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TNFR-Associated Factor 2 Deficiency in B Lymphocytes Predisposes to Chronic Lymphocytic Leukemia/Small Lymphocytic Lymphoma in Mice

Gema Pérez-Chacón,* David Llobet †,1 Constanza Pardo,*‡ José Pindado,†,3 Yongwon Choi,‡ John C. Reed,† and Juan M. Zapata*†

We have previously shown that transgenic (tg) mice expressing in B lymphocytes both BCL-2 and a TNFR-associated factor 2 (TRAF2) mutant lacking the really interesting new gene and zinc finger domains (TRAF2DN) develop small lymphocytic lymphoma and chronic lymphocytic leukemia with high incidence (Zapata et al. 2004. Proc. Nat. Acad. Sci. USA 101: 16600–16605). Further analysis of the expression of TRAF2 and TRAF2DN in purified B cells demonstrated that expression of both endogenous TRAF2 and tg TRAF2DN was negligible in Traf2-tg B cells compared with wild-type mice. This was the result of proteasome-dependent degradation, and rendered Traf2DN B cells as bona fide TRAF2-deficient B cells. Similar to B cells with targeted Traf2 deletion, Traf2DN-tg mice show expanded marginal zone B cell population and have constitutive p100 NF-κB2 processing. Also, TRAF3, X-linked inhibitor of apoptosis, and Bcl-XL expression levels were increased, whereas cellular inhibitors of apoptosis 1 and 2 levels were drastically reduced compared with those found in wild-type B cells. Moreover, consistent with previous results, we also show that TRAF2 was required for efficient JNK and ERK activation in response to CD40 engagement. However, TRAF2 was deleterious for BCR-mediated activation of these kinases. In contrast, TRAF2 deficiency had no effect on CD40-mediated p38 MAPK activation but significantly reduced BCR-mediated p38 activation. Finally, we further confirm that TRAF2 was required for CD40-mediated proliferation, but its absence relieved B cells of the need for B cell activating factor for survival. Altogether, our results suggest that TRAF2 deficiency cooperates with BCL-2 in promoting chronic lymphocytic leukemia/small lymphocytic lymphoma in mice, possibly by specifically enforcing marginal zone B cell accumulation, increasing X-linked inhibitor of apoptosis expression, and rendering B cells independent of B cell activating factor for survival. The Journal of Immunology, 2012, 189: 1053–1061.

T umor necrosis factor receptor-associated factors (TRAFs) constitute a family of trimeric adapter proteins that interact with the cytosolic regions of various members of the TNF-family receptors and with components of TLRs complexes. TRAFs function as docking molecules for kinases and other proteins involved in TNFR and TLR signaling. Furthermore, different members of the TRAF family also catalyze ubiquitination of various target proteins via their intrinsic E3 ubiquitin ligase activity. Thus, TRAFs can control the extent of the response by catalyzing the conjugation of a substrate with either lysine 48- or lysine 63-linked polyubiquitin chains, with differing consequences in terms of proteasome-dependent protein degradation and protein activation, respectively (1–3). Gene ablation studies in mice have demonstrated a critical role for different TRAF family members in regulating signaling by many TNFRs, and deregulation of these pathways has been shown to cause several autoimmune and inflammatory diseases, as well as cancer (reviewed in Ref. 4).

Chronic lymphocytic leukemia (CLL) is the most common leukemia in the Western world, and it is characterized by the gradual accumulation of quiescent, apoptosis-resistant B cells (5). Although CLL is seemingly a very uniform disease, new molecular data have highlighted unexpected heterogeneity among patients. This is also reflected in the variability of the clinical progression of this leukemia, with patients suffering an indolent disease that does not require immediate treatment, patients with aggressive disease, and patients who develop resistance to current treatments.

Abbreviations used in this article: BAFF, B cell activating factor; cIAP, cellular inhibitor of apoptosis; CLL, chronic lymphocytic leukemia; FO, follicular; IAP, inhibitor of apoptosis; MZ, marginal zone; NIK, NF-κB-inducing kinase; RING, really interesting new gene; SLL, small lymphocytic lymphoma; TRAF, TNFR-associated factor; TRAF2DN, TRAF2 mutant lacking the RING and zinc finger domains; tg, transgenic; WT, wild-type; XIAP, X-linked IAP.

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treatments. A need, therefore, exists to identify the critical modulators of CLL. B cell growth and survival toward the goal of identifying new targets for therapeutic invention.

Previous results from our group demonstrated that double-transgenic (tg) mice expressing in B cells both a mutant TRAF2 lacking the N-terminal region of the protein (TRAF2DN) encompassing the really interesting new gene (RING) and zinc finger domains and also the antiapoptotic protein BCL-2 develop CLL/small lymphocytic lymphoma (SLL) with high incidence (>85%) in adulthood (9–16 mo) (6). The cooperation between TRAF2DN and BCL-2 in promoting CLL/SLL was supported by the lack of significant incidence (<5%) of leukemia/lymphoma in single-tg mice carrying only the Traf2DN or the BCL-2 transgenes. B cells from these mice demonstrated a reduced rate of spontaneous apoptosis and resistance to apoptosis induced by chemotherapeutic drugs, but no increased proliferation, thus implying that resistance to apoptosis rather than deregulation of proliferation is responsible for the B cell accumulation in these mice.

Given the structural similarities between mutant TRAF2DN and TRAF1, both having highly conserved TRAF domains but lacking a RING domain, we proposed that TRAF2DN might mimic TRAF1 function and that the Traf2DN-tg mice might recapitulate the increased TRAF1 expression observed in CLL cells from patients (7). In this report, we have further studied the role of TRAF2DN in B cell transformation. We show that Traf2DN-tg B cells have very reduced expression of both TRAF2 and TRAF2DN compared with wild-type (WT) B cells, as a result of significant reduction in TRAF1 function and that the TRAF2 deficiency in B cells is responsible for the B cell accumulation in these mice.

Flow cytometry
Lymphocytes isolated as described earlier were incubated with 50 μg/ml horseradish peroxidase-labeled goat anti-mouse IgM (μ-chain specific; F(ab’)2 fragment; Jackson Laboratories, West Grove, PA) for the indicated times. After 1-h incubation at 4˚C, cells were washed in high-glucose DMEM (without phenol red; Irvine Scientific, Santa Ana, CA) containing 3% FCS. Flow cytometry analysis was accomplished using a FACSCalibur equipped with detectors for four colors (BD Biosciences, San Jose, CA).

DNA was isolated from tg mouse tails using the Maxwell 16 system and the Maxwell 16 system DNA enrichment kit (Promega Biotech Iberica, Madrid, Spain). A total of 300 ng DNA was used for amplification. Transgenes were amplified using GoTaq polymerase (Promega) and the following primers for Traf2 (forward, 5'-AGGTGAGGAGACGGTGACC-3'; reverse, 5'-ACTIN-3').

B cell proliferation and survival
Purified B cells (5 × 10^6) were lysed in TRIzol (Invitrogen Life Technologies, Grand Island, NY) and RNA was purified using the RNAeasy kit (Qiagen Iberica, Madrid, Spain), following the manufacturer’s instructions. Reverse transcription and PCR was carried out using the Superscript One-Step RT-PCR with platinum Taq kit from Invitrogen and primers for mouse Traf1 (forward, 5'-CTCAAAAGGAAG TGAGGC-3'; R 5'-CGTTGTCTCGTTGCAAGTAC-3'), Traf2 (forward, 5'-GTTCTCTGCGATGTTCCAC-3'), reverse, 5'-CCAATTCGCTTGTAGTAAAGG-3'), Traf3 (forward, 5'-CCTGCAACCACATCTTTFAtAAGGC-3'), reverse, 5'-CAATGCGGAGGAGGCTTTC-3').

Reagents and Abs
Abs used were against TRAF1 (C-20 and N-19), TRAF3 (C-20), TRAF1 (N-19), Iba1 (C-21), RELA (C-20), Santa Cruz Biotechnology, Santa Cruz, CA); BCL-XL, XIAP (BD Transduction Laboratories, Franklin, NJ); MCL-1 (Rockland, Gilbertsville, PA); JNK, phospho-JNK, ERK, phospho-ERK, p38, phospho-p38, AKT, phospho-AKT, p100/p52 NfκB2 (Cell Signaling Technologies, Danvers, MA); cellular inhibitors of apoptosis 1 and 2 (cIAP1/2), c-REL (R&D Systems, Abingdon, U.K.); and β-ACTIN (Sigma-Aldrich, St Louis, MO). Abs against human and mouse BCL-2 have been described previously (12). Rabbit polyclonal Abs against the cytosolic region of CD40 were prepared in the laboratory. Proteasome inhibitor MG-132 was from Calbiochem (La Jolla, CA). Bortezomib was kindly provided by Millenium Pharmaceuticals (Cambridge, MA).

Isolation and activation of B cells
Spleens from tg mice and WT littermates were mechanically processed, and mononuclear cells were isolated by Ficoll density centrifugation (Lympholyte-M; Cedarlane Laboratories, Burlington, NC). B cells were isolated by negative magnetic selection using the StemSep mouse B cells enrichment kit (StemCells Technologies, Vancouver, CA), following the manufacturer’s specifications. B cells were resuspended in RPMI 1640 medium supplemented with 10% FCS (Hyclone, Logan, UT), 50 μM 2-ME, 100 U/ml penicillin, 100 μg/ml streptomycin, 2 mM L-glutamine, and oxalacetate, pyruvate, and insulin (OP) media supplement (Sigma-Aldrich). Purified B cells (3 × 10^5 to 5 × 10^6) from age-matched sex-matched WT, and Traf2DN-tg littermates were left untreated or treated with the indicated concentrations of CD40L, BAFF, IL-4 (R&D Systems, and anti-mouse IgM (μ-chain specific; F(ab’)2 fragment; Jackson Laboratories, West Grove, PA) for the indicated times.

Materials and Methods
tg mice
Lymphocyte-specific tg mice expressing a 1D4-epitope–tagged TRAF2 deletion mutant lacking the N-terminal 240 aa encompassing the RING and zinc finger domains (TRAF2DN) (10), B cell-specific BCL-2-tg mice mimicking the (14;18)(q32;21) translocation involving BCL-2 and IgH found in human follicular (FO) lymphomas (11), and Traf2DN/BCL-2 double-tg mice (6) have been described. The animal protocols were approved by the Institutional Animal Care and Use Committees from the hosting institutions. All tg mice in the study were genotypically heterozygotes.

Genotyping
DNA was isolated from tg mouse tails using the Maxwell 16 system and the Maxwell 16 system DNA purification kit (Promega Biotech Iberica, Madrid, Spain). A total of 300 ng DNA was used for amplification. Transgenes were amplified using GoTaq polymerase (Promega) and the following primers for Traf2 (forward, 5'-GACCAGGACAAGATTGAGGC-3'; reverse, 5'-GACCAGGACAAGATTGAGGC-3').

Isolation and activation of B cells
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Flow cytometry
Lymphocytes isolated as described earlier were incubated with 50 μg/ml horseradish peroxidase–labeled goat to block FcRs. Then 10^6 to 5 × 10^7 cells were incubated with a combination of allopurinol-, FITC-, or PE-conjugated Abs recognizing various surface markers. After 1-h incubation at 4˚C, cells were washed in high-glucose DMEM (without phenol red; Irvine Scientific, Santa Ana, CA) containing 3% FCS. Flow cytometry analysis was accomplished using a FACSCalibur equipped with detectors for four colors (BD Biosciences, San Jose, CA).

Cell lysates and protein quantification
Cells were lysed in incomplete Laemmli buffer (0.125 M Tris pH 6.8; 4% SDS and 20% glycerol) supplemented with a mixture of protease inhibitors (Complete; Roche Diagnostics, Mannheim, Germany) and phosphatase inhibitors (PhosSTOP; Roche Diagnostics). Lysates were sonicated and protein concentration was determined by the bichinchoninic acid method (Pierce, Rockford, IL).

SDS-PAGE and immunoblotting
Protein samples (10–20 μg/condition) were prepared as described previously were supplemented with 10% 2-ME and 0.004% bromophenol blue, and SDS-PAGE analysis was performed as described previously (13). Ags were detected by ECL (Pierce) and either exposed on film or captured using the Gel Logic 1500 Image System and the Molecular Imaging Soft 4X Kodak software (Kodak Molecular Imaging Systems, New Haven, CT).

RNA isolation and RT-PCR
Purified B cells (5 × 10^5) were lysed in TRIzol (Invitrogen Life Technologies, Grand Island, NY) and RNA was purified using the RNAeasy kit (Qiagen Iberica, Madrid, Spain), following the manufacturer’s instructions. Reverse transcription and PCR was carried out using the Superscript One-Step RT-PCR with platinum Taq kit from Invitrogen and primers for mouse Traf1 (forward, 5'-CTCAAAAGGAAGTGAGGC-3'; R 5'-CGTTGTCTCGTTGCAAGTAC-3'), Traf2 (forward, 5'-GTTCTCTGCGAGATTCCACAC-3'), reverse, 5'-CCAATTCGCTTGTAGTAAAGG-3'), Traf3 (forward, 5'-CCTGCAACCACATCTTTFAtAAGGC-3'), reverse, 5'-CAATGCGGAGGAGGCTTTC-3').
ubiquitin ligase activity of TRAF2. As such, this truncated TRAF2 protein was conceived as a dominant inhibitor of endogenous, full-length TRAF2 (10). TRAF2DN expression was detectable by immunoblotting in spleen extracts from mice harboring the Traf2DN transgene (Traf2DN-tg and Traf2DN/Bcl-2 double-tg mice), although it could not be detected in extracts from spleens isolated from WT and Bcl-2-tg mice (Fig. 1A, top). However, as previously shown (6), endogenous TRAF2 expression was significantly reduced in splenocytes from Traf2DN-tg and Traf2DN/Bcl-2 double-tg mice compared with splenocytes from mice that did not contain the Traf2DN transgene (WT and Bcl-2; Fig. 1A, bottom). To further investigate these differences in TRAF2 expression, we purified B cells from Traf2DN-tg splenocytes and assessed the levels of expression of endogenous TRAF2 and mutant TRAF2DN. As shown in Fig. 1B, Traf2DN-tg B cells did not express significant levels of endogenous TRAF2 compared with WT B cells. Surprisingly, TRAF2DN expression was negligible in Traf2DN-tg B cells, thus indicating that Traf2DN-tg B cells had very reduced levels of both endogenous TRAF2 and mutant TRAF2DN expression (Fig. 1B). In contrast, TRAF3 expression was higher in Traf2DN-tg B cells compared with WT B cells (see later), whereas no differences in IκBα expression were observed (Fig. 1B). Consistent with this result, communoprecipitation experiments showed that activated CD40 failed to recruit TRAF2 in B cells isolated from Traf2DN-tg mice, whereas TRAF2 was readily recruited to CD40 in B cells from WT mice (Fig. 1C). In contrast, TRAF3 was recruited to the activated CD40 in B cells from both Traf2DN-tg mice and WT littermates (Fig. 1C).

To rule out that failure to detect TRAF2 was not caused by posttranslational modifications of this protein resulting in epitope masking, we used several anti-TRAF2 Abs against different regions of the molecule, but all failed to detect TRAF2 in B cells extracts from the Traf2DN-tg mice. Representative results obtained using two anti-TRAF2 polyclonal Abs against the C or the N terminus of the molecule are shown in Fig. 2A.

We next assessed the levels of Traf2 mRNA in B cells from Traf2DN-tg and WT mice. As shown in Fig. 2B, Traf2 mRNA levels were similar in both Traf2DN-tg and WT B cells, thus indicating that failure to express TRAF2 by Traf2DN-tg B cells was not the result of nonproductive Traf2/Braf2DN recombination and/or disruption of endogenous Traf2 gene transcription. These results prompted us to evaluate whether the expression of other members of the TRAF family was also altered in the Traf2DN-tg B cells. In this regard, we observed weak but consistent Traf1 expression in WT B cells. However, Traf1 was absent in Traf2DN-tg B cells (Fig. 2A). This was in sharp contrast with the levels of Traf1 mRNA, which were significantly higher in Traf2DN-tg B cells compared with those in WT B cells (Fig. 2B). This result suggests that Traf1 mRNA transcription is upregulated in Traf2DN-tg B cells, although it does not result in Traf1 accumulation.

We have previously described that Traf1 expression is upregulated in lymphocytes on activation (7). Therefore, to elucidate whether Traf1 could accumulate in activated Traf2DN-tg B cells, we incubated B cells from these mice and from WT littermates with anti-μ Ab to engage the BCR. Indeed, as shown

FIGURE 1. Endogenous TRAF2 is not expressed in B cells from Traf2DN-tg mice. (A) Splenocytes isolated from age-matched WT, Traf2DN-tg (T2DN), Bcl-2-tg, and Traf2DN/Bcl-2 double-tg (+/+ ) mice were lysed in Laemmli buffer, sonicated, and analyzed by SDS-PAGE and immunoblotting. Protein samples were normalized for protein content (25 μg) and blotted with anti-TRAF2 Abs. Cell lysate from the B cell line Ramos was used as control. Two different exposures of the same immunoblot are shown. (B) Purified B cells from spleens of Traf2DN-tg mice and WT littermates were analyzed as in (A), performing immunoblotting with Abs recognizing TRAF2, TRAF3, and IκBα. (C) Splenocytes (10⁶) isolated from Traf2DN-tg mice and WT littermates were preincubated on ice for 10 min with 6 μg/ml of an agonist anti-mouse CD40 αAb (Caltag, Burlingame, CA), followed by incubation at 37°C for the times indicated. Then, CD40+ cells were isolated using anti-rat Ab crosslinked to magnetic beads (Invitrogen, Carlsbad, CA). The recovered CD40+ B cells were lysed in isotonic buffer containing 1% Triton X-100. CD40-immunocomplexes were purified using a magnet and boiled for 3 min in Laemmli buffer. Immunocomplexes were analyzed by SDS-PAGE and immunoblotting using anti-TRAF3 and anti-TRAF2 Abs (Santa Cruz). L, Total splenocytes lysate (14 μg).

FIGURE 2. Patterns of expression of TRAF family members in B cells from WT and Traf2DN-tg mice. (A) Splenocytes and purified B cells from spleens from Traf2DN-tg mice and WT littermates were lysed in Laemmli buffer. A total of 14 μg protein from each sample was analyzed by SDS-PAGE and immunoblotting with the Abs indicated. (B) Total RNA was extracted from purified B cells from WT and Traf2DN-tg mice, and 1 μg RNA from each sample was used for retrotranscription followed by specific PCR amplification of the indicated cDNAs. (C) Purified B cells from Traf2DN-tg and WT splenocytes were left untreated or activated with 100 μg/ml anti-μ Ab for the indicated times. At the end of the incubation period, cells were collected and lysed in Laemmli buffer. Lysates from 10⁶ B cells from each condition were analyzed by SDS-PAGE and immunoblotting.
in Fig. 2C, TRAF1 upregulation was evident after 60 min of activation in both WT and Traf2DN-tg B cells, indicating no impediment of TRAF1 expression in activated TRAF2-deficient B cells. In contrast, expression of endogenous TRAF2 was not restored in BCR-activated Traf2DN-tg B cells, which would be consistent with our previous results (7) indicating that TRAF2 expression is not upregulated in activated B cells (Fig. 2C). In contrast, TRAF3 protein levels were higher in Traf2DN-tg B cells compared with WT B cells (Fig. 2A), whereas no differences in the amounts of TRAF3 mRNA were observed in B cells from both sources (Fig. 2B). TRAF3 accumulation in Traf2DN-deficient B cells would be consistent with previous results from Hostager and coworkers (14) showing that TRAF3 is ubiquitinylated by TRAF2 and subsequently degraded. Finally, IκBα and coworkers (14) showing that TRAF3 is ubiquitinylated by B cells would be consistent with previous results from Hostager and coworkers (14) showing that TRAF3 is ubiquitinylated by TRAF2 and subsequently degraded. TRAF3 accumulation in Traf2DN-tg B cells was comparable with that of BAFF-treated Traf2DN-tg B cells (p = 0.12). Notably, survival of WT B cells in the presence of BAFF was comparable with that of BAFF-treated Traf2DN-tg B cells (p = 0.67). Furthermore, BAFF failed to provide additional survival advantages to Traf2DN-tg B cells activated with anti-μ, in contrast with WT B cells (Fig. 4C). Altogether, these results suggest that Traf2DN-tg B cells are not dependent on BAFF for survival, most likely because Traf2DN-tg B cells have constitutively activated survival pathways that circumvent the requirement for BAFF, confirming previous results using B cell-specific Traf2−/− mice (8, 9). Furthermore, we observed that induction of B cell proliferation by CD40 engagement was significantly reduced in the Traf2DN-tg B cells compared with WT B cells (Fig. 4D), thus confirming that Traf2 is required for efficient CD40-mediated B cell proliferation (8, 14).

Constitutive p100 NFκB2 processing in Traf2DN-tg B cells

It was previously described that targeted deletion of Traf2 caused constitutive NF-κB2 activation in B cells (8, 9) and in other cell types (9, 16, 17). Consistent with prior results, we found that Traf2DN-tg B cells showed increased p100 NF-κB2 processing to active p52 (Fig. 5A, 6A). Interestingly, constitutive activation of NF-κB2 has been shown to promote MZ B cell differentiation (18), and BAFF-mediated MZ B cell expansion is reportedly dependent on NF-κB2 activation (19). Consequently, the accumulation of MZ B cells in the Traf2DN-tg mice might be explained by this constitutive NF-κB2 activity. In contrast, IκBα degradation in response to CD40 activation was similar in B cells from the Traf2DN-tg mice and WT littermates (Fig. 5A), and no differences in IκBα expression were noticed regardless the presence or absence of Traf2 (Fig. 6A), which is consistent with what has been described in B cells with targeted Traf2 deletion (14, 20). The levels of the NF-κB subunits c-REL and RELA were also similar in WT and Traf2DN-tg B cells (Fig. 6A).

**TRAF2 is differentially required for MAPK activation in response to CD40 and BCR stimulation**

To examine signaling alterations in B cells lacking TRAF2, we analyzed the activation of certain MAPKs in splenic B cells from Traf2DN-tg mice and WT littermates in response to CD40 and BCR engagement. As shown in Fig. 5A, CD40-mediated activation of JNK was significantly reduced in Traf2DN-tg B cells compared with WT B cells, confirming previous results (10). Moreover, activation or ERK1/2 was also significantly reduced in B cells lacking TRAF2. In contrast, CD40-mediated p38 MAPK activation was similar irrespective of the presence or absence of Traf2 (Fig. 5A). These differences in MAPK activation were not the result of differential expression of JNK, ERK, and p38, which was similar in Traf2DN-tg and WT B cells (Fig. 5). Altogether, these results are consistent with those found in Traf2−/− B cells (20).
BCR-mediated MAPK activation was also affected in B cells by TRAF2. Specifically, when anti-μ mAb was used to trigger BCR activation of B cells isolated from the Traf2DN−tg mice, we observed increased BCR-mediated ERK activation and significantly reduced p38 MAPK activation in these cells compared with WT B cells (Fig. 5B). In contrast, the level of JNK phosphorylation triggered by BCR engagement was similar regardless with WT B cells (Fig. 5B). In contrast, the level of JNK phosphorylation remained heavily phosphorylated in Traf2DN−tg B cells (data not shown). In contrast, BCR-mediated AKT activation was also independent of Traf2 (Fig. 5B).

**TRAF2 deficiency in B cells is associated with decline of cIAP1/cIAP2 expression and upregulation of XIAP**

We next assessed the effect of TRAF2 deficiency on the expression of various proteins relevant to CLL that are implicated in the control of apoptosis, including members of the BCL-2 and inhibitor of apoptosis (IAP) families. First, the analysis of the expression levels of BCL-2 and MCL-1 proteins in B cells isolated from the spleens of Traf2DN−tg mice and WT littermates by immunoblotting failed to show any significant difference (Fig. 6A). However, BCL-XL protein expression was upregulated in B cells from Traf2DN−tg mice (Fig. 6A), consistent with prior descriptions of Traf2−/− B cells (9). Furthermore, analysis of expression of IAP family members cIAP1, cIAP2, and XIAP by immunoblotting showed differential results depending on the presence or absence of TRAF2. Thus, cIAP1 and cIAP2 were absent in B cells from the Traf2DN−tg mice, although they were detected in WT B cells (Fig. 6A). This result is in agreement with Csomos and coworkers (21, 22), who have reported that cIAP1 and cIAP2 undergo autoubiquitination and subsequent proteasome degradation in the absence of TRAF2. In contrast, expression of caspase inhibitor XIAP was significantly upregulated in B cells lacking TRAF2 (Fig. 6A). Interestingly, cIAP1 has been shown to bind XIAP and to induce its proteasomal degradation by ubiquitin-dependent and -independent pathways (23, 24). Therefore, depletion of cIAP1 might underlie XIAP upregulation in the Traf2DN−tg B cells.

Next, we asked whether these differences in protein expression observed in Traf2DN−tg B cells were also found in Traf2DN/BCL-2 double-tg mice that had developed CLL/SLL. For that purpose, heterozygous Traf2DN−tg and BCL-2−tg mice were crossed to produce litters representing the four possible genotypes. Once Traf2DN/BCL-2−tg mice (+/++) had developed overt CLL/SLL, characterized by high B cells counts in blood (>10⁷ B cells/ml) and severe splenomegaly and lymphadenopathy, as de-
BCL-XL and reduced levels of MCL-1. BCL-2 expression, whereas the Traf2 (+/−) mice were left untreated (t = 0) or treated either with 1 μg/ml CD40L (A) or with 100 μg/ml anti-μ. F(ab′)2 mAb (B) for the indicated times (t). Cell lysates were prepared in Laemmli buffer, sonicated, and protein concentration was determined. A total of 10 μg protein from each sample was analyzed by SDS-PAGE and immunoblotting using Abs against the indicated Ags.

FIGURE 5. Analysis of CD40- and BCR-mediated signal transduction pathways in WT and Traf2DN-tg B cells. Purified B cells (A, 4 × 10⁶; B, 2 × 10⁷) from WT and Traf2DN-tg mice were left untreated (t = 0) or treated either with 1 μg/ml CD40L (A) or with 100 μg/ml anti-μ. F(ab′)2 mAb (B) for the indicated times (t). Cell lysates were prepared in Laemmli buffer, sonicated, and protein concentration was determined. A total of 10 μg protein from each sample was analyzed by SDS-PAGE and immunoblotting using Abs against the indicated Ags.

Discussion

The Traf2DN-tg mouse model was engineered to overexpress a TRAF2 deletion mutant lacking the RING and zinc fingers domains (Traf2DN) (10). This mutant was conceived as a dominant inhibitor of TRAF2 because it lacks the RING domain required for E3 ubiquitin ligase activity, but still contains the TRAF domain, thus retaining the ability to interact with TNFR family members and to trimerize with endogenous TRAF2 (26). However, our results indicate that Traf2DN-tg B cells not only fail to accumulate mutant Traf2DN protein, but also lack expression of endogenous TRAF2 protein, effectively turning Traf2DN-tg B cells into bona fide Traf2-deficient B cells.

These results strongly suggest that expression of the E3 defective Traf2DN mutant in B cells enforces continuous basal ubiquitination and subsequent proteasome-mediated degradation of both endogenous TRAF2 and mutant Traf2DN in B cells, as indicated by the restoration of TRAF2 and Traf2DN expression in Traf2DN-tg B cells upon incubation with the proteasome inhibitors bortezomib and MG-132. Although it remains unclear what protein is responsible for TRAF2 ubiquitination, a likely candidate is TRAF2 itself. Indeed, it has been described that on receptor activation, TRAF2 can catalyze its own K48-ubiquitination, thus targeting TRAF2 for proteasome-dependent degradation (15). Traf2DN ubiquitination could also be catalyzed by cIAP1 and cIAP2, which interact with TRAF2 and are recruited to various members of the TNFR family on activation. However, although signaling through TNFR2 induces cIAP1-dependent TRAF2 degradation (27), activation of CD30 triggers cIAP1 degradation as a result of TRAF2-mediated ubiquitination of cIAP (21). In contrast, other reports have described the ability of TRAF2 to activate cIAP1 and cIAP2 by catalyzing their K63-ubiquitination in response to receptor activation (28). Although seemingly contradictory, these results illustrate the complexity of TRAF biology, where variations in mechanisms can reflect processing, absence of detectable TRAF2, TRAF1, and cIAP1/2, and increased XIAP expression. Altogether, these results suggest that inhibition of cIAP1/2 expression, p100 NF-κB2 activation, and XIAP upregulation may contribute to the increased resistance to apoptosis observed in Traf2-deficient cells.
differences in cell types, specific ligand/receptor signaling systems, and the strength of the activation signal.

In any event, it remains an open question whether TRAF2 ubiquitination and degradation in Traf2DN-tg B cells are dependent on receptor activation. In this regard, it should be expected that if TRAF2 degradation was stimulus dependent, culturing Traf2DN-tg B cells in vitro in the absence of any stimulus should restore TRAF2 accumulation, but we have failed to detect Traf2DN in cultures of nonactivated Traf2DN-tg B cells (data not shown). Interestingly, we also discovered an absence of cIAP1 and cIAP2 proteins in Traf2DN-tg B cells. This result is consistent with previous data from Csomas and coworkers (22) describing that, in the absence of TRAF2, cIAP1 and cIAP2 undergo auto-ubiquitination and subsequent degradation. In further support of this hypothesis, we have confirmed that proteasome inhibition causes cIAP1/2 protein accumulation in Traf2DN-tg B cells (data not shown). Furthermore, cIAP1 depletion might underlie XIAP upregulation in Traf2DN-tg B cells, because it has been shown that cIAP1 targets XIAP for proteasomal degradation by ubiquitin-dependent and -independent pathways (23, 24).

The role of TRAF2 in control of B cell homeostasis is well established. The original description of the Traf2DN-tg mice that we used demonstrated that disrupting TRAF2 function causes splenomegaly and lymphadenopathy as a result of polyclonal expansion of B cells (10). We confirmed those observations and further demonstrated a role for TRAF2 as a B cell tumor suppressor, showing that disruption of TRAF2 function cooperates with BCL-2 to develop CLL/SLL (6). Additional evidence of the role of TRAF2 in B cell homeostasis was obtained by Brink and coworkers (8, 9) using mice with Traf2-deficient B cells. These B cell-specific Traf2−/− mice also developed splenomegaly and lymphadenopathy as a result of the expansion of mature B lymphocytes, in particular, cells with an MZ phenotype, as we have further confirmed in this report. Indeed, around 50% of splenic B cells from the Traf2DN-tg mice have a MZ phenotype. This result might be particularly relevant because it has been proposed that human CLL cells derive from MZ B cells (5).

B cell expansion in both Traf2DN-tg mice and B cell-specific Traf2−/− mice is the result of increased B cell survival rather than by deregulated proliferation. Our results concur with those of Gardam and coworkers (9) in that TRAF2 deficiency renders B cells independent of BAFF for their survival. Indeed, in vitro survival of nonstimulated Traf2DN-tg B cells was similar to that of BAFF-treated WT B cells, and no significant increase in Traf2DN-tg B cell survival was achieved by culturing these cells in the presence of BAFF. Furthermore, we previously showed that Traf2DN-tg B cells had reduced sensitivity to apoptosis induced by dexamethasone and fludarabine compared with WT B cells (6), further supporting that lack of TRAF2 provides survival advantages to B cells.

We have observed constitutive processing of p100 NF-κB2 into yield active p52 in Traf2DN-tg B cells, confirming previous results from Grech and coworkers (8) in Traf2−/− B cells. Both MZ differentiation (18) and BAFF-independent increased survival of Traf2-deficient B cells are likely consequences of this constitutive NF-κB2 activation. In this regard, the molecular mechanism controlling NF-κB2 activation in B cells has been previously elucidated, showing that, in resting B cells, p100 NF-κB2 processing is prevented by maintaining NF-κB-inducing kinase (NIK) levels low. The mechanism underlying NIK down-regulation involves its interaction with TRAF3, which acts as a bridge bringing NIK to the TRAF2/cIAP complex and thereby allowing cIAP1/2 to ubiquitinate NIK, thus promoting its degradation by the proteasome. In contrast, activation of the BAFF-R with BAFF triggers p100 NF-κB2 processing by recruiting TRAF3 to the cytosolic tail of the activated receptor and promoting TRAF2/cIAP-dependent TRAF3 degradation, thus preventing NIK degradation. Therefore, TRAF2, TRAF3, and cIAP1/2 work in tandem to repress NF-κB2 activation in the absence of appropriate stimuli, thus tightly controlling B cell homeostasis and differentiation, as has been shown in vivo in a variety of genetically modified mouse models (8, 9, 20, 28, 31).

In support of a role for BAFF in CLL/SLL, causative factors is the fact that BAFF cooperates with various oncogenes to promote CLL/SLL in mice. Indeed, either mice with B cells having constitutively activated BAFF-mediated pathways (as is the case of Traf2DN/Bcl-2 double-tg mice) or mice with B cells continuously exposed to high levels of circulating BAFF (Baff/Hsc-l and Baffc-Myc double-tg mice) (32, 33) develop CLL/SLL.

It is interesting to mention that, similar to Baff−tg mice (32–34), deregulation of NF-κB2 activation predisposes to either autoimmunity or CLL/SLL. In this regard, Zhang and coworkers (35) developed tg mice expressing in lymphocytes p80HT, a lymphoma-associated NF-κB2 mutant (36). These mice displayed a marked expansion of peripheral B cell populations and developed SLL. B cells from these mice were also resistant to apoptosis induced by cytokine deprivation and mitogenic stimulation. However, the same group also developed tg mice overexpressing in B cells p52, the proteolytic product of p100 NF-κB2 normally produced on activation (37). These mice did not develop SLL, but they were predisposed to inflammatory autoimmune disease. These results place NF-κB2 at the crossroads of autoimmunity and CLL/SLL in B cells, both of which are known to be promoted by defects in apoptosis. However, our results with the Traf2DN-tg mice showed that constitutive NF-κB2 activation may underlie MZ B cell expansion and might contribute to BAFF-independent B cell survival, but it is not sufficient to promote either B cell transformation or overt B cell-dependent autoimmunity in this model.

Notably, TRAF2 deficiency also has an impact in the signaling cascades activated by the BCR and by various members of the TNFR-family. Thus, we have observed significant differences in early MAPK activation by the BCR, with higher ERK and reduced p38 MAPK activation in the absence of TRAF2. It remains unclear how TRAF2 would control early BCR-mediated signaling, but altered BCR signaling in the TRAF2-deficient B cells might underlie the absence of autoimmune symptoms in these mice. However, these differences in BCR signaling might be the result of MZ B cell expansion, because it is well established that FO B cells and MZ B cells have different requirements for BCR activation (38).

Our data also indicate that, in the absence of TRAF2, CD40 engagement failed to efficiently activate JNK and ERK, although p38 MAPK activation and IκBα degradation remained intact, confirming previous reports (14, 20). We also showed that CD40L-mediated B cell proliferation was significantly reduced in the Traf2DN-tg B cells compared with that of WT B cells. Interestingly, recent evidence (39) has shown that CLL patients can be segregated in two distinct functional subsets according to their dependency on CD40L for leukemic expansion, with CD40L-independent CLL patients having a shorter time to progression. Thus, the CLL/SLL model developed by the Traf2DN/Bcl-2 double-tg mice might be the mouse counterpart of this CD40L-independent human CLL subset.

In this regard, it is interesting to compare the Traf2DN/Bcl-2 mouse model with the mechanisms believed to underlie the pathogenesis of human CLL. Most cases of CLL have aberrantly high levels of BCL-2 expression because of loss of gene encoding
microRNAs (miRs) that suppress expression of this antiapoptotic gene. Loss of the BCL-2–targeting miRs (miR15a and 16-1) as a consequence of 13q14 deletions is the most common genetic lesion thus far identified in CLL, occurring in >50% of cases. Our mouse model clearly recapitulates this circumstance. B cells from our Traf2Dn/blc-2 double-tg mice also contain increased levels of XIAP. High levels of XIAP expression have been found in malignant B cells from CLL patients (40), and targeting XIAP expression has been shown to induce apoptosis of CLL cells in culture (41-43). We also observed a decline in cIAP1 and cIAP2 protein levels in murine Traf2Dn/blc-2 double-tg B cells. In this regard, inactivating mutations in the human BIRC3 gene encoding cIAP2 have been found in CLL (44) and in other B lymphoid malignancies (45–47), and BIRC/MALT1 translocations are causative of mucosa-associated lymphoid tissue lymphoma (30). Thus, this mouse model also recapitulates additional features of human CLL.

Currently, there is no evidence of mutations of the Traf2 gene in CLL patients (45, 48, 49). However, there might be alternative mechanisms to inhibit Traf2 function leading to B cell transformation. In this regard, Thomas and coworkers (50) have shown that phosphorylation of Traf2 at Ser53 (within the RING domain), which is constitutively found in Hodgkin’s lymphoma samples, is deleterious for Traf2 activity (51). Finally, it is noteworthy that Traf1 is overexpressed in CLL cells, with higher Traf1 levels correlating with the development of refractory disease (7). Traf1 is the only member of the Traf family that lacks the RING domain; therefore, it lacks the ability to function as an E3 ubiquitin ligase. Traf1 can form heterotrimers with Traf2 (51), and there is evidence supporting a role for Traf1 as both a positive and negative regulator of Traf2 activities (reviewed in Ref. 52). These results suggest a role for Traf1 in the cause of this disease, maybe as a downregulator of Traf2 function. Further research on the role of Traf1 in CLL/SLL is warranted.

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References


