

Regulation and Function of Bcl-2 During Differentiation-Induced Cell Death in HL-60 Promyelocytic Cells

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Polymorphonuclear leukocytes are generated by differentiation of early myeloid precursors. Once fully differentiated, blood neutrophils are programmed to die rapidly and are removed by tissue macrophages. In normal myeloid cells, the death mechanism seems to be coupled to the differentiation pathway and is accomplished by a process termed apoptosis. In the present study, we have examined the role of Bcl-2 in the differentiation pathways of the promyelocytic cell line HL-60. Treatment of HL-60 with retinoic acid or phorbol ester, which induced neutrophil or macrophage-like cell differentiation, respectively, resulted in progressive loss of cellular viability and internucleosomal DNA degradation. In HL-60, differentiation and apoptosis were coupled to down-regulation of the Bcl-2 protein. Overexpression of Bcl-2 by gene transfer inhibited apoptosis triggered by terminal differentiation of HL-60. Yet, Bcl-2 did not alter the expression of surface markers or other phenotypic changes that are induced upon myeloid differentiation. In contrast to HL-60, another immature myeloid cell line, K562, did not produce Bcl-2 but expressed a related protein, Bcl-x₁, that functions as a repressor of apoptotic cell death. K562 has been shown to be relatively resistant to a variety of apoptotic stimuli. Incubation of HL-60 and K562 with inhibitors of macromolecular synthesis induced apoptosis, which appeared earlier in HL-60 than in K562. Interestingly, Bcl-2 overexpression protected K562 cells from apoptosis induced by inhibitor of macromolecular synthesis

but it had little or no effect on HL-60 cells. We conclude that although differentiation and apoptosis proceed simultaneously, they can be uncoupled by expression of Bcl-2. Down-regulation of Bcl-2 appears to be part of the differentiation pathway and may serve to facilitate the apoptotic response. (Am J Pathol 1995, 146:481-490)

Cellular homeostasis in vertebrates is regulated by cell proliferation as well as by cell death. The demise of cells that occurs during embryogenic and postnatal development is referred to as programmed cell death and usually occurs by apoptosis, a morphologically defined process that ultimately leads to activation of endogenous nucleases and DNA degradation.¹⁻⁴ Although the mechanism that induces and executes apoptosis is poorly understood, it is thought that in most instances cell death is controlled by a genetic program that is activated within the dying cell. The requirement for new DNA transcription and protein synthesis for induction of apoptosis in many cellular systems suggested that the demise of cells represents activation of a suicide program.^{5,6} However, it has been also found that inhibition of protein and RNA synthesis alone can induce apoptosis, arguing that in some cases apoptosis may be actively suppressed by proteins inside the cell.⁷ Apoptosis can be triggered by a variety of stimuli. They include deprivation of survival factors, signaling via certain surface receptors, and treatment with hormones such as glucocorticoids or DNA-damaging agents.^{8,9} In hematopoietic tissues, apoptosis is coupled to terminal differentiation of myeloid progeni-

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tors.¹⁰ Although the mechanism responsible for activation of apoptosis during myeloid maturation is poorly understood, the process serves to remove from the organism aging neutrophils. Moreover, apoptosis appears to play an important role in the disposal of polymorphonuclear leukocytes involved in the resolution of the acute inflammatory response.¹¹ In neutrophils, apoptosis appears to be suppressed by the stimulation of survival factors such as interleukin-3 (IL-3) and granulocyte-macrophage colony-stimulating factor (GM-CSF).^{12,13} It is generally thought that hematopoietic survival factors can maintain cell survival by inducing the synthesis of cellular proteins capable of suppressing the apoptotic mechanism.^{14,15} A candidate protein that functions as a repressor of apoptosis is the product of the *Bcl-2* proto-oncogene. *Bcl-2* is deregulated in 85% of follicular lymphomas as a consequence of the chromosomal translocation t(14;18) which juxtaposes *Bcl-2* and the Ig heavy chain locus.^{16,17} *Bcl-2* encodes a 26-kd integral membrane protein that localizes to outer mitochondria, smooth endoplasmic reticulum, and perinuclear envelope.^{18–20} *Bcl-2* protein expression appears widely distributed on tissues characterized by apoptotic cell death²¹ and protects hematopoietic cells from apoptosis induced by growth factor withdrawal and chemotherapeutic agents.^{22–24} Within the myeloid lineage, *Bcl-2* is expressed in early myeloid precursors but is absent in polymorphonuclear leukocytes of the blood.²⁵ Similarly, promyelocytic HL-60 cells induced to differentiate toward neutrophils down-regulate *Bcl-2*.²⁵ The correlation between expression of *Bcl-2* and differentiation suggests that down-regulation of *Bcl-2* may be part of the myeloid maturation pathway. To provide an experimentally useful model for examining the potential action of *Bcl-2* in the myeloid lineage, we have stably transfected two myeloid leukemic cell lines HL-60 and K562 with a *Bcl-2* expression vector.²⁶ Induction of HL-60 differentiation by retinoic acid or phorbol ester leads to down-regulation of *Bcl-2* protein and apoptotic cell death. Overexpression of *Bcl-2* inhibited differentiation-induced apoptosis but it failed to alter the maturation process.

Materials and Methods

Cell Cultures and Chemicals

K562 and HL-60 cells were maintained at $5-9 \times 10^5$ cell/ml in RPMI 1640 medium (Seromed Biochrom KG) supplemented with 10% heat-inactivated fetal calf serum (Flow Laboratories), nonessential amino acids, 2 mmol/L glutamine, 100 U/ml penicillin, and

100 µg/ml streptomycin. Viability and total cell counts were determined at various times by the trypan blue exclusion test by counting at least 200 cells from each individual culture. The following chemicals were used: actinomycin D (ActD) (Dactinomycin, MSD); cycloheximide (CHX) (Sigma Chemical Co., St. Louis, MO); arabinosyl-cytosine (Ara C) (Upjohn); puromycin (Sigma); phorbol-12-myristate-13-acetate (PMA) (Sigma) and all-*trans*-retinoic acid (RA) (Sigma). RA was dissolved and stored in DMSO at 5 mmol/L and diluted 1:5000 in culture medium to induce myeloid differentiation.

Cell Transfection

K562 and HL-60 cells were transfected by electroporation with the SFFV-Neo expression vector²⁶ containing the human *Bcl-2* open-reading frame driven by the long terminal repeat of the splenic focus-forming virus (SFFV-*Bcl-2*). As a control, transfections were performed with empty SFFV-Neo plasmid. For transfections, 20 to 40 µg of the plasmid was linearized with *NotI* (Pharmacia) and resuspended in Hebs buffer (20 mmol/L HEPES, pH 7.0; 137 mmol/L NaCl; 5 mmol/L KCl; 0.7 mmol/L Na₂PO₄H; 6 mmol/L dextrose) or in PBS buffer. K562 cells (10^7) were subjected to electroporation at 400 V, 500 µF and selected for resistance to neomycin by growth in the presence of 650 µg/ml G418 antibiotic (GIBCO). HL-60 cells (10^6) were electroporated at 450 V, 75 µF and selected in medium containing 1 mg/ml G418.

Western Blot and Flow Cytometry Analysis

Cell suspensions (2.5×10^6 cells) were lysed in a buffer containing 25 mmol/L Tris-HCl pH 8.0, 1% NP-40 (Sigma), 0.5% deoxycholate (Sigma), 144 mmol/L NaCl, 0.1% sodium dodecyl sulfate (SDS), 5 mmol/L dithiothreitol, 10 mmol/L iodoacetamide, and 0.5 mmol/L phenylmethylsulfonyl fluoride at 4°C. After a brief sonication, lysates were cleared by centrifugation at 17,000 rpm for 30 minutes and then boiled for 5 minutes in sample buffer (50 mmol/L Tris-HCl, pH 6.8; 8% glycerol; 1.6% SDS; 4% 2-mercaptoethanol; and 2% bromophenol blue) before being run on a SDS-12% polyacrylamide gel. Gels were transferred to nitrocellulose (Bio Rad), blocked with 3% BSA and then incubated for another hour with 25 µg/ml hamster anti-human *Bcl-2* antibody (6C8)¹⁸ or rabbit anti-*Bcl-2* antiserum (a gift of Dr. Craig Thompson, University of Chicago). Blots were incubated with secondary rabbit anti-hamster IgG (Jackson ImmunoResearch Lab,

Inc.) or goat anti-rabbit IgG-horseradish peroxidase (Amersham), washed, and developed with 0.6 mg/ml 3,3'-diaminobenzidine tetrahydrochloride dihydrate (DAB) (Bio Rad) in 50 mmol/L Tris, pH 8.0, containing H₂O₂ (1:1000) for Bcl-2 or ECL substrate for Bcl-x (Amersham).

Differentiation of myeloid cell lines was induced by addition of 20 ng/ml of PMA (macrophage-like cell phenotype) or 1 μ mol/L RA (granulocytic phenotype) and monitored by flow cytometry on a FACScan using antibodies to CD71, CD14, and CD11b antigens and a secondary FITC-conjugated goat anti-mouse IgG (Becton-Dickinson). To assess the expression of Bcl-2 by flow cytometric analysis, 10⁶ cells were washed twice with PBS/1% BSA, fixed with 2% paraformaldehyde (Merck) for 10 minutes at room temperature, and permeabilized with PBS/0.03% saponin (Sigma). Staining for Bcl-2 protein was performed as previously described.²⁷ Flow cytometric analysis was performed in a FACScan apparatus equipped with the Lysis II program.

DNA Fragmentation Analysis

Cells (1–3 \times 10⁶) were washed with PBS and pelleted by centrifugation at 200 \times g for 5 minutes. Cell pellets were resuspended in 750 μ l of lysis buffer (50 mmol/L Tris, pH 8.0; 10 mmol/L EDTA, pH 8.0; 0.5% SDS) and frozen at –70 C for 15 minutes. The lysates were then centrifuged at 14,000 \times g for 15 minutes and the supernatants were incubated with 0.5 mg/ml proteinase K (GIBCO-BRL) for 1 hour at 65 C. The DNA preparations were then extracted with buffered phenol, phenol:chloroform (1:1), and chloroform:isoamyl alcohol, and ethanol precipitated. Samples were air-dried and resuspended in 15 μ l of water containing 0.25 mg/ml RNase A (GIBCO-BRL). DNA samples were stained with 0.1% ethidium bromide and electrophoresed on a 2% agarose gel.

S1 Protection Analysis

Total RNA was prepared by the guanidinium thiocyanate method.²⁸ To construct a human *Bcl-x* probe, a 725-bp cDNA fragment containing the entire coding region of *Bcl-x_L* was inserted into the *Eco*RI polylinker site of pBluescript.²⁹ The 3' end of the antisense strand was labeled at the unique *Nco*I site of *Bcl-x_L* by filling with [³²P]CTP (6000 Ci/mmol) (Amersham) and Klenow (Promega). A control probe specific for the human (GAPDH) was prepared as previously described.³⁰ To assess mRNA expression, both *Bcl-x_L* and GAPDH-labeled probes (10⁵ cpm each) were hy-

bridized simultaneously with 10 μ g of total RNA in the same tube for 16 hours at 55 C and then digested with 200 U of S1 nuclease for 1 hour at 37 C. Protected fragments were size separated on a 6% sequencing gel, dried, and autoradiographed as previously described.³¹ Autoradiographs were quantified by densitometry scanning with a radioanalytic imaging system and AMBIS QuantProbe Software (AMBIS, Inc., San Diego, CA).

Results

Development of Myeloid Cell Lines Overexpressing Bcl-2

The Bcl-2 oncoprotein has been shown to function as a repressor of apoptosis in a variety of cellular systems.^{22–24} To determine whether Bcl-2 can exert a protective effect against apoptosis within the myeloid lineage, the myeloid cell lines HL-60 and K562 were stably transfected with the SFFV-*Bcl-2* plasmid containing the human *Bcl-2* open-reading frame. Control cells generated by transfection with the SFFV-Neo vector lacking the *Bcl-2* sequence were also developed. Bulk and clonal cell lines transfected with *Bcl-2* and control plasmid were generated by growth in medium containing G418. The expression of Bcl-2 protein in transfected cells was determined by flow cytometry and Western blot analysis. As shown in Figure 1, C and D, HL-60-Neo cells express moderate levels of endogenous Bcl-2 protein, which were increased four- to fivefold after transfection with the *Bcl-2* vector. Untransfected HL-60 cells displayed an identical pattern of Bcl-2 expression than HL-60-Neo cells (data not shown). The K562 cells expressed no detectable levels of endogenous Bcl-2 protein (Figure 1, A and B). Even polymerase chain reaction (PCR) analysis failed to detect trace amounts of *Bcl-2* mRNA (data not shown). After transfection with the *Bcl-2* plasmid, K562 expressed uniform levels of the 26-kd Bcl-2 in practically all cells (Figure 1B).

Bcl-2 Inhibits Apoptosis Induced by Myeloid Differentiation in HL-60 Cells

Differentiation of HL-60 toward neutrophils or macrophage-like cells can be induced by stimulation with RA or PMA, respectively.^{29,32,33} To assess the function of Bcl-2 in the differentiation pathway of HL-60 cells, control and Bcl-2-transfected HL-60 bulk cell lines were cultured in the presence of 1 μ mol/L RA (granulocytic differentiation) or 20 ng/ml PMA (macrophage-like cell differentiation) for various

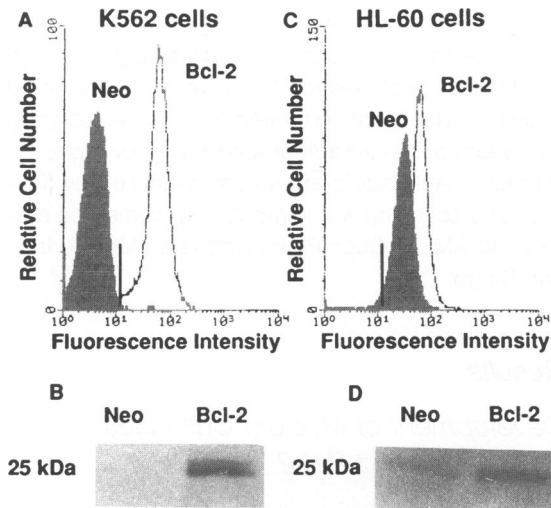


Figure 1. Expression of Bcl-2 protein in Neo and Bcl-2-transfected HL-60 and K562 cells. **A, C:** flow cytometric analysis of cell populations was performed as described in Materials and Methods. Bulk cell lines were stained with hamster anti-human Bcl-2 MAb (6C8) followed by biotin-conjugated goat anti-hamster Ab and PE-conjugated streptavidin. The line "cut-off" represents the highest level of background fluorescence obtained by staining with an isotype matched control hamster MAb. In the experiment shown the mean fluorescence intensity of Bcl-2 staining for K562-Neo was 20 HL-60-Neo 330 HL-60-Bcl-2 661 and 630 for K562-Bcl-2. **B, D:** Western blot analysis for Bcl-2. Cell lysates from 2.5×10^6 HL-60 or K562 cells were loaded onto a 12% polyacrylamide gel. After electrophoresis proteins were transferred to nitrocellulose and analyzed for Bcl-2 with 6C8 MAb followed by peroxidase-conjugated rabbit anti-hamster IgG.

times. The percentage of viable cells in the HL-60-Neo population fell dramatically by day 11 of RA treatment (20% viable) and dropped to less than 2% by day 15 (Figure 2A). In contrast, the great majority (94%) of the HL-60-Bcl-2 cells remained viable at day 11, and 76% of the cells continued viable by day 15 of RA treatment. Similarly, only 3% of the HL-60-Neo cells treated with PMA survived by 6 days (Figure 3A). By contrast cell death of HL-60-Bcl-2 was delayed, and about 45% of the cells were still viable after 6 days of incubation with PMA. Similar results were obtained using two separate HL-60-Bcl-2 clones (data not shown). This loss of viability observed after treatment with either RA or PMA was due to the activation of an apoptotic process. Thus, after treatment with RA or PMA, more than 70% of the cells became smaller and exhibited pyknotic and fragmented nuclei, which are morphological features of apoptosis (data not shown). Furthermore, as shown in Figures 2B and 3B, treatment with RA or PMA induced DNA fragmentation of genomic DNA in an oligonucleosomal pattern after 10 days of RA treatment (Figure 2B, lane 5), or 3 and 5 days of PMA treatment (Figure 3B, lanes 3 and 5). In contrast, genomic DNA from HL-60-Bcl-2 cells remained relatively unfragmented (Figures 2B and 3B, lanes 4 and 6). These experiments indicate that

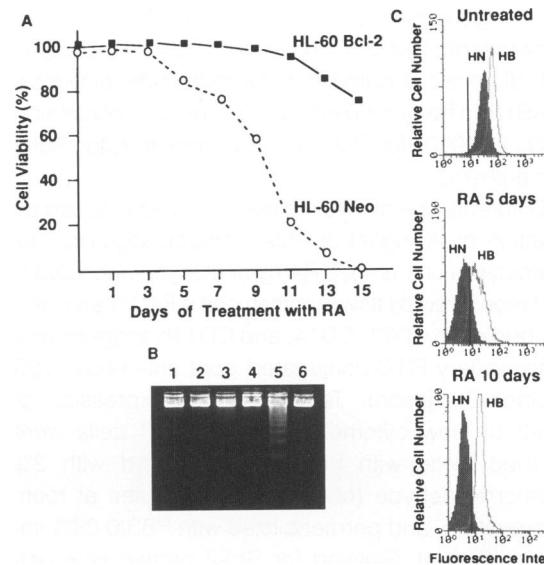


Figure 2. Inhibition of granulocytic differentiation-induced apoptosis in HL-60 by Bcl-2. **A:** Time course of cell viability as measured by exclusion of trypan blue dye after incubation with $1 \mu\text{mol/L}$ RA in HL-60-Neo cells (lanes 1, 3, and 5) and HL-60-Bcl-2 cells (lanes 2, 4, and 6) after induction of differentiation with RA. Before treatment (lanes 1 and 2) and after treatment for 5 days (lanes 3 and 4) and 10 days (lanes 5 and 6) DNA was prepared from cells as described in Materials and Methods and electrophoresed on a 2% agarose gel. **B:** Expression of Bcl-2 in HL-60-Neo (HN) and HL-60-Bcl-2 (HB) cell populations after treatment with RA. Histograms show staining with 6C8 MAb in the presence of saponin. The markers indicate the staining background of isotype match MAb 3F11.

in HL-60 cells, differentiation, and apoptosis occur simultaneously, and Bcl-2 can inhibit the differentiation-induced death process.

Down-Regulation of Endogenous Bcl-2 during Myeloid Differentiation

To assess whether the endogenous levels of Bcl-2 may regulate the apoptotic mechanism that is triggered by differentiation, the expression of Bcl-2 was examined before and after treatment with agents that induce myeloid differentiation. Incubation of HL-60 with RA or PMA was accompanied by a progressive decrease in the endogenous levels of the Bcl-2 protein in the SFFV-Neo-transfected HL-60 cells (HN) assessed by flow cytometric analysis (Figures 2C and 3C). In RA-treated cells, 39% remained Bcl-2 positive after 5 days and 11.4% after 10 days of treatment (Figure 2C). In PMA-treated HL-60 (HN), 74% of the cells remained Bcl-2 positive after 3 days, and only 1% of the cells were positive by 5 days of treatment (Figure 3C). In contrast, the expression of Bcl-2 remained positive in HL-60-Bcl-2 cells (HB) (Figures 2C and 3C), indicating that SFFV-driven Bcl-2 is not significantly down-regulated during differentiation.

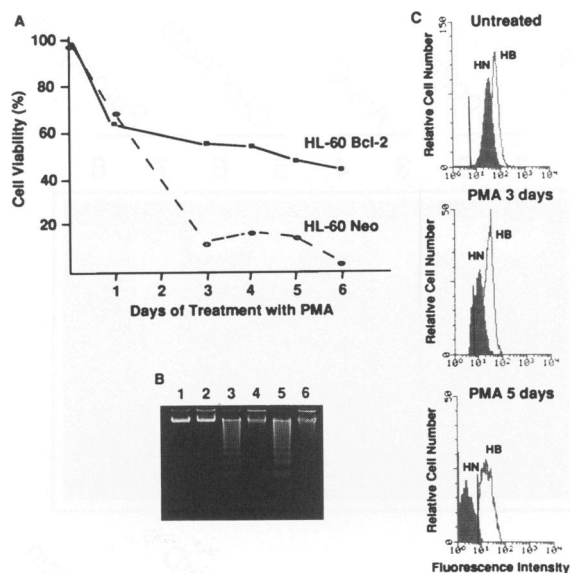


Figure 3. Inhibition of macrophage-like cell differentiation-induced apoptosis in HL-60 by Bcl-2. **A:** Time course of cell viability as measured by exclusion of trypan blue dye after incubation with 20 ng/ml PMA. Values shown represent the mean of triplicate cultures. Standard deviation of the mean was less than 15% of the mean value. **B:** Analysis of DNA fragmentation in HL-60-Neo cells (lanes 1, 3, and 5) and HL-60-Bcl-2 cells (lanes 2, 4, and 6) after induction of differentiation with PMA. Before treatment (lanes 1 and 2) and after treatment for 3 days (lanes 3 and 4) and 5 days (lanes 5 and 6) total DNA was prepared from cells as described in Materials and Methods and electrophoresed on a 2% agarose gel. **C:** Expression of Bcl-2 in HL-60-Neo (HN) and HL-60-Bcl-2 (HB) cell populations after treatment with PMA. Histograms show staining with 6C8 MAb in the presence of saponin. The markers indicate the staining background of the isotype match MAb 3F11.

Bcl-2 Overexpression Fails to Inhibit Differentiation in Myeloid Cell Lines

Because apoptosis is only a final step in the differentiation pathway of myeloid cells, we wished to determine whether Bcl-2 overexpression could have a more generalized effect on the differentiation process of HL-60 cells. To assess that, the expression of several cell surface markers (CD71, CD11b, CD14) known to be regulated during myeloid differentiation were examined in untreated and HL-60 cells incubated with RA for 10 days or PMA for 4 days. A common feature of HL-60 cells differentiating toward granulocytes or macrophage-like cells is the rapid internalization of surface transferrin receptor (CD71), which precedes the inhibition of proliferation and the acquisition of other differentiation markers (i.e., CD11b, CD14).^{34,35} As shown in Figure 4, there was no detectable difference in the expression of CD71, CD11b, and CD14 between control HL-60-Neo and HL-60-Bcl-2 cell populations after differentiation. As an additional criteria for differentiation, HL-60-Neo and HL-60-Bcl-2 cells were stained with Wright-Giemsa at different intervals after treatment with RA or

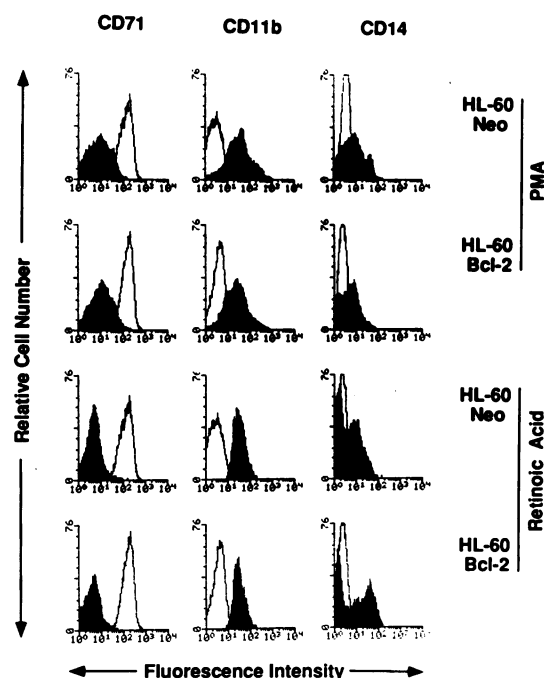


Figure 4. Expression of differentiation markers in HL-60-Neo and HL-60-Bcl-2 cell populations treated with PMA or RA. Cells untreated (open graphs) and treated with PMA (4 days) or RA (10 days) (shaded graphs) were stained with a primary antibody anti-CD71 anti-CD11b or anti-CD14 followed by a FITC-conjugated goat anti-mouse IgG.

PMA. The percentage of mature cells in the cultures was similar in HL-60-Neo and HL-60-Bcl-2 cells further confirming that Bcl-2 has no significant effect on terminal differentiation (data not shown).

Effect of Bcl-2 Overexpression on Apoptosis Induced by Inhibitors of Macromolecular Synthesis in HL-60 and K562 Cells

In many cellular systems, there is a requirement for *de novo* protein synthesis in the activation of an apoptotic response. However, in other systems such as HL-60, inhibition of RNA or protein synthesis induces apoptosis⁷ which argues for the presence of proteins within the cells that actively suppress the apoptotic mechanism. HL-60 and K562 cells were incubated with the protein synthesis inhibitor puromycin (6 μ mol/L), a combination of protein and RNA synthesis inhibitors, CHX (25 μ g/ml) and ActD (0.1 μ g/ml), or Ara C (100 μ mol/L), which interferes with DNA synthesis and has been shown to induce apoptosis in human myeloid leukemia cells.³⁶ Treatment of HL-60-Neo and K562-Neo with puromycin, the combination of CHX/Act D or Ara C induced a time-dependent loss

of cell viability (Figure 5). Noticeably, cell death induced by all drugs examined was detected much earlier in HL-60-Neo than in K562-Neo (Figure 5). During the first 3–6 hours, overexpression of Bcl-2 in HL-60 provided little or no protection from cell death induced by all drugs examined (Figure 5, F–H). In contrast, K562 overexpressing Bcl-2 were much more resistant than control cells to apoptosis triggered by the same inhibitors (Figure 5, B–D). To determine the cell death mechanism, genomic DNA was isolated and examined by agarose gel electrophoresis. Incubation of HL-60-Neo and K562-Neo cells with inhibitors of macromolecular synthesis induced degradation of DNA in an oligonucleosomal pattern which is characteristic of apoptosis (Figure 6, A and B, lanes 3, 5, and 7). Furthermore, the morphology of the cells treated with inhibitors of macromolecular synthesis revealed features which are characteristic of apoptosis (data not shown). Consistent with the viability results shown in Figure 5, overexpression of Bcl-2 did not inhibit significantly the degradation of genomic DNA in HL-60 cells incubated for 6 hours with either puromycin or

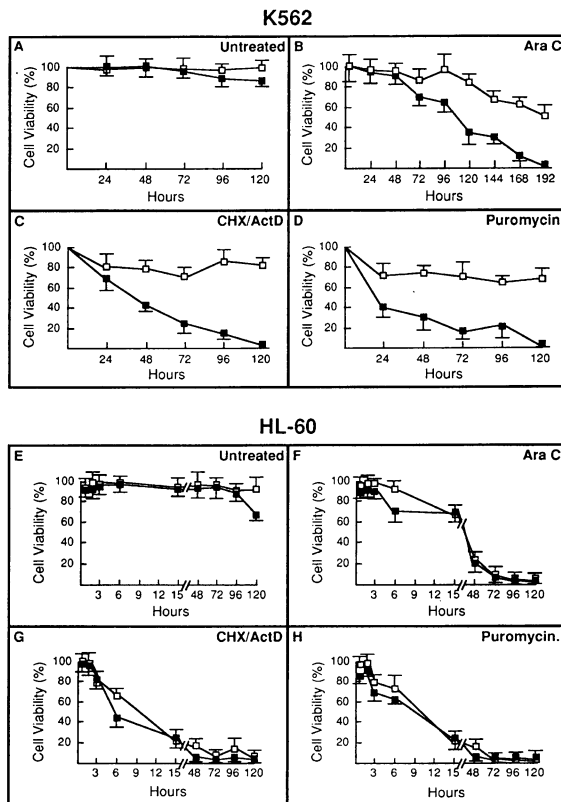


Figure 5. Viability of K562 and HL-60 cells incubated in the presence of macromolecular synthesis inhibitors Neo- (■) and Bcl-2- (□) transfected cells were incubated with Ara C (B and F), CHX/ActD (C and G) or puromycin (D and H) and at the indicated time points cell viability was measured by exclusion of trypan blue dye. All data points represent the mean of triplicate cultures ± standard deviation.

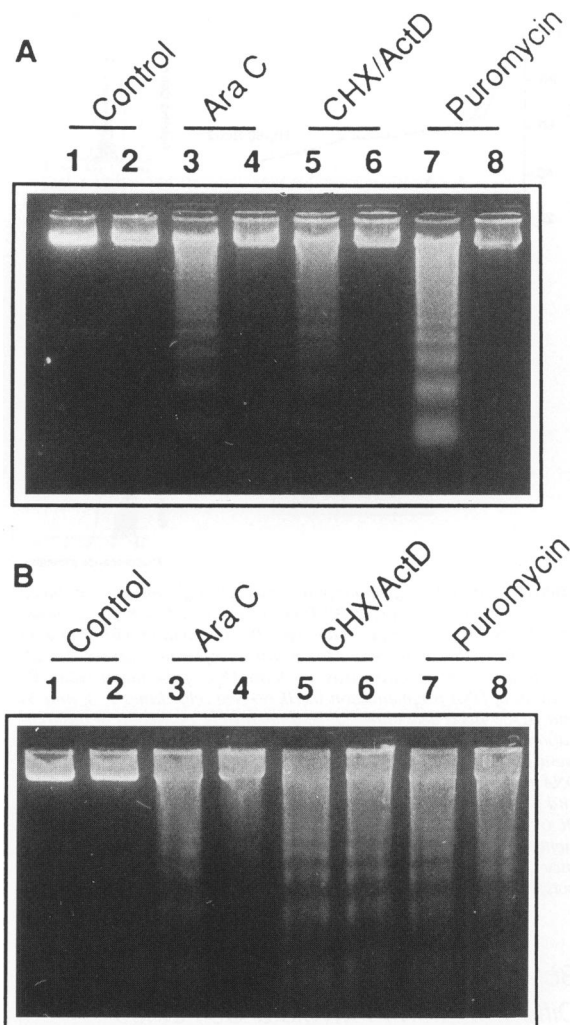


Figure 6. Analysis of DNA fragmentation in K562 and HL-60 cells following treatment with macromolecular synthesis inhibitors. **A:** K562-Neo (lanes 1, 3, 5, 7) and K562-Bcl-2 (lanes 2, 4, 6, 8) cells were incubated for 120 hours with Ara C 72 hours with CHX/ActD and 72 hours with puromycin. **B:** HL-60-Neo (lanes 1, 3, 5, 7) and HL-60-Bcl-2 (lanes 2, 4, 6, 8) cells were incubated for 6 hours with the same agents. DNA fragmentation was monitored by electrophoresis in a 2% agarose gel.

CHX/ActD (Figure 6B, lanes 6 and 8), although some protection was observed after incubation with Ara C for 6 hours (Figure 6B, lane 4). In contrast, the DNA from K562 overexpressing Bcl-2 remained uncleaved after treatment with the same macromolecular synthesis inhibitors (Figure 6A, lanes 4, 6, and 8).

Myeloid Cell Lines Can Express Bcl-x_L, a Bcl-2-Related Gene that Inhibits Apoptosis

The cell line K562 is relatively more resistant than HL-60 to a variety of stimuli capable of inducing apoptosis^{37,38} (Figure 5). The relative resistance of K562

to apoptosis is surprising, since it does not express endogenous Bcl-2 protein. One reasonable possibility is that the survival of K562 is maintained by anti-apoptotic genes other than *Bcl-2*. A candidate gene is *Bcl-x*, whose *Bcl-x_L* form is a powerful inhibitor of apoptosis in growth factor-dependent hematopoietic cell lines.³⁹ Because two mRNA species of *Bcl-x* with opposite biological function (*Bcl-x_L* and *Bcl-x_S*) have been described,³⁹ we developed a S1-nuclease assay capable of discriminating between both mRNA forms (Figure 7A). Hybridization of cellular RNA to an end-labeled *Bcl-x* probe protected a fragment of 455 nucleotides corresponding to *Bcl-x_L*, which was expressed threefold greater in K562 than in HL-60 (Figure 7B). The *Bcl-x_S* mRNA was not detectable in K562 and HL-60 (Figure 7B). The *Bcl-x_L* product was detected in whole cell lysates from K562 but not in HL-60 by Western blot analysis (Figure 7C), which is consistent with the expression pattern of *Bcl-x_L* mRNA shown in Figure 7B.

Discussion

The proto-oncogene *Bcl-2* localizes to membranes of the outer mitochondria, endoplasmic reticulum, and nuclear envelope and promotes cell survival by inhibiting the apoptotic mechanism. Although much of the work has been focused on the involvement of *Bcl-2* in lymphoid differentiation, this proto-oncogene is not lineage restricted. Bcl-2 is expressed in early hematopoietic progenitors and within myeloid cells is regulated in a differentiation-associated manner.²⁵ Because Bcl-2 is absent in polymorphonuclear leukocytes, it has been postulated that diminished expression of Bcl-2 may be a mechanism that triggers or facilitates the apoptotic mechanism that is coupled to terminal differentiation of myeloid progenitors.

In the present study we have examined the function of Bcl-2 in two myeloid leukemic cell lines HL-60 and K562. Induction of differentiation in HL-60 by RA or PMA leads to progressive loss of cell viability by activation of an apoptotic process. Thus, like in normal neutrophils, differentiation of HL-60 is coupled to apoptosis. Moreover, as it was previously reported by others, we find that differentiation of HL-60 is associated with a progressive diminution of Bcl-2 which is reminiscent of the developmental regulation of Bcl-2 observed in normal myeloid cells.²⁵ Importantly, we find that constitutive expression of Bcl-2 inhibits the apoptotic death triggered by differentiation. Significantly, however, enforced Bcl-2 expression did not affect the phenotypic changes that occur during myeloid maturation. These results suggest that although

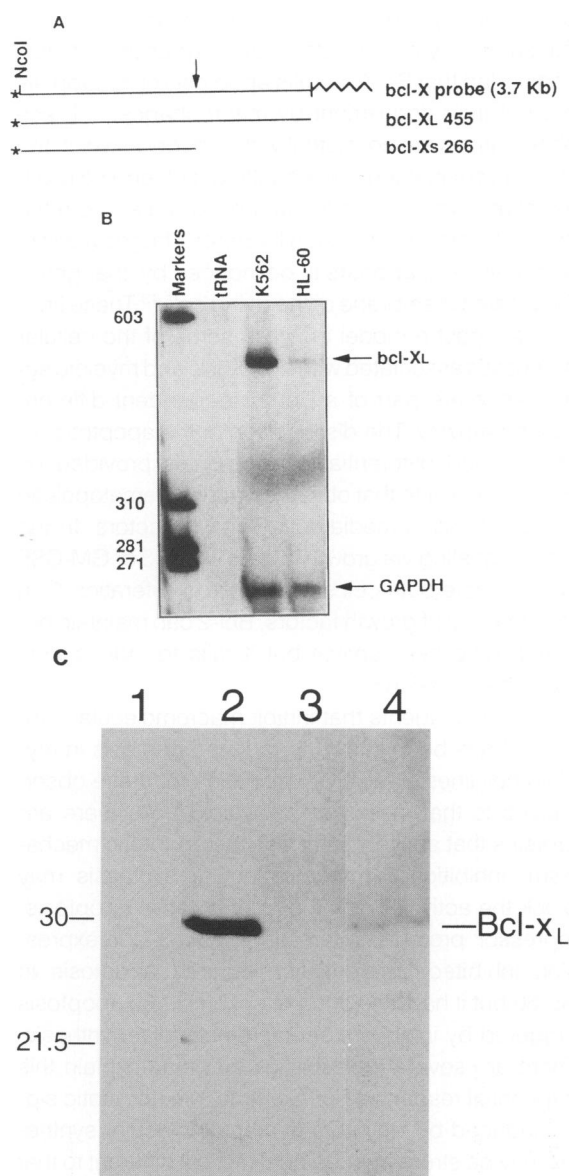


Figure 7. Expression analysis of *Bcl-x* in K562 and HL-60 cell lines. **A:** The antisense strand of the *Bcl-x* fragment was end-labeled at the NcoI site located in the coding region of the human *Bcl-x* cDNA³⁹ pBluescript sequences are indicated by a wavy line. The splice site utilized for the generation of *Bcl-x_S* is indicated by an arrow. Expected protected fragments for *Bcl-x_L* and *Bcl-x_S* mRNA forms are indicated in nucleotides. **B:** End-labeled *Bcl-x* and GAPDH S1-nuclease probes were simultaneously hybridized to total RNA samples (10 µg). Hybridization revealed a protected fragment of 455 (*Bcl-x_L*) nucleotides. The amount of *Bcl-x_L* signal was threefold greater in K562 than in HL-60 as determined by scanning densitometry (relative values were corrected according to the internal GAPDH standard). An expected fragment of 266 nucleotides corresponding to the *Bcl-x_S* form was not detected in K562 or HL-60. Size markers are in nucleotides. **C:** Detection of *Bcl-x_L* protein by Western-blot analysis. Protein lysates (2×10^6 cells/lane) from murine FL512 cells (lane 1) FL512 transfected with a human *Bcl-x_L* cDNA (lane 2) HL-60 (lane 3) and K562 (lane 4) are shown. Size markers are in kilodaltons.

apoptosis and differentiation proceed simultaneously in the myeloid lineage, they can be uncoupled by expression of Bcl-2, which confirms results recently

published by others.^{40,41} In other studies using a transgenic system of Bcl-2 overexpression, it was concluded that Bcl-2 inhibits apoptosis of neutrophils but not their engulfment by macrophages.⁴² These observations are consistent with a model in which the mechanism that triggers engulfment of terminally differentiated myeloid cells can be separated from the apoptotic process inhibited by Bcl-2. Phagocytosis of apoptotic cells appears to be induced by changes in the plasma membrane of the dying cell.⁴³ These findings suggest a model in which some of the cellular processes associated with apoptosis and myeloid senescence are part of a Bcl-2-independent differentiation pathway. The dissociation of the apoptotic response and differentiation by signals provided by Bcl-2 is similar to that observed during hematopoietic cell proliferation mediated by growth factors. In the latter, signaling via growth factors like IL-3 or GM-CSF can promote both cell survival and proliferation.²² In the absence of growth factors, Bcl-2 can maintain hematopoietic cell survival but it fails to induce cell cycle progression.²²

Chemical agents that inhibit macromolecular synthesis have been shown to induce apoptosis in myeloid cell lines.⁷ A likely explanation for these observations is that in leukemic myeloid cells there are proteins that actively suppress the apoptotic mechanism. Inhibition of macromolecular synthesis may block the activity or synthesis of putative apoptosis-repressor proteins. Interestingly, Bcl-2 overexpression inhibited differentiation-induced apoptosis in HL-60 but it had little or no effect on HL-60 apoptosis triggered by inhibitors of macromolecular synthesis. There are several possibilities that may explain this differential response. For example, the apoptotic signal induced by inhibitors of macromolecular synthesis may be stronger or be qualitatively different to that generated during differentiation in HL-60 cells. These observations are not too surprising as the ability of Bcl-2 to inhibit apoptosis in lymphoid cells differs depending on the apoptotic stimulus.^{44,45} The cellular proteins involved in controlling apoptosis in the myeloid lineage are not well understood. It is likely that down-regulation of Bcl-2 in myeloid cells facilitates the apoptotic process triggered by terminal differentiation. Recently, another *Bcl-2*-related gene, *mcl-1* has been isolated from human myeloid cells treated with PMA and it appears to be regulated during differentiation.⁴⁶ In the present work, we provide evidence that another *Bcl-2* family member, *Bcl-x*, is expressed in the early myeloid cell line, K562. The predicted Bcl-x_L protein shares a remarkable amino acid and structural homology to Bcl-2 and its expression suppresses apoptosis induced by growth factor

withdrawal.³⁹ Our preliminary studies suggest that the expression of Bcl-x_L in K562 may account at least in part for the relative resistance of this cell line to apoptotic cell death.^{37,38} However, additional experiments will be needed to firmly establish a role for *Bcl-x* within myeloid cells.

The mechanism by which Bcl-2 and other Bcl-2-related proteins inhibits apoptosis is poorly understood. Recent evidence suggests that Bcl-2 may prevent apoptosis through the regulation of an antioxidant pathway.²⁰ However, other experimental data indicate that Bcl-2 may inhibit apoptosis by modulating Ca²⁺ fluxes through intracellular organelles⁴⁷ or by regulating protein trafficking across the nuclear membrane.^{48,49} Bcl-2 appears to be expressed as a part of an intracellular protein complex. For example, Bcl-2 has been shown to interact with at least two cellular proteins, BAX⁵⁰ and r-Ras p23,⁵¹ although the significance of these protein interactions is not well understood. At least four genes of the *bcl-2* family, *Bcl-2*, *Bcl-x*, *bax*, and *mcl-1*, can be expressed at some point during myeloid differentiation. Together, these results indicate that the regulation of apoptosis within myeloid cells is complex and modulated by multiple proteins.

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