



Review

Permeabilization of the mitochondrial inner membrane during apoptosis: impact of the adenine nucleotide translocator

HLA Vieira¹, D Haouzi¹, C El Hamel¹, E Jacotot¹,
A-S Belzacq², C Brenner² and G Kroemer^{*,1}

¹ Centre National de la Recherche Scientifique, UMR1599, Institut Gustave Roussy, 39 rue Camille-Desmoulins, F-94805 Villejuif, France

² Centre National de la Recherche Scientifique, UMR6022, Université Technologique de Compiègne, F-60205 Compiègne, France

* Corresponding author: G Kroemer, 19 rue Guy Môquet, B.P. 8, F-94801 Villejuif, France. Tel: 33-1-49 58 35 13; Fax: 33-1-49 58 35 09; E-mail: kroemer@infobiogen.fr

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Abstract

Mitochondrial membrane permeabilization can be a rate limiting step of apoptotic as well as necrotic cell death. Permeabilization of the outer mitochondrial membrane (OM) and/or inner membrane (IM) is, at least in part, mediated by the permeability transition pore complex (PTPC). The PTPC is formed in the IM/OM contact site and contains the two most abundant IM and OM proteins, adenine nucleotide translocator (ANT, in the IM) and voltage-dependent anion channel (VDAC, in the OM), the matrix protein cyclophilin D, which can interact with ANT, as well as apoptosis-regulatory proteins from the Bax/Bcl-2 family. Here we discuss that ANT has two opposite functions. On the one hand, ANT is a vital, specific antiporter which accounts for the exchange of ATP and ADP on IM. On the other hand, ANT can form a non-specific pore, as this has been shown by electrophysiological characterization of purified ANT reconstituted into synthetic lipid bilayers or by measuring the permeabilization of proteoliposomes containing ANT. Pore formation by ANT is induced by a variety of different agents (e.g. Ca^{2+} , atractyloside, thiol oxidation, the pro-apoptotic HIV-1 protein Vpr, etc.) and is enhanced by Bax and inhibited by Bcl-2, as well as by ADP. In isolated mitochondria, pore formation by ANT leads to an increase in IM permeability to solutes up to 1500 Da, swelling of the mitochondrial matrix, and OM permeabilization, presumably due to physical rupture of OM. Although alternative mechanisms of mitochondrial membrane permeabilization may exist, ANT emerges as a major player in the regulation of cell death. *Cell Death and Differentiation* (2000) 7, 1146–1154.

Keywords: apoptosis; Bcl-2; mitochondria; permeability transition

Abbreviations: ANT, adenine nucleotide translocator; IM, inner membrane; OM, outer membrane; PTPC, permeability transition pore complex; SIMPs, soluble intermembrane space proteins; VDAC, voltage dependent anion channel

Introduction

Mitochondrial membrane permeabilization (MMP) appears to be a near-to-general phenomenon associated with apoptosis.^{1–3} Schematically, three phases of the apoptotic process can be distinguished. During a pre-mitochondrial phase pro-apoptotic second messengers are activated and factors acting on mitochondrial membranes accumulate and/or translocate to mitochondria. Prominent pro-apoptotic proteins directly acting on mitochondria include the pro-apoptotic members of the Bcl-2/Bax family, as well as kinases and phosphatases which induce covalent modification of Bcl-2/Bax family members, thereby influencing their function and/or subcellular localization. p53 has also recently been shown to translocate to mitochondria.⁴ Non-protein factors acting on mitochondria include Ca^{2+} , reactive oxygen species, NO, and ganglioside GD3 (reviewed in^{3,5–7}). During the mitochondrial phase, MMP occurs, presumably through a limited set of mechanisms which are discussed in this special issue of *Cell Death and Differentiation*. Finally, during the post-mitochondrial phase, the functional consequences of MMP namely bioenergetic failure and/or release of potentially harmful proteins normally sequestered in mitochondria causes cell death.

The signs of MMP include the release of soluble proteins from the mitochondrial intermembrane space (e.g. cytochrome *c*, apoptosis inducing factor) through the outer membrane (OM), as well as a partial permeabilization of the inner membrane (IM) for solutes up to ~1500 Da, leading to a reduction of the mitochondrial transmembrane potential ($\Delta\Psi_m$). IM permeabilization appears to be a less constant feature of apoptosis than OM permeabilization. Although cytochrome *c* release through OM is mostly associated with a permanent loss of $\Delta\Psi_m$,⁸ this $\Delta\Psi_m$ reduction may be transient, indicating IM ‘resealing’.^{9–11} Moreover, in some cases cytochrome *c* release may occur in cells whose mitochondria have an apparently normal^{1,12} or even an increased $\Delta\Psi_m$.¹³

The mechanism of OM permeabilization is controversial. OM permeabilization has been proposed to occur independently from that of IM, e.g. due to the OM insertion and oligomerization of Bax-like molecules, which may or may not cooperate with the OM protein VDAC (voltage-dependent anion channel) to form large protein-permeable

conduits.^{14,15} Alternatively, primary IM permeabilization to small ions and water may cause osmotic matrix swelling and consequent OM rupture, resulting because the surface area of the IM with its folded cristae exceeds that of the OM. Accordingly, matrix swelling and herniation of IM through OM, with consequent physical rupture of OM, has been observed at the ultrastructural level in a variety of models of apoptosis (Table 1), including in hepatocytes exposed to CD95 crosslinking *in vivo*.¹⁶ Of note, matrix swelling is a feature of apoptosis which can only be observed transiently, before the cytoplasm (including mitochondria) undergoes apoptotic shrinkage.¹⁷

The present review will focus on one particular molecule involved in MMP, namely the IM protein ANT (adenine nucleotide translocator). We will advance several arguments why we believe ANT to be a key player in the regulation of cell-death associated MMP.

Normal structure and function of ANT

ANT, a ~30 kDa protein exclusively localized to the IM, is involved in the specific exchange of ADP and ATP.¹⁸ ANT is an antiporter whose function is strictly required for ATP produced on the matrix side of IM by the F₀/F₁ ATP synthase to be exported to the rest of the cell. Genetic inactivation of ANT therefore results into a severe metabolic impairment.¹⁹ Transport is driven by the $\Delta\Psi_m$ leading to the net import of one positive charge per reaction cycle (exchange of ATP⁴⁻ by ADP³⁻). In particular circumstances, when the respiratory chain (which normally generates the $\Delta\Psi_m$) is blocked, ANT may function in the opposite direction and import ATP into the matrix while exporting ADP (a reaction which then contributes to the generation of the $\Delta\Psi_m$), ATP consumption being mediated by the F₀/F₁ ATP synthase functioning in its ATPase mode (which pumps protons out of the matrix while consuming ATP, thus generating a $\Delta\Psi_m$). As a result, the activity of ANT and F₀/F₁ ATP synthase may be expected to be tightly coupled among each other.

In humans and rodents, three and two ANT isoforms exist, respectively, and are expressed in a strictly tissue-specific fashion.²⁰ The human ANT2 isoform is selectively expressed in proliferating cells.²¹ In non-proliferating cells ANT2 expression appears to be negatively regulated by the general transcription factor Sp1,²² as well as specific hexanucleotide silencer element in the ANT2 promoter.²³ All ANT isoforms are members of the family formed by the carriers of the mitochondrial IM. Proteins from this family are characterized by a tripartite structure with three repeated segments of about 100 amino acid residues each.²⁴⁻²⁶ Each of the repeated segments contains two peaks of hydrophobicity corresponding to two transmembrane helices (six in total), separated by a stretch of amino acids that protrude to the matrix (three in total). The N-terminus and the C-terminus of the ANT molecule are located on the intermembrane face of IM, and the linker regions between each of the repeated segments (two in total) form loops protruding into the intermembrane space.¹⁸ ANT is a basic protein whose excess cationic changes are at least partially compensated by close interaction with the acidic lipid cardiolipin,²⁷ a lipid which is exclusively found within the IM. The native ANT is probably a dimer or an oligomer with an even number of molecules, based on the observation that a covalent tandem dimer of yeast ANT (generated by fusion of the C-terminus of the first repeat to the N-terminus of the second repeat) is functional.²⁸

Two pharmacological ANT inhibitors interact with distinct binding sites of ANT. Bongkrekic acid (BA) binds to the matrix face of ANT, whereas carboxyatractyloside (or atractyloside, Atr) binds to the intermembrane side of the molecule. Interaction with BA forces ANT to adopt its m-state conformation, whereas Atr induces the c-state conformation. During the ADP/ATP exchange, the ANT molecule is thought to undergo major conformational changes, which probably are reflected by the m- and c-states respectively.²⁹ These conformational changes are

Table 1 Examples of mitochondrial swelling and outer membrane disruption in cell death

Model	Swelling	Outer membrane rupture	Reference
Apoptosis induced <i>in vitro</i> by IL-3 withdrawal or α CD95	+	+	75
Hepatocyte apoptosis induced by α CD95 or D-galactosamine and TNF- α <i>in vivo</i>	+	+	16,78
Hepatocyte death induced by hydrazine chloramphenicol, or chloroform <i>in vivo</i>	+	N.D.	79,80
Castration induced prostate cell apoptosis	+	+	81
Traumatic axonal injury <i>in vivo</i>	+	+	82
Leukocytes exposed to Pasteurella haemolytica leukotoxin	+	+	83
Thymocytes treated with dexamethasone	+	N.D.	17
Ischemia reperfusion of intestine	+	N.D.	84
Auditory epithelial cells after injection of gentamycin	+	N.D.	85
Ceramide-treated HUT78 cells	+	N.D.	86
H ₂ O ₂ -stressed astrocytes	+	N.D.	87
Hippocampal injury by hypoglycemia	+	N.D.	88
Motoneurons of mice with transgenic SOD-1 mutations	+	N.D.	62
NO-treated HeLa and PC12 cells	+	N.D.	89
Capsaicine-induced neuronal death in neonatal rats, <i>in vivo</i>	+	N.D.	90

N.D. denotes not detected

likely to involve the rearrangement of charged sites within the membrane.^{30,31} On the matrix side of ANT, ADP is likely to interact with the second matrix loop, since Lys162 of the bovine heart ANT interacts with radiolabelled 2-azido-ADP.¹⁸ Moreover, 7-azido-5-isopropyl-acridone, which reacts with Cys159, displaces ADP from its binding site.³² Oxidative stress induced by *tert*-butylhydroperoxide or diamide (which crosslinks Cys56 in the first matrix loop) reduces the affinity of ANT for ADP.³³ Monovalent derivatization of Cys56 by the thiol-reactive agent methyl methanethiosulfonate causes an irreversible extrusion of the first loop facing the matrix and freezes the ANT in its m-state conformation.³⁴ Intermolecular crosslinking of Cys56 residues by bifunctional dimaleimides only causes dimerization of ANT in its m-state, but not in its c-state,³⁵ and inhibits the antiporter activity of ANT. Dimerization can be achieved with dimaleimide in which the distance between the two maleimide groups ranges from 8 to 17 Å, with an optimum at 12 Å, suggesting a (regulatory?) fluctuation of the loop containing Cys56.³⁵

ANT as a pore-forming protein

The biochemical features of ANT can be best studied by reconstituting the purified protein into synthetic lipid bilayers, either in proteoliposomes or in planar membranes. Hydrophilic compounds with a relative mass < 1500 Da (e.g. malate, ³H-glucose, calcein, 4-methylumbelliferone phosphate) can be encapsulated in proteoliposomes and their release can be quantitated via a variety of different techniques (enzymatically in the case of malate, radioactivity in the case of ³H-glucose, fluorescence dequenching in the case of calcein, alkaline phosphatase-mediated conversion to a fluorescent product, 4-methylumbelliferone, in the case of 4-methylumbelliferone phosphate).^{36–38} Using this experimen-

tal set-up, it has been shown that ANT proteoliposomes but not control liposomes lacking ANT become permeabilized in response to atractyloside,³⁷ Ca²⁺,³⁶ the thiol crosslinker diamide,³⁸ the ROS donor *tert*-butylhydroperoxide, Bax,³⁷ and viral protein R (Vpr) encoded by human immunodeficiency virus-1 (HIV-1).³⁹ These data indicate that ANT can mediate permeabilization in response to several agents which reportedly induce mitochondrial membrane permeabilization and apoptosis. Of note, non-specific pore formation has also been reported for other members of the mitochondrial carrier family. Thus, following treatment with thiol-specific chemical reagents, the aspartate/glutamate carrier can be converted from an obligatory exchange antiporter to a channel-like uniporter.⁴⁰ After deletion of a stretch of nine amino acid in the third matrix loop, uncoupling protein (UCP) becomes a non-specific pore.⁴¹ Whether native UCP also may form a pore in a more physiological context, however, remains elusive.

Electrophysiological experiments confirm that ANT can form channels (Table 2). Single channel current measurements of excised patches with reconstituted purified ANT indicate that Ca²⁺ can induce the formation of large channels with multiple subconductance states varying from 70 to 600 pS, depending on the ion concentration.^{42,43} Channel formation is inhibited by low pH (<5.2), ADP and bongkrekate.⁴² Single channel recordings revealed that ANT can also form relatively small channels (30 pS) in response to its ligand Atr.⁴³ A mixture of Bax and ANT (molar ratio 1:4) has a higher probability of Atr-induced pore openings and exhibits two different conductance levels (30 and 80 pS), as well as cation specificity (whereas Bax alone forms an anion-selective channel). When employed at relatively low doses (1 nM), Bax does not yield any major macroscopic conductance, unless combined with ANT treated with Atr. Thus, the combination of ANT+Atr+Bax forms a much more efficient membrane

Table 2 Electrophysiological characteristics of ANT, Bax, and Bcl-2

Protein (s)	Unit conductance (pS)	pH	Salt (nM)	Selectivity	Reference
Bax	5.6; 26; 80; 180; 250; 2000	7.0	125 NaCl	Cation	91
	27; 77	4.0	125 NaCl		91
	329	7.0	450/150 KCl	Anion	92
	22 to 730	4.0	450/150 KCl		
	200	7.4	100 KCl	Anion	43
	20; 250	7.4	500/100 NaCl	Cation	93
Bcl-2	20; 40; 90	7.4	500 KCl	Cation	46
	80 to >1900	4.0	450/150 KCl	Cation	92
	1080	7.0	450/150 KCl		
ANT	35	7.4	100 KCl	Cation	43
	0	7.2	100 KCl	–	42
	0	7.4	100 KCl	–	43
ANT+Ca ²⁺	300 to 600	7.2	100 KCl	Cation	42
	70; 250	7.4	100 KCl	Cation	43
ANT+Atr	30	7.4	100 KCl	Cation	43
ANT+Bax	200	7.4	100 KCl	–	43
ANT+Bax+Atr	30; 80	7.4	100 KCl	Cation	43
ANT+Bax Δα5/6+Atr	30	7.4	100 KCl	–	43
ANT+Bax DIGDE+Atr	30	7.4	100 KCl	–	43
ANT+Bcl-2+Atr	0	7.4	100 KCl	–	43
ANT+Bcl-2 Δα5/6+Atr	30	7.4	100 KCl	–	43
ANT+Bcl-2 G145A+Atr	0	7.4	100 KCl	–	43
ANT+Bax+Bcl-2+Atr	0	7.4	100 KCl	–	43

permeabilizing channel than do the combinations ANT+Atr, ANT+Bax, or Atr+Bax. The ANT/Bax cooperation is not observed when wild type Bax is replaced by two mutant proteins which have lost their apoptogenic potential:^{44,45} Bax Δ IGDE, which lacks a homodimerization domain in the BH3 region, and Bax $\Delta\alpha$ 5/6, which lacks a putative pore forming domain. Preincubation of ANT with its physiological ligand ATP completely inhibits the channel activity mediated by ANT+Atr+Bax.⁴³ The combination of ANT plus Bcl-2 (molar ratio 1 : 1) results in a virtual cessation of Atr-induced ion movement indicative of the closure of both ANA and Bcl-2 channels.⁴³ If Bcl-2 is replaced by a mutant protein (Bcl-2 $\Delta\alpha$ 5/6) lacking a putative pore formation domain,^{45,46} the inhibition of ANT-mediated conductance is suboptimal (Table 2). In conclusion, Bax and ANT can cooperate by forming a new class of channels which acquire distinct electrophysiological properties as well as a far higher probability of opening than either of the two compounds on its own. Moreover, Bcl-2 and ANT exhibit mutual inhibition of ion channel formation *in vitro*.

ANT-interacting, apoptosis-regulatory proteins

ANT can interact with a large number of proteins involved in the regulation of MMP and apoptosis (Figure 1). Thus, ANT is part of a multiprotein ensemble, the permeability transition pore complex (PTPC), which forms in the contact site between IM and OM.⁴⁷ In this section, we will briefly enumerate proteins that have been shown to physically interact with ANT.

Cyclophilin D

Cyclophilin D is the mitochondrial target of cyclosporin A (CsA) and the non-immunosuppressive CsA derivative and N-methyl-4-Val-CsA, both of which inhibit the PTPC and can

inhibit apoptosis in various *in vitro* and *in vivo* models.^{16,48} When immobilized on a column, purified recombinant cyclophilin D specifically retains ANT among triton-solubilized IM preparations⁴⁹ and ANT plus VDAC among whole mitochondrial membrane extracts.⁵⁰ Binding of cyclophilin D to purified mitochondrial IM is inhibited by CsA and enhanced by treatment with tert-butylhydroperoxide and by diamide,⁵¹ suggesting that the cyclophilin-D-ANT interaction favors mitochondrial membrane permeabilization.

Proteins from the Bcl-2/Bax family

ANT has been shown to interact directly with Bcl-2, Bcl-XL, Bax and Bak by three independent techniques: co-purification, co-immunoprecipitation and yeast-two-hybrid screening.^{37,47} This latter technique revealed that a short stretch of human ANT2 (amino acids 105–156) suffices for the interaction with Bcl-2-related proteins.³⁷ As discussed above, it appears that Bax can cooperate with ANT to form pores, whereas Bcl-2 prevents the ANT-dependent pore formation in synthetic membranes. Bax-induced MMP can be inhibited by the ANT ligand bongkreikic acid,^{37,52} underlining the probable relevance of the ANT-Bax interaction.

VDAC

VDAC binds to ANT.⁵³ VDAC is generally considered as the principal OM protein allowing for the OM transit of metabolites < 5000 kDa. VDAC has been suggested to be the mitochondrial target of the pro-apoptotic proteins Bax and Bcl-2, which would allow VDAC to form a cytochrome *c*-permeant conduit.¹⁴ Intriguingly, the VDAC1 gene is transcriptionally upregulated in a model of γ -irradiation-induced apoptosis.⁵⁴

Peripheral benzodiazepin receptor

The peripheral benzodiazepin receptor (PBR, also called mitochondrial diazepam binding receptor) co-purifies with ANT and VDAC.⁵⁵ PBR, an OM protein, is a pharmacological target for cytotoxic drugs. Thus PBR ligands such as PK111195 (1-(2-chlorophenyl)-N-methyl-N-(1-methylpropyl)-isoquinolinecarboxamide), FGIN-I-27 (N,B-di-n-hexyl 2-(4-fluorophenyl)indole-3-acetamide), and chlorodiazepam enhance the apoptogenic effects of a variety of agents including TNF,⁵⁶ ceramide, doxorubicin, etoposide,⁵⁷ arsenite,⁵⁸ and lonidamine⁵⁹ and overcome the cytoprotective effects of Bcl-2.^{57–59}

Creatine kinase

Creatine kinase co-purifies with ANT and VDAC. It appears that the creatine kinase octamer can inhibit pore formation by ANT.⁶⁰ Creatine and creatine phosphate may have cytoprotective effects in some models of cell death.^{61,62}

The protein kinase src

An N-terminally myristylated peptide derived from src binds to ANT *in vitro*.⁶³ However, at present it is not clear whether

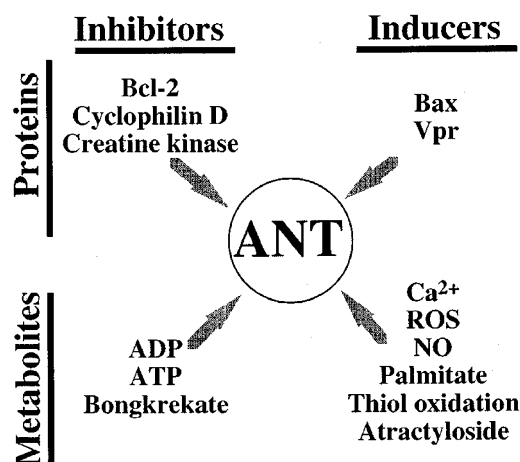


Figure 1 Molecules influencing ANT-mediated pore formation in chemically defined systems. The upper part lists proteins affecting the pore function of ANT, whereas the lower part focuses on non-protein molecules. Data are from references^{36–39,43,60}

intact protein kinases from the src family bind to mitochondria in intact cells.

Viral effectors

The anti-apoptotic protein vMIA, a product of the cytomegalovirus UL37 gene, has been shown to specifically interact with ANT.⁶⁴ Similarly, viral protein R (Vpr), a pro-apoptotic protein encoded by human immunodeficiency virus-1 (HIV-1) specifically binds to ANT with an affinity in the nanomolar range.³⁹

Pharmacological and genetic evidence that ANT participates in cell death regulation in intact cells

Bongkreikic acid, a specific ANT ligand which prevents pore formation by ANT, can inhibit the induction of apoptosis in a number of different experimental systems (Table 3). Pharmacological evidence suggests that ANT itself is the target of several apoptosis-inducing agents. Thus, MMP and apoptosis induction by means of the thiol-crosslinking agent diamide correlates with oxidation of Cys56 of ANT, as well as with ANT dimerization.^{38,65} Fatty acid anions (e.g. palmitate or stearate), including a non-metabolizable analogue β,β' -methyl substituted hexadecane α,ω -dioic acid, uncouple mitochondria via an effect on ANT,⁶⁶ who facilitates their electrophoretic translation from the inner to the outer leaflet of IM.⁶⁷ Palmitate also induces apoptosis when added to intact cells and this effect is inhibited by BA, indicating the involvement of ANT.⁶⁸ Some non-steroidal anti-inflammatory drugs (e.g. diclofenac) both induce PTPC opening and inhibit ANT activity in purified mitochondria.⁶⁹ The unsaturated aldehydes 4-hydroxynonenal and 4-hydroxyhexenal, which arise as a by-product of lipid peroxidation and have potent cytotoxic and MMP-inducing activities, also inhibit the antiport activity of ANT reconstituted into liposomes.⁷⁰

More convincingly, genetic experiments confirm the participation of ANT in the control of cell death. Yeast cells in which the three ANT isoenzymes have been inactivated by homologous recombination are relatively resistant against killing by Bax³⁷ and Vpr.³⁹ Inactivation of

the ANT isoenzyme 2 alone suffices to render yeast cells relatively resistant to Bax.⁷¹ Inactivation of $F_{1/0}$ ATPase subunits also yields Bax-resistant cells.^{71,72} On theoretical grounds, it may be speculated that the suppression of mitochondrial ATP synthesis/consumption should paralyse the antiporter function of ANT (and perhaps reduce the probability that ANT adopts the pore-forming conformation). Transfection-enforced overexpression of mouse ANT1 (but not ANT2) induces apoptosis in mammalian cells. This is not due to a non-specific toxic effect of the overexpressed protein, because ANT1-induced apoptosis is abolished by co-transfection with cDNA coding for cyclophilin D.⁷³ The N-terminal half of ANT-1 (aa 1–141) conserves its cytotoxic potential. However, further truncation of ANT-1, from aa 102 to the C-terminus, abolishes its apoptogenic effect. Hence, a critical region of ANT1 (aa 102–141) is required for apoptosis induction. Intriguingly, this region overlaps with the Bcl-2/Bax binding site of ANT (aa 105–156)³⁷ and contains a Vpr-binding peptide motif (WXXF; aa 110–114;⁷⁴) within the C-terminal half of the first intermembrane loop (aa 103–115) (Figure 2). It is tempting to speculate that the apoptosis-regulatory domain of the ANT protein (aa 103–142), which comprises the third transmembrane domain (aa 116–134), may participate in ANT-mediated pore formation. Intriguingly, the Bcl-2/Bax binding site also overlaps with the region of ANT (aa 148–156) in which the three ANT isoforms exhibit the strongest level of divergence, suggesting an iso-form specific regulation of ANT at this level.

Open questions and perspectives

At least in some models of apoptosis, a transient $\Delta\Psi_m$ increase precedes the later $\Delta\Psi_m$ collapse.⁷⁵ According to a recent study,⁷⁶ overexpression of Bax induces alkalization of the mitochondrial matrix accompanied by cytosolic acidification,⁷⁶ as well as an increase in the $\Delta\Psi_m$ before the $\Delta\Psi_m$ drops.⁷⁶ This effect is observed both in mammalian and in yeast cells and can be recapitulated in mammalian cells exposed to the universal apoptosis inducer staurosporin.⁷⁶ Given the fact that Bax can inhibit the ATP/ADP antiporter function of ANT (A-S Belzacq and C Brenner, unpublished

Table 3 Models of apoptosis inhibited by the ANT ligand bongkreikic acid

Model of cell death induction	Reference
Glucocorticoid receptor occupancy of thymocytes	94
Protoporphyrin IX treatment of thymocytes	95
Microinjection of recombinant Bax protein into fibroblasts	37
B-cell receptor crosslinking in WEHI-231 cells	96
TNF-induced killing of L929 cells	97
TNF-induced apoptosis of primary hepatocytes	98
CD95 crosslinking of neutrophil granulocytes	99
H ₂ O ₂ treatment of T cells	100
Betulinic acid acting on neuroblastoma cells	101
Valinomycin added to BAF-3 pre-B cells	102
NMDA-induced apoptosis of cerebrocortical neurons	103
Palmitate or tributyltin treatment of Jurkat cells	68, 104
Osteoclast anikis	105
Sindbis virus infection	106
Vpr-induced killing of Jurkat cells	39

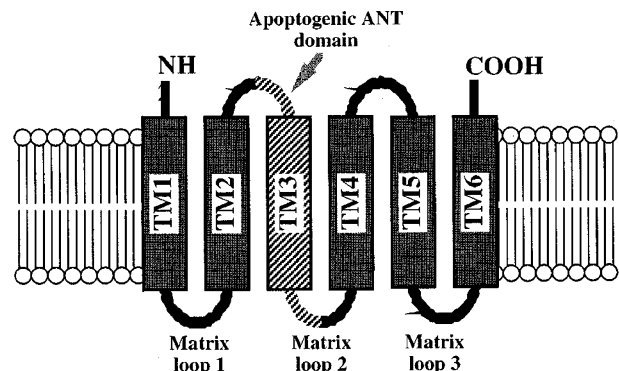


Figure 2 Topology of ANT in the inner membrane. TM, transmembrane

observations), and that the ATP/ADP exchange reaction is compromised in mitochondria from pre-apoptotic cells,⁷⁷ the following scenario becomes plausible (Figure 3): Early during apoptosis, Bax (and perhaps other pro-apoptotic members of the Bcl-2 family) would translocate to mitochondria and interact with ANT to inhibit its antiporter activity, before facilitating ANT-mediated pore formation. Indeed, pore formation by Bax+ANT in artificial membranes requires the action of additional factors (e.g. atractyloside, Vpr) which impinge on the conformation of ANT.^{37,39,43} As a net result of Bax-mediated antiporter inhibition, ATP would accumulate in the matrix, while matrix ADP would decline until the $F_{1/0}$ ATPase would be forced to operate in its ATPase mode, thereby increasing the $\Delta\Psi_m$ and generating phosphate (which via activation of the hydroxide/phosphate carrier would cause matrix alkalinization). Accordingly, $F_{1/0}$ ATPase inhibition by oligomycin prevents the bax-induced $\Delta\Psi_m$ increase, matrix alkalinization, cytosolic acidification, and apoptosis.⁷⁶ During later stages of the process, matrix alkalinization, local imbalances in the ATP/ADP concentration, increases in the production of ROS etc. would favor pore formation by ANT, aided by Bax, thereby favoring the $\Delta\Psi_m$ loss and complete loss of mitochondrial function. This scenario provides an exciting working hypothesis (Figure 3) which fits well the existing experimental data, yet requires further exploration in cell-free systems.

Although ANT is probably a major pore-forming/pore-regulating protein involved in the control of apoptosis, it appears clear that other proteins contained within the PTPC (VDAC, Bax, Bcl-2 etc.) may also function as pore-forming units, perhaps independently of ANT. Resolving the question to which extent individual PTPC proteins can function in the control of MMP and apoptosis will require thorough investigation of their function by multiple methods, including their reconstitution into lipid bilayers and genetic modifications in mammalian cells. Furthermore, numerous questions remain without response. How is it possible that

proteins that are generally thought to be confined to OM (Bcl-2, Bax) can interact with the IM protein ANT? Do they translocate to IM? Or do protruding domains of IM-anchored Bcl-2/Bax protein (or OM-anchored ANT) bind to OM (or IM, respectively), within the OM/IM contact sites? Do all ANT (and VDAC) molecules participate in the control of apoptosis, or is this function restricted to the small fraction of molecules localized in the contact site? What are the exact conformational changes explaining cooperative channel formation by sessile mitochondrial proteins and Bax? What submolecular events do determine the switch from the antiporter mode to the pore-forming mode? In which specific signal transduction pathways does ANT participate at MMP, and when is it dispensable for MMP to occur? Are there differences in the pore-forming function between distinct ANT isoforms? Can other members of the mitochondrial carrier protein family participate in MMP regulation? Answering to these questions may provide tantalizing insights into cell death control mechanisms and open therapeutic avenues to the specific pharmacological manipulation of apoptosis.

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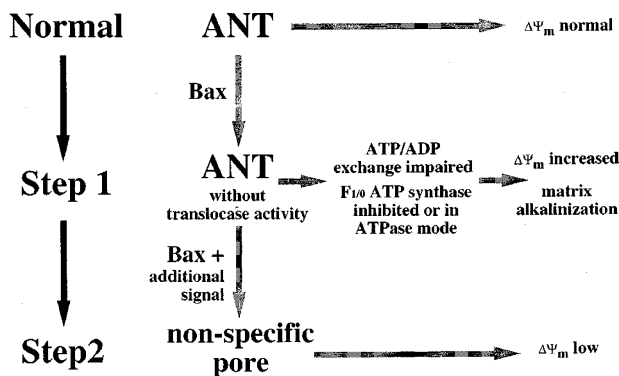


Figure 3 Hypothetical implication of ANT in a two-step model of apoptotic mitochondrial changes. During an early step (step 1), only the translocase activity of ANT would be inhibited. In contrast during a second step (step 2), ANT would convert into a non-specific pore. It is possible that the period required for the transition of step 1 to step 2 varies in different models of apoptosis, thereby creating the impression that OM permeabilization precedes or accompanies the loss of the $\Delta\Psi_m$

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