Relaxed Negative Selection in Germinal Centers and Impaired Affinity Maturation in \(bcl-x_L\) Transgenic Mice

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Summary

The role of apoptosis in affinity maturation was investigated by determining the affinity of (4-hydroxy-3-nitrophenyl)acetyl (NP)-specific antibody-forming cells (AFCs) and serum antibody in transgenic mice that overexpress a suppressor of apoptosis, \(bcl-x_L\), in the B cell compartment. Although transgenic animals briefly expressed higher numbers of splenic AFCs after immunization, the \(bcl-x_L\) transgene did not increase the number or size of germinal centers (GCs), alter the levels of serum antibody, or change the frequency of NP-specific, long-lived AFCs. Nonetheless, the \(bcl-x_L\) transgene product, in addition to endogenous Bcl-x\(_L\), reduced apoptosis in GC B cells and resulted in the expansion of B lymphocytes bearing VDJ rearrangements that are usually rare in primary anti-NP responses. Long-lived AFCs bearing these non-canonical rearrangements were frequent in the bone marrow and secreted immunoglobulin G\(_1\) antibodies with low affinity for NP. The abundance of noncanonical cells lowered the average affinity of long-lived AFCs and serum antibody, demonstrating that Bcl-x\(_L\) and apoptosis influence clonal selection/maintenance for affinity maturation.

Key words: Bcl-x\(_L\) • apoptosis • affinity maturation • germinal center • clonal selection

A distinct property of humoral immune responses to T cell–dependent antigens is a progressive increase in antibody affinity known as affinity maturation (1, 2). Affinity maturation is achieved by two key events: the generation of antibody variants by V(D)J hypermutation and the subsequent selection of those variants that bind antigen strongly (3, 4). It is widely believed that the selective accumulation of high-affinity B cells is mediated by inter- and intraclonal competition for antigen retained on follicular dendritic cells (FDCs)\(^1\) in germinal centers (GCs) (5–7). However, little is known about the cellular and molecular mechanisms underlying this selection.

GCs serve as a crucial site for antigen-driven V(D)J hypermutation (8, 9). Clonal selection and affinity maturation within this mutated population can be followed by a variety of methods (10, 11) to show that increased affinity is achieved by both preferential retention of higher-affinity B cells (positive selection) and loss of low-affinity B cells (negative selection). Although positive selection can only result from an active process, i.e., selective proliferation, negative selection can arise passively. For example, limiting amounts of antigen may be insufficient to activate B cells with low-affinity receptors (12) or to support their interaction with T lymphocytes (13). Such clones would be rapidly overgrown in the GC population by higher-affinity competitors. Nonetheless, negatively selected GC B cells are believed to die by apoptosis, because GCs are sites of considerable cell death, and in vitro, GC B cells undergo programmed cell death in the absence of activating stimuli (14). Furthermore, administration of large amounts of soluble antigen sharply elevates the number of apoptotic B cells in GCs, an experiment thought to mimic the negative selection of autoreactive mutants (15–17).

Several molecules that regulate apoptosis have been proposed to modulate negative selection during affinity maturation. Bcl-2, an inhibitor of apoptotic cell death, is selectively downregulated in GC B cells (18), and human GC B cells rapidly become apoptotic in ex vivo culture. How-
ever, stimulation of human GC B cells with antibody to membrane Ig (mlg) or CD40 extends the survival of cultured GC cells and upregulates Bcl-2 (14). Reciprocally, a positive regulator of apoptotic cell death, Fas (CD95), is highly expressed in GC B cells (18, 19), and GC B cells are susceptible to Fas-mediated apoptosis in vitro (20, 21). Despite these in vitro models, studies of genetically modified mice do not support major roles for Bcl-2 or Fas in affinity maturation. Neither the overexpression of Bcl-2 nor the lack of Fas has detectable effects on the affinity maturation of serum antibodies (19, 22). These findings raise the possibility that affinity maturation is achieved solely by positive selection, or that other apoptosis-regulatory molecules are involved in the negative selection process.

A homologue of bd-2, bd-x, also suppresses apoptosis through its Bcl-x<sub>L</sub> product (23). Bcl-x<sub>L</sub> is highly expressed in pre-B cells but is downregulated when B cells enter the mature pool (24, 25). While Bcl-2 plays a critical role in the survival of mature naive lymphocytes (26), Bcl-x<sub>L</sub> is important for the survival of immature lymphocytes (27). Interestingly, cross-linking of mlg or CD40 on splenic B cells upregulates the expression of Bcl-x<sub>L</sub> (25, 28). Human GC B cells are also known to reexpress Bcl-x<sub>L</sub>, with expression confined to the centrocyte subset in which clonal selection is thought to occur (29, 30). These data and the many shared characteristics of immature and GC B cells (31) suggest that Bcl-x<sub>L</sub> might control life-or-death decisions in the GC compartment.

To examine the roles of apoptosis and Bcl-x<sub>L</sub> in affinity maturation, we tracked the affinity of antibody-forming cells (AFCs) in the bone marrow (BM) and serum antibody of bd-x<sub>L</sub> transgenic mice and their congenic wild-type controls, during the clonally restricted antibody response to the (4-hydroxy-3-nitrophenyl)acetyl (NP) hapten (32). Our study revealed that overexpression of Bcl-x<sub>L</sub> did not change the magnitude of the GC response or the frequency of AFCs in the BM. However, apoptotic cell death in GCs was significantly reduced in bd-x<sub>L</sub> transgenic mice and led to the persistence of many B cells carrying VDJ rearrangements that are normally rare in the later stages of the primary anti-NP response and generally encode lower-affinity antibody (11, 12, 32). Affinity maturation of serum IgG<sub>1</sub> antibody was reduced in transgenic mice by the persistence of low-affinity BM AFCs. Selective apoptosis, rather than the overgrowth of high-affinity clones, appears to be the prime agency by which low-affinity B cells are lost from humoral responses.

Materials and Methods

Antigens and Antibodies. The succinic anhydride ester of NP was reacted with chicken γ-globulin (G<sub>C</sub>; Sigma Chemical Co.) or BSA (U.S. Biochemical Corp.) as described (32). The coupling ratio of each conjugate was determined spectrophotometrically. Antibodies specific for IgM<sub>1</sub> (AF6-78) and mouse λ<sub>1</sub> L chain (Ls136) were purified over protein G-Sepharose (Amersham Pharmacia Biotech) from culture supernatants. Horseradish peroxidase (H<sub>R</sub>P)-conjugated goat anti-mouse IgG<sub>1</sub> and biotinylated anti-IgD antibodies were purchased from Southern Biotechnology Associates. Anti-FcγRI/II (2.4G2), FITC-labeled GL-7, PE-conjugated anti-B220, biotinylated anti-M<sub>ζ</sub>α-1, -Gr-1, -Thy1.2, -CD4, -CD8, and -Ter119, and PE-conjugated anti-CD138 (syndecan) antibodies were purchased from PharMingen. Anti-Bcl-x<sub>L</sub> and anti-Bcl-2 mAbs were purchased from Transduction Laboratories.

Mice and Immunizations. bd-x<sub>L</sub> transgenic mice were generated as described previously (24) and backcrossed with the C57BL/6 strain (The Jackson Laboratory). Ig<sub>H<sub>2</sub></sub><sub>2</sub> progeny were used in all experiments. bd-x<sub>L</sub> transgenic or transgene-negative littermate controls were immunized intraperitoneally with 50 μg of an NP<sub>20</sub>-CG conjugate precipitated in alum.

Enzyme-linked Immunospot Assay and Affinity Estimates. The frequencies of N<sub>P</sub>-specific AFCs in spleen and BM were estimated by enzyme-linked immunospot (ELISPOT) assay using two different coupling ratios of NP-BSA (11). In brief, splenocytes (10<sup>5</sup> cells/well) or BM cells (5 × 10<sup>5</sup> cells/well) were incubated on nitrocellulose filters coated with NP<sub>23</sub>-BSA, NP<sub>23</sub>-BSA, or BSA alone at 37°C, 5% CO<sub>2</sub> for 2 h. After washing, filters were stained with HRP-conjugated anti-IgG<sub>1</sub> antibodies, and HRP activities were visualized using 3-aminohexyl carbazol. The frequencies of high-affinity and total AFCs were determined from NP<sub>23</sub>-BSA- and NP<sub>23</sub>-BSA–coated filters after background on BSA-coated filters was subtracted.

ELISA Titration of Serum IgG<sub>1</sub> Antibody and Affinity Estimates. IgG<sub>1</sub> specific for the NP hapten was detected by ELISA using two different coupling ratios of N<sub>P</sub>-BSA as described (11). In brief, serially diluted sera were added to plates coated with NP<sub>20</sub>-BSA or NP<sub>23</sub>-BSA and incubated at 4°C overnight. After washing, HRP-conjugated goat anti–mouse IgG<sub>1</sub> was added, and HRP activity was visualized using a TMB peroxidase substrate kit (Bio-Rad Laboratories). The concentrations of anti-NP IgG<sub>1</sub> antibodies were estimated by comparison with standard curves created from the H33γ1/λ1 control antibody on each plate (12). To estimate the affinity of N<sub>P</sub>-binding antibody in the sera, ratios of N<sub>P</sub>-binding antibody to N<sub>P</sub>23-binding antibody were calculated.

Histology. All histological procedures were conducted as described previously (32). The number of λ<sub>1</sub> GCs was determined by staining sections with biotinylated Ls136, followed by alkaline phosphatase–conjugated streptavidin (Southern Bio-technology Associates) and HRP-conjugated peanut agglutinin (PNA). Apoptotic cell death in GCs was estimated by terminal deoxynucleotidyl transferase–mediated dUTP–biotin nick end labeling (TUNEL) as described (17). TUNEL<sup>+</sup> cells in GCs were counted at 200× magnification by systematic scanning. Cell proliferation in GCs was determined by the incorporation of 2-bromodeoxyuridine (BrdU) as described (17). In brief, 10 d after immunization, bcl-x<sub>L</sub> transgenic and control mice were given 1.0 mg BrdU by intraperitoneal injection; 2 h later, the mice were killed and their spleens prepared for histology. Proliferation indices were determined by microscopic inspection as the fraction (%) of PNA-binding (PNA<sup>+</sup>) cells that exhibited nuclear BrdU incorporation.

Sequence Analysis of VDJ Rearrangements from GC B Cells. λ<sub>1</sub> GC cells were microdissected from day 12 spleen sections of bd-x<sub>L</sub> transgenic mice and control mice. VDJ DNA was amplified by PCR and cloned into Bluescript plasmid (34). The frequency of VDJ genes using the V186.2 gene segment was estimated by colony hybridization using oligonucleotides specific for V186.2 and one specific for the framework 3 region of the mouse V<sub>H</sub>2, V186.2 and V3 subfamilies of the J558 group (32, 35). Plasmid DNA was extracted from ≤3 bacterial colonies from each GC, and V<sub>H</sub> gene sequences were determined by automated sequencing.

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Flow Cytometry. Single cell suspensions of splenocytes and BM cells were prepared as described (11). Cells were then washed in PBS (pH 7.4) containing 2% FCS and 0.08% sodium azide at 4°C for cytometric analysis, or washed with deficient RPMI 1640 (Irvine Scientific) containing 2% FCS for sorting. The enumeration of GC B cells and sorting of BM AFCs were carried out as described (11).

To collect GC B cells, splenocytes pooled from four mice were blocked with anti-FcγRI/RII and then stained with biotinylated anti-IgM, -M Ac-1, -Gr-1, -Thy1.2, -CD4, -CD8, and -Ter119 antibodies for 30 min. After three washes, cells were incubated with streptavidin-conjugated microbeads (Miltenyi Biotec) for 15 min. Cells attached to microbeads were depleted by passage through a C5 column (Miltenyi Biotec) in a magnetic field based on the manufacturer’s protocol. Recovered cells were stained with FITC-labeled GL-7, PE-conjugated anti-B220, TRICOLOR-conjugated streptavidin (Caltag Laboratories), and 7-aminoactinomycin D (7-AAD). Finally, GL-7 FITC-conjugated streptavidin, PE-conjugated anti-B220, and 7-amino actinomycin D (7-AAD) were loaded (10^5 cells/well) into 96-well plates and cultured in medium containing 1% FCS for 96 h. Viable cells present in triplicate cultures were enumerated by trypan blue exclusion at the indicated times; each point represents the mean number (± SD) of viable B lymphocytes.

Western Blots. Cells were lysed in a buffer containing 137 mM NaCl, 1 mM MgCl₂, 0.1 mM CaCl₂, 20 mM Tris-HCl (pH 9.0), 1% NP-40, and 10% glycerol. After homogenization, cells were centrifuged and supernatants were recovered. The cell lysates were loaded (10 µg protein) onto 12% SDS polyacrylamide gel and resolved by electrophoresis. The proteins were then transferred by electrophoresis onto polyvinylidene fluoride membranes. After blocking with TBS (Tris-buffered saline) containing 5% nonfat dry milk, the membranes were incubated with 1:500 diluted anti-Bcl-x or anti-Bcl-2 mAbs, then washed five times with TBS containing 0.1% Tween-20. After incubation with 1:20,000 diluted HRP-conjugated goat anti-mouse Ig antibodies (Amersham Pharmacia Biotech), the reaction was developed by enhanced chemiluminescence using the ECL kit (Amersham Pharmacia Biotech) and detected by exposure to X-ray film.

Results

bd-x₁ T transgene Protects B Cells from Passive Apoptotic Death. Spleens of mice carrying the bd-x₁ transgene are ~50% larger and contain 30% more mononuclear cells than those of nontransgenic littermates. This increased cellularity is due to a near doubling in the number of mature IgM⁺ B220⁺ cells (Fig. 1 A). Flow cytometric analyses of splenic B cells from transgenic mice revealed that expression of IgM, IgD, CD19, CD21, CD22, CD23, and CD24 was identical to that of control littermates (data not shown). Despite the increased numbers of peripheral B lymphocytes, transgenic animals displayed normal levels of serum IgM (1,242 ± 351 vs. 1,295 ± 379 µg/ml) and IgG (1,341 ± 101 vs. 1,777 ± 379 µg/ml) as measured by specific ELISA. As expected (24), the thymic and peripheral T cell compartments of transgenic mice were normal in size and cellular composition (Fig. 1 A, and data not shown).

Initial assays were performed to assess the ability of transgene-bearing B cells to survive in culture medium containing little FCS. Purified splenic B cells from transgenic mice showed a significant survival advantage over control cells.
when cultured in medium containing 1% (Fig. 1 B) or 0.1% serum (not shown), indicating their strong resistance to the effects of serum starvation.

Despite their resistance to serum starvation, transgenic B cells displayed no evidence for increased proliferation in response to CD40 cross-linking or T cell help in vitro (Fig. 1 C). In addition, proliferative responses and antibody production in cultures containing LPS were the same for both transgenic and control splenocytes.

Expression Pattern of Endogenous and Transgenic Bcl-x<sub>L</sub> in Splenic Lymphocytes. The product of the bd-x<sub>L</sub> transgene carries a short epitope tag at its N<sub>H</sub>2 terminus and migrates more slowly in SDS-PAGE gels than endogenous Bcl-x<sub>L</sub>, which runs as a doublet at ~31 and 32 kDa. Fig. 2 A illustrates that transgenic Bcl-x<sub>L</sub> is expressed almost exclusively in the B220<sup>+</sup> fraction of splenic lymphocytes. To determine transgene expression in B cells participating in an immune response, C57BL/6 mice were immunized with NP-CG, and 12 d later splenic B220<sup>+</sup> cells were sorted into GL-7<sup>+</sup>- and GL-7<sup>-</sup> fractions to identify follicular and GC B cells, respectively (31). The expression of endogenous Bcl-2 and of endogenous and transgenic Bcl-x<sub>L</sub> in these populations were then compared (Fig. 2 B).

Follicular B (GL-7<sup>+</sup>-B220<sup>+</sup>) cells from wild-type mice are positive for Bcl-2 but express little Bcl-x<sub>L</sub>. Both proteins are abundant in the follicular population of mice carrying the bd-x<sub>L</sub> transgene. In contrast, GC B cells (GL-7<sup>+</sup>-B220<sup>+</sup>) isolated from both wild-type and transgenic mice abundantly express Bcl-x<sub>L</sub> but little or no Bcl-2. This observation is consistent with studies of GCs in humans (18, 30). Thus, the reciprocal expression of Bcl-x<sub>L</sub> and Bcl-2 observed in pre-B cells holds for GC B cells (24, 25). Interestingly, although transgenic Bcl-x<sub>L</sub> is strongly expressed in follicular B cells, only modest amounts of tagged Bcl-x<sub>L</sub> could be demonstrated in GC B cells. Reverse transcription PCR studies confirm lower steady state levels of transgenic Bcl-x<sub>L</sub> message in GC B cells (data not shown). This biased expression of transgenic Bcl-x<sub>L</sub> may represent distinct E<sub>45</sub> activity in each B cell compartment (the density of mlg on GC B cells is ~10% of that found on follicular B cells [29]) or downregulation of the transgene’s herpes TK promoter in activated cells (24).

GCs Develop Normally in bd-x<sub>L</sub> Transgenic Mice. To assess the effects of the bd-x<sub>L</sub> transgene on GC development, we compared the GC reaction of transgenic and control mice at day 12 after immunization with NP-CG. This antigen elicits a characteristic hapten-specific antibody that bears a L chain and an H chain encoded by a canonical VDJ gene rearrangement (32). We identified L<sup>+</sup> GCs in spleen sections by labeling with PNA and anti-L antibody (32) and determined the average number of L<sup>+</sup> GCs per section from groups of transgenic and control mice (Fig. 3 A). Differences in the number or size (data not shown) of GCs were not observed between the groups, nor did the mean frequency of L<sup>+</sup> GCs significantly differ between transgenic (35.4%) and wild-type mice (41.7%). When transgenic mice were immunized with carrier protein alone, the average frequency of L<sup>+</sup> GCs was 7.6%. Thus, frequent L<sup>+</sup> GCs in transgenic mice result from immunization with NP rather than altered L chain expression.

The frequencies of splenic GC B cells (GL-7<sup>+</sup>-B220<sup>+</sup> fraction) in transgenic and control mice were also determined by flow cytometry. Both groups supported equivalent and typical GC responses (Fig. 3 B): in transgens, the frequency of GC B cells peaked at an average of 2.46% of splenocytes compared with 2.39% in controls at day 12 after immunization. Proliferative activity in the GC compartments of both transgens and controls was also equivalent; 10 d after immunization, 21 vs. 24% of PNA<sup>+</sup> GC cells were labeled by a 2-h pulse of BrdU (not shown).

Transgenic Bd-x<sub>L</sub> Increases Splenic AFC Numbers but not Their Longevity or Serum Antibody Titer. T cell–dependent antigens induce two distinct populations of AFC, a short-lived splenic population that generates the earliest primary antibody and a long-lived set in the BM that maintains the serum response (10, 11). Frequencies of NP-specific, IgG1, AFCs in the spleen and BM of transgenic and control mice were determined by ELISPOT assay 12, 35, and 69 d after immunization (Fig. 3 C). The kinetics of AFC production were virtually identical in both groups of mice, but splenic AFCs were threefold more abundant in transgenic mice than in controls. This increase may reflect the approximately twofold increase in the number of B cells in the spleens of transgenic mice (Fig. 1 A). Despite their greater
numbers, splenic AFCs in transgenic mice were lost at the same rate as in control animals. This rapid decline contrasts with bcl-2 transgenic mice, which support higher numbers and longer-lived splenic AFCs (22). Frequencies and kinetics of specific BM AFCs were indistinguishable between transgenic and control mice (Fig. 3 C).

The expanded splenic AFC pool in transgenic mice resulted in a minor increase in serum antibody titers on day 12, but later levels of antibody did not differ significantly between transgenic and control mice (Fig. 3 C).

**Figure 3.** bcl-xL transgenic mice produce GC and IgG1 antibody responses that are similar to control animals. Splenocytes were recovered from transgenic mice or wild-type controls at various times after immunization with NP-CG. (A) The numbers of λ1+ GCs were determined by histological staining with anti-λ1 antibody and PNA. Each point represents the average number of λ1+ GCs per histologic section (≥ 3 sections representing ≥ 2/3 splenic area) in single transgenic (open circles) or wild-type (filled circles) mice. (B) The percentage of GC B cells in live lymphocytes was assessed by flow cytometry using anti-B220 and anti-GL-7 antibodies. Each point represents the frequency mean (± SD) of GC B cells (percentage of total lymphoid gate) in single transgenic (open circles) and control (filled circles) mice 8, 12, and 35 d after immunization. (C) Numbers of NP-specific AFCs from BM (circles) and spleen (squares) of bcl-xL transgenic (open) or littermate control mice (filled) were determined by ELISPOT using NP23-BSA as the capture antigen. Frequencies of AFCs in naive mice (day 0) from both groups were <0.2 × 10^−5. (D) NP-specific serum antibody from transgenic (open) or wild-type control mice (filled) was determined by ELISA using NP23-BSA. The average values (± SD) for serum antibody concentrations from five to seven individual mice per time point are presented.

**GC B Cells Using Noncanonical VDJ Rearrangements Are More Frequent in bcl-xL Transgenic Mice.**

bd-xL Transgenic Mice Have Fewer A apoptotic Cells in GCs. GCs contain more apoptotic lymphocytes as determined by TUNEL than other regions of spleen (17). These TUNEL+ cells are thought to represent lymphocytes that have been negatively selected during the GC response. We performed TUNEL assays on spleen sections from transgenic and control mice to determine if the small addition of transgenic Bcl-xL expressed in GC B cells was sufficient to reduce programmed cell death. TUNEL+ cells in GCs from both groups were counted by microscopic examination, and the frequency of TUNEL+ cells per unit area was calculated. These frequencies were subdivided into 12 categories, and the distribution histogram for each category was plotted (Fig. 4). GCs from bd-xL transgenic mice contained fewer TUNEL+ cells per unit area (P < 0.01) than those from control mice (Fig. 4). The most common apoptotic index in wild-type animals was 2.0–2.5 TUNEL+ cells/unit area but only 1.0–1.5 in the bd-xL transgenics. Perhaps more significantly, >20% of GCs in control mice contained >3 TUNEL+ cells/unit area, whereas only 5% of GCs in bd-xL transgenic mice had 3.0–4.0 apoptotic cells/unit area with no GCs in the 4.5–6.0 categories. Thus, a modest addition of Bcl-xL in transgene-bearing GC B cells leads to a readily detectable decrease of TUNEL+ cells.
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These hybridization data were confirmed by sequencing VDJ inserts from representative bacterial colonies (Table I). From normal C57BL/6 control mice, 79% (11/14) of sequenced VDJ rearrangements contained the V186.2 gene segment, confirming our hybridization analysis and prior sequence studies (33). In contrast, only 47% (17/36) of sequenced VDJ fragments from bcl-x<sub>L</sub> transgenics carried the canonical V186.2 element (Table I). Noncanonical rearrangements from both control and transgenic mice contained other V<sub>H</sub> genes from the V186.2 and V3 subfamilies (35) commonly recovered in early primary anti-NP responses (12, 34).

The use of noncanonical VDJ rearrangements by immunized transgenic mice was not due to altered usage of VH gene segments in naive λ<sub>1</sub> B cells. We recovered splenic λ<sub>1</sub>B220<sup>+</sup> cells from unimmunized, transgenic, and wild-type mice by fluorescence-activated cell sorting, amplified their VDJ rearrangements with the PCR primers used to study GC populations, and determined the ratios of VDJ rearrangements containing V186.2 versus related V<sub>H</sub> genes. There was no significant difference in the percentage of V186.2 genes used by naive Bcl-x<sub>L</sub> transgenic mice (14%; 12/88) and naive controls (16%; 12/74). These observations suggest that even slight overexpression of Bcl-x<sub>L</sub> in GC B cells leads to lower numbers of TUNEL<sup>+</sup> GC cells and the persistence of clones bearing noncanonical VDJ rearrangements that commonly encode low-affinity antibodies present early in the primary response to NP.

The abundance of noncanonical VDJ rearrangements was not associated with impaired positive selection. Patterns of mutation in VDJ rearrangements containing the

**Figure 4.** bcl-x<sub>L</sub> transgenic mice show reduced numbers of TUNEL<sup>+</sup> cells in GCs. Spleen sections were prepared from transgenic mice (white bars) and wild-type control mice (black bars) at day 12 after immunization. TUNEL assays were performed with staining by PNA to identify GCs. The number of TUNEL<sup>+</sup> cells present and the area of each GC were determined under 200× magnification from >500 GCs. Frequencies of TUNEL<sup>+</sup> GC cells/area were then calculated, and each frequency was placed into 1 of 12 categories. The distributions of categories for transgenic and wild-type controls are plotted.

**Table I.** Somatic Genetics of λ<sub>1</sub> GC Cells in bcl-x<sub>L</sub> Transgenic and Wild-type Mice 12 d after Immunization

<table>
<thead>
<tr>
<th></th>
<th>bd-x&lt;sub&gt;L&lt;/sub&gt;</th>
<th>Wild-type</th>
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<tr>
<td>V186.2 (% of total)</td>
<td>17 (47%)</td>
<td>11 (79%)</td>
</tr>
<tr>
<td>Other (% of total)</td>
<td>19 (53%)</td>
<td>3 (21%)</td>
</tr>
<tr>
<td>Average no. of mutations in V186.2</td>
<td>3.5</td>
<td>4.3</td>
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<tr>
<td>R/S ratio</td>
<td></td>
<td></td>
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<tr>
<td>CDR1 (14.0/1)*</td>
<td>8.0/1</td>
<td>&gt;1.0/1</td>
</tr>
<tr>
<td>CDR2 (4.3/1)</td>
<td>&gt;15.0/1</td>
<td>4.8/1</td>
</tr>
<tr>
<td>FW (3.1/1)</td>
<td>1.3/1</td>
<td>2.4/1</td>
</tr>
<tr>
<td>DFL16.1 (%)‡</td>
<td>59</td>
<td>64</td>
</tr>
<tr>
<td>YYGS (%)§</td>
<td>24</td>
<td>18</td>
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All mice were immunized with NP-CG. Complete sequence data are available from EMBL/GenBank/DDJB under accession nos. AF065315-31 (bd-x<sub>L</sub>) and AF065332-42 (wild-type).

*R/S ratio of V<sub>H</sub> V186.2 given random mutagenesis.

†Percentage of rearrangements using DFL16.1 gene segments in all rearrangements of V<sub>H</sub> V186.2.

‡Percentage of rearrangements encoding YYGS in CDR3 in all rearrangements of V<sub>H</sub> V186.2.
canonical V186.2 gene segment were similar in transgenic and control mice, with no significant difference (P > 0.05) in the ratios of replacement versus silent mutations (R/S ratios) in CDRs (Table I). Other characteristics indicative of high-affinity, NP-specific B cells, e.g., the fraction of rearrangements containing DFL16.1 and the YYG motif, were also similar in both groups. Thus, cellular recruitment, V(D)J hypermutation, and positive selection in GCs are unaffected by the bcl-xL transgene.

Transgenic Bcl-xL Leads to Impaired Affinity Maturation in the BM AFC Compartment and Serum Antibody. Serum antibody is maintained by long-lived BM AFCs that depend on the GC differentiation pathway (10, 11). Affinity maturation of serum antibody and the BM AFC compartment can be monitored by differential binding to ELISA or ELISPOT substrates with sparse (NP2) or dense (NP23) hapten coatings (10, 11). High-affinity antibody from serum and AFCs binds equally well to both hapten densities, whereas low-affinity binding is evident only on the NP23 substrate.

The high-affinity compartment of BM AFCs in wild-type mice rapidly increased between days 12 (30.3%) and 35 (75.6%) of the response, with a more gradual increase up to day 69 (88.4%) (Fig. 5 A). This kinetic is typical of normal responses (11). At day 12, high-affinity AFCs were as common in the BM of transgenic mice (34.3%) as in controls. However, this population expanded more slowly in animals with the bcl-xL transgene, reaching only 57.5% and 60.6% by days 35 and 69, respectively (Fig. 5 A). Remarkably, at day 69 of the response three transgenic mice had a larger high-affinity AFC compartment than were present at day 35, indicating little or no proliferation/survival advantage for high-affinity cells even when antigen concentrations should be minimal.

The average affinity of NP-specific serum antibody was determined for the same mice by ELISA (Fig. 5 B). In wild-type controls, early (day 12) serum antibody contained little or no high-affinity component; by day 35 roughly half of the serum antibody displayed high-affinity binding, and by day 69 this value increased to ~90% (Fig. 5 B). The average affinity of serum antibody in transgenic mice also increased from day 12 to day 69, but again the extent of affinity maturation was only ~60% of controls. Overexpression of Bcl-xL led to diminished affinity maturation in both BM AFCs and the serum antibody.

Impaired Affinity Maturation in Transgenic Mice Is Reflected in the Somatic Genetics of the BM AFCs. To determine the cause of decreased affinity in the BM AFCs of transgenic mice, we recovered the λ+ BM AFC populations from immunized wild-type (n = 5) and transgenic (n = 5) mice by cell sorting (11). Typically, at day 69 after immunization >50% of sorted cells from both groups of mice secreted IgG1 antibody specific for NP. Enriched BM AFC populations were subjected to a reverse transcription PCR that preferentially amplifies cDNA representing rearrangements of the V186.2 and V3 subfamilies of VH gene segments. To determine the identity of rearrangements present in BM AFCs, we recovered the V186.2 and V3 subfamilies of VH gene segments used and any mutations present. Table II summarizes this work and shows that only half (11/21) of the VDJ sequences recovered from bcl-xL transgenic mice used the V186.2 gene segment. In contrast, nearly all (16/17) VDJ rearrangements from wild-type mice contained the V186.2 gene segment. Thus, the high frequency of B cells bearing noncanonical VDJ rearrangements present in day 12 GCs (47%; Table I) was maintained in the day 69 BM AFC population (53%) of mice with the bcl-xL transgene. The reduced average affinity of BM AFCs in bcl-xL transgenic mice results from the retention of B cells bearing noncanonical VDJ rearrangements. Interclonal competition in both

Figure 5. bcl-xL transgenic mice show relaxed affinity maturation of NP-specific IgG1 BM AFCs and serum antibody. The average affinities of BM AFCs (A) and serum antibodies (B) produced by transgenic (open circles) and control (filled circles) mice at different time points were estimated. (A) The frequencies of NP2- and NP23-specific IgG1 AFCs from BM were determined by ELISPOT. Ratios of NP2 versus NP23-specific AFCs were then calculated and plotted. AFC affinities are significantly (P < 0.05) lower in transgenic animals at 35 and 69 d after immunization. (B) Concentrations of NP2- and NP23-specific IgG1 antibody were determined by ELISA, and the ratios of NP2 versus NP23-specific IgG1 antibody were plotted. Each point represents the ratio determined in a single mouse. The average affinity of serum antibody in transgenic mice is significantly (P < 0.05) lower than that of controls at 69 d after immunization.
Table II. Somatic Genetics of BM AFCs in bd-x_L Transgenic and Wild-type Mice 69 d after Immunization

<table>
<thead>
<tr>
<th></th>
<th>bd-x_L</th>
<th>Wild-type</th>
</tr>
</thead>
<tbody>
<tr>
<td>V186.2 (% of total)</td>
<td>11 (52%)</td>
<td>16 (94%)</td>
</tr>
<tr>
<td>Other (% of total)</td>
<td>10 (48%)</td>
<td>1 (6%)</td>
</tr>
<tr>
<td>Average no. of mutations</td>
<td></td>
<td></td>
</tr>
<tr>
<td>in V186.2</td>
<td>10.3</td>
<td>4.3</td>
</tr>
<tr>
<td>R/S ratio</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CDR1 (14.0/1)*</td>
<td>1.8/1</td>
<td>14.0/1</td>
</tr>
<tr>
<td>CDR2 (4.3/1)</td>
<td>3.1/1</td>
<td>8.2/1</td>
</tr>
<tr>
<td>FW (3.1/1)</td>
<td>2.1/1</td>
<td>1.5/1</td>
</tr>
<tr>
<td>DFL16.1 (% of total)‡</td>
<td>46</td>
<td>69</td>
</tr>
<tr>
<td>YYGS (% of total)§</td>
<td>27</td>
<td>44</td>
</tr>
<tr>
<td>W→L33 (% of total)†</td>
<td>18</td>
<td>25</td>
</tr>
</tbody>
</table>

All mice were immunized with NP-CG. Complete sequence data are available from EMBL/GenBank/DDBJ under accession nos. AF065343-63 (bd-x_L) and AF065364-80 (wild-type).

* R/S ratio of V_H V186.2 given random mutagenesis.
† Percentage of rearrangements using DLF16.1 gene segments in all rearrangements of V_H V186.2.
‡ Percentage of rearrangements encoding YYGS in CDR3 in all rearrangements of V_H V186.2.
§ Percentage of all V_H V186.2 rearrangements bearing a W→L mutation in codon 33.

Discussion

In this report, we have demonstrated that a bd-x_L transgene reduces apoptosis in the GC reaction and impairs affinity maturation by sparing cells normally lost from the primary response. This transgene also enhances the survival of peripheral B cells in response to serum starvation in vitro and rescues developing B lymphocytes with aberrant VDJ rearrangements. These effects represent supplementation of endogenous Bcl-x_L activity; although Bcl-x_L is abundant in the GL-7+ B220+ GC cells of wild-type mice, Bcl-2 is not (Fig. 2 B). Similar observations have been reported for human GC cells where Bcl-x_L rather than Bcl-2 mediates the CD40-dependent survival of centrocytes ex vivo (30).

This result contrasts with that of Bcl-2 overexpression, which does not interfere with affinity maturation (22) but permits the survival of mature autoreactive B cells in the periphery (41). The bd-x and bd-2 transgenes also act differently during negative selection in immature B cells, as transgenic Bcl-x_L has the ability to block negative selection and promote developmental maturation, whereas autoreactive cells transgenic for bd-2 remain arrested in development (42, 43). Given the similar reciprocal expression of bd-2 and bd-x in GC B cells and pre-B cells, bd-x may have a distinct role in regulating the survival of B cells undergoing selection via IgM or the pre-B cell antigen receptor (BCR) (24, 30). Bcl-x_L becomes abundant in B cells after cross-linking IgM or CD40 (25, 28), and the fate of GC B cells is controlled by these same signals (40). We speculate that the degree or quality of IgM signaling in low-affinity B cells does not induce Bcl-x_L expression as effectively as in high-affinity cells, and that this deficit leads to apoptosis. That even a slight addition of transgenic Bcl-x_L to the higher levels of the endogenous protein in GC B cells leads to significant effects on cell death and affinity maturation is indicated that GC B cells are quite sensitive to small changes in levels of this death antagonist. The fate of lower-affinity GC B cells appears to be determined by a regulatory threshold of Bcl-x_L.

R relaxation negative selection and the retention of low-affinity B cells in transgenic mice did not alter the duration of affinity maturation.
or magnitude of the GC response in bcl-x<sub>L</sub> transgenic mice (Fig. 3). At 35 d after immunization, the splenic GC reaction had ended both in transgenic (0.33% GL-7<sup>+</sup>B220<sup>+</sup> spleen cells) and control (0.37%) animals. This is the earliest time after immunization that the numbers of splenic GL-7<sup>+</sup>B220<sup>+</sup> cells return to preimmune levels in normal mice (11). Thus, the GC response appears to be regulated by factors beyond affinity-driven competition and selective apoptosis. The rise and fall of GCs depend on the presence of antigen, sustained cell–cell interactions, and cues for cellular location (40, 44–47). It is not surprising that this important immunological response is controlled by finer means than that afforded by Darwinian competition alone.

Nie et al. (37) have reported that immunization of C57BL/6 mice with complexes of antibody and antigen elicits lower-affinity serum antibody and a genetically diverse GC reaction similar to that we observe in bcl-x<sub>L</sub> transgenic mice. These authors hypothesize that immune complexes decorated with C3d efficiently recruit the CD21/CD19/CD81 coreceptor to antigen-binding BCRs to reduce the threshold of B cell activation. Lowered activation thresholds would result in reduced levels of affinity-driven recruitment of Bcl-x<sub>L</sub> transgenic B cells to return to preimmune levels in normal mice (11). Thus, the GC response appears to be regulated by factors beyond affinity-driven competition and selective apoptosis. The rise and fall of GCs depend on the presence of antigen, sustained cell–cell interactions, and cues for cellular location (40, 44–47). It is not surprising that this important immunological response is controlled by finer means than that afforded by Darwinian competition alone.

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A possible mechanism for continued selection by apoptosis outside of GCs is competition among memory B cells for restimulation (48, 49). However, memory B cells are thought to regain Bcl-2 expression, and it would be surprising if their survival depended also on Bcl-x<sub>L</sub> (18). Alternatively, selective competition among BM AFCs for antigen might drive sustained affinity maturation. BM AFCs express low levels of mIg (11) and could interact with antigen deposits in a Bcl-x<sub>L</sub>-dependent fashion. Indeed, plasmacytomas express Bcl-x<sub>L</sub> (50), and human plasma cells exhibit high levels of Bcl-x<sub>L</sub> but low levels of Bcl-2 (51), although it is unclear if these cells represent long- or short-lived AFCs. It will be important to learn how BM AFCs integrate the usually antagonistic processes of differentiation to antibody secretion and cellular longevity so as to maintain protective levels of serum antibody over long time periods.

Our data provide strong evidence of a continuing role for antigen in the maintenance of the long-lived AFC pool. However, Manz et al. (38) have reported that the transfer of BM AFCs into unimmunized recipients reconstitutes long-term serum antibody and conclude that antigen is unnecessary for the survival of these cells. Such experiments are complicated by the possibility of coincidental transfer of residual antigen (6, 7, 48), but we cannot exclude the possibility that post-GC selection acts on precursors of the long-lived AFC pool. In this case, the characteristic somatic genetic changes observed in BM AFCs (11; Tables I and II) would first occur in the precursor population. Such selection would be antigen dependent and affinity driven. Recent work on the longevity and affinity of BM AFCs and serum antibody (our unpublished studies) support the importance of antigen retention and/or BCR signaling in shaping the long-lived AFC pool. What remains unchanged is that affinity maturation of serum antibody continues for months after primary immunization (1, 2, 11; Fig. 5). Although this progressive increase in affinity could be programmed in the early phase of the response, we suggest that in some way antigen continues to exert selection on the responding B cells.

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