Receptor Editing in Self-reactive Bone Marrow B Cells

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Summary

A central paradigm of immunology is clonal selection: lymphocytes displaying clonally distributed antigen receptors are generated and subsequently selected by antigen for growth or elimination. Here we show that in mice transgenic for anti-H-2Kk,b antibody genes, in which a homogeneous clone of developing B cells can be analyzed for the outcome of autoantigen encounter, surface immunoglobulin M + immature B cells binding to self-antigens in the bone marrow are induced to alter the specificity of their antigen receptors. Transgenic bone marrow B cells encountering membrane-bound Kb or Kk proteins modify their receptors by expressing the V(D)J recombinase activator genes and assembling endogenously encoded immunoglobulin light chain variable genes. This (auto)antigen-directed change in the specificity of newly generated lymphocytes is termed receptor editing.

Each B lymphocyte bears a unique antigen receptor composed of a single Ig light chain and a single heavy chain, despite its potential to simultaneously produce two different heavy chains and six different light chains (two κ's and four λ's). This so-called "allelic exclusion" is thought to be important in conferring on the B cell receptor a high degree of antigen specificity, which is critical for the process of clonal selection (1, 2). In adult mice, B cell production and V gene assembly occur in the bone marrow (3). Rearrangement and expression of the Ig genes is a highly ordered process (4), initiated by DNA rearrangement at the heavy chain loci in pro-B cells, where D elements are specifically ligated to J elements. Vλ-to-DJ rearrangement then ensues, completing heavy chain gene assembly and leading to functional μ heavy chain protein synthesis. The resulting pre-B cells then rearrange light chain genes, leading to their expression of surface IgM. Light chain rearrangement appears to occur first at the κ locus and, because the light chain loci have no D minigenes, involves only V to J rearrangement (5, 6). λ light chain V-to-J gene rearrangement also occurs at this stage of development, but cells rearranging and expressing λ light chains generally have previously undergone nonproductive rearrangements at the κ locus, such as RS recombination; thus, λ rearrangement may represent a salvage pathway (7, 8). In developing B cells, expression of membrane-bound μ heavy chains mediates allelic exclusion by feedback inhibition of heavy chain gene rearrangement (9-12). Light chain rearrangement is believed to be blocked by the expression of membrane IgM that results from the assembly of heavy and light Ig chain proteins (11, 13-15). However, the recent finding that circular DNAs excised by nested κ gene rearrangements frequently contain rearranged VJs that are in frame and potentially functional (16) contradicts this notion and suggests that light chain gene rearrangement often continues in IgM + cells.

Immature lymphocytes that have successfully recombined receptor genes display their antigen receptors on the cell surface where they are then selected by antigen for activation, inactivation, or elimination. Autoreactive lymphocytes are probably produced continuously in the primary lymphoid organs. How are such autoreactive lymphocytes controlled? To study negative selection of autoreactive B cells in the mouse, many model systems have been used. These have included the treatment of immature B cells from normal mice with tolerogens or antibodies specific for IgM (reviewed in reference 17) and the generation of transgenic mice bearing functional, rearranged Ig genes encoding autoantibodies (reviewed in reference 18). These studies have yielded a wealth of information supporting the idea that B cells can be tolerized to self-antigens and suggest that more than one mechanism may play a role in this tolerance. Experiments using transgenic mice have shown that one way that autoreactive B lymphocytes are selected against in vivo is "clonal deletion" (19-25). In the bone marrow, encounter with cell membrane-associated self-antigens, capable of crosslinking Ig receptors on B cells with high avidity, leads to their elimination from secondary lymphoid tissues. However, a large pool of self-reactive
sIgMlow B cells is present in the bone marrow, suggesting that immature B cells are developmentally blocked (19, 20, 24). In this paper we address the mechanism by which deletion occurs in B cells reactive to membrane-bound autoantigens. We test the hypothesis that receptor selection, rather than clonal selection, occurs in immature, bone marrow B cells, and present data in support of this hypothesis indicating that immature autoreactive B cells encountering self-antigen attempt, and often succeed, in altering their specificities through secondary Ig light chain gene rearrangement.

Materials and Methods

Mice and Bone Marrow Chimeras. 3-83μ/δ transgenic mice were produced as described (23). This transgenic mouse line bears approximately four copies of a 42-kb heavy chain genomic construct containing the genomic VDJ3.4 containing R1 fragment upstream of a genomic Cμ-C6 construct and approximately three copies of an 18-kb genomic fragment containing the intact VJ3.4-Cκ light chain gene. The light and heavy chain transgenes cosegregate in an 18-kb genomic fragment containing the intact VJ3-s3-Cκ light chain gene. The light and heavy chain transgenes cosegregate in breeding experiments and are probably integrated at the same locus (our unpublished results). 3-83μ/δ transgenic mice were bred and maintained in the animal care facility at the National Jewish Center for Immunology and Respiratory Medicine. MT-Kb mice (26) were backcrossed twice onto a BALB/c (H-2d) background. 3-83μ/δ transgenic mice were bred three generations onto B10.D2/oSnJ (H-2a), C57BL/10J (H-2b), B10.A/SgSnJ (H-2KkDa), MRL/1 (our unpublished results). 3-83μ/δ transgenic mice were bred and maintained in the animal care facility at the National Jewish Center for Immunology and Respiratory Medicine. MT-Kb mice (26) were backcrossed twice onto a BALB/c (H-2d) background.

Bone marrow chimeras were prepared as follows. Femurs were removed aseptically, ground in a mortar containing 10 ml ice-cold, sterile, HBSS (Gibco Laboratories, Grand Island, NY), and filtered through cotton to remove bone and debris. The cells were depleted of erythrocytes using Gey's solution, washed twice in HBSS, and incubated for 30 min on ice in HBSS containing a cocktail of anti-Thy-1 and anti-CD4 antibodies. Cells were then centrifuged, resuspended in rabbit complement (Cedarlane, Hornby, Canada), incubated for 30 min on ice in HBSS containing a cocktail of anti-Thy-1 and anti-CD4 antibodies. Cells were then centrifuged, resuspended in HBSS, filtered through cotton, washed twice in HBSS, and counted. Viable cell concentration was adjusted to 5 x 10^9/ml in HBSS and 0.1 ml was injected intravenously per irradiated recipient. Aliquots of cells taken from the final cross were analyzed. As the results with (Tg-B10.D2 x B10.A/SmJ (H-2a), C57BL/10J (H-2b), B10.A/SgSnJ (H-2KkDa), MRL/1 (our unpublished results). 3-83μ/δ transgenic mice were bred and maintained in the animal care facility at the National Jewish Center for Immunology and Respiratory Medicine. MT-Kb mice (26) were backcrossed twice onto a BALB/c (H-2d) background. 3-83μ/δ transgenic mice were bred three generations onto B10.D2/oSnJ (H-2a), C57BL/10J (H-2b), B10.A/SgSnJ (H-2KkDa), MRL/1 (our unpublished results). 3-83μ/δ transgenic mice were bred and maintained in the animal care facility at the National Jewish Center for Immunology and Respiratory Medicine. MT-Kb mice (26) were backcrossed twice onto a BALB/c (H-2d) background.

Detection of mRNA. RNA preparation was as described (31). For PCR detection of mRNA, cDNA was synthesized from total RNA using a kit (SuperScript; Bethesda Research Laboratories, Gaithersburg, MD) according to the instructions of the manufacturer. In the cell sorting experiments, cDNA was synthesized in a 20-μl reaction volume containing RNA from 10^6 cell equivalents. 1 μl of this reaction mixture was amplified with 18 cycles of PCR, run on 1.5% agarose gels, transferred to a Zetaprobe membrane (Bio-Rad Laboratories, Richmond, CA), and hybridized with probes recognizing gene transcripts of the GTP-binding protein Gs (32), and recombinase activator gene (RAG)-1 (33), RAG-2 (34), or terminal transferase (dTT) (35). PCR reactions were done in a final volume of 30 μl containing 1 μl of reverse transcription reaction, 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM MgCl₂, 20 μg/ml gelatin (0.3 mM each of dATP, dCTP, dGTP, and dTTP, 1 μM of each oligonucleotide primer, and 1 U of Taq polymerase (Perkin-Elmer Corp., Norwalk, CT). Except for the first cycle, which had a 2-min 94°C denaturation step, each cycle consisted of 30 s at 94°C, 30 s at 62°C, and 1.5 min at 72°C. A thermal cycler was used (Twinblock System; Ericomp, San Diego, CA). The appropriate cloned cDNAs were used as hybridization probes after labeling with α-32PdCTP. PCR primers were: RAG-1, primers P3 and R6 (36); RAG-2, 101F and 102R (36); Gs primers were as in Russell et al. (23); TdT, 7T (766-786); 5'-GCTGTGTTAAATGATGAGCAGA-Y; and P35 (1115-1134), 5'-GTGGCTTCTGGGCTGGTAAT-3' (35). PCR product sizes were: RAG-1, 562 bp; RAG-2, 472 bp; Gs, 820 bp; TdT, 369 bp. Control experiments showed that the dose-response of the RNA PCR assay is linear, and mock cDNA synthesis controls verified that the amplified material was not the result of DNA contamination from genomic DNA or other sources. The ubiquitous Gs message served as an internal control for the efficiency of cDNA synthesis and PCR amplification. All of the primer pairs we used span introns and thus distinguish between genomic DNA and cDNA based on the predicted sizes of the amplified fragments.

Excision Product PCR Detection Assays. PCR reactions were done in a final volume of 30 μl containing 1 μl of purified DNA solution (at the concentration indicated) in PCR reaction buffer (10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM MgCl₂, 20 μg/ml gelatin 0.3 mM each of dATP, dCTP, dGTP, and dTTP, 1 μM of each oligonucleotide primer, and 1 U of Taq polymerase [Perkin-Elmer Corp.]). VJ₅588-to-D excision products were detected using the following primers: P5 (conserved 3' of VJ₅588), 5'-TGAGGA-

Abbreviations used in this paper: RAG, recombinase activator gene; TdT, terminal transferase.
GGAGGTAATAAATGGACA-Y (37); P71 (conserved 5' of DQβ1.6/ DQβ2.1), 5'-TCAAAGCACAATGCCTGGCTTGGG-Y (38). Each PCR cycle consisted of 30 s at 94°C, 30 s at 62°C, and 1.5 min at 72°C. A thermal cycler was used (Ercomp). 1/~g of input DNA was subjected to 27 amplification cycles under these conditions. The amplified product was 563 bp long. Vα1-to-Jα excision products were detected using the following primers: P46 (3' of Vα1), 5'-GCTGCATACATCACAGATGC-Y; P47 (5' of Jα3), 5'-CAATGATTCTATGTTGTGCC-Y (39). DQα2-to-Jα excision products were detected using the following primers: P25 (3' of DQα2), 5'-AAGACCTGTCCACAGTAACTCG-3'; P24 (5' of jα), 5'-ATA-GGAGCAGGAGGACAGA-3' (40).

For PCR amplification of Vα1-to-Jα and DQα2-to-Jα excision products each cycle consisted of 60 s at 94°C, 2 min at 64°C and 2 min at 72°C. 0.1/~g of input DNA was subjected to 27 amplification cycles under these conditions. The amplified products are 290 bp for Vα1-to-Jα excision product and 182, 502, 883, and 1,451 bp for DQα2-to-Jα,1,2,3,4, respectively. PCR products were run on 1.5% agarose gels and transferred onto zeta probe membranes (Bio-Rad Laboratories) in 0.4 N NaOH. The appropriate cDNA or PCR products were used as hybridization probes after labeling with α-[32p]dCTP using the hexamer labeling method (41). Filters were hybridized with probes for 16 h at 68°C in 0.5 M NaPO4 (pH 7.2), 1 mM EDTA, 7% SDS. Filters were washed to a final stringency of 0.1x SSC (15 mM NaC1, 1.5 mM sodium citrate [pH 7.4]), 0.1% SDS at 65°C, and then exposed to X-ray film.

Linear dose-response of the excision product assays was verified by including different input amounts of normal mouse bone marrow DNA in the assays and measuring the amounts of PCR product detected in Southern blotting by 32P radioactivity quantitation using a PhosphorImager (Molecular Dynamics, Inc., Sunnyvale, CA).

**Results**

Membrane Autoantigens Expressed on Peripheral Cells or on Cells throughout the Whole Body Delete Autoreactive B Cells. To analyze the mechanism of B cell tolerance we produced transgenic mouse bearing functional, rearranged heavy and light chain genes encoding the H-2Kα anti-body specificity 3-83 (19, 23). In this study we used the 3-83αβ transgenic line, which encodes 3-83 Ig of the IgM and IgD isotypes (23). 3-83αβ mice that were H-2d (nondeleting mice) were virtually monodonal with respect to B cells, with >95% bearing the 3-83 idiotype (23). In contrast, when membrane Kα or Kβ autoantigen was present on the whole body (centrally deleting mice) most B cells, including virtually all idiotype-positive B cells, were deleted from the spleen and lymph nodes (Table 1), but were present in the bone marrow (Table 2). Cell surface immunofluorescence staining with mAb to the pan B cell marker B220 confirmed that autoreactive B cells were deleted from the peripheral lymphoid organs and retained in the bone marrow (compare Tables 1 and 2). A similar profound deletion of autospecific B cells in the lymph nodes, and to a lesser extent in the spleen, was observed in 3-83αβ mice bred with MT-Kβ transgenic mice (26), in which the

| Mouse type (n) | Lymph nodes | Spleens |
|---------------|-------------|---------|
|               | B220        | λ       | κ       | id |
|               |             |         |         |    |
|               |             | %       | %       |    |
| Unmanipulated mice* | | | | |
| H-2d Tg (9) (nondeleting) | 24.4 ± 5.7 | 0.08 ± 0.05 | 24.6 ± 5.8 | 24.4 ± 5.7 |
| H-2d Tg × MT-Kβ (7) (peripherally deleting) | 0.9 ± 0.8 | 0.07 ± 0.07 | 0.6 ± 0.3 | 9.6 ± 4.3 |
| H-2d Tg × H-2b (7) (centrally deleting) | 1.5 ± 0.8 | 0.6 ± 0.6 | 1.0 ± 0.5 | 6.4 ± 4.3 |
| H-2d Tg × H-2β (4) (centrally deleting) | 3.7 ± 1.8 | 1.1 ± 0.4 | 2.4 ± 1.4 | 13.5 ± 6.7 |
| Non-Tg (7) (normal) | 29.0 ± 5.9 | 1.0 ± 0.33 | 29.1 ± 6.7 | 51.5 ± 7.6 |
| Bone marrow chimeras† | | | | |
| H-2d Tg→H-2d (3) (nondeleting) | 58.9 ± 10.8 | 0.13 ± 0.05 | 53.1 ± 15.4 | 50.7 ± 16.4 |
| H-2 Tg→H-2α/β (4) (centrally deleting) | 4.4 ± 1.5 | 1.0 ± 0.20 | 3.4 ± 1.2 | 0.1 ± 0.2 |
| Non-Tg→H-2α/β (3) (normal) | 51.9 ± 1.6 | 3.5 ± 0.5 | 52.3 ± 5.2 | 57.7 ± 8.9 |
| Non-Tg→H-2β (3) | 67.7 ± 3.4 | 4.5 ± 0.6 | 64.4 ± 0.7 | 67.7 ± 3.4 |

* Mean ± SD from four to six experiments. Mice were 2 mo. old.
† Mean from three experiments. Mice were analyzed 21-26 d after transfer in three independent experiments.

Table 1. Increased Number of λ Light Chain-bearing B Cells in Centrally Deleting, but Not in Peripherally Deleting, Transgenic Mice
Figure 1. Elevated expression of RAG-1 and RAG-2, but not TdT, in the bone marrow of centrally deleting mice detected using a PCR assay.

(A) cDNA synthesized from the bone marrow RNA of an 8-wk-old B10.D2 nontransgenic littermate mouse was subjected to various numbers of PCR amplification cycles as described in Materials and Methods using pairs of oligonucleotide primers specific for RAG-2 and the ubiquitous GTP-binding protein, Gas. Synthesized fragments were detected by Southern blotting, and the amount of probe hybridized was quantitated. Based on these results 18 cycles of amplification using the conditions described in Materials and Methods were chosen for the subsequent quantitation experiments.

(B and C) Various amounts of cDNA synthesized from the bone marrow RNA were subjected to 18 cycles of the PCR with primers specific for RAG-2 and Gas. (B) Autoradiogram of Southern blot used to detect specific amplification of RAG-2 and Gas. (C) Measurement of radioactivity in the visualized bands of B. Dilution of input cDNA: lane a, undiluted; lane b, 1:5; lane c, 1:10; lane d, 1:25. The RAG-2 cpm/Gas cpm ratios were very similar at all cDNA dilutions tested: 0.52, 0.53, 0.47, 0.56 for a-d, respectively.

(D) Comparison of recombinase message levels in bone marrow RNA of individual transgenic and nontransgenic mice. PCR detection of RAG-l, RAG-2, and TdT mRNA in bone marrow cells was performed as described in Materials and Methods. Shown are autoradiograms of Southern blots used to detect PCR products. (Left) Samples were from 5-wk-old mice; (right) samples were from 8-wk-old mice.

Table 2. Increased Abundance of Bone Marrow RAG mRNA and B Cells in Centrally Deleting, but Not in Peripherally Deleting, Transgenic Mice

| Mouse type | RAG-2 mRNA* (n) | % B220+cells† (n) | % Ig+cells† (n) |
|------------|-----------------|-------------------|----------------|
| H-2d Tg (non deleting) | 1.0 ± 0.38 (5) | 11.7 ± 1.9 (5) | 9.7 ± 1.4 (5) |
| H-2d Tg × MT-Kb (peripherally deleting) | 1.2 ± 0.38 (4) | 13.3 ± 5.9 (4) | 10.6 ± 4.7 (4) |
| H-2d Tg × H-2b (centrally deleting) | 3.4 ± 0.75 (4) | 19.1 ± 4.9 (3) | 16.0 ± 5.7 (3) |
| H-2d Tg × H-2k (centrally deleting) | 8.3 ± 2.1 (2) | 15.2 ± 0.9 (3) | 11.7 ± 0.7 (3) |
| Non-Tg (normal) | 11.6 ± 6.5 (6) | 23.8 ± 6.9 (3) | 6.4 ± 2.0 (3) |

* PCR detection of RAG-2 mRNA was performed as described in Materials and Methods using detection of Gas mRNA as internal control. Relative abundance was calculated as: (cpm RAG-2 probe hybridized/cpm Gas probe hybridized)maximal/(cpm RAG-2 probe hybridized/cpm Gas probe hybridized)mean of nontreating samples. Data shown are expressed as mean relative abundance. All mice were 2 mo old.
† Percent of total viable bone marrow cells.
‡ As the sIg+ cells in this group had a very low level of staining, this value is only approximate.
Kb antigen is only detectably expressed on the surfaces of hepatocytes, exocrine pancreatic cells, and kidney tubules (peripherally deleting mice) (Table 1) (see also reference 23). As shown below, comparison of the peripherally and centrally deleting mice provided insights into the mechanism of deletion.

Elevated RAG Expression in Bone Marrow IgM+ Cells of Centrally Deleting Mice. To examine the possibility that secondary Ig gene rearrangements are induced upon encounter of B cells with tolerogen, we measured RAG-1 and RAG-2 (33, 34) expression in bone marrow cells using a quantitative PCR assay (Fig. 1). Nondeleting, H-2d 3-83μ/β mice have greatly reduced levels of both RAG-1 and RAG-2 relative to nontransgenic littermates, presumably because of the feedback regulation that maintains allelic exclusion (15) (Fig. 1 D, lanes Ig-Tg, and Table 2). Peripherally deleting mice showed similar low levels of RAG-1 and RAG-2 (Fig. 1 D, lanes Ig-Tg/H-2Kb periphery, and Table 2). In striking contrast, and consistent with the possibility that secondary Ig gene rearrangements are induced in B cells by interaction with autoantigen, centrally deleting mice had greatly increased RAG-1 and RAG-2 levels that approached the levels in nontransgenic mice (Fig. 1 D, lanes Ig-Tg/H-2d and Ig-Tg/H-2k, and Table 2).

To determine which cells in the bone marrow of centrally deleting mice were responsible for the elevated RAG expression, we separated idiotype-positive and idiotype-negative cells and measured their RAG-1 and RAG-2 levels. For these experiments we chose to analyze centrally deleting mice bearing the antigen Kb, which is a low affinity ligand for the 3-83 antibody, because the level of idiotype detected on the surface of bone marrow B220+ cells is higher in these mice than in H-2k centrally deleting mice and thus allows a cleaner cell separation. Fig. 2 A shows that the idiotype-positive cells were highly enriched for RAG-2 expression and accounted for most of the bone marrow RAG-2 message, as demonstrated by the depletion of RAG-2 in the idiotype-negative cells. The lack of RAG expression in the idiotype-negative cells is confirmed by the autoradiogram of Southern blot used to detect PCR products in Fig. 2 A (Bottom). Fig. 2 B shows a similar analysis for bone marrow cells from a normal, nontransgenic mouse sorted on the basis of slgM expression. Fig. 2 C shows RAG-2 expression analysis of sorted nondeleting, peripherally deleting, and centrally deleting mouse bone marrow cells. In this experiment Gas probe of lower specific activity was used to better reveal the RAG-2 signal.

Figure 2. Most RAG-2 mRNA from H-2k centrally deleting bone marrow is contained in slgM+ cells. (A) 3-83 idiotype-positive cells were stained with the anticonotype antibody 34.1/biotin, followed by PE-avidin, and sorted as described in Materials and Methods. RNA was isolated from sorted and nonsorted populations and PCR detection was carried out as in Fig. 1. (Bottom) Autoradiogram of Southern blot used to detect PCR products. (RT, +/-) Addition or omission of reverse transcription during the cDNA synthesis procedure before PCR amplification. (B) A similar analysis as in A for bone marrow cells from a normal, nontransgenic mouse sorted on the basis of slgM expression. (C) RAG-2 expression analysis of sorted nondeleting, peripherally deleting, and centrally deleting mouse bone marrow cells. In this experiment Gas probe of lower specific activity was used to better reveal the RAG-2 signal.
negative cells was not the result of selective death of pre-B cells, because in normal mouse bone marrow cells that were sorted similarly using anti-IgM antibodies most, but not all, of the RAG-2 mRNA was present in the slgM- population (Fig. 2 B). The idiotype-positive cells of the nondeleting and peripherally deleting transgenic mice were also enriched in RAG-2 mRNA, but this message was present at a lower level than in the idiotype-positive cells isolated from centrally deleting mouse bone marrow (Fig. 2 C). These results reflect the relative amounts of RAG-2 message seen in the total mouse bone marrow RNA preparations (Table 2). The significance of the residual RAG expression in the slg- cells of the nondeleting and peripherally deleting mice is unclear, as these cells demonstrate little functional Ig gene rearrangement (see below). Because binding by the antidiotype antibody is dependent on coexpression of the transgenic light and heavy chains, these experiments demonstrate that bone marrow B cells bearing intact surface (s)lgM can express RAG-1 and RAG-2, and that the levels of RAG mRNAs are highest in cells that have bound (auto)antigen in the bone marrow. Interestingly, centrally deleting mice bearing the high affinity ligand Kk expressed more RAG-1 and RAG-2 in their bone marrow, but had no more bone marrow B cells than centrally deleting mice expressing the low affinity ligand Kbb (Table 1). This suggests that the affinity of the antigen–receptor interaction affects the probability that a bone marrow IgM+ cell will express recombinase.

Elevated Light Chain Gene Recombination in Centrally Deleting Bone Marrow Cells. To test whether or not the elevated RAG expression in centrally deleting bone marrow cells reflected

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Figure 3. PCR detection of Ig gene rearrangement excision products. (A) General strategy for the PCR detection of Ig gene rearrangement excision products. Filled and open rectangles represent Ig gene coding segments. Open and filled triangles represent rearrangement signal sequences with 12- and 23-bp spacers, respectively. Primers a and b are oligonucleotides that initiate DNA synthesis on opposite DNA strands in the indicated directions. (B) Amplification of VxV-to-Jb joining excision product from purified normal, nontransgenic mouse bone marrow DNA. Effect of altering the number of PCR cycles on the amount of amplified product. Based on these results 27 cycles of amplifications on the amount of amplified product. Based on these results 27 cycles of amplifications using the conditions described in Materials and Methods was chosen for the subsequent quantitation experiments. (C) Dose-response of input normal bone marrow DNA amount on VxV-to-Jb excision product signal detected after 27 cycles of amplification. Similar linear dose-response curves were seen in experiments detecting the other types of excision product (not shown). (D–G) Detection of Ig gene rearrangement excision products in bone marrow DNA. Bone marrow DNA from 8-wk-old mice was analyzed for excision products of: (D and G) VxV-to-Jb joining (D, comparison of a number of individual 2-mo-old mice; G, comparison of one mouse of each group using different starting amounts of bone marrow DNA); (E) VxV-to-Jb joining; (F) Dqs2-to-Js joining. PCP, products were visualized by Southern blotting followed by autoradiography.
increased V(D)J recombination, we measured the levels of Ig gene rearrangement excision products in bone marrow DNA using a PCR assay (Fig. 3). This assay takes advantage of the fact that during recombination the heptamer-nonamer signal sequences flanking the two joined Ig gene coding elements are themselves ligated, and the resulting structure can be detected and amplified using PCR with appropriately designed oligonucleotide primers (shown schematically in Fig. 3A). The strength of this approach, at least for V\textsubscript{\textgamma}-to-D, DQ52-to-J\textsubscript{\textlambda}, and V\textsubscript{\textkappa}-to-J\textsubscript{\textlambda} rearrangements, is that these excision products, unlike the corresponding coding products that are retained by the chromosome, are always deleted from the chromosome and so their quantity should not be affected by the possible subsequent growth of the cells. In addition, because each cell has a limited number of loci that can rearrange, the amount of excision product detected is likely to reflect the fraction of cells undergoing gene rearrangement. These experiments showed that the level of \lambda\textsubscript{l} light chain excision products in bone marrow DNA preparations were extremely high in centrally deleting but not peripherally deleting or nondeleting mice (Fig. 3, D and G). Thus, autoantigen expression in the bone marrow is correlated with increased Ig gene recombination activity. Similar results were obtained with \lambda\textsubscript{\textkappa}-specific assays (not shown). By contrast, V\textsubscript{\textkappa}-to-D excision products were not elevated in bone marrow cells of centrally deleting mice, indicating that light chain, but not heavy chain, rearrangement is induced in the centrally deleting mice (Fig. 3E).

Interestingly, increased levels of DQ52-to-J\textsubscript{\textkappa} excision products were detected in the bone marrow cells of centrally deleting mice, relative to the levels seen in the bone marrow cells of nondeleting and peripherally deleting control mice (Fig. 3F). The appearance in centrally deleting B cells of D\textsubscript{\textkappa}-to-J\textsubscript{\textkappa} joining, but not V\textsubscript{\textkappa}-to-D joining, is similar to the IgH rearrangement patterns seen in T cell lines (42) and probably reflects a less restrictive control of the accessibility of the elements needed for D\textsubscript{\textkappa}-to-J\textsubscript{\textkappa} joining compared with the control of the accessibility of elements needed for V\textsubscript{\textkappa}-to-D rearrangements.

Bone marrow DNA preparations also were analyzed for V\textsubscript{\textkappa}-to-J\textsubscript{\textkappa} rearrangements by the excision product assay. As for the \lambda loci tested, the bone marrow cells of centrally deleting mice had greatly elevated levels of detectable excision products, relative to the bone marrow cells of peripherally deleting or nondeleting transgenic mice (data not shown). These results support the idea that \kappa light chain genes are also induced to rearrange in centrally deleting mice. However, these data are more difficult to interpret for \kappa than for the other loci tested, because in \kappa, in contrast to the other Ig loci, many Vs rearrange by inversion. In the case of inversion the signal joints that our assay recognizes are retained on the chromosome upstream of the Ck, and their quantity is therefore potentially subject to subsequent cellular selection.

**Elevated \lambda Light Chain Expression in Centrally Deleting Mice.** In deleting transgenic mice small numbers of B cells that lack the autoreactive specificity escape deletion and appear in the peripheral lymphoid organs. A large fraction (\textasciitilde1/3) of the B cells found in centrally deleting mouse lymph nodes expressed \lambda light chains (Table 1). These \lambda chains must have been the result of rearrangement and expression of endogenous \lambda loci because the transgenic light chain is \kappa. Lymph node cells of centrally deleting mice had \textasciitilde10-fold more \lambda\textsuperscript{+} cells than lymph node cells of peripherally deleting and of nondeleting mice, both in terms of the absolute numbers of \lambda\textsuperscript{+} cells and in terms of the percentage of total lymph node cells. This high frequency of \lambda\textsuperscript{+} cells in the centrally deleting mice was not a simple result of selective outgrowth of idioype-negative cells, because peripherally deleting mice, which had even more profoundly depressed lymph node B cell levels, had as few \lambda-bearing lymph node cells as the nondeleting 3-83\mu/\delta mice. Although the peripherally deleting mice had nearly twofold more \lambda-bearing cells in the spleen than the nondeleting mice (0.5 vs. 0.3%), this increase was relatively slight compared with the 8–16-fold increase seen in the spleens of centrally deleting mice (Table 1). We note that the slight increase in the percentages of B220\textsuperscript{+} cells in the lymph nodes of centrally deleting mice, relative to that percentage in peripherally deleting mice, can be largely accounted for by the increase in the fraction of \lambda-bearing cells. These data document the increased rearrangement of endogenous light chain genes in the B cells of centrally deleting mice at the level of light chain protein expression.

To more directly examine the potential of bone marrow B cell precursors developing in deleting or nondeleting environments to give rise to \lambda-bearing cells, we constructed radiation chimeras. Aliquots of bone marrow cells from nondeleting, H-2\textsuperscript{d} 3-83\mu/\delta mice were used to reconstitute lethally irradiated H-2\textsuperscript{d} or H-2\textsuperscript{k/b} recipients. 3–4 wk after transfer the mice were analyzed. Again, centrally deleting mice demonstrated a greatly increased frequency of \lambda-bearing cells, while the nondeleting transgenic chimeras demonstrated excellent light chain isotype exclusion (Table 1). These cells were of donor origin because double staining of peripheral B cells with anti-I-A\textsuperscript{b} and anti-B220 antibodies revealed that >95% of the B cells in all samples were donor derived and virtually all detectable bone marrow B cells in the deleting chimeras had low levels of 3-83 idiotype (not shown). Since the transgenic donor bone marrow was H-2\textsuperscript{d}, this experiment also shows that for the induction of \lambda\textsuperscript{+} B cell production in these chimeras the B cell receptor had to emerge onto the cell surface and receive an antigenic signal from another cell. This result is important because pre-B cells and B cells express class I MHC molecules and might have conceivably required autoantigen expression internally, for example in the endoplasmic reticulum, to induce \lambda production. It also suggests that any antigen that is present in the bone marrow, and is capable of crosslinking B cell receptors with sufficient avidity, can induce recombinase expression and secondary light chain rearrangement in sigM\textsuperscript{+} cells.

**In Centrally Deleting Mice \lambda Chain-bearing B Cells Arise from Self-reactive B Cells.** To determine whether or not \lambda\textsuperscript{+} B cells from centrally deleting mice arose from autoreactive precursors, we analyzed bone marrow cells by two-color immunofluorescence with antiidiotype and anti-\lambda antibodies (Fig.
BONE MARROW

Figure 4. Detection of idio-
type \(\lambda^+\) B cells in the bone mar-
row of a centrally deleting mouse.

Figure 5. Peripheral \(\lambda^+\) light chain-bearing B cells in a centrally deleting
mouse coexpress transgenic heavy chain genes and they support the \(V_\mu\)-to-D excision product data, suggesting that receptor editing involves assembly of light
chain, but not heavy chain, \(V\) genes (Fig. 3).

Discussion

Although Ig receptor generation and antigenic selection in B cells have been generally thought to be independent
processes, we find that in immature, IgM\(^+\) bone marrow B lymphocytes these processes are intimately linked. Bone
marrow B cells expressing receptors that are crosslinked by autoantigen express high levels of recombinase gene mRNAs
and continue to rearrange Ig light chains. Evidence for rearrangement activity in bone marrow cells of centrally deleting
mice came from experiments demonstrating: (a) elevated levels of RAG-1 and RAG-2 mRNA in bone marrow cells of cen-
trally deleting mice; (b) elevated expression of these recom-
binase genes in slgM\(^+\) bone marrow cells of centrally
deleting mice; (c) elevated levels of light chain rearrangement
excision products in bone marrow cells of centrally deleting
mice; and (d) expression of endogenously encoded light chain
protein in cells expressing transgenic Ig in bone marrow cells
of centrally deleting mice. These results suggest that autoreac-
tive bone marrow B cells are often rescued from elimination
by an induced alteration of the structure and specificity of
their antigen receptors. While our results in a sense reinforce
the concept of clonal selection, as cells with autoreactive
specificities do indeed disappear in our system, the receptor
editing idea represents an important conceptual departure from
the prevailing dogma of clonal selection, which holds that
selection against self-reactive clones requires their functional
or physical elimination. In essence, the distinction between
clonal selection and receptor editing is that in receptor editing
the fates of the autoreactive B cell and its receptor are un-
coupled.

The Case against Feedback Regulation. The elevated expres-
sion of RAG-1 and RAG-2 accompanied by increased \(\lambda\) light
chain gene rearrangement in the bone marrow of centrally

drafting.
deleting mice raises the question of feedback in hematopoiesis. It could be argued that a paucity of B cells in the periphery or in the bone marrow induces elevated RAG expression in bone marrow cells of centrally deleting mice as a consequence of an overall increase in B cell production. We think this is unlikely for several reasons: (a) the peripherally deleting mice, which are highly B cell deficient, fail to demonstrate RAG upregulation (Fig. 1); (b) the cells that are enriched for RAG expression in bone marrow of centrally deleting mice are not pre-B cells, as would be predicted by a feedback model, but slgM+ cells (Fig. 2); (c) expression of terminal transferase, a pro-B stage-specific gene, is not elevated in bone marrow cells of centrally deleting mice (Fig. 2); (d) rearrangement in bone marrow B cells of centrally deleting mice occurs at the light chain loci, but not detectably at the heavy chain loci (Fig. 3); (e) in mixed bone marrow chimeras, in which an excess of normal, nontransgenic B cells of all developmental stages develops alongside a minority population of transgenic B cells, the autoreactive transgenic B cells continue to demonstrate elevated λ light chain rearrangement (data not shown); (f) a simple feedback model cannot explain the different λ/κ ratios in peripherally deleting and centrally deleting mice; and (g) studies on anti-IgM-suppressed mice, SCID mice, and SCID mice bearing active Ig transgenes indicate that depletion of mature and immature B cells, late-pre-B cells, or late pro-B cells does not increase the rate of formation, or steady-state levels, of their precursors in the bone marrow (3, 43, 44).

The Receptor Editing Hypothesis. Based on these results we have formulated the following model for the role of Ig gene rearrangement in B cell tolerance (Fig. 6). Cells at the pre-B to B cell transitional stage of development in the bone marrow are undergoing κ rearrangement. The appearance of IgM on the cell surface normally turns off further recombination. We propose that if the newly emerging or recently emerged receptors are autoreactive, and their surface IgM is crosslinked by membrane-bound autoantigen, the following sequence of events takes place. (a) Recombinase levels in the autoreactive B cells are high, either because expression fails to be shut down or because the recombinase machinery is newly expressed. (b) Because recombinase is now expressed in a cell with recombinase-accessible light chain V genes, but not recombinase-accessible heavy chain V genes, secondary rearrangement occurs in the κ locus. (c) If light chain rearrangement is successful, the previously active κ VJ is rendered inactive by nested rearrangement and deletion, or by inversion, which places the VJ far away from Ck. Rearrangement continues until a new, functional VJ is generated, or until the Cκ loci are inactivated by using up the available Jκ's or by RS recombination. The functional light chain must fail to result in an autoreactive receptor or the editing process will be resumed, starting at step a. It is also possible at this stage that a new light chain that pairs preferentially with the cell's μ chain can in some cases extinguish the B cell's anti-self-specificity without eliminating the active, autospecific VJ on the other chromosome. This has been clearly shown by Gay et al. (45) in their anti-DNA transgenic mouse system. Their work also underscores the importance of editing in eliminating potentially pathogenic specificities. (d) Those cells that have activated RS recombination, which deletes the Cκ locus, now make λ loci available for rearrangement and expression. In the mouse, further editing of active λ light chain loci that encode autoantibodies is not generally possible, given the organization of the λ genes; however, in other species, such as humans, nested secondary VκJκ rearrangements that can eliminate active VκJκ's may be possible.

The Importance of Secondary Ig Gene Rearrangements. Secondary Ig gene rearrangements are defined as rearrangements caused by the V(D)J recombinase system in loci that have already undergone V region gene assembly. In the case of nonfunctional rearrangements, such as out-of-frame coding joints, secondary (and higher order) rearrangements can allow multiple attempts at generating functional Ig genes. Mouse Ig gene organization has a number of interesting features that may be important in limiting, or facilitating, such secondary rearrangements. The heavy chain V, D, and J minigene are in the same transcriptional orientation (46). Thus, VDJ recombination deletes the intervening DNA between the active Vα and Dα segments and that between the rearranged Dα and Jα segments. This results in the loss of all other D's from that allele of the Ig locus and eliminates the possibility of further rearrangements using conventional signal sequences. By contrast, the κ locus has V genes in different orientations relative to the J's, and thus can rearrange by deletion or inversion of the intervening DNA (47-49). Because in the κ locus the V's recombine directly to J's, and there are four functional Jκ's, nested rearrangement is possible. Furthermore,
Secondary Rearrangement of Ig Genes in B Cells Can Alter Specificity. How can the concept of receptor editing be reconciled with the observation of allelic exclusion? There are a number of well-documented reports of secondary Ig gene rearrangements in murine B cell tumor lines already expressing intact IgM on the cell surface (54–56). These rearrangements can create new, functional light or heavy chain genes, effectively changing the antigen specificity of the cells in the process. Two groups demonstrated a novel form of recombination at the IgH locus, called V gene replacement, in which coding sequences of the rearranged, functional V gene are replaced by upstream germline V gene segments (54, 57). This V~to-V.DJ recombination appears to be mediated by cleavage and recombination in a highly conserved heptamer in the 3' portion of the rearranged V~ coding sequence. This heptamer is identical to, and in the same orientation as, that found 5' of D elements, suggesting that in V~ to V.DJ replacement, the same enzymatic machinery that mediates the familiar V~to-DJ recombination is involved. It has not been determined whether or not this process occurs in normal cells. Nevertheless, we cannot exclude a role for V~ gene replacement in receptor editing. Evidence for a functional secondary rearrangement at the light chain locus has been provided by Levy et al. (55): independent idioype variants of the surface IgM+ tumor 38C13 were shown to have deleted and replaced the rearranged, functional V.DJK by recombination between upstream V~'s and downstream J~'s. This type of nested rearrangement has been observed frequently in myelomas and hybridomas in situations where the rearrangement was inversiveional (48–50). In normal B cells, circular DNAs excised by nested k gene rearrangements have been demonstrated. Interestingly, these circles frequently contain rearranged VJs, about one-third of which are in-frame and potentially functional (16). Finally, in the NPS-5 tumor, under conditions in which it expresses surface IgM (μ,κ), λ light chain rearrangement may occur. The λ protein product competes efficiently for binding to heavy chain with the functional κ protein, extinguishing surface κ expression (56). In all the above examples, not only do the rearrangements create a new specificity, but they extinguish the original specificity of the B cells. Secondary rearrangements have been thought to occur in developing B cells that fail to make functional Ig receptors; the data presented in this paper suggest that autoreactive B cells can similarly be rescued and made nonautoreactive by secondary Ig gene rearrangement.

Our model may help to explain exceptions to the paradigm of feedback inhibition of Ig gene rearrangement. For example, Storb and her colleagues (58, 59) have observed that in k chain transgenic mice, in which feedback inhibition of k rearrangement is effective in most B cells, a subset of B cells appears to ignore the expressed transgene and continues to rearrange endogenous k and λ light chains. We predict that in this subset of B cells the transgenic light chain paired with the cell's μ heavy chain confers autoreactive specificity that is sufficient to activate the receptor editing process.

Antigen Receptor Selection in the Primary Lymphoid Organs. Recent work on T lymphocyte selection suggests that thymic-positive selection or TCR crosslinking can terminate ongoing TCR α chain gene rearrangement in immature TCR+ T cells (60, 61), providing another example of a link between antigen receptor crosslinking in immature lymphocytes and V(D)J recombinase regulation. Our results demonstrating secondary light chain rearrangement in immature B cells encountering autoantigen in the bone marrow differ substantially from the results with T cells, however, because we find that receptor crosslinking in immature B cells turns recombinase on, rather than off. However, sIgM+ lymphomas generated in Eμ-N-myc transgenic mice downregulate RAG expression upon Ig crosslinking (62). It is possible that B cells are uniquely adapted to use the receptor editing mechanism for the elimination of potentially harmful autoreactive B cells, whereas T cells make use of receptor editing to increase their chances of being positively selected. We assume that the receptor editing we detect in transgenic mice reflects a process occurring in normal cells as suggested by the presence of a subset of sIgM+/RAG+ cells in normal bone marrow (62) and the abundance of in-frame Vκ joins in circular excised B cell DNA from normal mice (16). In both B and T lymphocytes receptor editing could relieve developmental "bottlenecks," in which large numbers of cells are selected against, by providing a means of rapidly generating cells with appropriate specificities at an early developmental stage through the sequential alteration and testing of their antigen receptors.

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