

# Chapter 3

## Roles of Apoptosis-Regulating Bcl-2 Family Genes in AML

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**Abstract** Among the cardinal features of malignancy is abrogation of cell death mechanisms, thus endowing cancer and leukemia cells with a selective survival advantage relative to normal cells. Genetic and epigenetic lesions that result in defects in cell death regulation represent an essential characteristic of acute myeloid leukemia (AML), promoting accumulation of leukemia cells by conferring tolerance to oncogene activation, cell cycle checkpoint defects, and genetic instability. Defects in cell death mechanisms also greatly contribute to resistance to cytotoxic anticancer drugs. Bcl-2 family proteins are central regulators of cell life and death, impacting both apoptotic and non-apoptotic cell death. The Bcl-2 family includes both cell survival- and death-promoting members, with the relative levels and activities of these proteins becoming imbalanced in favor of cell survival in AML and most other malignancies. The fundamental mechanisms of Bcl-2 family proteins and some of their roles in AML are reviewed in this chapter.

**Keywords** Bcl-2 · Cell death · Apoptosis · Cell stress · Autophagy · Chemoresistance

### 3.1 Introduction

Defects in the normal apoptosis mechanisms that keep blood cell numbers in check commonly occur during the pathogenesis and progression of hematopoietic malignancies. Most physiological cell death occurs via apoptosis, a type of programmed cell death essential for normal development and adult tissue homeostasis. In addition to promoting clonal cell expansion by extending cell life span, apoptosis defects also contribute to myriad aspects of tumor biology, including (1) factor-independent growth, allowing hematopoietic cells to survive in absence of trophic support from lymphokines or colony-stimulating factors (CSFs); (2) oncogene activation, negating the pro-apoptotic activity of oncoproteins such as c-Myc and Cyclin-D1 that drive cell division and cell death unless complemented by anti-apoptotic mechanisms; (3) tissue infiltration, where invasive properties of leukemias and lymphomas are supported by promoting cell survival in extra-vascular and extra-nodal

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M. Andreeff (ed.), *Targeted Therapy of Acute Myeloid Leukemia*,  
Current Cancer Research, DOI 10.1007/978-1-4939-1393-0\_3

locations; (4) resistance of immune surveillance mechanisms, especially blunting the pathways that cytolytic T-cells (CTL) and natural killer (NK) cells rely upon for killing tumor target cells; and (5) chemoresistance, where defects in cell death mechanisms raise the threshold for cytotoxicity resulting from macromolecule-damaging drugs that attack DNA, microtubules, and other cellular structures. Thus, restoring sensitivity to apoptosis is an attractive strategy for eliminating malignant cells, which takes advantage in part of the intrinsic abnormalities in neoplastic cells to selectively trigger their death.

From an understanding of the core components of the apoptosis machinery at the molecular and structural levels, and from an emerging knowledge of the signal transduction pathways that link to this core machinery, many potential new therapies for leukemia are beginning to emerge, and new insights into the mechanisms by which currently available therapies work (and why they fail) are accumulating. This knowledge base provides the foundation upon which more effective therapies for hematopoietic malignancies may become a near-term reality.

### 3.1.1 *Apoptosis Inducers and Effectors*

Apoptosis is caused by the activation of intracellular proteases, known as caspases. These cysteine proteases cleave their cellular targets at aspartic acid residues residing in the context of tetrapeptide motifs within polypeptide substrates (Boatright and Salvesen 2003). The human genome encodes ten caspases (Reed et al. 2004; Saleh et al. 2004). Numerous cellular substrates of caspases have been identified, which in aggregate produce the characteristic morphology we call “apoptosis” when cleaved. Several pathways for triggering caspase activation exist, though two have been elucidated in great detail and have been the center of much attention in recent years. These two pathways for apoptosis are commonly referred to as the *intrinsic* and the *extrinsic* pathways (Salvesen 2002).

The intrinsic pathway centers on mitochondria as initiators of cell death. Multiple signals converge on mitochondria, including DNA damage, hypoxia, and oxidative stress, causing these organelles to release cytochrome *c* (cyt *c*) and other apoptogenic proteins into cytosol. In the cytosol, cyt *c* binds caspase-activating protein Apaf1, triggering its oligomerization into a heptameric complex that binds pro-caspase-9, forming a multi-protein structure known as the “apoptosome” (Salvesen and Renatus 2002). Physical binding of Apaf1 to pro-caspase-9 is mediated by their caspase recruitment domains (CARDs), through homotypic CARD–CARD binding. Activation of apoptosome-associated cell death protease caspase-9 then initiates a proteolytic cascade, where activated caspase-9 cleaves and activates downstream effector proteases, such as pro-caspase-3.

In contrast, the extrinsic apoptotic pathway relies on tumor necrosis factor (TNF) family death receptors for triggering apoptosis. A subgroup of the TNF family receptors contains a cytosolic death domain (DD) that enables their intracellular interaction with downstream adapter proteins, which link these receptors to specific

caspsases. Upon ligand binding, TNF family receptors containing cytosolic DDs (e.g., Fas, TNFR, TRAIL-R1, and TRAIL-R2) cluster in membranes, recruiting caspase-binding adaptor proteins, including the bipartite adapter Fas-associated protein with death domain (FADD) that contains both a DD and a death effector domain (DED) (Wallach et al. 1999). The DED of FADD binds DED-containing procaspases (e.g., caspases-8 and -10), forming a “death-inducing signaling complex” (DISC) and resulting in caspase activation by an “induced proximity” mechanism (Boatright and Salvesen 2003).

Aside from the intrinsic and extrinsic pathways, multiple additional routes to caspase activation are possible, though for some the pathophysiological relevance is less well established (reviewed in (Reed 2005; Xu et al. 2005)). Also it is important to note that while these and the aforementioned can all lead to caspase activation and apoptosis, some of them also trigger parallel caspase-independent cell death mechanisms, which nevertheless kill cells via non-apoptotic mechanisms. For example, mitochondria not only release caspase-activating proteins such as *cyt c*, but also release endonuclease G (Endo G) and a chromatin-modifying protein apoptosis-inducing factor (AIF) that promote genome digestion and cell death independent of caspases (Penninger and Kroemer 2003). Thus, some types of cell death stimuli can induce parallel paths to apoptotic (caspase-dependent) and non-apoptotic (caspase-independent) cell demise.

### 3.1.2 *Apoptosis Blockers*

Given the critical importance of making the correct choices about cell life–death decisions in complex multicellular organisms, it is not surprising that the pathways governing caspase activation are under exquisite control by networks of proteins that directly or indirectly communicate with these proteases. A delicate balance between pro-apoptotic and anti-apoptotic regulators of apoptosis pathways is at play on a continual basis, ensuring the survival of long-lived cells and the proper turnover of short-lived cells in a variety of tissues, including the bone marrow, thymus, and peripheral lymphoid tissues. However, imbalances in this delicate dance of pro- and anti-apoptotic proteins occur in disease scenarios, including cancer where the scales tip in favor of anti-apoptotic proteins and endow cells with a selective survival advantage that promotes neoplasia and malignancy.

The anti-apoptotic proteins responsible for creating roadblocks to apoptosis have been mapped to specific pathways, providing insights into the defective cell death mechanisms that contribute to malignancy. Among these apoptosis blockers are members of the Bcl-2 family, a large group of proteins ( $n \geq 25$  in humans) that control mitochondria-dependent steps in cell death pathways (Reed et al. 2004), including dictating whether *cyt c* is or is not released from these organelles. These proteins control the intrinsic pathway (Kroemer and Reed 2000). Bcl-2 family proteins however are also capable of modulating other cell death and cell survival pathways and mechanisms, including the endoplasmic reticulum (ER) pathway for

cell death (Demaurex and Distelhorst 2003), the extrinsic (death receptor) pathway, and autophagy (see below).

The Bcl-2 family proteins can be contrasted with other types of anti-apoptotic proteins known to create apoptosis roadblocks in cancer cells, which are discussed in other chapters in this book. Examples of alternative blockers of apoptosis include (a) c-FLIP, a protein that competes with pro-caspase-8 and -10 for interactions with TNF/Fas family death receptors complexes (Tschopp et al. 1998), and (b) IAP family proteins that thwart cell death by directly binding to and suppressing the activity of certain caspases (Deveraux and Reed 1999; Deveraux et al. 1999; Salvesen and Duckett 2002), in addition to other mechanisms.

### 3.2 The Bcl-2 Family—Diversity of Players

The human genome encodes at least 25 Bcl-2 family proteins. Only six of these are anti-apoptotic and thus represent logical targets for cancer therapy. The six anti-apoptotic members of the family are Bcl-2, Bcl-XL, Mcl-1, Bcl-W, Bfl-1, and Bcl-B. Overexpression of several of these anti-apoptotic Bcl-2-family proteins has been documented in various hematopoietic malignancies (reviewed in Kitada et al. 2002). The anti-apoptotic members of the Bcl-2 are comprised of alpha-helical bundles with structural similarity to the pore-forming proteins of bacteria (e.g., colicins, diphtheria toxin, etc.). Sequence homology motifs called Bcl-2 homology (BH) domains are recognizable in these proteins, with anti-apoptotic members possessing BH1, BH2, BH3, and BH4 domains. These family members typically also have a C-terminal hydrophobic transmembrane domain that anchors them into intracellular membranes—primarily mitochondria and ER membranes.

Pro-apoptotic Bcl-2 family members can be subgrouped into different categories based on sequence, structure, and function properties, making this type of Bcl-2 family member much more diverse than the anti-apoptotic branch of the family. By definition, all pro-apoptotic family members possess the BH3 domain, an amphipathic alpha-helix that mediates their interactions with anti-apoptotic family members. One subset, characterized by Bax, Bak, and probably Bok, appears to have evolved directly from the same ancestor gene as the anti-apoptotic branch of the family, giving these proteins a similar 3D structure (namely alpha-helical bundles with similar to pore-forming bacterial proteins) and possessing several BH domains (typically BH1, BH2, and BH3, but not BH4). This pro-apoptotic group of the family is sometimes called the “multidomain” branch (reviewed in Reed 2006). The other subset of pro-apoptotic Bcl-2 family proteins typically has little overall structural similarity, with the BH3 domain representing the only commonality. This branch of the family has thus been dubbed the “BH3-only” proteins (reviewed in Bouillet and Strasser 2002). Among the BH3-only proteins are those that (a) bind to the anti-apoptotic family members to neutralize them and (b) those that bind to both anti-apoptotic and the multidomain pro-apoptotic family members, antagonizing the anti-apoptotic and activating the pro-apoptotic proteins.

### 3.3 Dimerization of Bcl-2 Family Proteins

Bcl-2 family proteins participate in hand-to-hand combat to control cell life-and-death decisions. The surface of the anti-apoptotic members of the family forms a crevice that serves as a receptor-like structure for binding the ligand-like BH3 domains of the pro-apoptotic proteins. The BH3 domain consists of an amphipathic alpha-helix that binds this hydrophobic crevice on anti-apoptotic Bcl-2-family members, negating their cytoprotective activity (Fesik 2000). Proof-of-concept experiments using BH3 peptides have suggested that compounds docking at this regulatory site on Bcl-2 and its related anti-apoptotic proteins could provide a route to effective suppression of these proteins, thereby promoting apoptosis of malignant cells (Holinger et al. 1999). Indeed, several chemicals have been identified that bind this pocket on anti-apoptotic Bcl-2-family proteins and that promote apoptosis (reviewed in Reed 2005; Pellecchia and Reed 2004; Reed 2008). Small-molecule inhibitors that directly interact with Bcl-2 or related anti-apoptotic proteins via the BH3-binding pocket have entered clinical trials for cancer and leukemia, a topic reviewed elsewhere in this book.

Additionally, some pro-apoptotic BH3-only members of the family use their BH3 domains to activate multidomain pro-apoptotic proteins Bax and Bak (Reed 2006). The structural basis for this protein interaction has been elucidated (Gavathiotis et al. 2010), thus suggesting a possible path to production of agonists of Bax and Bak for oncology therapeutics development.

Various BH3-mimicking compounds have been reported as a strategy for therapeutics development (Vogler et al. 2009; Kang and Reynolds 2009). A critical but unanswered question about the various chemical antagonists of Bcl-2 is to what extent they inhibit various anti-apoptotic members of the Bcl-2-family ( $n = 6$ ), and whether broad-spectrum versus selective inhibitors would provide the optimal path forward for clinical applications, where efficacy is balanced against toxicity. Moreover, the structure activity relation (SAR) characteristics of the optimal compound may vary depending on the type of cancer or leukemia one wishes to attack, given that the repertoire of Bcl-2 family proteins differs among different types of malignancies. For instance, for optimal treatment of acute myeloid leukemia (AML), one might anticipate that the best compounds will have SAR characteristics that consistently promote apoptosis of AML cells (especially chemorefractory AML cells) but that do not kill normal hematopoietic stem cells.

### 3.4 Phenotype Conversion by Bcl-2 Family Proteins

Conditions have been identified where anti-apoptotic Bcl-2 family members can seemingly switch their phenotype, converting into pro-apoptotic proteins. The mechanism underlying this phenomenon involves exposure of the BH3 domain, which in proteins such as Bcl-2 and Bcl-XL is normally buried in the protein, with the interaction surface of the BH3 domain oriented towards the hydrophobic core

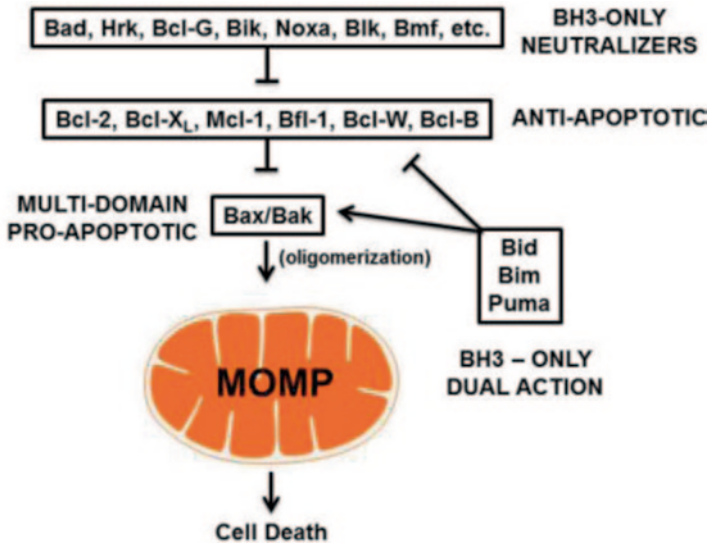
of the protein. Mechanisms for phenotypic conversion include proteolytic cleavage and interactions with other proteins that promote conformational changes in anti-apoptotic Bcl-2 family proteins. Cleavage of Bcl-2 and Bcl-XL, for example, by caspases removes the N-terminal region containing the BH4 domain, presumably causing an opening of the protein structures that exposes the BH3 domain. Interaction of Bcl-2 with the orphan nuclear receptor, Nur77 (also known as TR3 and NR4A1), has also been identified as a mechanism for phenotype conversion. Stimuli that cause Nur77 to leave the nucleus and traffic to mitochondria cause apoptosis in a Bcl-2-dependent manner (Li et al. 2000). In the cytosol, Nur77 binds the Bcl-2 protein, thus accounting for accumulation of this nuclear receptor on the surface of mitochondria. Nur77 induces a profound conformational change of Bcl-2, causing exposure of this BH3 domain, and converting Bcl-2 from a protector to a killer (Lin et al. 2004). The Nur77-mediated mechanism of phenotypic conversion of Bcl-2 may be particularly relevant to AML, given that Nur77 is frequently epigenetically silenced in AML and considering that double knockout of Nur77 and its close relative Nor1 in mice causes AML (Mullican et al. 2007).

The revelation that the Bcl-2 protein can have two opposing phenotypes, depending upon its interactions with other proteins such as Nur77, suggests a possible explanation for the paradoxical association of higher Bcl-2 levels with favorable (not worse) clinical outcome in some types of cancer (Reed 1996), including some subtypes of AML (Kornblau et al. 1999). Examination of Bcl-2 and Nur77 expression in clinical specimens may help to select patients most likely to benefit from therapeutic strategies designed to stimulate the Nur77 pathway for Bcl-2 conversion, since cells with higher Bcl-2 are more sensitive to Nur77 activators (Lin et al. 2004).

### **3.5 Mitochondrial Mechanisms at the Core of Bcl-2 Family Function**

Though Bcl-2 family proteins possess diverse mechanisms by which they can impact cell life-and-death decisions (see below), their central mechanism is believed to relate to regulation of permeability of the outer mitochondrial membrane, thus controlling the release (or sequestration) of apoptogenic proteins stored in the inner membrane space between the inner and outer mitochondria membranes (reviewed in (Chipuk and Green 2008)). When activated, multidomain pro-apoptotic Bcl-2 family members Bax and Bak insert in the outer membrane, oligomerize, evidently forming lipid pores directly or indirectly, cause release of proteins from mitochondria, thus constituting the phenomenon of mitochondrial outer membrane permeabilization (MOMP) (reviewed in Reed 1997; Jurgensmeier et al. 1998; Qian et al. 2008).

Anti-apoptotic Bcl-2 family proteins bind Bax and Bak, preventing their oligomerization in mitochondrial membranes (Fig. 3.1). The BH3-only proteins bind anti-apoptotic proteins, thus neutralizing them and preventing them from binding to and negating the pore-forming proteins Bax and Bak. In addition, a few of the BH3-only proteins (e.g., Bid, Bim, and Puma) not only antagonize the anti-apoptotic



**Fig. 3.1** Hierarchy of Bcl-2 family interactions in the regulation of mitochondrial outer membrane permeabilization (*MOMP*)

members of the family (e.g., Bcl-2 and Bcl-XL), but also bind to and activate the multidomain pro-apoptotic Bax and Bak proteins, stimulating their oligomerization in mitochondrial membranes.

Some studies have also suggested a role for Bcl-2 family proteins in regulating aspects of inner mitochondrial membrane function, particularly as pertains to perturbations in the electrochemical gradient (Chen et al. 2011). This aspect of Bcl-2 protein function is still poorly understood. Roles for interactions of Bcl-2 family proteins with resident mitochondrial proteins such as the voltage-dependent anion channels (VDACs) have also been implicated in mitochondrial control of apoptosis, but their overall importance is unclear (Cheng et al. 2003; Shimizu et al. 1999). Bcl-2 family proteins such as pro-apoptotic Bax have also been reported to impact mitochondrial ultrastructure by regulating membrane fission/fusion proteins such as Opal and Dynamin, a feature that has been correlated with remodeling of cristae of mitochondria to affect accessibility of cyt *c* for release (Yamaguchi et al. 2008; Cassidy-Stone et al. 2008).

### 3.6 Bcl-2 Family Proteins at the ER

The ER also plays an important role in regulating cell life-and-death decisions in the context of various cell stress scenarios. At least two aspects of ER biology are relevant. First, the ER is the major storage site for intracellular  $\text{Ca}^{2+}$ . Control of release of  $\text{Ca}^{2+}$  from the ER has a number of important implications for cell death

regulation (reviewed in Demarex and Distelhorst 2003; Kim et al. 2008a). Second, conditions that cause accumulation of unfolded proteins in the lumen of the ER invoke an evolutionarily conserved signaling program, called the unfolded protein response (UPR). Signaling proteins involved in the UPR are connected to the Bcl-2 family. These mechanisms are described below.

Conversely, the ER appears to be capable of regulating the functions of Bcl-2 family proteins. For example, sphingolipids derived from the ER and delivered into mitochondrial membranes (at sites of direct contact of ER with mitochondria) have been implicated in creating conditions in mitochondrial membranes that are permissive for pore formation by Bax and Bak (Chipuk et al. 2012; Lee et al. 2011).

### **3.6.1 $Ca^{2+}$ Regulation**

Disturbances in intracellular  $Ca^{2+}$  regulation contribute to cell life and death. For example, acute release of  $Ca^{2+}$  from the ER can trigger a variety of signaling mechanisms that promote cell death (Kim et al. 2008b). Conversely, pulses of  $Ca^{2+}$  delivered via inositol triphosphate receptors (IP3Rs) at contact sites of ER with mitochondria promote mitochondrial bioenergetics, sustaining adenosine triphosphate (ATP) and cell survival (Cardenas et al. 2010). Several Bcl-2 family members, particularly the anti-apoptotic members of the family, reside within ER membranes. At least some Bcl-2 family proteins regulate ER  $Ca^{2+}$  homeostasis, with anti-apoptotic proteins Bcl-2 and Bcl-XL reducing the steady-state levels of luminal [ $Ca^{2+}$ ] (Chae et al. 2004; Xu et al. 2008; Kim et al. 2008a; Hunsberger et al. 2011). Various studies have shown that Bcl-2 and Bcl-XL increase passive leak of  $Ca^{2+}$  ions from the ER via a mechanisms that is dependent upon IP3Rs. A picture has emerged that envisions anti-apoptotic Bcl-2 proteins associating with IP3Rs, causing passive leak of  $Ca^{2+}$  to achieve a lower resting (free)  $Ca^{2+}$  concentration in the ER (Rong et al. 2008). In contrast, Bax and Bak increase ER  $Ca^{2+}$  levels (Oakes et al. 2005).

Bcl-2 and Bcl-XL interact in ER membranes with BI-1 (Bax inhibitor-1), a multi-membrane ER protein that also regulates ER  $Ca^{2+}$  homeostasis, in a manner that largely phenocopies Bcl-2 (Chae et al. 2004; Xu et al. 2008). Interestingly, gene ablation studies suggest that BI-1 is required for ER  $Ca^{2+}$  regulation by Bcl-XL (Xu et al. 2008). BI-1 also reportedly binds IP3Rs (Kiviluoto et al. 2012) and controls  $Ca^{2+}$  transport from ER to mitochondria via IP3Rs (Sano et al. 2012). Thus, BI-1 appears to collaborate with Bcl-2/Bcl-XL to regulate ER  $Ca^{2+}$ . The impact of ER  $Ca^{2+}$  on tumor cell survival during ER and metabolic stress requires further investigation.

### **3.6.2 UPR Regulation**

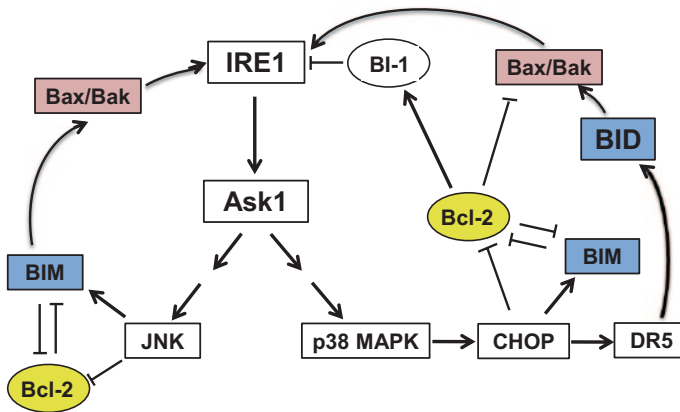
Accumulation of unfolded proteins in the ER stimulates the UPR, also called the ER stress response. ER stress can be induced by myriad stimuli that perturb protein



folding, including hypoxia and oxidative stress (via effects on protein disulfide bonding), nutrient perturbations (hypoglycemia/hyperglycemia), and disturbances to cellular protein homeostasis that overwhelm proteasome function and molecular chaperones (Kim et al. 2008b; Ma and Hendershot 2004). (Dong et al. 2005; Shuda et al. 2003; Fernandez et al. 2000). While UPR signaling events clearly help cells (malignant and normal) to adapt to inhospitable microenvironments (Jamora et al. 1996; Li and Lee 2006; Lee 2007; Romero-Ramirez et al. 2004), when sustained or excessive, ER stress triggers cell death, usually by apoptosis but also by non-apoptotic mechanisms (Xu et al. 2005; Kim et al. 2008). Therefore, malignant cells often develop barriers to ER stress-induced apoptosis, providing novel targets for therapeutic intervention. For example, ER stress is causally involved in the cytotoxic activity of proteasome inhibitors used for cancer treatment (Lee et al. 2003). Also, some experimental agents now in clinical testing induce ER stress as their primary mechanism of action (Zou et al. 2008).

While three major signal transduction nodes have been identified as components of the UPR (initiated by IRE1, PERK, ATF6), it is the IRE1 that has been most clearly linked to the mechanism of Bcl-2 family proteins IRE1 $\alpha$  is a transmembrane protein that contains both a Ser/Thr-kinase domain and an endoribonuclease domain, the latter of which processes an intron from X box-binding protein-1 (XBP-1) mRNA to produce the 41 kDa XBP-1 protein (a bZIP family transcription factor). XBP-1 binds to promoters of several genes involved in UPR and ERAD (ER-assisted degradation) (Rao and Bredesen 2004), and thus seems to be generally protective. In contrast, the protein kinase activity of IRE1 $\alpha$  has been linked to cell death induction, initiated by apoptotic signaling kinase-1 (Ask1), which causes Jun-N-terminal kinase (JNK) activation (Nishitoh et al. 2002).

Bax and Bak reportedly bind IRE1 and activate it, thus inducing a cascade of stress kinase activation (Hetz et al. 2006) (Fig. 3.2). Within these kinase cascades, among the apoptosis-relevant substrates of JNK are Bcl-2 and Bim, which are inhibited and activated, respectively, by JNK phosphorylation (Lei and Davis 2003; Putcha et al. 2003; Srivastava et al. 1998; Wei et al. 2008). Substrates of p38 mitogen-activated protein kinase (MAPK) include transcription factor C/EBP homologous protein (CHOP), which represses expression of the gene encoding Bcl-2 and induces expression of genes encoding Bim and DR5 (TRAIL-R2) (Zou et al. 2008; Lei and Davis 2003; Putcha et al. 2003; McCullough et al. 2001; Puthalakath et al. 2007; Wang and Ron 1996). Prolonged CHOP activity can also promote non-apoptotic cell death via induction of ER oxidase-1a (ERO1a) (Li et al. 2009; Ozcan and Tabas 2012; Marciniak et al. 2004). Thus, IRE1 is a focal point for the ER-relevant activities of Bcl-2-family proteins, with pro-apoptotic Bax and Bak proteins interacting with and activating IRE1 (Hetz et al. 2006). Conversely, cytoprotective Bcl-2-interacting ER membrane protein, BI-1 (Tmbim6) (Xu and Reed 1998; Reimers et al. 2008) binds to and suppresses IRE1 signaling in cultured cells and in mice (Bailly-Maitre et al. 2006; Lisbona et al. 2009; Bailly-Maitre et al. 2010).



**Fig. 3.2** Networks connecting Bcl-2 family proteins to the UPR (ER stress) machinery. MAPK mitogen-activated protein kinase, *CHOP* C/EBP homologous protein, *JNK* Jun-N-terminal kinase, *Ask1* apoptotic signaling kinase-1

### 3.7 Autophagy

Autophagy is a catabolic cellular process for lysosome-mediated degradation of senescent proteins and organelles (Bernales et al. 2006; Kruse et al. 2006). Autophagy is implicated in cancer primarily as a survival mechanism, where it provides substrates for maintaining ATP levels during times of nutrient deprivation and hypoxia. However, autophagy that is excessive in nature may also contribute or induce to cell death in some contexts (Levine and Yuan 2005; Kroemer et al. 2010). Among the Bcl-2-interacting proteins is beclin (ATG6), an essential component of the autophagy machinery. The beclin protein has a BH3-like domain that mediates interactions with Bcl-2. Bcl-2 inhibits beclin's participation in protein complexes that generate autophagic vesicles. Phosphorylation of Bcl-2 by JNK provides a means of freeing beclin to allow autophagy to proceed (Wei et al. 2008), in addition to displacement of beclin from Bcl-2 by various pro-apoptotic BH3-containing proteins.

Interestingly, ER stress also induces autophagy (Bernales et al. 2006; Momoi 2006; Yorimitsu et al. 2006; Ogata et al. 2006), potentially involving a diversity of mechanisms, including (a) changes in ER  $\text{Ca}^{2+}$ , perhaps mediated by IP3Rs (Hoyer-Hansen and Jaattela 2007; Criollo et al. 2007; Lam et al. 2008; Vicencio et al. 2009); (b) activation of  $\text{Ca}^{2+}$ -dependent kinases, including CamKK and DAPK1 (Gozuacik et al. 2008; Zalckvar et al. 2009; Sakaki et al. 2008); and (c) JNK-mediated phosphorylation of Bcl-2 (which causes its release of Beclin-1) occurring downstream of IRE1 signaling (Pattingre et al. 2005; He et al. 2012). Thus, the ability of Bcl-2 family proteins to regulate ER  $\text{Ca}^{2+}$  via interactions with IP3Rs and to modulate UPR signaling via interactions with IRE1 appears to establish a complex network of regulatory mechanisms that link the Bcl-2 family to autophagy and cellular resilience.

### 3.8 Interacting Proteins and Posttranslational Modifications

A plethora of proteins have been reported to interact with Bcl-2 family members, suggesting that the Bcl-2 family connects to a variety of protein networks and cellular processes as a mechanism for sensing the cellular status. Bcl-2-interacting proteins range from nuclear receptors that exit the nucleus to bind Bcl-2 and promote apoptosis (Nur77, SHP), to molecular chaperones and co-chaperones (FK506-binding proteins, FKBP; BAG family Hsp70/Hsc70 co-chaperone) that collaborate with Bcl-2 to promote cell survival, to NLR family innate immunity proteins involved in activation of pro-inflammatory caspases, to kinases and phosphatases (reviewed in Chipuk et al. 2010). Pro-apoptotic family members such as Bax have been reported to interact with Hsp27 family chaperone clusterin, innate immunity adapter protein ASC, the cytoprotective peptide humanin, cathepsin family proteases, and more (reviewed in Reed 2006). Much remains unknown about the cellular contexts in both health and disease where these various protein interactions play fundamentally important roles in cell life-and-death decisions.

Post-translational modifications of Bcl-2 family proteins have not been systematically studied, but multiple examples are found in the literature. For example, phosphorylation of Bcl-2 has been shown to modulate its activity (Konopleva et al. 2002), with MEK1 inhibitors suppressing Bcl-2 phosphorylation and displaying robust synergy with chemical inhibitors of Bcl-2 in AML cells (Milella et al. 2002). Akt (PKB) and several other kinases phosphorylate pro-apoptotic protein BAD (a BH3-only protein), causing its sequestration in a complex with 14-3-3 proteins (Khawaja 1999). Dephosphorylation of pro-apoptotic Bak protein on specific tyrosines has been reported to be required for its activation (Fox et al. 2010).

Proteolytic cleavage of Bcl-2 family proteins is another functionally important post-translational modification, with cleavage of pro-apoptotic BH3-only protein Bid serving as a prime example. Bid becomes activated by caspase-8-mediated cleavage in the context of signaling by TNF family death receptors (extrinsic pathway), resulting in its translocation from cytosol to mitochondrial membranes and exposure of its BH3 domain to enable interaction with other Bcl-2 family members (reviewed in Korsmeyer et al. 2000). Bid is also cleaved and activated by other classes of intracellular cysteine proteases in various pathological contexts (Droga-Mazovec et al. 2008; Upton et al. 2008; Stoka et al. 2001; Chen et al. 2001).

Deamidation of Bcl-XL, converting asparagine to isoaspartic acid residues, has been associated with DNA damage responses (Deverman et al. 2002). Deamidation of Bcl-XL impairs its ability to bind various BH3-containing proteins and to reduce its anti-apoptotic activity. Interestingly, defects in Bcl-XL deamidation have been associated with myeloproliferative disorders (Zhao et al. 2008).

Ubiquitination is an important post-translational modification for regulating the stability of Bcl-2 family proteins. For example, anti-apoptotic protein Mcl-1 is the substrate of an E3 ligase (MULE/ARF-BP1) that contains a BH3-like domain, mediating Mcl-1 degradation in the context of DNA damage (Zhong et al. 2005).

Phosphorylation impacts Mcl-1 protein stability, with phosphorylation by Erk1 slowing and GSK3 $\beta$  accelerating degradation (Domina et al. 2004; Maurer et al. 2006). In contrast, ubiquitination of Bfl-1 occurs constitutively, keeping levels of Bfl-1 protein low—a mechanism that becomes defective in lymphomas (Fan et al. 2010).

### 3.9 Deregulated Expression of Bcl-2 Family Genes in AML

Many examples exist of alterations in the expression of either apoptosis-suppressing or apoptosis-inducing members of the Bcl-2 family in human cancers (reviewed in Reed et al. 2004; Levine and Yuan 2005; Kroemer et al. 2010; Momoi 2006). The explanations for overexpression of anti-apoptotic proteins of the Bcl-2 family in cancer and leukemia cells vary, but documented mechanisms include chromosomal translocations, gene amplification, loss of microRNAs that target Bcl-2 family genes, gene hypomethylation, transcriptional upregulation, and perhaps altered protein stability (reviewed in (Kitada et al. 2002)).

Bcl-2, Bcl-XL, Mcl-1, and, occasionally, other anti-apoptotic members of the Bcl-2 family are commonly overexpressed in AML (Kornblau et al. 1999; Andreeff et al. 1999; Campos et al. 1993; Konopleva and Andreeff 2002; Kasimirbauer et al. 1998; Deng et al. 1998; Lauria et al. 1997; Schaich et al. 2001). In AML, higher levels of Bcl-2 protein or mRNA have been associated with poor responses to chemotherapy and/or shorter overall survival (Campos et al. 1993; Kasimirbauer et al. 1998; Deng et al. 1998; Lauria et al. 1997; Bincoletto et al. 1999; Campos et al. 1997; Rochitz et al. 1999; Maung et al. 1994; Karakas et al. 1998).

Conversely, pro-apoptotic genes that oppose these cytoprotective proteins can become inactivated in malignant cells, through gene deletion, somatic mutation, gene hypermethylation, and transcriptional downregulation and probably other mechanisms. For example, inactivating mutations in the pro-apoptotic Bcl-2 family gene *Bax* occur in some hematological malignancies including AML (Meijerink et al. 1995; Brimmell et al. 1998; Meijerink et al. 1998).

The tumor microenvironment undoubtedly contributes to the regulation of Bcl-2 family proteins in AML. Several cytokines, including granulocyte colony-stimulating factor (G-CSF) and Flt3, have been reported to upregulate expression of Bcl-2 and promote apoptosis resistance in freshly isolated AML cells *in vitro*, implying that the Bcl-2 gene is subject to regulation by inputs from cytokine/lymphokine receptor pathways of the tumor microenvironment (Lisovsky et al. 1996; Bradbury et al. 1994). Lymphokines that activate STAT3 stimulate expression of Bcl-XL. Retinoids also can modulate the expression of Bcl-2 family proteins, including downregulating Bcl-2 and Bcl-XL in AML (Andreeff et al. 1999; Ahmed et al. 1999; Elstner et al. 1996; Dipietrantonio et al. 1996; Delia et al. 1995). Thus, numerous signal transduction and transcriptional pathways may be capable of modulating the expression of Bcl-2 family genes in AML.

### 3.10 Cytotoxic Chemotherapy and Bcl-2 Family Proteins

In many instances, cell death induced by anticancer drugs appears to occur via the mitochondrial pathway that involves release of cytochrome *c*. It remains unclear how damage induced to DNA or other macromolecules by anticancer drug triggers mitochondrial release of cyt *c*. However, some specific mechanisms have been revealed in recent years. For example, in some types of cells, DNA-damaging agents can induce activation of p53, which in turn binds to cis-acting elements located within the Bax gene (Miyashita and Reed 1995) and the Bax-activity gene Puma and Bim. The p53 protein has also been reported to modulate the activity of Bcl-2 family proteins in the cytosol and on the surface of mitochondria. Another example of how anticancer drugs activate the mitochondrial (intrinsic) pathway is found in the pro-apoptotic Bcl-2 family protein Bim, which can be activated by anti-microtubule drugs. The Bim protein is normally sequestered at microtubules but can be released into the cytosol when it translocates to the surface of mitochondria, heterodimerizing with Bcl-2 or Bcl-XL and triggering cytochrome *c* release.

### Conclusions

Bcl-2 family proteins are intricately involved in the biology of AML. From pathogenesis to progression and resistance to therapy, Bcl-2 family proteins are inextricably linked to AML. The advent of experimental therapeutics targeting anti-apoptotic Bcl-2 family proteins (small molecules) and mRNA (antisense) creates hope that are more effective strategies for treating AML may be near.

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