene (463 bp).

The EVI-15 D segment does not match any published D segment (47) and is one of the longest D regions described to date. The junctional V-D amino acid, asparagine (GAT), was probably formed by the addition of the T (from either the D gene element or added by terminal transferase) to the GA that has been seen in the germ line of an unrearranged, related V<sub>H</sub>I gene (48).

The J<sub>H</sub> gene segment used in EVI-15 can be classified as a J<sub>H</sub>6 (49). The nucleotide and amino acid sequence differences from the germ line J<sub>H</sub>6 can be explained by single base substitutions. Alternately, EVI-15 uses a J<sub>H</sub>6 segment that is one codon shorter than the germ line J segment, similar to that seen in the heavy chain variable region exon cloned from a human plasma cell line, ARH-77 (50). The 783 rearranged gene, which also uses a J<sub>H</sub>6 gene element, is three nucleotides longer (5') and is more closely related to the genomic nucleotide sequence of J<sub>H</sub>6.

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GATCCTGGTTTAGTTAAAGAGGATTTTATTCACCCCTGTGTCTCTCCACAG GT GTC CAG -4
      V Q
S Q V Q L V Q S G A E V K K P G
TCC CAG GTG CAG TTG GTG CAG TCT GGG GCT GAG GTG AAG AAG OCT GGG +45
S S V K V S C K A S G G T F S S
TCC TGG GTG AAG GTC TCC TGC AAG GCT TCT GGA GGC ACC TTC AGC AGT +93
Y A F S W V R Q A P G Q G L E W
TAT GCT TTC AGC TGG GTG CCA CAG GCC OCT GGA CAA GGG CIT GAG TGG +141
M G G I I P F L G T T H Y A Q K
ATG GGA GGC ATC ATC OCT TTC TTA GGG ACA ACA CAC TAC GCA CAG AAA +189
F Q D R V T I T T D E S T R T A
TTC CAG GAC AGA GTC ACG ATT ACC ACG GAC GAA TOC ACG GCG ACA GCC +237
Y M E L H I L R S E D T A I Y Y
TAT ATG GAA CTA CAC ATC TTG AGA TCT GAG GAC ACG GOC ATA TAT TAT +285
C A R D Q S L E N I E V V P L D
TGT GCG AGA GAT CAG TOC CTC GAG AAT ATT GAA GTG GTG CCA CIT GAC +333
P N Y F Y D G M D V W G Q G T T
OCT AAT TAC TTC TAC GAC GGT ATG GAC GTC TGG GGC CAA GGG ACC ACG +381
V T V S S
GTC ACC GTC TOC TCAGGT +399

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Figure 2. The nucleotide sequence of the heavy chain Bam HI-Hind III fragment of EVI-15. Amino acids are designated by the single-letter code. The CDRs are boxed.



**Table I. Reactivity of Antiidiotypic Sera/Antibodies and Anti-peptide Antisera to EV1-15 and Members of the Wa Idiotypic Family of Rheumatoid Factors, BOR and KAS and RIV, a non-Wa RF**

Antisera/MAB idiotypic	Human monoclonal Igs			
	EV1-15	BOR	KAS	RIV
Wa	—*	++	++	—
EV1-15 (private)	++	—	—	—
1-15 (B)	++	+++	+++	—
Light chain determinants				
Anti-PSL2	++ <sup>‡</sup>	++	+	—
Anti-PSL3	++	+	++	—
B12	+*	+++	+++	—
C7	++	+++	+++	—
17-109	—	++	++	—
G8	—	++	—	—
Heavy chain determinants				
Anti-PSH3	—	++	—	—
G8	—	++	—	—
G6	—	++	++	—

\* ELISA results: —, <0.05; +, 0.05–0.5; ++, 0.5–1.0; +++, >1.0.

<sup>‡</sup> Results with anti-peptide (PSL2, PSL3, and PSH3) antisera based on autoradiographic detections on Western blots.

appeared to be interchangeable and could form hybrids with either heavy chain with subsequent expression of the idiotype associated with the parent molecule from which the heavy chain was isolated. The 1-15(B) idiotype could not be detected on intact Wa RFs SIE and WOL, which have the V<sub>K</sub>IIIb light chain but not the V<sub>H</sub>Ia heavy chain, lending further support to the hypothesis that for this idiotype to be expressed, a specific heavy chain variable region must be present. The V<sub>K</sub>IIIa light

**Table II. Expression of Idiotype by Hybrid Immunoglobulins from Homologous and Heterologous Recombinations of Heavy and Light Polypeptide Chains from the Anti-CMV Antibody EV1-15, and Two RFs, BOR\* and RIV<sup>‡</sup>**

Recombination		Expression of idiotype		
Heavy chain	Light chain	Wa	EV1-15	1-15 (B)
EV1-15	None	—	—	—
EV1-15	EV1-15	+	++	++
EV1-15	BOR	—	++	+
EV1-15	RIV	ND	+	—
BOR	None	—	ND	—
BOR	BOR	+	—	++
BOR	EV1-15	++	—	+++
BOR	RIV	—	ND	—
RIV	RIV	—	ND	—
RIV	BOR	—	ND	—

+, 0.1–0.2; ++, 0.2–0.3; +++, 0.3–0.4 OD units, when assayed at 20 µg/ml.

\* Wa idiotypic family.

<sup>‡</sup> By structural analysis similar to the Po idiotypic family (33).

chain of RIV (another RF, structurally similar to the Po family [33]) appeared not to form hybrids capable of expressing either the Wa or the shared 1-15(B) idiotypes with either BOR or EV1-15 heavy chains. Weak expression of the private EV1-15 idiotype was detected on the hybrid formed from the EV1-15 heavy chain and the RIV light chain.

**Rheumatoid factor activity and expression of EV1-15 Idiotype in patients with RA or IDDM or normal individuals.** Patients with RA (90%), some normal individuals (5%), and patients with IDDM (5%) were found to have detectable IgM RFs (Table III). The 1-15(B) idiotype was detected in 20% of normal controls and 50% of patients with RA and IDDM. Antibodies expressing the private EV1-15 idiotype were not detected in the sera from 20 patients with RA, 20 patients with IDDM, or 40 normal controls (data not shown). Only EV1-15 was positive for the private idiotype in the assay when controlled with the irrelevant goat anti-mouse sera. In contrast, it appeared that 62% of RA patients, 45% of IDDM patients, and 15% of normal controls had antibodies that were reactive with several goat sera (this reactivity could be either RFs or anti-Fab antibodies).

## Discussion

These data document a striking serologic and primary structural similarity between a human anti-CMV antibody and the RFs of the Wa cross-reactive idiotype group. Three of the five gene elements, representing > 95% of the primary structures of these two sets of antibodies, are derived from the same or very similar germ line gene segments. While an important reservation concerning these data is that only a single human anti-CMV antibody has been sequenced, the data have important implications for our understanding of the use of the human immunoglobulin gene repertoire, and provide information concerning the importance of D and J segments in the Wa cross-reactive idiotype. Additionally, the results suggest a potentially important interrelationship between viral infections and RA and provide a possible framework to investigate the network concept of immunoregulation.

The light chain variable region of EV1-15 is closely related to the light chains of IgM Wa idiotypic RFs. Chain recombination experiments document that the light chains of the anti-CMV antibody and RFs are interchangeable without affecting RF binding specificity. Both the Wa- and EV1-15-associated idiotypes could be restored to isolated heavy chains (Table II) by heterologous light chains. No antiviral activity could be

**Table III. Detection of Rheumatoid Factor and the Expression of the 1-15(B) Idiotype in Patients with RA, IDDM, and in Normal Controls**

Patients/normal controls	No.	RF*	IgM RF	1-15 (B) idiotype
		Positive (%)	Positive (%)	Positive (%)
Normal	40	5 (13)	2 (5)	8 (20)
RA	20	18 (90)	18 (90)	10 (50)
IDDM	20	10 (50)	2 (5)	10 (50)

\* Detected with antihuman kappa.

detected in any of the recombined hybrid molecules. It is likely that the proper refolding of the very large heavy chain CDRIII of EVI-15 is critical for such activity. There is a striking similarity between the nucleotide sequence of EVI-15 light chain and the published sequence of the related germ line KIIIa genes, 305 and 321 (55), the latter of which may be a KIIIb. The EVI-15 light chain V region is 120 nucleotides longer than 305 (5' of coding). Within the untranslated region, including the leader sequences (440 bp), the two sequences (305 and EVI-15) are 97% identical. There is 95% identity in the coding region. The 321 gene, which is thought to be more closely related to the RF KIIIb, has 96% nucleotide identity (164 bp) with EVI-15. The KIIIb light chain has been shown to be primarily associated with the IgM isotype in normal human sera (56).

There has been considerable controversy concerning the significance of the highly restricted use of KIIIb light chains, primarily in autoantibodies (21, 24, 54, 55). Since EVI-15 exhibits potent anti-CMV activity, it is apparent that the restriction of the KIIIb light chain to autoantibodies is not exclusive. It appears that, based on the strong reactivity of the anti-PSL2 serum to the EVI-15 light chain, this antiserum probably recognizes a stretch of amino acids between positions 54 and 61, which is predominantly framework III. Clearly, this anti-peptide serum is able to recognize antibodies that do not have RF activity, confirming the observations of Agnello et al. (57). EVI-15, however, is the first antibody not selected for autoreactivity that reacts with this antiserum. The CDRIII of the light chain of EVI-15 is indistinguishable from an RF CDRIII. The anti-peptide antiserum that is reactive with this region is equally reactive with SIE RF and EVI-15 molecules.

EVI-15 uses the  $J_{\kappa 1}$  gene element, which is also most commonly used by the Wa idiotypic RFs (21, 22). The junctional amino acid arginine, between the V-J in EVI-15, is also the most commonly seen amino acid in this position. There thus is a striking similarity between the  $V_{\kappa}$  and  $J_{\kappa}$  gene segments used by EVI-15 and the major (Wa) class of human RFs.

*The heavy chain variable region of EVI-15 is highly related to the heavy chain variable region of Wa family RFs.* The EVI-15  $V_H$  region is 85% identical to the Wa RFs of the  $V_{H1a}$  subgroup and by definition EVI-15 is a member of this  $V_H$  subgroup. The amino acid substitutions in CDRI and II of EVI-15 are limited in number and conservative and as such are unlikely to account for the differences in antigen specificity. The D and J regions (CDRIII), however, are very different between the anti-CMV antibody and the RFs (Fig. 5) and most likely account for the difference in the antigen binding characteristics, as well as the observed differences in the expression of idiotype. This difference lends further support to the importance of the D-J4 region (22, 25, 58) of the RFs, both for expression of the Wa idiotype and for antigen binding. Until other related anti-CMV antibodies with the same specificity are described, no firm conclusions about the importance of parts of the variable regions to anti-CMV activity can be made. When compared with the RFs, however, it is clear that the D-J6 region is important for both the anti-CMV binding activity and the expression of the idiotype associated with EVI-15.

Most of the structural and serological information about RFs has been derived from the study of monoclonal IgM RFs isolated from patients with mixed cryoglobulinemia. The rele-

vance of this information to the polyclonal RFs has been established by several studies that have identified antibodies similar to the monoclonal RFs, based on their expressed idiotype (Wa) in individuals with RA (26-30, 52, 54).

*The serologic and structural similarity of the major idiotypic family of RF antibodies and the anti-CMV antibody, EVI-15, may provide a link between the immune response to a common virus and RA.* Several possibilities are suggested: (a) that CMV causes RA in a genetically susceptible host. (Several studies have shown a clear association of RA with HLA, in particular DR4, [59, 60] and it is likely that other genes may also be involved. In these individuals, the immune response to CMV that produces a viral neutralizing anti-CMV antibody may also induce autoantibodies.); (b) that CMV does not cause RA, but when a patient with RA is exposed to CMV, the immune response also produces autoantibodies; and (c) that the structural homology that exists between RFs and EVI-15 is coincidental and only reflects the limited human germ line antibody repertoire.

In addressing the first possibility, it is clear that not all patients with RA have been exposed to CMV. Although this virus is ubiquitous and several studies have shown that up to 75% of patients with RA have antibodies to CMV, this may not be significantly different from normal controls (13, 61). There has, however, been one report of the isolation of cytomegalovirus from synovial cells of a patient with RA (12).

The second possibility, that a CMV infection in a patient with established RA results not only in anti-viral antibodies, but also in RFs, suggesting a possible malfunctioning network system, is also feasible. The fact that RFs have been detected in persons with infections such as bacterial endocarditis, syphilis, leprosy, tuberculosis, and AIDS (62, 63) suggests that some individuals with an activated immune system may respond to such an infectious agent and also produce autoantibodies.

The third possibility, that there is a limited immunoglobulin repertoire in man, is unlikely. There is no evidence that the ability to produce diverse antibody specificities is limited relative to other mammals, in which the estimated repertoire is  $10^7$  to  $10^8$  antibodies. It is possible, however, that the number of human germ line variable segment genes commonly used is limited and that antibody diversity is generated primarily by selection among many D segment genes, as well as by junctional and N-segment mechanisms operating on V-D-J recombination. The similarity of EVI-15 to Wa RFs thus may indicate that although V segment genes are the major components of variable regions, they may not be the primary determinants of precise binding specificity. If this explanation is correct, the serendipitous findings described herein support the notion that different immune responses may use the same gene segments. The data we report do not directly address the possible role of viral infections in the pathogenesis of autoimmune diatheses.

The striking similarity between the anti-CMV antibody and RF autoantibodies is not without precedent. In a mouse MAb system, two immunoglobulins differing by a single amino acid have been described. The parent antibody has antibacterial (specifically phosphorylcholine) activity, whereas the antibody differing by one amino acid no longer binds phosphorylcholine, but instead binds DNA (64). It is clear that the EVI-15 antibody and the Wa idiotypic family of RFs are more distantly related. Another parallel may exist in the production of a specific idiotypic family of anti-DNA antibodies

after pulmonary tuberculosis or *Klebsiella pneumoniae* infections (65–67). Nonetheless, the striking serologic and structural similarity of these distinct antibodies may provide a crucial link between an antiviral response and an autoimmune disease.

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