

# N-Region Addition in Immunoglobulin Kappa Light Chains in B Cell Subsets in Rheumatoid Arthritis: Evidence for Over-expression of TdT in B Lineage

Choong Won Lee<sup>1</sup> and S. Louis Bridges, Jr<sup>2</sup>

<sup>1</sup>Division of Rheumatology, Department of Internal Medicine, Wallace Memorial Baptist Hospital, Busan, Korea, and <sup>2</sup>Division of Immunology and Rheumatology, University of Alabama at Birmingham, Birmingham, Alabama, U.S.A

## ABSTRACT

**Background:** Unusually high amounts of N region addition and CDR3 length diversity were found in immunoglobulin (Ig) light chain Vk and Jk joins in patients with rheumatoid arthritis (RA). We sought to determine whether this finding is due to excessive activity of the enzyme responsible for N region addition (terminal deoxynucleotidyl transferase [TdT]) in B lineage cells in bone marrow or from positive antigenic selection of B cells with long CDR3 lengths. **Methods:** We used FACS to isolate IgM<sup>+</sup>/IgD<sup>+</sup> B cells (predominantly naive) and IgMIgD<sup>-</sup> B cells (predominantly class-switched) B cells from peripheral blood of a patient with RA known to have enrichment for long Vk CDR3s and from that of two normal controls. RT-PCR of VkIII transcripts was performed, followed by sequencing of individual cDNA clones. We analyzed the CDR3 lengths and N region additions in 97 clones. **Results:** There was enrichment for long CDR3 lengths (11 or 12 amino acids) in both IgM<sup>+</sup>/IgD<sup>+</sup> and IgMIgD<sup>-</sup> B cells in RA compared to B cell subsets in the normal controls. The IgM<sup>+</sup>/IgD<sup>-</sup> B cell subset in RA was markedly enriched for N region addition and was similar to that seen in the IgM/IgD<sup>-</sup> subset. **Conclusion:** These data suggest that enrichment for N region addition and long CDR3 lengths in RA may result from unusually high or prolonged activity of TdT in bone marrow. (*Immune Network* 2003;3(2):89-95)

**Key Words:** Rheumatoid arthritis, N region, CDR3

## Introduction

Rheumatoid arthritis (RA) is a systemic disease marked by synovial inflammation and hyperplasia that often destroys involved joints (1,2). Infiltration of the synovium by antibody secreting plasma cells is a hallmark of the disease (3,4). Immunoglobulins are heteromeric proteins consisting of two heavy and two light chains, each of which is divided into a variable domain (V) that defines the antigen specificity of the molecule. V domains contain 3 hypervariable intervals of the complementary-determining regions (CDR1, CDR2, and CDR3) that are divided into 3 relatively constant domains of the framework regions (FR1,

FR2, and FR3)(5-7). The V<sub>H</sub>-D<sub>H</sub>-J<sub>H</sub> and V<sub>L</sub>-J<sub>L</sub> and non-germline-encoded (N) nucleotides additionally define CDR3. The CDRs are usually directly involved in antigen binding, with CDR3 at the center of antigen binding sites (6).

Previous studies showed high levels of non-germline encoded nucleotides (N regions) in VJ joins of kappa light chain from RA synovia and unsorted cells of RA peripheral blood (PB)(8,9). N-nucleotides enhance antibody diversity by encoding additional amino acid residues in CDR3. This finding may be due to positive antigenic selection or rearrangement abnormality from the bone marrow or lymph nodes.

In order to clarify these matters, we separated IgM<sup>+</sup> IgD<sup>+</sup> B cells, which come from bone marrow without contacting antigen, and IgMIgD<sup>-</sup> B cells (presumably IgG<sup>+</sup> or IgA<sup>+</sup>) in order to compare CDR3 and N-nucleotides between RA and normal individuals. We choose the IgM<sup>+</sup> IgD<sup>+</sup> B cells subset as a precursor of GC B cells and the IgMIgD<sup>-</sup> cells

Correspondence to: Choong Won Lee, Division of Rheumatology, Department of Internal Medicine, Wallace Memorial Baptist Hospital, Gumjung-gu P.O Box 100, Namsan-dong, Geumjeong-gu, Busan 609-340, Korea. (Tel) 051-580-1257, (Fax) 051-583-7114, (E-mail) choong@wmbh.co.kr

subset as GC derived memory B cells. To clarify whether abnormal N-nucleotides and CDR3 in RA comes from rearrangement abnormality or positive antigen selectivity, we compared N-nucleotides and CDR3 in those B cells subsets through sequencing of the V light chain.

## Materials and Methods

*Patient and control characteristics and cell separation of peripheral blood mononuclear cells (PBC).* PBC from patient AS, a 46-year-old black female with a 10-year history of RF-positive RA, and from two normal healthy individuals, a 35-year-white female SB and a 37-year old Asian male CL, were isolated by Ficoll-Isopaque density centrifugation. PBC were incubated with anti-CD19-microbeads for 15 min at 4°C. CD19<sup>+</sup> B cells were enriched by magnetic cell separation using the MiniMACS system (Miltenyi Biotec, Auburn, CA, USA). B cells were enriched 98% by a single step of magnetic sorting for analysis by immunofluorescence staining with anti-human CD19 FITC (PharMingen, San Diego, CA, USA). Cells of the CD19-enriched fraction were incubated with anti-human IgM-PE (PharMingen, San Diego, CA, USA) and anti-human IgD-FITC for 20 min on ice, then sorted into IgM<sup>+</sup>IgD<sup>+</sup> and IgM<sup>+</sup>IgD<sup>-</sup> fractions on a FACS advantage SE (Becton Dickson, Franklin lakes, NJ, USA).

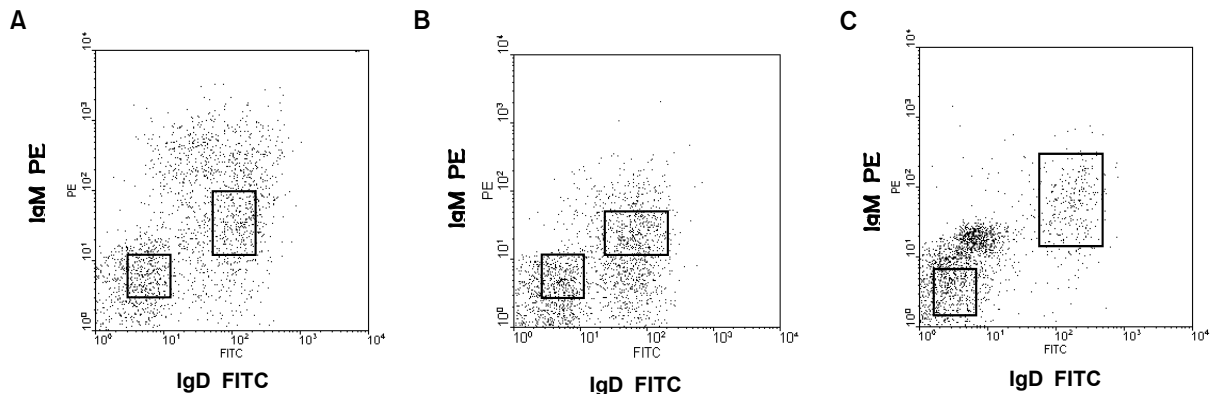
*Generation of cDNA and PCR amplification of  $\kappa$ -containing transcripts.* Total RNA was isolated from each IgM<sup>+</sup>IgD<sup>+</sup> subset and from IgM<sup>+</sup>IgD<sup>-</sup> subset B cells using Tri-zol reagent (Molecular Research Center, Inc., Cincinnati, OH, USA). Oligo d(T)-primed first-strand cDNA was generated from total RNA using SuperScript II for RNase H<sup>-</sup> Reverse transcriptase kit (GibcoBRL, Gaithersburg, MD, USA). PCR amplifications were performed on 2- $\mu$ l aliquots of first-strand cDNA, using *Taq* DNA polymerase.

PCR conditions were: 35 cycles of denaturation at 94°C for 2 min, annealing at 55°C for 30 sec, extension at 72°C for 1 min, with a final extension at 72°C for 7 min. PCR amplifications were designed to  $\kappa$  sequence as an anti-sense 3' primer (LSK-19: 5'-GCGCCGTCTAGAATTAACACTCTCCCCTGTTGA-3') and the leader and FR1 of germline *Humkv325* as a sense 5' primer (LSK-16: 5'-CCACCGGAGAGCTCGTGTTGACGCAGTCTCCA-3'). To control for possible contamination, a mock PCR reaction mixture, lacking a template and containing products of the first strand cDNA reaction without reverse transcriptase were prepared. None of the controls contained amplified product as assessed by ethidium-stained agarose gel electrophoresis.

*Cloning, transformation and sequencing of PCR products.* Aliquots of PCR products were subcloned with pGEM-T vector using TA cloning kit (Promega, Madison, WI, USA). Plasmids were transformed into DH5 $\alpha$  *E. coli* by 37°C heat shock. For colonies that were digested with EcoRI restriction enzyme, plasmid DNA was obtained and sequenced by dye terminator cycle sequencing using an automated sequencer (Applied Biosystems, Inc., Model ABI373, Foster, CA, USA).

*Sequence analysis.* Sequences were analyzed with a sequence alignment (DNAPLOT) and SAW (Sequences Analysis Workshop) software (10). Nucleotide exchanges in  $\kappa$  were considered for the analysis of somatic mutation. Levels of somatic hypermutation were assessed by comparing the number of nucleotides from the codon 20 of FR1 throughout the CDR3 domains (6). Non-germline encoded nucleotides at the  $\kappa$ - $\kappa$  joint, which represent N-region insertion, and P nucleotides, which are palindromic to terminal nucleotides of the coding sequence, were not counted as somatic mutations (11).

*Statistical analysis.* The results are presented as the

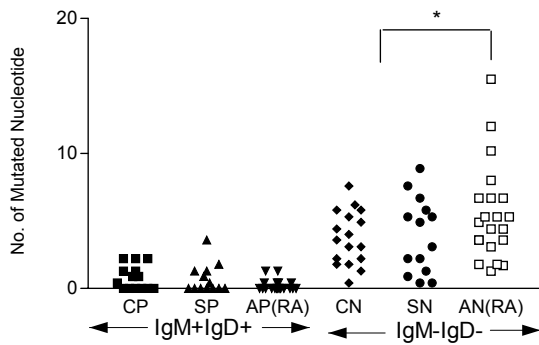


**Figure 1.** Fluorescence analysis and gate for sorting of B cell subsets derived from peripheral lymphocytes of the rheumatoid arthritis (A) and normal controls (B and C).

mean±SD. Differences in the amounts of somatic mutation, N-region addition, and CDR3-length heterogeneity between RA patients and normal individuals were analyzed using the Chi-square test, Fisher exact test (two-tailed), or Student *t*-test, as appropriate.

**Results**

*Vκ* transcripts from PBC of IgM<sup>+</sup>IgD<sup>+</sup> B cells had no, or fewer, somatic mutations than those from IgM<sup>+</sup>IgD<sup>-</sup> B cells. Following enrichment of CD19<sup>+</sup> B cell by microbeads magnetic cell separation, IgM<sup>+</sup>IgD<sup>+</sup> and IgM<sup>-</sup>IgD<sup>-</sup> B cells were purified by fluorescence activated cell sorting (Fig. 1). The levels of somatic mutation, as reflected by divergence from germline, among the transcripts from the different samples are shown in Fig. 2. The transcripts from IgM<sup>+</sup>IgD<sup>+</sup> B cells of the RA patient and normal individuals (AS, CL and SB, n=46) were significantly less mutated (0.54±0.12%) than their transcripts from IgM<sup>+</sup>IgD<sup>-</sup> B cells (4.51±0.42%, n=52) (*P*<0.0001). Somatic mutation level of the IgM<sup>+</sup>IgD<sup>-</sup> B cells (memory cells) in RA was also significantly higher than those in the two normal controls (*P*=0.04).



**Figure 2.** Somatic mutation in IgM<sup>+</sup>IgD<sup>+</sup> and IgM<sup>+</sup>IgD<sup>-</sup> B cells between rheumatoid arthritis (AP, AN) and normal controls (CP, CN, SP and SN). \**P*=0.04: AN versus CN & SN.

Twenty-seven (59%) of 46 *Vκ* transcripts from IgM<sup>+</sup>IgD<sup>+</sup> B cells were completely germline in the *Vκ* region, compared with none of 52 colonies from IgM<sup>+</sup>IgD<sup>-</sup> B cells.

*N-region addition.* The nucleotide sequences of N regions of each clone in RA are shown in Fig. 3. The percentages of clones with at least one nucleotide of N region addition in IgM<sup>+</sup>IgD<sup>+</sup> B cells were: SB 2 of 13 (15%), CL 3 of 13 (23%), and AS 10 of 19 (53%). Those of N region addition in IgM<sup>+</sup>IgD<sup>-</sup> B cells were: SB 4 of 14 (29%), CL 7 of 17 (41%), and AS 12 of 21 (57%) (Table I). The nucleotides of N-region addition in the RA patient (1.3±0.3, n=40) were significantly higher than those of the two normal controls (0.4±0.1, n=58) (*P*=0.0003), as in previous report (9) (Fig. 3). The nucleotides of N region addition in IgM<sup>+</sup>IgD<sup>+</sup> B cells in the RA patient (1.5±0.4) were significantly higher than those of the two normal individuals (0.3±0.1) (*P*=0.0004). But those in IgM<sup>+</sup>IgD<sup>-</sup> B cells did not differ significantly between RA and normal controls.

*CDR3 lengths of Vκ transcripts.* The *Vκ* repertoires of the RA patient are compared with those of the normal controls in Table I and Fig. 4, in order to demonstrate CDR3 length. Clones with unusually long CDR3s (one 11 and two 12 amino acid codons) were found in 3 of 40 (7.5%) transcripts from the RA patient, but in none of 58 transcripts from the normal controls. One 11 and one 12 amino acid codons were found in 19 transcripts of IgM<sup>+</sup>IgD<sup>+</sup> B cells (naive cells) in RA (Fig. 5). One 12 amino acid codons was also found in 21 transcripts of IgM<sup>+</sup>IgD<sup>-</sup> B cells in RA. Each of 3 long CDR3s came from *Humkv325*, *Vg*, and *Humkv328* *Vκ* gene segments.

*Germline derivation of κ light chains amplified with Humkv325 and CK primers.* The majority of transcripts amplified with *Humkv325* and *CK* primers were derived from *Humkv325* (A27) (36%). Most of the remaining clones were derived from two other members of the *Vκ* III family, 29% from *Humkv328* (L2) and 21% from *Vg* (L6). One clone, AN22, was

**Table I.** N region addition and CDR3 length in IgM<sup>+</sup>IgD<sup>+</sup> and IgM<sup>+</sup>IgD<sup>-</sup> cells in the rheumatoid arthritis (RA) and normal controls.

	B cell subset	CDR3>10 aa	Avg. CDR3	N addition	Avg. No. of "N"
RA	IgM <sup>+</sup> /IgD <sup>+</sup>	2/19 (10%)	9.3 aa	10/19 (53%)	1.0
	IgM <sup>+</sup> /IgD <sup>-</sup>	1/21 (5%)	9.3 aa	12/21 (57%)	1.1
Normal 1	IgM <sup>+</sup> /IgD <sup>+</sup>	0/13 (0%)	9.0 aa	2/13 (15%)	0.2
	IgM <sup>+</sup> /IgD <sup>-</sup>	0/14 (0%)	9.2 aa	4/14 (29%)	0.4
Normal 2	IgM <sup>+</sup> /IgD <sup>+</sup>	0/13 (0%)	9.2 aa	3/13 (23%)	0.3
	IgM <sup>+</sup> /IgD <sup>-</sup>	0/17 (0%)	9.0 aa	7/17 (41%)	0.7

aa: amino acid.



**A**

Ig M+Ig D+	CDR3							P <-N >	P	Fram ework 4										Length of aa codo			
Codon	89	90	91	92	93	94	95			96	97	98	99	100	101	102	103	104	105	106	107		
<u>HumnkV325</u>	CAG	CAG	TAT	GGT	AGC	TCA	CCT	CC		G	TGG	ACG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	J k 1
AP3	---	---	---	---	---	---	---	---	AG	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 1
AP25	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---	---	---	---	---	---	J k 1
AP1	---	---	---	---	---	---	---	g		TG	TAC	ACT	TTT	GGC	CAG	GGG	ACC	AAG	CTG	GAG	ATC	AAA	J k 2
AP7	---	---	---	---	---	---	---		a	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 2
AP19	---	---	---	---	---	---	---		CGG	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 2
AP23	---	---	---	---	---	---	---		TTC C	G	CTC	ACT	TTC	GGC	GGA	GGG	ACC	AAG	GTG	GAG	ATC	AAA	J k 4
AP4	---	---	---	---	---	---	---			G	ATC	ACC	TTC	GGC	CAA	GGG	ACA	CGA	CTG	GAG	ATT	AAA	J k 5
AP13	---	---	---	---	---	---	---			---	---	---	---	---	---	---	---	---	---	---	---	---	J k 5
<u>HumnkV328</u>	CAG	CAG	TAT	AAT	AAC	TGG	CCT	CC		G	TGG	ACG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	J k 1
AP8	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---	---	---	---	---	---	J k 1
AP15	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---	---	---	---	---	---	J k 1
AP17	---	---	---	---	---	---	---	---	TG	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 1
AP2	---	---	---	---	---	---	---	---	CCT C	G	ATC	ACC	TTC	GGC	CAA	GGG	ACA	CGA	CTG	GAG	ATT	AAA	J k 5
AP16	---	---	---	---	---	---	---	---		---	---	---	---	---	---	---	---	---	---	---	---	---	J k 5
<u>Vg</u>	CAG	CAG	CGT	AGC	AAC	TGG	CCT	CC		TG	TAC	ACT	TTT	GGC	CAG	GGG	ACC	AAG	CTG	GAG	ATC	AAA	J k 2
AP10	---	---	---	CC	A	---	---	---	GAA	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 2
AP18	---	---	---	---	---	---	---	---	CT	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 2
AP11	---	---	---	---	---	---	---	---	TCC A	G	CTC	ACT	TTC	GGC	GGA	GGG	ACC	AAG	GTG	GAG	ATC	AAA	J k 4
AP22	---	---	---	---	---	---	---	---	CT	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 4
AP5	---	---	---	---	---	---	---	gg	GGG	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 5
AP12	---	---	---	---	---	---	---	g		---	---	---	---	---	---	---	---	---	---	---	---	---	J k 5

**B**

Ig M-Ig D-	CDR							P <-N >	P <---	Jk	Fram ework 4										Length of aa codo		
Codon	89	90	91	92	93	94	95			96	97	98	99	100	101	102	103	104	105	106	107		
<u>HumnkV325</u>	CAG	CAG	TAT	GGT	AGC	TCA	CCT	CC		G	TGG	ACG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	J k 1
AN3	---	---	-G	---	---	---	T	---	C	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 1
AN16	---	---	---	C	---	---	---	---		---	---	---	---	---	---	---	---	G	---	---	---	---	J k 1
AN7	---	---	---	---	---	---	T	---	G	TG	TAC	ACT	TTT	GGC	CAG	GGG	ACC	AAG	CTG	GAG	ATC	AAA	J k 2
AN21	---	---	---	---	---	---	T	---	G	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 2
AN11	-A	---	---	---	GA	---	---	---		A	TTC	ACT	TTC	GGC	CCT	GGG	ACC	AAA	GTG	GAT	ATC	AAA	J k 3
AN13	---	---	---	---	T	---	T	---		---	---	---	---	---	---	---	---	---	---	---	---	---	J k 3
AN12	-A	-A	C	---	GA	---	G	---	TCT GG	G	CTC	ACT	TTC	GGC	GGA	GGG	ACC	AAG	GTG	GAG	ATC	AAA	J k 4
AN20	---	---	---	C	---	---	---	---		---	---	---	---	---	---	---	---	G	---	A	C	---	J k 4
<u>HumnkV328</u>	CAG	CAG	TAT	AAT	AAC	TGG	CCT	CC		G	TGG	ACG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	J k 1
AN6	-A	---	---	C	G	---	---	---	G	---	---	---	---	---	---	---	---	---	---	---	G	---	J k 1
AN14	-A	---	---	C	G	---	---	---	G	---	---	---	---	---	---	---	---	---	---	---	G	---	J k 1
AN17	-A	---	---	C	G	---	---	---	G	---	---	---	---	---	---	---	---	---	---	---	G	---	J k 1
AN9	---	---	---	---	G	---	---	---	C	TG	TAC	ACT	TTT	GGC	CAG	GGG	ACC	AAG	CTG	GAG	ATC	AAA	J k 2
AN1	---	---	T	C	---	---	---	---	ACG GCC	A	TTC	ACT	TTC	GGC	CCT	GGG	ACC	AAA	GTG	GAT	ATC	AAA	J k 3
AN24	---	---	---	T	G	G	---	---	CC	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 3
AN8	---	G	---	---	T	---	---	---		G	CTC	ACT	TTC	GGC	GGA	GGG	ACC	AAG	GTG	GAG	ATC	AAA	J k 4
AN19	---	---	---	C	---	---	---	---		---	---	---	---	---	---	---	---	---	---	---	---	---	J k 4
<u>Vg</u>	CAG	CAG	CGT	AGC	AAC	TGG	CCT	CC		G	CTC	ACT	TTC	GGC	GGA	GGG	ACC	AAG	GTG	GAG	ATC	AAA	J k 4
AN2	---	---	---	C	G	---	---	g	g	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 4
AN4	---	---	---	---	---	---	---	---	g	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 4
AN5	---	---	---	C	G	---	---	g	g	---	---	---	---	---	---	---	---	---	---	---	---	---	J k 4
AN18	---	---	---	TA	---	---	---	tt	C	---	---	---	---	---	---	---	---	G	---	---	---	---	J k 4
<u>HumnkV305</u>	CAG	CAG	TAT	GGT	AGC	TCA	CCT	CC		G	TGG	ACG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	J k 1
AN22	---	G	---	C	---	C	---	---	GCG	---	T	---	---	---	TG	---	---	---	---	---	---	---	J k 1

**Figure 5.** Nucleotide sequences of CDR3 regions of clones in IgM<sup>+</sup>IgD<sup>+</sup> B cells (A) and those of clones in IgM<sup>+</sup>IgD<sup>-</sup> B cells (B) in rheumatoid arthritis.

fraction of CD27-expressing B cells (16). The memory B-cell compartment in humans consists of somatically mutated, class-switched, which represent

IgM<sup>+</sup>IgD<sup>-</sup> such as IgG<sup>+</sup> and IgA<sup>+</sup> PB cells, and IgM bearing B cells (17).

If B cells succeed in generating a functional,

non-autoreactive, antigen receptor, they come into the peripheral B cell pool as naive cells. Upon encountering antigen, the antibodies expressed by a B cell are modified by class-switch recombination and somatic hypermutation (18,19). Somatic hypermutation appears to B cells proliferating within the microenvironment of germinal center (GC)(20,21). Thus somatic mutation of V-region gene is a hallmark of GC B cell and their descendants.

*V $\kappa$  transcripts from IgM<sup>+</sup>IgD<sup>-</sup> B cells of a patient with RA is higher somatically mutated than those from normal individuals.* The V genes of human PB IgM<sup>+</sup>IgD<sup>-</sup> lymphocytes, which are thought to be GC-derived memory B cells, are highly diversified by somatic mutation and independent of the age of an individual (13,22). We also found high levels of somatic mutation among V $\kappa$  transcripts derived from the IgM<sup>+</sup>IgD<sup>-</sup> B cells of the two normal individuals (3.93% and 3.74%), similar to the 3.9% reported for V $\kappa$  gene of IgM<sup>+</sup>IgD<sup>-</sup> B cells of a 67-year-old female (13). But the somatic mutation level of those cells was significant higher in the RA patient than in the normal controls (5.5%,  $P=0.04$ ). Differences in the proportions of different B cell subsets between RA and normal individuals may explain the increase in somatic mutation in IgM<sup>+</sup>IgD<sup>-</sup> B cells in the RA patient. RA may have a higher proportion of circulating memory B cells that have been exposed to antigen, which are more likely than naive cells to express mutated antigen receptor.

*Abnormal CDR3 regions encoding 11 or 12 amino acids of V $\kappa$  expressed in IgM<sup>+</sup>IgD<sup>-</sup> B cells in RA.* We found that V $\kappa$  transcripts of the RA patient contain distinctively long CDR3 regions (Fig. 4). Data from other investigators show that V $\kappa$  CDR3 regions with more than 10 codons were very rare in normal individuals (6,12,13,23). Most data showed less than 5% of CDR3 domains of 11 amino acids from normal PB. Nobody has reported CDR3 domains of 12 amino acids in V $\kappa$  transcripts. Our data also showed no CDR3 domains of 11 or 12 amino acids among the 59 V $\kappa$  transcripts of two normal controls. However, there were two CDR3 domains of 12 amino acids and one of 11 amino acids expressed among the 40 V $\kappa$  transcripts (7.5%) of the RA patient. Our previous data from unsorted peripheral B cells in the same RA patient (AS) showed two CDR3 domains of 10 sequences with 11 amino acids (9). Interestingly, two of 3 abnormally long CDR3 domains in RA were expressed in IgM<sup>+</sup>IgD<sup>-</sup> B cells (memory B cells).

Three factors influence the number of nucleotides at the V $\kappa$ -J $\kappa$  join and thus determine the CDR3 length: the rearrangement site of the V $\kappa$  gene segment, that of the J $\kappa$  gene segment, and the

presence of N nucleotides. Since abnormally long CDR3 was expressed in IgM<sup>+</sup>IgD<sup>+</sup> B cells (naive B cell), the mechanism responsible for generation of CDR3 regions of unusual length in RA maybe unusual V $\kappa$  and J $\kappa$  rearrangement or abnormal N region addition in bone marrow. But we couldn't exclude peripheral antigen selection because of the 2 abnormally long CDR3 in IgM<sup>+</sup>IgD<sup>-</sup> B cells in RA. *N-region addition is extensively higher in IgM<sup>+</sup>IgD<sup>+</sup> B cells in RA than those in normal individuals.* Insertion of non-germline encoded nucleotides (N-regions) during Ig gene rearrangement was first described as a mechanism for the generation of junctional diversity in heavy chain CDR3 (24,25). A previous study with unsorted PBC in normal individuals and the same RA patient has shown N-region addition was present in kappa light chains with a similar proportion (9). In our present study with sorted IgM<sup>+</sup>IgD<sup>+</sup> B cells in RA, N-region addition was extensively higher than in normal controls. There are several possible explanations for the presence of non-germline encoded nucleotides at the V-J junctions of light chains. Most likely, TdT in an amount sufficient to introduce N regions into the light chains junction is expressed from the pro-B cell to pre-B cell stage (26,27). Alternatively, light chain rearrangement can potentially precede heavy chain rearrangement in normal pro-B cells that express TdT (28). Thus, this high proportional N-nucleotides addition of IgM<sup>+</sup>IgD<sup>+</sup> B cells in RA may result from abnormal regulation of TdT or light chain rearrangement in bone marrow level.

In conclusion, these data suggest that enrichment for N region addition and long CDR3 lengths in RA may be from unusually high or prolonged activity of TdT in bone marrow B lineage cells.

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