

## **Somatic Hypermutation Shapes the Antibody Repertoire of Memory B Cells in Humans**

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### **Abstract**

High-affinity antibodies produced by memory B cells differ from antibodies produced in naive B cells in two respects. First, many of these antibodies show somatic hypermutation, and second, the repertoire of antibodies expressed in memory responses is highly selected. To determine whether somatic hypermutation is responsible for the shift in the antibody repertoire during affinity maturation, we analyzed the immunoglobulin lambda light chain (Ig $\lambda$ ) repertoire expressed by naive and antigen-selected memory B cells in humans. We found that the Ig $\lambda$  repertoire differs between naive and memory B cells and that this shift in the repertoire does not occur in the absence of somatic hypermutation in patients lacking activation-induced cytidine deaminase (AID). Our work suggests that somatic hypermutation makes a significant contribution to shaping the antigen-selected antibody repertoire in humans.

Key words: immunoglobulin repertoire • activation-induced cytidine deaminase • somatic hypermutation • memory B cell • affinity maturation

### **Introduction**

The affinity of antibodies for their cognate antigens increases during immune responses (1). In depth analysis of hybridoma antibodies specific for influenza hemagglutinin or for small chemical haptens such as 2-phenyl-5-oxazolone or 4-hydroxy-3-nitrophenyl acetyl (NP) revealed that somatic hypermutation is one of the mechanisms that produce this increased affinity (2–9). For example, the V<sub>H</sub>186–2 + Ig $\lambda$  antibodies dominate the initial antibody response to NP, and mutation from Trp<sup>H33</sup> to Leu<sup>H33</sup> brings about a 10-fold increase in affinity of these V<sub>H</sub>186–2 + Ig $\lambda$  antibodies (8, 10–13). Increased affinity is also accompanied by a shift in the antibody repertoire, and secondary high-affinity responses to NP are dominated by Ig $\kappa$  antibodies and not Ig $\lambda$ , suggesting that repertoire shifts contribute to affinity maturation (3, 10, 14, 15). Little is known about this shift in the repertoire and how it relates to somatic hypermutation.

Activation-induced cytidine deaminase (AID) is a germinal center B cell–restricted molecule that carries cytidine

deaminase activity and is required for switch recombination and somatic hypermutation in mice and humans (16–18). In the absence of AID, B cells are unable to undergo somatic hypermutation or produce secondary antibodies despite germinal center formation (17, 18). Here we report on the Ig $\lambda$  antibody repertoire in humans deficient in AID. We find that AID is essential for the shift in repertoire between naive and antigen-selected memory B cells.

### **Materials and Methods**

*Patient Samples and Cell Preparation.* AID-deficient patients and AID mutations have been described (18). Patients P1, P13, P14, P17, and P18 were 10, 11, 4, 14, and 2 yr old, respectively at the time of blood donation, and they did not suffer from chronic infections. They were treated with intravenous Ig supplementation. Control donors C1, C2, C3, C4, C5, C6, and C7 were healthy and 32, 11, 35, 2, 28, 41, and 33 yr old, respectively when blood samples were obtained. Blood mononuclear cells were isolated on Ficoll gradients. Control CD19<sup>+</sup> B cells were fractionated into naive CD19<sup>+</sup>IgM<sup>+</sup>CD27<sup>–</sup> and memory CD19<sup>+</sup>IgM<sup>+</sup>CD27<sup>+</sup> B cells by cell sorting on FACS Vantage<sup>TM</sup>. Due to absence of secondary isotypes in AID-deficient patients, AID B cells are all IgM<sup>+</sup> and were therefore sorted into naive CD19<sup>+</sup>CD27<sup>–</sup> and memory CD19<sup>+</sup>CD27<sup>+</sup> B cells without IgM staining. Antibodies used for staining were FITC–anti-CD19,

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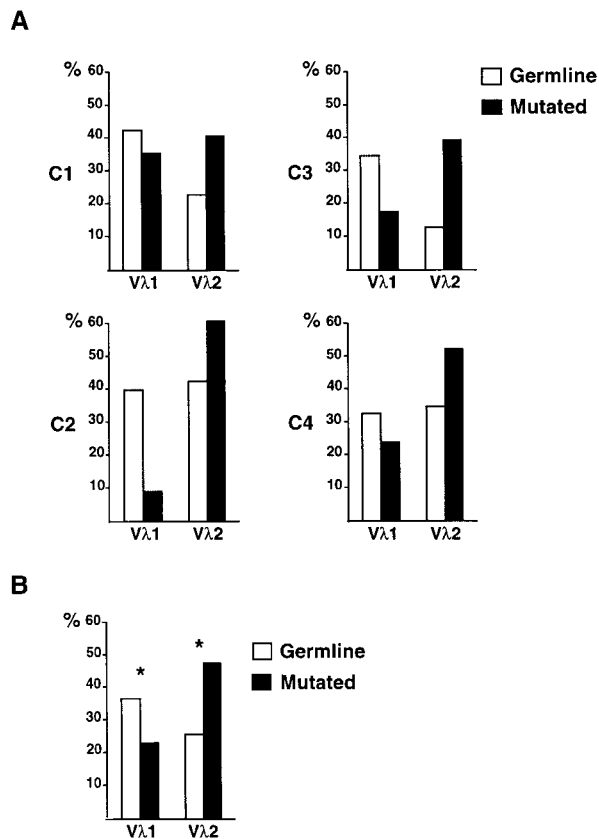
PE-anti-CD27 (Immunotech/Beckman Coulter), and biotin-conjugated anti-IgM mAb (PharMingen), which was visualized with Streptavidin Red 670 (GIBCO BRL).

**Reverse Transcription PCR, Cloning, and Sequencing.** Total RNA was extracted from  $10^4$ – $10^5$  purified cells using TRIzol Reagent (GIBCO BRL) and reverse transcribed in a 10- $\mu$ l reaction with Superscript II (GIBCO BRL). For reverse transcription (RT)-PCR reactions, 1  $\mu$ l of cDNA was amplified for 30–35 cycles of 30 s at 94°C, 30 s at 58°C ( $V_{H1}$ -C $\mu$ ) or at 55°C ( $V_{\lambda}$ -C $\lambda$ ) and 30 s at 72°C with a final 10-min extension at 72°C using HotStarTaq™ DNA polymerase (QIAGEN) and the following primers:  $V_{\lambda 1-8}$  family consensus sense, 5'-GGG(G/A)TC(T/C)CTGA(C/T/G)CG(A/C/G)TTCTCTGG(C/G)TCC-3';  $V_{\lambda 9}$  sense, 5'-ATCCCTGATCGCTTCTCAGTCTTG-3';  $V_{\lambda 10}$  sense, 5'-GATCTCAGAGAGATTATCTGCATCC-3'; and C $\lambda$  antisense, 5'-CACAC(T/C)AGTGTGGCCTTGTG-GCTTG-3'. Sense FR1  $V_{H1}$  and antisense C $\mu$  primers were as described previously (19, 20). RT-PCR products were run on 2% agarose gels, and PCR products were gel purified (Qiaquick™; QIAGEN) and cloned into TA vectors (Invitrogen). Double-stranded DNA sequences were obtained using anti-

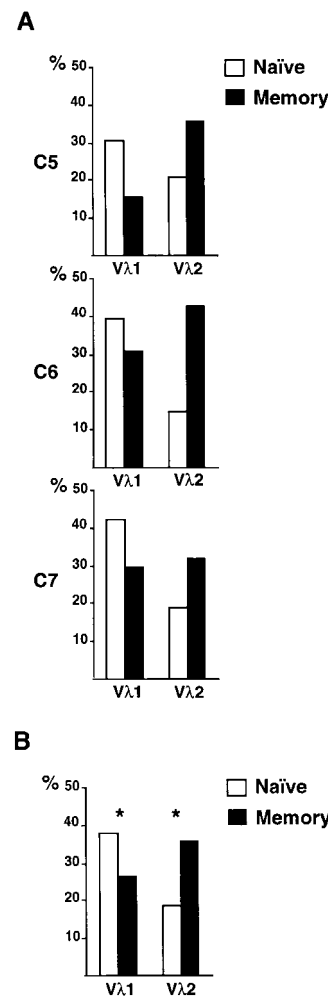
sense C $\mu$  or C $\lambda$  primers and Dye Terminator Cycle Sequencing (PE Applied Biosystems). Sequences were analyzed using Ig BLAST®. When two or more identical sequences were found, they were counted as a single clone. Sequences were considered mutated when they displayed two or more nucleotide differences from their germline counterparts. Differences in gene distribution between naive and memory B cells were analyzed with chi-square tests (Cochran-Mantel-Haenszel test) adjusted by the Bonferroni method for multiple testing and they were considered significant when *P* values were equal to or less than 0.05.

## Results and Discussion

To determine whether there is a shift in repertoire between naive and antigen-selected B cell compartments in humans, we compared the unmutated germline Ig $\lambda$  sequences to mutated Ig $\lambda$  sequences obtained from CD19<sup>+</sup> peripheral B cells from four control donors. In humans, Ig $\lambda$  light chains are found in 30–40% of all antibodies, and among the 10  $V_{\lambda}$  gene families three ( $V_{\lambda 1}$ ,  $V_{\lambda 2}$  and  $V_{\lambda 3}$ ) represent >80–90% of all  $V_{\lambda}$  genes (21, 22). We found that the distribution of  $V_{\lambda 1}$  and  $V_{\lambda 2}$ , two of the most frequently used human  $V_{\lambda}$  families, differs between germline-encoded and mutated antibodies (Fig. 1 A; total of 239 individual sequences):  $V_{\lambda 1}$  is decreased and  $V_{\lambda 2}$  increased



**Figure 1.** Ig $\lambda$  repertoire expressed in peripheral B cells from control donors. (A)  $V_{\lambda 1}$  and  $V_{\lambda 2}$  gene usage in germline-encoded (open bars) and mutated (solid bars) sequences from CD19<sup>+</sup> peripheral B cells in four unrelated controls. 25, 15, 46, and 34 germline  $V_{\lambda J_{\lambda}}$  sequences from donors C1, C2, C3, and C4 were compared with 33, 23, 33, and 29 mutated  $V_{\lambda J_{\lambda}}$  sequences from the same individuals. The percent  $V_{\lambda}$  utilization is indicated on the y axis. (B) Combined total of  $V_{\lambda 1}$  and  $V_{\lambda 2}$  gene usage in germline-encoded and mutated  $V_{\lambda J_{\lambda}}$  sequences from control donors. 121 germline-encoded and 118 mutated sequences were obtained from the four control donors. Asterisk (\*) indicates statistically significant difference ( $V_{\lambda 1}$ , *P* = 0.022;  $V_{\lambda 2}$ , *P* = 0.0004).



**Figure 2.** Ig $\lambda$  repertoire expressed in naive and memory B cells from control donors. (A)  $V_{\lambda 1}$  and  $V_{\lambda 2}$  gene usage in naive CD19<sup>+</sup>IgM<sup>+</sup>CD27<sup>-</sup> (open bars) and memory CD19<sup>+</sup>IgM<sup>+</sup>CD27<sup>+</sup> (solid bars) B cells in three unrelated controls. 33, 33, and 52  $V_{\lambda J_{\lambda}}$  sequences from naive B cells from donors C5, C6, and C7, respectively were compared with 39, 42, and 63  $V_{\lambda J_{\lambda}}$  sequences from memory B cells from the same individuals. The percent  $V_{\lambda}$  utilization is indicated on the y axis. (B) Combined total  $V_{\lambda 1}$  and  $V_{\lambda 2}$  gene usage in CD19<sup>+</sup>IgM<sup>+</sup>CD27<sup>-</sup> and CD19<sup>+</sup>IgM<sup>+</sup>CD27<sup>+</sup> B cells. Asterisk (\*) indicates statistically significant difference ( $V_{\lambda 1}$ , *P* = 0.035; and  $V_{\lambda 2}$ , *P* = 0.0017).

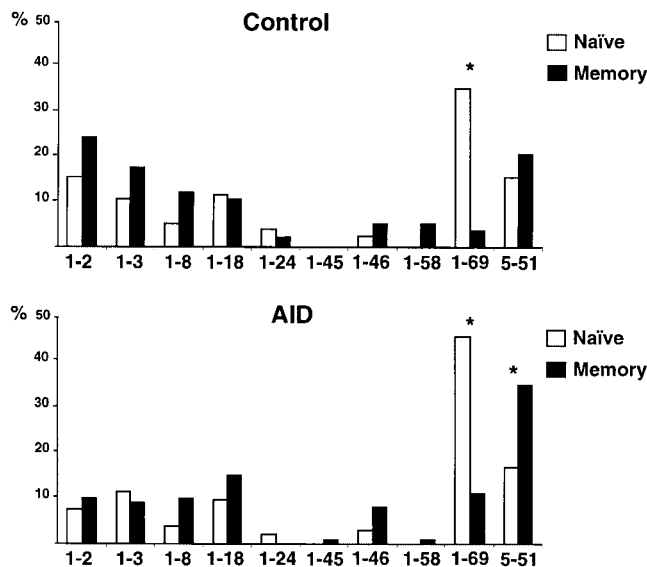
among mutated Igλs, and this difference is independent of the age of the donors (Fig. 1, A and B).

To further analyze the shift in Igλ repertoire between naive and memory B cells, we fractionated peripheral B cells using CD27 memory marker and isolated naive (CD19<sup>+</sup>IgM<sup>+</sup>CD27<sup>-</sup>) and memory (CD19<sup>+</sup>IgM<sup>+</sup>CD27<sup>+</sup>) B cells from control donors (23, 24). The difference in Vλ distribution was also found when comparing naive and memory B cell compartments (Fig. 2; total of 262 sequences). Antibodies cloned from memory B cells were predominantly mutated and showed decreased Vλ1 and increased Vλ2 gene usage (Fig. 2, A and B). We conclude that there is a shift in the Igλ repertoire between the naive and antigen-selected memory B cell compartments in humans.

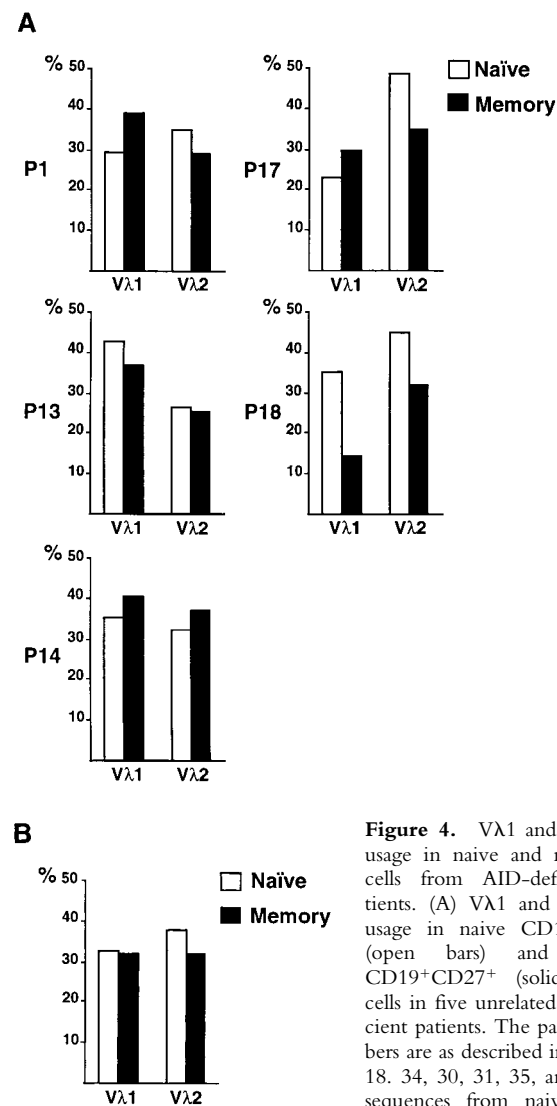
To determine whether the shift in Igλ repertoire between the naive and memory compartments is related to somatic hypermutation, we analyzed the Igλ genes expressed in naive and memory B cells from patients lacking activation-induced deaminase (AID) (17, 18). AID has been shown to be essential for both hypermutation and switch recombination but does not appear to be necessary for normal B cell development in mice and humans (17, 18). Patients with AID deficiency showed no secondary antibodies and no somatic mutation; nevertheless, these individuals displayed enlarged tonsils with germinal centers and showed normal numbers of CD19<sup>+</sup>CD27<sup>+</sup> B cells (18). The CD27<sup>+</sup>IgM<sup>+</sup> B cells found in AID-deficient patients resembled authentic CD27<sup>+</sup>IgM<sup>+</sup> memory B cells in that they showed normal selection against V<sub>H</sub>1-69, a V<sub>H</sub> gene that is frequently found in B lymphoid chronic lym-

phocytic leukemias producing autoreactive antibodies (Fig. 3) (19, 25, 26). However, the antibodies expressed in antigen-selected memory B cells in five AID-deficient patients differed from the three controls in that they showed no mutations, and there was no shift in the Vλ repertoire between naive B cells and antigen-selected memory B cells (compare Figs. 2 and 4; total of 330 sequences). In particular, there was no increase in Vλ2 gene expression and no relative decrease in Vλ1 (Fig. 4). In addition, V<sub>H</sub>5-51 gene usage was favored in the memory CD27<sup>+</sup> B cells from AID-deficient patients but not in normal controls (Fig. 3).

Somatic hypermutation is known to increase antibody affinity during immune responses. However, the contribution of mutation to shaping the antibody repertoire has not been determined. We have found a global shift in the Igλ



**Figure 3.** V<sub>H</sub>1 and V<sub>H</sub>5 repertoire analysis of naive and memory B cells from control donors and AID-deficient patients. 77 control C5, C6, and C7 (top) and 105 AID (bottom) V<sub>H</sub>1 and V<sub>H</sub>5 sequences from naive B cells (open bars) are compared with 58 control and 112 AID sequences from memory B cells (solid bars). The percent V<sub>H</sub>1 and V<sub>H</sub>5 utilization is indicated on the y axis. Asterisk (\*) indicates statistically significant difference (V<sub>H</sub>1-69,  $P < 0.0001$  for both controls and AID-deficient patients; V<sub>H</sub>5-51,  $P = 0.03$  for AID-deficient patients).



**Figure 4.** Vλ1 and Vλ2 gene usage in naive and memory B cells from AID-deficient patients. (A) Vλ1 and Vλ2 gene usage in naive CD19<sup>+</sup>CD27<sup>-</sup> (open bars) and memory CD19<sup>+</sup>CD27<sup>+</sup> (solid bars) B cells in five unrelated AID-deficient patients. The patient numbers are as described in reference 18. 34, 30, 31, 35, and 31 V<sub>λ</sub> sequences from naive B cells from AID-deficient patients P1, P13, P14, P17, and P18, respectively were compared with 31, 35, 32, 37, and 34 V<sub>λ</sub> sequences from memory B cells from the same individuals. The percent V<sub>λ</sub> utilization is indicated on the y axis. (B) Combined total Vλ1 and Vλ2 gene usage in CD19<sup>+</sup>CD27<sup>-</sup> and CD19<sup>+</sup>CD27<sup>+</sup> B cells for AID-deficient patients.

antibody repertoire between naive and memory B cells from normal donors. This shift in repertoire is associated with somatic hypermutation and is AID dependent. We conclude that AID and hypermutation make a significant contribution to shaping the antigen-selected memory B cell repertoire in humans.

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