Human Germinal Center B Cells Express the Apoptosis-inducing Genes Fas, c-myc, P53, and Bax but Not the Survival Gene bcl-2

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Summary

During T cell-dependent antibody responses, B cells within germinal centers (GC) alter the affinity of their antigen receptor by introducing somatic mutations into variable region of immunoglobulin (IgV) genes. During this process, GC B cells are destined to die unless positively selected by antigens and CD40-ligand. To understand survival/death control of germinal center B cell, the expression of four apoptosis-inducing genes, Fas, c-myc, Bax, and P53, together with the survival gene bcl-2, has been analyzed herein among purified tonsillar naive, GC, and memory B cells. IgD+CD38- naive B cells were separated into CD23- (mature B cell (Bm) 1) subset and CD23+ (Bm2), IgD+CD38+ GC B cells were separated into subsets of CD77+ centroblasts (Bm3) and CD77- centrocytes (Bm4), whereas IgD-CD38- cells represented the Bm5 memory B cell subset. Sequence analysis of IgV region genes indicated that somatic hypermutation was triggered in the Bm3 centroblast subset. Here we show that bcl-2 is only detectable with naive (Bm1 and 2) and memory B cell (Bm5) subsets, whereas all four apoptosis-inducing genes were most significantly expressed within GC B cells. Fas was equally expressed in Bm3 centroblasts and Bm4 centrocytes, whereas Bax was most significantly expressed in Bm4 centrocytes. c-myc, a positive regulator of cell cycle, was most significantly expressed in proliferating Bm3 centroblasts, whereas P53, a negative regulator of cell cycle, was most significantly expressed in nonproliferating Bm4 centrocytes. The present results indicate that the survival/death of GC B cells are regulated by the up- and downregulation of multiple genes, among which the expression of c-myc and P53 in the absence of bcl-2 may prime the proliferating Bm3 centroblasts and nonproliferating Bm4 centrocytes to apoptosis.
centrocytes (Bm4) may undergo isotype switching (16) and differentiate into either plasma cells or into IgD⁻CD38⁻ memory B cells (Bm5) (17).

In this study, we have analyzed the apoptotic propensity of the five B cell subsets, together with the expression of four apoptotic-inducing genes (Bax, c-myc, P53, and Fas) and a survival gene, bcl-2 (7–10). The Fas gene–encoded surface receptor is a member of the tumor necrosis factor (TNF) receptor family. It is expressed on many activated lymphoid cells including GC B cells. Fas triggering on lymphocytes either by monoclonal antibody or by Fas-ligand induces rapid apoptosis. Natural mutation in either Fas gene or Fas-ligand gene results in abnormal lymphoproliferation in lpr/lpr autoimmune or in gld/gld mice (18, 19). The cellular protooncogene c-myc–encoded protein is a positive regulator of cell cycle progression. Expression of c-myc is required for apoptosis in many situations, including activation–induced apoptosis in T cell hybridomas and growth factor deprivation–induced apoptosis in factor-dependent cell lines (20, 21). The tumor suppressor gene P53-encoded protein is a negative cell cycle regulator that arrests cells in G1. DNA damage within cells induced by ionizing radiation rapidly upregulates P53 expression, which is required for the subsequent apoptosis of irradiated cells (22, 23). Bax is a member of an expanding bcl-2 gene family that has the ability to dimerize with itself or with Bcl-2 and promote apoptotic cell death (24).

Here, we present evidence that the molecular mechanism contributing to spontaneous apoptosis is turned on within GC centroblast (Bm3), possibly as a result of the high levels of expressions of c-myc, P53, Bax, and Fas in the absence of bcl-2.

Materials and Methods

Isolation of Five Tonsillar B Cell Subsets (Bm1–Bm5). Total B cells were prepared as previously described (13). Briefly, tonsils taken from patients during routine tonsillectomy were finely minced and the resulting cell suspension was subjected to two rounds of depletion of non-B cells: (a) T cells were depleted by rosetting with sheep red blood cells; (b) the residual non-B cells were depleted by T cell–specific antibodies (CD2, CD3, and CD4; Immunotech, Marseille, France) followed by magnetic beads coupled with anti–mouse IgG (Dynabeads; Dynal, Oslo, Norway). The resulting cells from all the experiments contain >98% CD19⁺ positive B cells.

Some tonsil B cells were further separated into high density and low density B cells by centrifugation through 15, 60, and 65% Percoll gradient (Pharmacia/LKB, Uppsala, Sweden) at 400 g, 20°C for 20 min. Whereas dead cells remained on the surface of 15% Percoll, low density B cells were collected on the surface of 60% Percoll. High density B cells that penetrated through the 60% Percoll were recovered (13).

For isolation of Bm1 and Bm2 subsets, high density B cells were stained by goat anti-IgD–biotin (Sigma Chemical Co., St. Louis, MO) and mouse anti-CD3–FITC (Serotec, Oxford, UK) for 30 min. After washing twice, the cells were incubated with streptavidin–PE and goat anti-IgD–FITC for 30 min. The stained cells were washed and sorted into CD38⁺CD77⁺ (Bin3) and CD38⁻CD77⁻ (Bm4) subsets.

For isolation of Bm5 subset, total tonsillar B cells were incubated with goat anti–human IgD–biotin (Sigma Chemical Co.) and mouse anti-CD3–FITC (Immunotech) for 30 min. After washing twice, the cells were incubated with sheep anti–rat IgM–FITC for 30 min. The stained cells were washed and sorted into CD38⁺CD77⁺ Bm3 and CD38⁻CD77⁻ Bm4 subsets.

Quantiﬁcation of Spontaneous Apoptosis. Cells were cultured in RPMI 1640 medium containing 10% heat-inactivated fetal calf serum, 80 µg/ml gentamicin, and 2 mM glutamine (all from Flow Laboratories, Inc., McLean, VA) at 37°C for 16 h. 10⁶ cells from each subset after culture were cytospun for 5 min at 500 rpm on a microscope slide. Slides were fixed in ethanol for 5 min and then stained with Giemsa staining solution (BDH Chemicals, Ltd., Poole, UK) diluted 1:5 with distilled water (12).

Immunohistology. A frozen tonsil section was stained with mouse anti-Ki67 proliferating antigen (Dako, Glostrup, Denmark), followed by the alkaline phosphatase–antialkaline phosphatase (APAAP) system. Two other serial sections were stained by mouse anti-Bcl-2 and mouse anti-Fas, respectively, followed...
Results

Both GC Centroblasts (Bm3) and Centrocytes (Bm4) Undergo Rapid Apoptosis In Vivo. Our previous study on five tonsillar B cell subsets showed the IgV\textsubscript{n} genes from two naive B cell subsets Bm1 and Bm2 to be in germline configuration and the IgV\textsubscript{n} genes from GC centroblasts Bm3, centrocytes Bm4, and memory B cells Bm5 to be mutated (15). To determine their propensity to enter into spontaneous apoptosis, B cells from each of the five subsets were cultured in medium for 16 h. Fig. 2 shows that >90% of GC centroblasts (Bm3) and centrocytes (Bm4) displayed apoptotic figures, whereas <10% of naive (Bm1, Bm2) and memory B cells (Bm5) displayed apoptotic figures after 16 h of culture. This indicates that the molecular mechanisms underlying both somatic mutation as well as spontaneous apoptosis are turned on within the GC dark zone (Bm3). In addition, spontaneous apoptosis is not terminated in the light zone (Bm4).

The Expression of bcl-2 and Fas Transcripts Correlates with the Expression of Their Proteins in GC B Cells. To determine the feasibility of analyzing the expression of survival/death-related genes by a RT-PCR, the bcl-2 and Fas transcripts were amplified among 500 B cells from each subset. Fig. 3 A shows that the Bcl-2 transcripts are selectively detected within Bm1, Bm2, and Bm5 subsets, but not within Bm3 and Bm4 subsets. In contrast, the Fas transcripts are detected within Bm3 and Bm4 subsets, but not in Bm1, Bm2, and Bm5 subsets. To control for the amplification sensitivity and intersubset purity, the mRNA for bcl-2 and Fas were also amplified from 1,000 and 5,000 cells, and the same patterns of expression were observed (data not shown). Equal amounts of RNA template per B cell subset were routinely verified by overall IgH chain RT-PCR, using consensus IgV\textsubscript{n}-J\textsubscript{\alpha} primers (Fig. 3 B). Thus, the selective expression of Fas transcripts in GC Bm3 centroblasts, Bm4 centrocytes, and Bcl-2 transcripts in Bm1 and Bm2 naive B cells correlates with the patterns of Fas and Bcl-2 protein expression detected by immunohistology (Fig. 4) and flow cytometry (data not shown) (13). This established the validity of mRNA analysis in low numbers of cells from highly purified B cell subsets.

c-myc Is Predominantly Expressed in Bm3 Centroblasts, Whereas p53 and Bax Are Predominantly Expressed in Bm4 Centrocytes. To investigate whether the expression of c-myc, p53, and Bax is developmentally regulated during the differentiation pathway from naive B cells (Bm1 and 2) to GC B cells (Bm3 and 4) and then memory B cells (Bm5), their mRNA were amplified by RT-PCR, followed by Southern blot hybridization. Fig. 5 shows that c-myc is strongly expressed in GC centroblasts (Bm3) and weakly in GC centrocytes (Bm4) and memory B cells (Bm5). p53 and Bax are mainly expressed in GC B cells, more importantly in centrocytes (Bm4) than in centroblasts (Bm3). Bax is also observed at low level in memory B cells (Bm5).

Discussion

The GC reaction is a hallmark of T cell–dependent antibody responses (3, 4, 27). It allows the rare antigen–specific B cells to expand rapidly and to increase the affinity of their antigen receptor by introducing somatic mutations into
Figure 2. (A) Giemsa staining of cytospin preparations of five B cell subsets after 16 h of culture in RPMI 1640 medium. Apoptotic figures are characterized by nuclear condensation and fragmentation, which are present in Bm3 (centroblast) and Bm4 (centrocyte) subsets. (B) The percentage of apoptotic cells among 400 total cells was counted; and B represents one out of four identical experiments.

Figure 3. (A) Bcl-2 and Fas gene expression analysis by RT-PCR by mature B cell subsets. The lanes depict each of the five distinct Bm subsets. PCR amplification was carried out using five-μl RT-cDNA aliquots (see Materials and Methods) from 500 cells of each subset and analyzed on ethidium bromide-stained agarose gels. (Arrow) Predicted 560-bp Fas PCR product, which was further confirmed by sequencing (not shown). (B) Similar expression of VDJ among five B cell subsets.

their IgV genes, followed by affinity selection (28-31). In established GC, proliferation and somatic mutation seem to occur mainly in the GC dark zones, whereas affinity selection mainly occurs in the GC light zone (3, 4).

In agreement with these two functional compartments, c-myc gene, which is a positive regulator in cell cycle control (18, 19), was most significantly detected in proliferating centroblasts (Bm3) within the GC dark zone. The differen-
infection of the c-myc gene into EBV-transformed B cells results in the generation of centroblast-like cells that express CD10 and CD38 but not CD23 or CD39 and become sensitive to spontaneous apoptosis (32).

An important experimental signal inducing p53 expression is DNA damage or single-stranded DNA generated by ionizing radiation. p53 induce G1 cell cycle arrest thereby allowing DNA repair or induction of cell death program (22, 23). As c-myc is dominant over p53-mediated cell cycle arrest in mouse fibroblasts (23), the low expression of p53 in centroblasts (Bm3) and its further upregulation in centrocytes (Bm4) suggest that centroblasts (Bm3) may come out of cell cycle and differentiate into centrocytes (Bm4) as a result of downregulation of c-myc and upregulation of p53. Upregulation of p53 in GC B cells may also directly contribute to the downregulation of bcl-2 and upregulation of Bax within GC, because p53 is a direct transcriptional activator of Bax gene (33), as well as a transcriptional inhibitor of bcl-2 gene (34).

Whereas our recent experiments showed that triggering Fas by monoclonal antibodies can accelerate the rate of spontaneous apoptosis of GC B cells (13), the function of Fas expression on GC B cells remains to be established. Fas-mediated apoptosis in both activated human and mouse B cells were shown to be prevented by antigen receptor triggering but not by T cell cytokines or CD40-ligand (35-37). Thus, Fas-ligand-expressing T cells may discriminate high affinity B cells from autoreactive or low affinity B cells by the occupancy of their antigen receptors with follicular-dendritic cell-bound antigens, and selectively kill autoreactive or low affinity B cells. In this context, upregulation of Fas on GC B cells may facilitate the rapid elimination of autoreactive or low affinity B cells generated by somatic hypermutation within GC. It will be important to determine if GC T cells or other GC cell types express Fas-ligand.

![Figure 4. Expression of proliferating nuclear antigen Ki67, Fas, and Bcl-2 in situ on serial tonsil sections. (A) Blue Ki67 nuclear staining within a GC; (B) Red Fas staining within the same GC; and (C) most of the B cells within the same GC do not express Bcl-2.](image)

![Figure 5. Bax, c-myc, P53, and IgH RT-PCR determination on the five distinct Bm subsets. Shown here is the selective expression of Bax, c-myc, and P53 by corresponding Bm subsets, after amplification, Southern blotting, and hybridization (see Materials and Methods). Also depicted here, is the expression of overall Ig heavy chain (IgH), systematically used as an internal control to evaluate equivalent mRNA input per B cell subset.](image)
In conclusion, by selective B cell subset gene expression analysis, our data show that the genes related to cell cycle, apoptosis, and DNA repair are tightly regulated during the affinity maturation of peripheral B cells. Such regulation results in a high rate of GC B cell proliferation, which favors the introduction of point mutations into IgV region genes, and promotes the propensity of GC B cell to die, thus allowing for positive selection of high affinity mutants.

References


