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Review

BCL2A1: the underdog in the BCL2 family

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B-cell lymphoma 2 (BCL2) proteins are important cell death regulators, whose main function is to control the release of cytochrome *c* from mitochondria in the intrinsic apoptotic pathway. They comprise both pro- and anti-apoptotic proteins, which interact in various ways to induce or prevent pore formation in the outer mitochondrial membrane. Due to their central function in the apoptotic machinery, BCL2 proteins are often deregulated in cancer. To this end, many anti-apoptotic BCL2 proteins have been identified as important cellular oncogenes and attractive targets for anti-cancer therapy. In this review, the existing knowledge on B-cell lymphoma 2-related protein A1 (BCL2A1)/Bcl-2-related gene expressed in fetal liver (Bfl-1), one of the less extensively studied anti-apoptotic BCL2 proteins, is summarized. BCL2A1 is a highly regulated nuclear factor κB (NF-κB) target gene that exerts important pro-survival functions. In a physiological context, BCL2A1 is mainly expressed in the hematopoietic system, where it facilitates survival of selected leukocytes subsets and inflammation. However, BCL2A1 is overexpressed in a variety of cancer cells, including hematological malignancies and solid tumors, and may contribute to tumor progression. Therefore, the development of small molecule inhibitors of BCL2A1 may be a promising approach mainly to sensitize tumor cells for apoptosis and thus improve the efficiency of anti-cancer therapy.
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Facts

- B-cell lymphoma 2-related protein A1 (BCL2A1) is particularly important in the hematopoietic system and exerts its anti-apoptotic function by sequestering pro-apoptotic B-cell lymphoma 2 (BCL2) proteins.
- In different types of cancer including leukemia and lymphoma an increased expression of BCL2A1 was described.
- Enhanced expression of BCL2A1 can result in resistance to chemotherapeutic drugs.
- Nuclear factor κB (NF-κB) is an important inducer of BCL2A1 expression.

Open Questions

- Is BCL2A1 induced upon inflammasome formation and important for cellular survival during inflammation?
- Does BCL2A1 have a function or interaction partners outside of the BCL2 family?
- Which E3 ligase mediates the proteasomal degradation of BCL2A1?
- Can small molecule inhibitors of BCL2A1 be used clinically as anti-cancer treatments?

Overview of the BCL2 Family

Apoptosis or programmed cell death can be either triggered by death receptor ligation on the cell surface (the extrinsic pathway) or alternatively upon cellular stress at the mitochondria (the intrinsic pathway). While death receptor ligation results in the formation of the death-inducing signaling complex, in the intrinsic pathway the release of cytochrome *c* from the mitochondrial intermembrane space into cytosol triggers the formation of the apoptosome and caspase-9 activation. The extrinsic pathway appears to be mainly regulated by the caspase-8 inhibitory protein FLIP, which was first identified by Jurg Tschopp and co-workers.[1,2] However, in the intrinsic pathway the critical step is the release of cytochrome *c* from mitochondria, which is regulated by the BCL2 proteins.[3] The BCL2 protein family consists of both pro- and anti-apoptotic members, which all share sequence homology in their BCL2 homology (BH) domains. The pro-apoptotic proteins comprise the multidomain proteins BAX and BAK as well as the BH3-only proteins. By forming a pore in the outer mitochondrial membrane, BAX and BAK have an essential role in mediating cytochrome *c* release and thus their activation is tightly controlled by the other BCL2 proteins. The BH3-only proteins are highly regulated on the transcriptional and post-transcriptional level and can be induced by multiple stress signals.[4] Upon activation, the BH3-only proteins can activate BAX and BAK, thereby triggering cytochrome *c* release and apoptosis. The main function of the anti-apoptotic BCL2 proteins is to counteract the activation of BAX and BAK. Thus they can either inhibit BAX and BAK directly, or sequester and inactivate BH3-only proteins. So far,

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Abbreviations: BCL2, B-cell lymphoma 2; BCL2A1, B-cell lymphoma 2-related protein A1; BH, BCL2 homology; Bfl-1, Bcl-2 related gene expressed in fetal liver; GRS, Glasgow rearranged sequence; NF-κB, nuclear factor κB; TNF, tumor necrosis factor; NuBCP-9, Nur77-derived BCL2-converting peptide with nine amino acids; PRP, pattern recognition receptor
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multiple anti-apoptotic BCL2 proteins have been described, namely BCL2, BCL-X_L, BCL-w, MCL1, BCL-B and BCL2A1 (also called Bcl-2 related gene expressed in fetal liver (Bfl-1) or Glasgow rearranged sequence (GRS)). Many of these proteins have been identified as important cellular oncogenes that not only promote tumorigenesis but also contribute to the resistance to chemotherapeutic drugs and failure of anti-cancer treatments. The importance of BCL2 proteins for cancer progression has recently been highlighted by a genome-wide screen, which identified BCL-X_L and MCL1 as highly amplified in cancer cells.[5] However, although BCL2, BCL-X_L and MCL1 are well studied, less is known about the exact function of BCL-w, BCL-B and BCL2A1. Here, the published knowledge on BCL2A1 is reviewed with a particular focus on its role in cancer biology.

Structure of BCL2A1

The human gene *BCL2A1* is located on chromosome 15q24.3 and contains three exons.[6,7] The most common mRNA for *BCL2A1* is transcribed from exons 1 and 3, resulting in a 175 amino-acid protein, which consists of nine α-helices. Crystal structures of BCL2A1 in complex with BH3-peptides (Protein Data Bank: 3MQP, 3I1H, 2VM6) revealed that it displays a similar hydrophobic groove as found on all related anti-apoptotic BCL2 proteins.[8] In addition, it contains four BH-domains (BH1–4) (Figure 1). In contrast to other anti-apoptotic BCL2 proteins, BCL2A1 does not display a well-defined C-terminal transmembrane domain. However, its C-terminus is of importance for the anti-apoptotic function and the subcellular localization of BCL2A1.[9]

An additional isoform named Bfl-1S was described, which contains all three exons with an early stop codon in exon 3.[10] This isoform is expressed in lymph nodes and spleen and the resulting 163 amino-acid protein has an altered and shorter C-terminus, which results in nuclear rather than cytoplasmic or mitochondrial localization. However, the physiological function of this alternative splice variant is only poorly understood and whether there is a nuclear function for Bfl-1S remains to be investigated.

Mouse *Bcl2a1* contains two exons and is encoded on chromosome 9. In contrast to the human gene, it contains four copies (*A1-a, A1-b, A1-c, A1-d*). Although *A1-a*, *A1-b* and *A1-d* are nearly identical, *A1-c* contains a point mutation resulting in a truncated transcript.[11] Overall, murine and human BCL2A1 share 72% amino-acid identity and display very similar structures[8,12] (Figure 1).

Interaction Partners of BCL2A1

A shared characteristic of all anti-apoptotic BCL2 proteins is the sequestration of pro-apoptotic BCL2 proteins including the

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                                        BH4
HUMAN BCL2A1                MTDCEFGYIYRLAQDYLQCVLQIPQPGSGPSKTSRVLQNVAFSVQKEVEK 50
HUMAN GRS*                  MTDCEFGYIYRLAQDYLQCVLQIPQPGSGPSKTSRVLQNVAFSVQKEVEK 50
HUMAN BCL2A1-short          MTDCEFGYIYRLAQDYLQCVLQIPQPGSGPSKTSRVLQNVAFSVQKEVEK 50
MOUSE BCL2A1-a              MAESELMHIHSLAEHYLQYVLQVPAFESAPSQACRVLQRVAFSVQKEVEK 50
MOUSE BCL2A1-b              MAEYEFMYIHSLAEHYLQYVLQVPAFESAPSQACRVLQRVAFSVQKEVEK 50
MOUSE BCL2A1-c              MAEYELMHIHSLAEHYLQYVLQVPAFESAPSQAFRVLQRVAFSVQKEVGK 50
MOUSE BCL2A1-d              MSEYEFMYIHSLAEHYLQYVLQVPAFESAPSQACRVLQRVAFSVQKEVEK 50
                            *:: *: :*: **:.*** ***:*   *.**:: ****.********* *

                                BH3                             BH1
HUMAN BCL2A1                NLKSCLDNVNVVSVDTARTLFNQVMEKEFEDGIINWGRIVTIFAFEGILI 100
HUMAN GRS*                  NLKSCLDNVNVVSVDTARTLPTQVMEKEFEDGIINWGRIVTIFAFEGILI 100
HUMAN BCL2A1-short          NLKSCLDNVNVVSVDTARTLFNQVMEKEFEDGIINWGRIVTIFAFEGILI 100
MOUSE BCL2A1-a              NLKSYLDDFHVESIDTARIIFNQVMEKEFEDGIINWGRIVTIFAFGGVLL 100
MOUSE BCL2A1-b              NLKSYLDDFHVESIDTARIIFNQVMEKEFEDGIINWGRIVTIFAFGGVLL 100
MOUSE BCL2A1-c              NLKSYLDDFHVESIDTTRIIFNQVMEKEFEDGIINWGRIVTIFAFGGVLL 100
MOUSE BCL2A1-d              NLKSYLDDFHVESIDTARIIFNQVMEKEFEDGIINWGRIVTIFAFGGVLL 100
                            **** **:.:* *:**:* :************************ *:*:

                                                        BH2
HUMAN BCL2A1                KKLLRQQIAPDVDTYKEISYFVAEFIMNNTGEWIRQNGGWENGFVKKFEP 150
HUMAN GRS*                  KKLLRQHIAPDVDTYKEISYFVAEFIMNNTGEWIRQNGGWENGFVKKFEP 150
HUMAN BCL2A1-short          KKLLRQQIAPDVDTYKEISYFVAEFIMNNTGEWIRQNGGWGKWHNHTP-- 148
MOUSE BCL2A1-a              KKLPQEQIALDVCAYKQVSSFVAEFIMNNTGEWIRQNGGWEDGFIKKFEP 150
MOUSE BCL2A1-b              KKLPQEQIALDVGAYKQVSSFVAEFIINNTGEWIRRNGGWEDGFIKKFEP 150
MOUSE BCL2A1-c              KKTSTR-------------------------------------------A 107
MOUSE BCL2A1-d              KKLPQEQIALDVGAYKQVSSFVAEFIMNNTGEWIRRNGGWEDGFIKKFEP 150
                            **    .

HUMAN BCL2A1                KSGWMTFLEVTGKICEMLSLLKQYC 175
HUMAN GRS*                  KSGWMTFLEVTGKICEMLSLLKQYC 175
HUMAN BCL2A1-short          -----MLVESVAHKKRKMAL----- 163
MOUSE BCL2A1-a              KSGWLTFLQMTGQIWEMLFLLK--- 172
MOUSE BCL2A1-b              KSGWLTFLQMTGQFWEMLFLLK--- 172
MOUSE BCL2A1-c              DCPGCTCLQTSFQFWGRIHNE---- 128
MOUSE BCL2A1-d              KSGWLTFLQMTGQIWEMLFLLK--- 172
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Figure 1 Protein sequence alignment of human and mouse BCL2A1. Besides full-length human BCL2A1 (Q16548), the variant GRS[49] and the alternative splicing isoform BCL2A1-short/Bfl1-S (Q86W13) are displayed. Mouse BCL2A1 is encoded on four copies named A1-a (O07440), A1-b (O55177), A1-c (O55178) and A1-d (O55179). Protein IDs refer to the UniProt knowledgebase. Alignment was done using ClustalW2 from the European Bioinformatics Institute (Cambridge, UK). The BH domains as well as intraspecies single amino-acid variants are highlighted by color

multidomain proteins BAK/BAX and the BH3-only proteins. The interaction of BCL2A1 with BAX and BAK has been investigated in many different studies, with rather conflicting results. In this regard, BCL2A1 has been found to bind both BAK and BAX in yeast-two-hybrid screens.[13–15] Recombinant BCL2A1 showed a weak interaction with BAX and not with BAK in a GST-pulldown assay, but binding to both BAK and BAX BH3-peptides by fluorescence polarization assay with an EC_{50} of 45.5 and 17.3 nM, respectively[16] (Figure 2). In mammalian cells, overexpressed mouse BCL2A1 was found to bind BAK but not BAX.[17] Similarly, human BCL2A1 selectively bound to BAK and overexpressed but not endogenous BAX.[18] However, others have not found either interaction with BAK or BAX.[19,20] Thus, it appears that in cellular systems, BCL2A1 binds to BAK more prominently than to BAX, and contrasting results reported in the individual studies may be explained by the investigated expression system and different assay sensitivities.

In regards to binding of BH3-only proteins, it appears clear that BCL2A1 interacts with tBID.[18,19] BH3 profiling indicated that among the BH3-only proteins, BCL2A1 binds only to BIM (Figure 2), BID and PUMA BH3-peptides.[21] Using a different approach, binding of BCL2A1 to BH3-peptides was investigated by fluorescence polarization assay, when BCL2A1 was found to interact with BIM, BID and PUMA, but also to a weaker extent with BIK, HRK and NOXA (Figure 3), indicating a similar binding profile as displayed by MCL1.[22] Binding of BCL2A1 and NOXA by fluorescence polarization assay was confirmed in a different study.[23] Therefore, in terms of binding to BH3-only proteins, BCL2A1 is often grouped together with MCL1, whereas BCL2, BCL-X_L and BCL-w form another group capable of binding BAD but not NOXA.[24]

HA-tagged overexpressed BCL2A1 also interacts with the BH3-like protein Beclin-1, thus potentially contributing to inhibition of autophagy.[25] In addition, an interaction of BCL2A1 with Nur77-derived BCL2-converting peptide with nine amino acids (NuBCP-9) has been described. In that study, NuBCP-9 converted BCL2 into a pro-apoptotic molecule by binding to its loop region, which resulted in exposure of the BCL2 BH3 domain.[26] However, as that study was focussed on BCL2, no data for BCL2A1 other than the co-immunoprecipitation of the tagged proteins were reported, and it remains to be proven whether, by analogy to BCL2, binding of NuBCP-9 may also convert BCL2A1 into a pro-apoptotic protein (Figure 3).

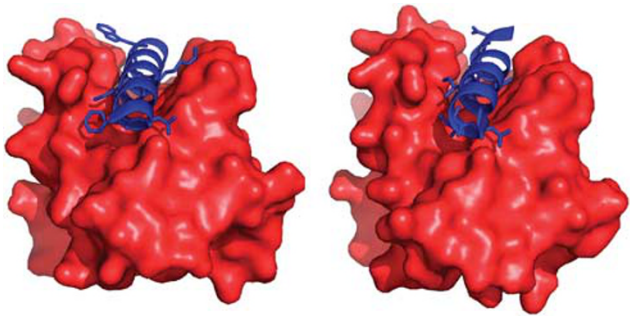

Figure 2 Structure of BCL2A1 in complex with BH3 peptides. Binding of human BCL2A1 (in red) to BIM (left, PDB: 2VM6) and BAK (right, PDB: 3I1H) BH3-peptides was illustrated in Pymol (Schrodinger Inc., Portland, OR, USA). The residues of the BH3-peptides (blue) directly interacting with the hydrophobic pockets of BCL2A1 are displayed as sticks

Regulation of BCL2A1

The transcription of *BCL2A1* is highly regulated. It was originally identified by Prystowsky's group[27,28] as a gene induced by GM-CSF and LPS, suggesting that it may be an early-response gene. Later on it was found to be inducible by tumor necrosis factorα[29,30] and identified as an NF-κB target gene.[31] Simultaneously, *BCL2A1* transcription was reported to be induced in response to antigen receptor stimulation.[32] Since then, several reports have demonstrated the importance of *BCL2A1* upregulation for B-lymphocyte survival upon CD40 signaling.[33–35] In addition to CD40 signaling, PI3K and ERK signaling initiated by ICAM-1 binding have been found to induce NF-κB and subsequently *BCL2A1* expression[36] (Figure 4). Interestingly, both hyperoxia[37] and low levels of reactive oxygen species[38] were described to increase *BCL2A1* transcription, possibly in an NF-κB-dependent manner. In both situations, *BCL2A1* exerted a pro-survival function to prevent cell death.

Besides NF-κB, several other transcription factors have been implicated in *BCL2A1* transcriptional regulation, including all-trans retinoic acids[39,40] or retinoic X receptor agonists,[41] the (−EX5/−KTS) isoform of WT-1[42] and the transcriptional enhancer Spi-1/PU.1.[43] On the other hand, *BCL2A1* transcription is repressed by the plasma cell transcription factor PRDI-BF1/Blimp-1[44] (Figure 4).

In addition to the transcriptional regulation, BCL2A1 is also controlled at the post-translational level. In this regard, BCL2A1 is regulated by the ubiquitin/proteasome pathway

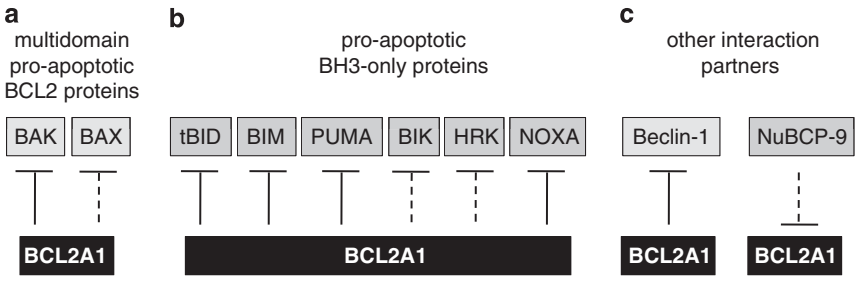

Figure 3 Interaction partners of BCL2A1. Binding by BCL2A1 can inhibit or neutralize pro-apoptotic multidomain BCL2 proteins (**a**) and BH3-only proteins (**b**). In addition, BCL2A1 can sequester Beclin-1 (**c**). Binding by NuBCP-9 may inhibit the anti-apoptotic function of BCL2A1

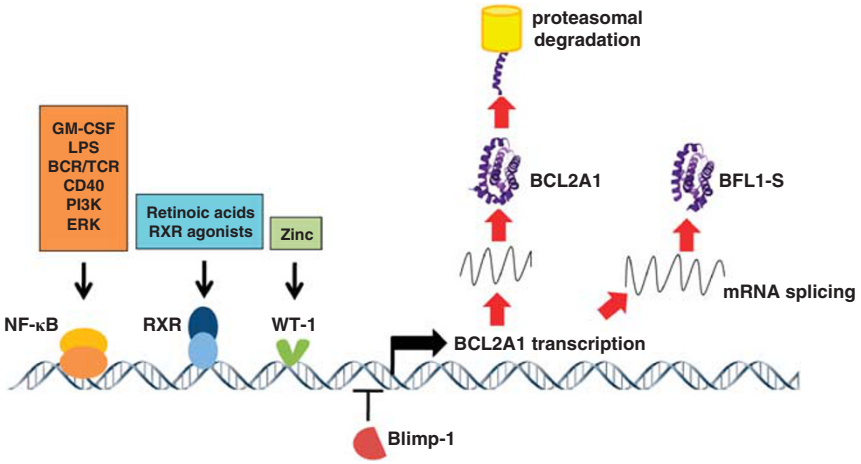

Figure 4 Regulation of BCL2A1. BCL2A1 transcription is induced by NF-κB, retinoic X receptors (RXR) and WT-1, but repressed by the plasma cell transcription factor Blimp-1. Differential splicing can result in transcription of either BCL2A1 or BFL1-S. The stability of BCL2A1 protein is regulated by proteasomal degradation

and undergoes constitutive proteasome-mediated turnover, resulting in a short half-life of the protein.[45,46] However, so far no E3-ligase for BCL2A1 has been identified. Whether the proteasomal degradation of BCL2A1 can also be controlled by certain pro-or anti-apoptotic stimuli, for example, via phosphorylation events, has not been investigated yet but may provide an extra layer of regulation. In addition to the proteasomal turnover, cleavage by μ-calpain can convert BCL2A1 from an anti- into a pro-apoptotic protein.[46]

Expression and Function of BCL2A1 in Normal Tissues

There are conflicting reports on the tissue distribution of BCL2A1, possibly due to differences in the expression pattern of mouse and human *BCL2A1* mRNA. Although mouse mRNA appears to be mainly expressed in hematopoietic cells, in humans a more widespread tissue distribution was found, also including lung, small intestine, testis and smooth muscle cells.[30] The human *BCL2A1* gene was identified and cloned by three different groups using distinct and independent approaches. Firstly, it was identified from fetal liver and thus named 'Bcl-2 related gene expressed in fetal liver' (Bfl-1), highlighting its involvement in early hematopoiesis.[47] Secondly, it was discovered as a gene induced upon cytokine treatment in activated endothelial cells.[30] This study indicated that BCL2A1 exhibits an important pro-inflammatory function. Further support for the importance of BCL2A1 expression in endothelial cells was provided by the findings that monocytes can induce BCL2A1 upregulation in endothelial cells to protect them from cell death.[48] Thirdly, BCL2A1 was found to be involved in a chromosomal rearrangement in a chronic myeloid leukemia patient linking it to fibroblast growth factor 4, thus also named GRS.[49] This rearranged BCL2A1 displayed three mutations in sequence, the importance of which is not clear (Figure 1). Mouse *Bcl2a1* mRNA is induced during myeloid differentiation,[28] mast cell activation upon an allergic reaction,[50–52] lymphocyte development,[53–55] and lymphocyte and macrophage activation,[28,56] emphasizing the importance of BCL2A1 in the immune system. BCL2A1 was downregulated in plasma cells,[57,58] possibly due to its transcriptional repression by plasma cell transcription factors.[44]

The identification of BCL2A1 as an NF-κB target gene further indicates an important function of BCL2A1 during inflammation. Inflammation is an important part of the innate immune response and involves the ligation of pattern recognition receptors (PRPs) including the NOD-like receptors that participate in the formation of the inflammasomes, first described by Jurg Tschopp and colleagues.[59,60] One of the major signaling pathways induced by PRPs is the activation of NF-κB and the upregulation of pro-inflammatory genes. Thus it appears possible that formation of inflammasomes may also induce the expression of BCL2A1, thus contributing to the survival of the pro-inflammatory cells during an immune response.

Interestingly, a physiological function of BCL2A1 in mammary cell differentiation has been reported. In this regard, *Bcl2a1* mRNA is upregulated in pregnant mice upon weaning, and pregnancy prevents mammary gland involution by apoptosis, a function that may be mediated by the increased BCL2A1 levels.[61] However, there may be differences in the regulation of *Bcl2a1* during mammary gland involution in different mouse strains.[62]

Genetic Modification of *Bcl2a1* in Mice

To further study the function of BCL2A1, transgenic and knockout mice have been generated. Lymphocyte-specific transgenic *Eμ-Bcl2a1* mice show extended survival of thymocytes and early B-cells together with a prolonged pro-B stage, indicating an impairment of pro- to pre-B-cell transition due to BCL2A1 overexpression.[63] The importance of BCL2A1 for T-cell survival was confirmed in *lck-Bcl2a1* transgenic mice, which displayed increased BCL2A1 expression predominantly in T-cells. Overexpression of BCL2A1 resulted in higher T-cell numbers in the thymus and spleen as well as reduced apoptosis.[64] In a similar study, *CD2-Bcl2a1* transgenic mice showed increased thymic cellularity due to enhanced survival of $CD4^+CD8^+$ double positive T-cells.[65] Interestingly, transgenic *Bcl2a1* mice do not develop

lymphomas,[63] suggesting that in contrast to other anti-apoptotic proteins like BCL2,[66] BCL2A1 overexpression alone is not sufficient to induce tumorigenesis.

Although the genetic deletion of *Bcl-X* and *Mcl-1* is lethal,[67,68] the overall phenotype of *Bcl2a1*-knockout animals appears to be rather normal with only hair loss observed during ageing.[69] However, genetic deletion of *Bcl2a1* is complicated by the occurrence of multiple gene copies, which are differentially expressed in different cell types.[11] The genetic deletion of one copy of the murine *Bcl2a1* gene (*A1-a*) resulted in enhanced apoptosis in peripheral blood neutrophils.[69] In addition, a reduced response to allergenic stimuli was found and *Bcl2a1-a* knockout mice displayed 50% less mast cells in the skin upon allergenic challenge.[50] In order to silence multiple copies of the *Bcl2a1* gene, a conditional transgene-driven shRNA for *Bcl2a1* was used to simultaneously knock down *A1-a*, *A1-b* and *A1-d*. However, the RNAi efficiency varied between tissues, and although efficient knockdown of the *Bcl2a1* mRNA was achieved in thymocytes, the gene silencing was inefficient in mature lymphocytes and no obvious phenotype was found.[70] Taken together, the studies performed with transgenic and knockout mice support a pro-survival function of BCL2A1 in the hematopoietic system especially during maturation and differentiation of specific lymphocytes subsets.

Expression of BCL2A1 in Cancer

Due to its important function in the hematopoietic system it is not surprising that increased expression of BCL2A1 is associated with different forms of leukemia and lymphoma (Table 1). As compared with healthy controls, overexpression of *BCL2A1* mRNA was described in acute lymphoblastic and chronic lymphocytic leukemia.[71] In chronic lymphocytic leukemia, high BCL2A1 expression was found to correlate with more severe cases, indicating a prognostic function of BCL2A1 in this very heterogeneous patient group.[72] In addition, BCL2A1 was highly expressed in mantle cell lymphoma [71] and multiple types of large B-cell lymphoma,[73–75] especially the OxPhos subgroup of diffuse large B-cell lymphoma.[76]

When first identified, human *BCL2A1* mRNA was overexpressed in stomach cancer as compared with normal tissue, indicating a possible function of BCL2A1 also in solid tumors.[47] High mRNA expression in solid tumor tissues was confirmed in other studies, for example, by northern blot analysis in stomach and colon cancer.[77] Among a panel of solid tumor tissues of different origins, including breast, colon, lung, ovarian and prostate, the highest expression of *BCL2A1* mRNA was detected in breast cancer samples.[78] Interestingly, in advanced breast cancer a higher expression of *BCL2A1* mRNA was found when compared with less advanced tumors,[79] suggesting an association of BCL2A1 expression with later and more severe disease stages. Furthermore, *BCL2A1* expression was associated with metastatic disease in melanoma[80] and hepatocellular carcinoma.[81] Transcriptional profiling indicated *BCL2A1* as highly expressed in squamous cell carcinoma of the skin,[82] and later on, *BCL2A1* was observed to be overexpressed in oral squamous cell carcinoma.[83] In summary, BCL2A1 has been identified as overexpressed in a variety of hematological malignancies as well as solid tumors and appears to be predominantly associated with advanced or metastatic disease stages (Table 1). However, so far most studies have

Table 1 Expression of BCL2A1 in human tumor samples

Tumor type	*N*	mRNA	Protein	Expression in a selective patient group	Method	Reference
Acute lymphoblastic leukemia	16	X			PCR	71
Acute lymphoblastic leukemia	9	X		Higher in cortical T-ALL than in pre-T ALL	PCR	85
Chronic lymphocytic leukemia	32	X		Higher in 11q del patients	PCR	71
Chronic lymphocytic leukemia	14	X		Higher in fludarabine-resistant patients	Microarray, PCR	72
Chronic lymphocytic leukemia	37	X		Higher in chemotherapy-resistant patients	PCR	92
Chronic lymphocytic leukemia	5		X		IHC	95
Chronic lymphocytic leukemia	12		X		Western blot	103
Acute myeloid leukemia	27	X			PCR	71
Acute myeloid leukemia	14/19	X			PCR	42
Chronic myeloid leukemia	12	X			PCR	71
Mantle cell lymphoma	19	X			PCR	71
Mediastinal large B-cell lymphoma	176	X			Microarray	73
Diffuse large B-cell lymphoma	9	X			Microarray	74
Diffuse large B-cell lymphoma	176	X		Higher in OxPhos patient group	Microarray	76
Stomach cancer	8	X			Northern blot	56
Stomach cancer	28	X		Higher in metastatic tumors	Northern blot	77
Colon adenoma	15	X			Northern blot	77
Colon cancer	3/9	X			PCR	78
Breast cancer	8/9	X			PCR	78
Breast cancer	30	X		Higher in advanced tumors	PCR	79
Breast cancer	150	X		Associated with poor treatment outcome	Microarray	93
Melanoma	82	X		Higher in metastatic tumors	Microarray	80
Hepatocellular carcinoma	32	X		Higher in metastatic tumors	Microarray, PCR	81
Skin squamous cell carcinoma	5	X			Microarray	82
Oral squamous cell carcinoma	43	X	X		Microarray, IHC	83

Abbreviations: IHC, immunohistochemistry; *N*, number of primary tissue samples. Overview of the studies investigating the expression of BCL2A1 mRNA and proteins in human tumor samples.

analyzed mRNA expression levels, and only little data are available on BCL2A1 protein expression in tumors, possibly due to the limitations of commercially available antibodies for human BCL2A1.

A Function of BCL2A1 in Tumorigenesis

The increased BCL2A1 expression in advanced tumor stages indicates that BCL2A1 may facilitate tumor progression. Indeed, a contribution of BCL2A1 to tumorigenesis was demonstrated in anaplastic large cell lymphoma, where the transformation by anaplastic lymphoma kinase was dependent on BCL2A1.[75] Additional support for the ability of BCL2A1 to transform tumor cells was provided by another study in which BCL2A1 increased E1A-induced transformation.[84] Similarly, Mandal *et al.*[85] suggest that upon deregulated T-cell receptor signaling, BCL2A1 may contribute to the transformation of pre T-cell to cortical acute lymphoblastic leukemia. Ubiquitin-resistant and hence more stable mutants of BCL2A1 have been described to promote lymphoma, highlighting the importance of post-translational regulation of BCL2A1 in a physiological context.[86] Although not tumorigenic by itself in mice,[63] enforced expression of BCL2A1 was found to accelerate *myc*-induced leukemogenesis upon engraftment in mice. However, when compared with other anti-apoptotic BCL2 proteins, the effect of BCL2A1 overexpression on the survival of leukemic mice was less pronounced.[78] As indicated by a genome profiling study, BCL2A1 may have an important function in squamous cell carcinoma.[82] Support for an important role of BCL2A1 in oral squamous cell carcinoma was provided by the description of increased expression of BCL2A1 in a stem-cell like side population of oral squamous cell carcinoma, highlighting a potential pro-survival function of BCL2A1 in cancer stem cells.[87] Taken together, several studies have shown that BCL2A1 may contribute to tumor progression, probably by preventing apoptosis in the advanced tumor cells, which may display more genetic abnormalities and thus may be more dependent on the protection by anti-apoptotic BCL2 proteins.

The Role of BCL2A1 in Chemotherapy Resistance

Besides a potential role of BCL2A1 in tumorigenesis, a central function of BCL2A1 is to suppress apoptosis upon toxic insults and consequently to prevent cell death upon chemotherapy. In this regard, overexpression of BCL2A1 in cell lines has been shown to mediate resistance to etoposide,[88] staurosporine[89] or cisplatin.[90] Conversely, silencing of BCL2A1 by gene knockdown was found to sensitize malignant B-cell lines to apoptosis induced by chemotherapy or the therapeutic antibody rituximab.[91] Besides the modulation of expression levels in cell lines, high expression of BCL2A1 in tumor samples has been correlated with *in vivo* chemoresistance, for example, in chronic lymphocytic leukemia[92] or breast cancer.[93] Similarly, BCL2A1 was described to be highly expressed in cisplatin-resistant bladder cancer cell lines.[94] In a different context, overexpression of BCL2A1 can mediate the resistance to ABT-737,[95,96] a specific inhibitor of BCL2, BCL-X_L and BCL-w, indicating that expression of BCL2A1 may be very important to consider for the successful application of BCL2 inhibitors as novel cancer therapy.

The Potential of BCL2A1 Inhibitors for Cancer Therapy

Due to their important anti-apoptotic function, BCL2 proteins have been identified as valuable targets for anti-cancer therapy. To this end, several small molecule inhibitors of BCL2 proteins have been developed and are currently tested in clinical trials for multiple malignancies including chronic lymphocytic leukemia. So far, either compounds which inhibit BCL2, BCL-X_L and BCL-w, but do not bind MCL1 or BCL2A1, have been presented (ABT-737, Navitoclax), or broad-spectrum BCL2 protein inhibitors which bind all anti-apoptotic BCL2 proteins although with varying affinities (eg Obatoclax, apogossypol, TW-37).[97] However, the specificity of many of these compounds with the exception of ABT-737 and Navitoclax has not been demonstrated, and many potential BCL2 inhibitors might have additional cellular targets resulting in BCL2 protein-independent cell death.[98] In regards to their toxicity, it may be beneficial to consider selective inhibitors of individual BCL2 proteins rather than broad-spectrum BCL2 inhibitors. In a small compound screen for inhibitors of BCL2A1, gambogic acid was identified as a potential lead compound.[99] However, gambogic acid also induced cell death in cells that were deficient in the main effector molecules of the BCL2 family, BAX and BAK. Similarly, *N*-aryl maleimides have been identified as potential BCL2A1 inhibitors by high-throughput screening of 66 000 compounds and may serve as lead compounds for the development of specific BCL2A1 inhibitors.[100] Besides these novel potential inhibitors, several apogossypol derivatives may target BCL2A1,[101] although their specificity for BCL2A1 remains to be demonstrated. Recently, peptide aptamers that specifically target BCL2A1 have been presented, which sensitized malignant B-cells to chemotherapeutic drugs,[102] indicating that a peptide-based targeting strategy might be a promising alternative to small molecule inhibitors. In conclusion, although BCL2A1 is overexpressed in many different types of cancer and the inhibition of BCL2A1 by small molecule inhibitors may be a highly promising strategy for the development of novel anti-cancer therapeutics, so far very few specific and potent inhibitors of BCL2A1 have been described. The lack of selective inhibitors may be explained by the difficulties in targeting specific protein–protein interactions with small molecules and the similarity of the hydrophobic groove found on all anti-apoptotic BCL2 proteins. Therefore, further work is required to fully investigate the potential of BCL2A1 inhibitors for anti-cancer therapy, especially in comparison with other selective inhibitors, for example, for MCL1 or BCL2.

Conflict of Interest

The author declares no conflict of interest.

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