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Physiological roles of the mitochondrial permeability transition pore

Nelli Mnatsakanyan¹, Gisela Beutner², George A. Porter², Kambiz N. Alavian³, and Elizabeth A. Jonas¹

¹Department Internal Medicine, Section of Endocrinology, Yale University, New Haven, CT, USA

²Department of Pediatrics (Cardiology), University of Rochester Medical Center, Rochester, NY, USA

³Division of Brain Sciences, Department of Medicine, Imperial College London, London, UK

Abstract

Neurons experience high metabolic demand during such processes as synaptic vesicle recycling, membrane potential maintenance and Ca^{2+} exchange/extrusion. The energy needs of these events are met in large part by mitochondrial production of ATP through the process of oxidative phosphorylation. The job of ATP production by the mitochondria is performed by the F_1F_0 ATP synthase, a multi-protein enzyme that contains a membrane-inserted portion, an extra-membranous enzymatic portion and an extensive regulatory complex. Although required for ATP production by mitochondria, recent findings have confirmed that the membrane-confined portion of the c-subunit of the ATP synthase also houses a large conductance uncoupling channel, the mitochondrial permeability transition pore (mPTP), the persistent opening of which produces osmotic dysregulation of the inner mitochondrial membrane, uncoupling of oxidative phosphorylation and cell death. Recent advances in understanding the molecular components of mPTP and its regulatory mechanisms have determined that decreased uncoupling occurs in states of enhanced mitochondrial efficiency; relative closure of mPTP therefore contributes to cellular functions as diverse as cardiac development and synaptic efficacy.

Keywords

Mitochondria; Permeability transition pore; Synaptic transmission; Synaptic plasticity; ATP synthase

Calcium re-release from mitochondria after synaptic activity determines short term plasticity

 Ca^{2+} re-release from mitochondria determines short term synaptic plasticity in many neuronal synapses (Zucker & Regehr, 2002). During neuronal activity, Ca^{2+} enters across the plasma membrane through glutamate receptors and voltage gated Ca^{2+} channels. Ca^{2+}

Correspondence to: Elizabeth A. Jonas.

clearance from the cytosol is performed by the actions of Ca^{2+} ATPases at the plasma membrane and by buffering through uptake by intracellular stores including the endoplasmic reticulum (ER) and mitochondria (Rizzuto et al., 2012; Lopreiato et al., 2014); these processes reset the normally low Ca^{2+} levels present in resting neurons or neuronal synapses. The Ca^{2+} that is buffered by mitochondria is rapidly re-released within the presynaptic cytosol, providing for residual Ca^{2+} within presynaptic endings. Residual Ca^{2+} increases total Ca^{2+} levels during subsequent neuronal activity, enhancing the amount of neurotransmitter released for a given stimulus (Neher & Sakaba, 2008; Jonas, 2006) (Figs. 1 and 2). In squid presynaptic terminal, the high level of Ca^{2+} contained in sea water causes a marked synaptic depression which masks short term synaptic potentiation. Upon lowering extracellular Ca^{2+} , short term potentiation after a tetanus reappears, and is dependent on synaptic mitochondria, as in other synapses (Jonas et al., 1999).

Ca²⁺ - sensitive ligand gated channels in mitochondrial membranes are widely conserved in species from invertebrates to mammals although in many cases their molecular identity and or Ca²⁺ binding domains is/are not known. These channels open in response to elevated Ca²⁺ within the mitochondrial matrix and comprise part of the machinery that maintains residual Ca²⁺ levels for enhanced presynaptic vesicle fusion. In the example of the squid presynaptic terminal, the opening of a Ca^{2+} – activated mitochondrial channel in response to neuronal activity enhances neurotransmitter release from presynaptic endings (Jonas et al., 1999; Jonas et al., 1997), consistent with a role for this channel in re-releasing mitochondrially-buffered Ca²⁺ within the presynaptic terminal after a phase of increased neuronal activity (Fig. 2). Electrophysiological recordings of mitochondrial membranes within the squid presynaptic terminal demonstrate that the conductance of mitochondrial membranes is low at rest (Jonas et al., 1999) but that mitochondrial membrane ion channel activity increases at about 1 s after the onset of neuronal activity and persists after neuronal activity has ended (Fig. 3a). Furthermore, mitochondrial activity and short term increases in post stimulation synaptic transmitter release are abrogated by applying the uncoupler FCCP (carbonyl cyanide *p*-trifluoromethoxyphenylhydrazone), which depolarizes mitochondria, preventing Ca²⁺ handling (Jonas et al., 1999; Tang & Zucker, 1997; Friel & Tsien, 1994) (Fig. 3b, c).

Is the calcium sensitive channel of synaptic mitochondria the mitochondrial permeability transition pore (mPTP)?

In order to begin to determine a molecular identity for the calcium release channel in presynaptic mitochondria, a comparison can be made to another known channel with Ca²⁺ sensitivity in the inner membrane, the mitochondrial permeability transition pore (mPTP). Permeability transition (PT) of the mitochondrial inner membrane has been extensively studied for its role in ischemic injury in brain, heart and other organs as well as in neurodegenerative conditions (10). In the heart, data suggest that opening of the mPTP during early reperfusion after ischemia is a harmful event that precipitates further damage to the myocardium (Griffiths & Halestrap, 1995). However additional data also suggest that transient mPTP opening during preconditioning can be protective, thus serving a physiological role even during injury (Hausenloy et al., 2004).

Another type of mitochondrial channel that also increases mitochondrial permeability is formed by proteins of the Bcl-2 family. Programmed cell death (apoptosis) in vertebrate cells may be initiated by signaling at the plasma membrane or by intracellular pathways that lead to changes in mitochondria (Kinnally et al., 2006). The final common pathway for programmed cell death in many systems is mitochondrial outer membrane permeabilization (MOMP) (Dejean et al., 2005; Dejean et al., 2006; Antonsson et al., 2000; Adams & Cory, 2007), which is activated by formation of an outer membrane channel called MAC (Dejean et al., 2005; Dejean et al., 2006; Pavlov et al., 2001). Pro-apoptotic Bcl-2 family members such as Bax regulate MOMP by inducing the formation of large outer membrane pores comprised of activated oligomerized pro-apoptotic Bcl-2 proteins, aided by other proapoptotic moieties (Dejean et al., 2005; Antonsson et al., 2000; Kim et al., 2006). In their canonical role, the anti-apoptotic Bcl-2 family proteins such as Bcl-x_L protect cells against MOMP by interacting with, and inhibiting the pore forming properties of the pro-apoptotic family members (Adams & Cory, 2007; Kim et al., 2006; Galonek & Hardwick, 2006).

MOMP leads to the release of several inter-membrane space proteins such as cytochrome *c* (Green & Kroemer, 2004; Martinez-Caballero et al., 2005). The resultant decrease in cytochrome *c* levels compromises the ability of mitochondria to maintain the mitochondrial inner membrane potential and to produce ATP (Gottlieb et al., 2002). In addition, cytochrome *c* released into the cytoplasm activates downstream cytosolic enzyme pathways including effector caspases that execute cell death (Youle & Strasser, 2008). Whether the Bcl-2 proteins that regulate MOMP may also regulate mPTP activity and how these two activities are linked has been heretofore poorly understood. In addition, it is now well understood that caspase activity serves physiological roles (Li et al., 2010; Tang et al., 2015), raising the issue of whether MOMP, along with, or separate from, physiological opening of mPTP may occur reversibly.

Physiological and metabolic role of the permeability transition pore

To determine if mPTP may play a physiological role in Ca^{2+} buffering and re-release in presynaptic terminals, it is helpful to identity the pore region or channel of mPTP. This will enable studies to determine 1) if channel opening or PT occurs under physiological conditions and 2) how cellular processes regulate and are regulated by PT. To begin to narrow down the possible molecules that could form the pore, we considered the known regulators of mPTP in isolated mitochondria and in cells. Pathologically, mPTP opening is induced by elevated mitochondrial matrix Ca²⁺, ROS, inorganic phosphate, and intracellular acidification (Szabo et al., 1992; Giorgio et al., 2013). In contrast, PT is inhibited by ATP/ADP and Mg²⁺ (Kowaltowski et al., 1998; Crompton, 1999). Recent reports have also confirmed increased propensity toward PT caused by the presence of polyphosphates, chains of 10s to 100 s of repeating phosphates linked by ATP-like high energy bonds (Abramov et al., 2007; Seidlmayer et al., 2012; Holmstrom et al., 2013; Stotz et al., 2014). The actions of Ca²⁺ may also require polyhydroxybutyrate (PHB), which enters mitochondria and enhances the ability of Ca^{2+} to induce PT (Elustondo et al., 2013). Although the above conditions occur under pathological circumstances, evidence for physiological opening of the mPTP has been described including flickering short of permanent opening (Hausenloy et al., 2004; Crompton, 1999; Huser & Blatter, 1999; Korge et al., 2011; Petronilli et al., 1999; Wang et

al., 2008; Ichas & Mazat, 1998; Jouaville et al., 1998). An association between transient mPTP opening and "superoxide flashes" has been observed in striated muscle mitochondria (Wang et al., 2008). It has been hypothesized that transient opening of the mPTP may release mitochondrial matrix Ca^{2+} to maintain mitochondrial homeostasis (Elrod et al., 2010) although this function of the mPTP has recently been questioned (De Marchi et al., 2014). These studies provide a possible link between mPTP and a Ca^{2+} re-release channel that regulates physiological processes.

Metabolic pathways also regulate PT. Electron transport chain activity that increases mitochondrial membrane polarization inhibits PT, while membrane depolarization (a fall in membrane potential) enhances it (Haworth & Hunter, 1979; Hunter & Haworth, 1979; Di Lisa et al., 2011). Components of the glycolytic pathway may also control opening of the mPTP, as the binding of hexokinase II to the OMM in cardiac myocytes inhibits MOMP and PT (Pasdois et al., 2013). Furthermore, a complex of ANT, VDAC, hexokinase, and mitochondrial creatine kinase (mtCK) regulates PT (Beutner et al., 1998; Beutner et al., 1996). These data suggest that mitochondrial electron transport, mitochondrial use of substrates and ADP/ATP (or creatine kinase) govern the opening of mPTP. Finally, major pharmacologic agents used to manipulate the mPTP also target metabolic pathways. For example, inhibitors of ANT can either attenuate (bongkrekic acid) or enhance (atractyloside) mPTP opening (Haworth & Hunter, 1979). The pharmacological agent most efficient at inhibiting PT is cyclosporine A (CsA), an immunosuppressant drug which binds to cyclophilin D (CypD) and inhibits the channel activity associated with PT (Szabo & Zoratti, 1991; Giorgio et al., 2009). CyPD binds to ANT, F1F0 ATP synthase, and the phosphate carrier, further suggesting a role for metabolic components in the regulation of mPTP (Giorgio et al., 2009).

Electrophysiologic properties of the mPTP

Combining the role of mPTP as a mitochondrial ion channel and as an entity involved intimately in cellular Ca^{2+} management and metabolic regulation provides clues to its molecular identity. We will first describe its biophysical features as a mitochondrial ion channel and will then describe its metabolic functions in neurons and heart with reference to possible roles in health and disease.

PT most likely begins as the opening of a Ca^{2+} sensitive ion channel in the inner mitochondrial membrane. Such a Ca^{2+} release channel is heavily regulated; therefore it is assumed that only after prolonged opening does pathological PT (followed by MOMP) occur (Bernardi, 1999). The conversion of a physiological Ca^{2+} extrusion mechanism into a pathological channel opening may be correlated with cellular energy failure and arrest of energy dependent Ca^{2+} extrusion mechanisms in the mitochondrion; nevertheless, the factors that regulate the transition from physiological to pathophysiological ion channel opening in the mitochondrion are not completely understood.

Description of the biophysical properties of the pore that opens in the inner mitochondrial membrane during PT (the mPTP) provide support for the notion that PT is initiated by the opening of an ion channel. The first patch clamp recordings of mitochondrial inner

membrane were published in 1987. This early report highlighted a ~100 pS channel recorded by patch-clamping giant mouse liver mitochondria produced by cuprizone application (Sorgato et al., 1987). In the late 1980s, a putative mPTP was recorded by patchclamping mitochondrial inner membrane or mitoplast preparations (Petronilli et al., 1989). The activity occurred at positive potentials of the patch pipette and was found either in whole organelle mode or in single channel recordings in the organelle-attached configuration. The activity was slightly anion over cation selective with multiple subconductance states ranging from 30 pS to a peak single channel conductance of 1.3 nS. Lower conductances were attributed to substates of the larger channel openings because of long periods lacking activity followed by periods of multi-conductance behavior (Petronilli et al., 1989). Conductances of 550 pS were frequently observed at positive potentials. Gating was less common at negative potentials but this observation was consistent with the presence of prolonged openings and fewer sub-conductance steps at negative patch potentials contrasted with increased flickering at positive potentials. The authors concluded that conductance levels were not sharply defined, consistent with the existence of many varied conductance levels of the channel.

Also in 1989, Kinnally et al. recorded a similar mitochondrial multiconductance channel (MMC) in mouse liver mitoplasts (Kinnally et al., 1989). This channel changed over time, with low activity at the onset of the recording followed by progressively higher activity at later times during the recording. The channels were sometimes open more frequently at negative potentials but at times rectification occurred in the opposite direction (more frequently open at positive potentials). Channel activity displayed multiple conductances ranging from 10 to 1000 pS and was weakly cation-selective. These early studies began to establish expected criteria for activity of mPTP.

Shortly after the first recordings of the putative mPTP were performed, similar inner membrane activity was found to be inhibited by CsA. In patch clamp experiments performed in liver mitochondria, channel activity was rapidly inhibited by submicromolar concentrations of CsA in a manner consistent with the expression of the binding site on the matrix side of the inner membrane. Ca^{2+} – activated large conductance channel activity up to 1.3 nS was inhibitable, but a 107 pS inner membrane conductance similar to the first recorded inner mitochondrial membrane channel was also observed in the recordings. This smaller conductance was resistant to CsA, suggesting that this activity might be due to a separate ion channel (Szabo & Zoratti, 1991). The large conductance channel was sensitive to Mg^{2+} , Mn^{2+} , Ba^{2+} and Sr^{2+} in that order, which inhibited the activity in a competitive manner with Ca^{2+} , the main activator of the channel (Szabo et al., 1992).

Metabolic functions of the mPTP in cells: Characterization of a metabolic molecular complex surrounding the pore

The recent identification of a molecular structure matching the biophysical properties of mPTP was aided by several reports showing that regulators of the pore bind to the ATP synthase. CypD, which had been known for many years to regulate PT, was found to bind to the stator arm of ATP synthase, specifically on the OSCP subunit (Giorgio et al., 2013;

Giorgio et al., 2009). More recently we described that $Bcl-x_L$ enhances metabolic efficiency (decreases uncoupling) by binding to the β -subunit of the ATP synthase (Alavian et al., 2011; Chen et al., 2011). The third finding suggested that closure of the mPTP is related to the level of CypD activity in a developmentally regulated manner such that its activity falls at the onset of respiration in mammalian heart (Hom et al., 2011). This final report found that ATP synthase assembles into a very large complex with several proteins that may regulate the mPTP (Beutner et al., 2014). Since the first set of findings has been described in detail elsewhere, we will herein concentrate on the physiological and developmental regulation of an inner membrane uncoupling pore within the ATP synthase.

Narrowing down the possibilities for mPTP structure: Bcl-x_L regulates metabolic efficiency by binding to the β -subunit of the ATP synthase

Inefficiency of metabolism is correlated with cell death under conditions of neurodegeneration or acute cellular injury such as occurs during PT (Beal, 2007; Dodson & Guo, 2007; Brand, 2005). In contrast, a highly efficient state of metabolism requires maximally decreased uncoupling of the inner membrane. In neurons as in other cells, calcium entry into mitochondria regulates ATP production and the efficiency by which calcium causes this effect may indeed be crucial to normal synaptic function (Chouhan et al., 2012). It has been found recently that Bcl-2 family proteins regulate efficiency of ATP production by binding directly to the ATP synthase (Alavian et al., 2011; Chen et al., 2011; Hockenbery et al., 1990). Although it was known previously that Bcl-2 family proteins regulate mitochondrial outer membrane permeability (Galonek & Hardwick, 2006; Jonas, 2009), it now seems possible that Bcl- x_L forms part of a large protein complex that regulates mPTP and cell death at the inner mitochondrial membrane. This implies that it may fine tune metabolism in a physiological role in neurons.

During the initiation of cell death an important function of Bcl- x_L , in addition to protection from MOMP, is to increase the release of ATP through enhanced VDAC opening (Gottlieb et al., 2002; Vander Heiden et al., 2000). This decreases the probability of MOMP in cancer cell lines by providing extra ATP to overcome cell death stimuli (Gottlieb et al., 2002; Vander Heiden et al., 2001). In the neuronal synapse, injection of either Bcl- x_L or ATP enhances synaptic transmitter release (Jonas et al., 2003), suggesting that Bcl- x_L increases ATP levels in the synapse (Hickman et al., 2008).

In support of a role for Bcl-x_L in metabolic regulation in healthy cells, hippocampal neurons overexpressing Bcl-x_L show a large increase in cytoplasmic ATP levels. Surprisingly, this increase in ATP accompanies a decrease in neuronal oxygen uptake and aerobic glycolysis, but an increase in synapse number, size and use (Li et al., 2008; Li et al., 2013) including an increase in mitochondrial targeting to synapses (Li et al., 2008; Berman et al., 2009) consistent with the notion that Bcl-x_L overexpression increases mitochondrial bioenergetic efficiency (Alavian et al., 2011; Chen et al., 2011). Bcl-x_L depletion reverses these effects on metabolism, decreasing ATP production and increasing oxygen uptake by resting cells (Alavian et al., 2011; Chen et al., 2011). The regulation of inner membrane coupling by Bcl-x_L also may increase the efficiency of recovery of releasable vesicle pools in synapses that

have undergone synaptic vesicle depletion. Studies show that inhibition of $Bcl-x_L$ slows vesicle recovery to a Ca^{2+} /calmodulin dependent readily releasable pool but not to the reserve or recycling pools (Jonas et al., 2003; Hickman et al., 2008; Li et al., 2013), consistent with a role for mitochondria and/or $Bcl-x_L$ in vesicle docking at release-ready sites (Fig. 4).

Regulatory molecules do not form the pore of mPTP

We have found that $Bcl-x_L$ regulates neuronal metabolism by interacting with the β -subunit of the ATP synthase (Alavian et al., 2011; Chen et al., 2011). A likely scenario is that $Bcl-x_L$ enhances the efficiency of ATP production by closing a leak or pore within the F_1F_O ATP synthase itself; such a pore may also form mPTP. In support of this, F_1F_O ATP synthase interacts with a large number of proteins many of which closely regulate mPTP such as ANT (Woodfield et al., 1998), CypD (Halestrap & Davidson, 1990), VDAC (Crompton et al., 1998), hexokinase, mitochondrial creatine kinase (mtCK) (Beutner et al., 1998; Beutner et al., 1996) and PiC (Leung & Halestrap, 2008), all of which have been touted as candidates for mPTP identity. Although genetic deletions of ANT1 and 2, PiC and VDAC demonstrate that these proteins are not essential to mPT pore formation, the studies still support regulatory roles for these molecules (Gutierrez-Aguilar et al., 2014; Kokoszka et al., 2004; Kwong et al., 2014; Gunter & Sheu, 2009; Kinnally et al., 2011).

Evidence suggests that the regulatory molecules including $Bcl-x_L$ form large macromolecular structures with F_1F_O ATP synthase in the inner mitochondrial membrane. ANT and PiC form a complex with F_1F_O ATP synthase called the synthasome (Chen et al., 2004). In addition, the large complex of ANT, VDAC, hexokinase and mtCK is likely also involved in the regulation of ATP synthesis (Beutner et al., 1998; Beutner et al., 1996). Therefore, each of these molecules may regulate the structure and activity of F_1F_O ATP synthase, and, in so doing, modulate the opening of the mPTP.

The c-subunit of F_1F_0 ATP synthase comprises the PT pore

These various reports all agree that F_1F_0 ATP synthase is a major factor in the formation of the mPTP, and recent evidence suggests that the F_0 or membrane portion of F_1F_0 ATP synthase in fact forms the pore (Bonora et al., 2014; Bonora et al., 2013; Alavian et al., 2014; Azarashvili et al., 2014; Karch & Molkentin, 2014; Chinopoulos & Szabadkai, 2014). Mammalian F_1F_0 ATP synthase is a ~600 kDa complex of 15 subunits. The membrane portion, or F_0 , contains a ring of 8 very hydrophobic c-subunits and subunits a, b, e, f, g, and A6L. A stalk composed of the δ , ε , and γ subunits connects the c-subunit ring to the catalytic F_1 component made of a hexamer of alternating α and β subunits, where ATP synthesis and hydrolysis occur. Finally, a stator containing the b, d, F6, and OSCP subunits connects the lateral portion of F_0 to the top of the F_1 . Movement of protons between the csubunit and the a-subunit causes rotation of the c-subunit ring, the energy of which is transferred to F_1 to synthesize ATP (Carbajo et al., 2005; Pedersen, 1994; Jonckheere et al., 2012; Walker, 2013; Wittig & Schagger, 2009).

Age-dependent structural and functional alterations of F_1F_O ATP synthase in rat brain and heart mitochondria support the idea that an isolated F_O portion of the ATP synthase may form the actual pore of mPTP (Guerrieri et al., 1992). In myocytes in the early embryonic mouse heart the inner membrane is leaky, but this leak is not associated with any form of cell death. However, by mid-embryonic stage, the leak is closed (Hom et al., 2011). This closure coincides with activation of complex I of the electron transport chain, assembly of electron transport chain supercomplexes called respirasomes, and activation of oxidative phosphorylation (Beutner et al., 2014). These changes cause a fall in mitochondrial-derived ROS that signals the myocyte to undergo further differentiation (Hom et al., 2011). The evidence that this developmentally regulated leak is the mPTP comes from studies that show that manipulating mPTP changes the course of cardiac development. Indeed, pharmacologically inhibiting mPTP with cyclosporine A or deleting CypD enhances myocyte differentiation, while in contrast opening mPTP inhibits differentiation (Hom et al., 2011). These findings have been confirmed in cardiac stem cells (Cho et al., 2014; Fujiwara et al., 2011).

Even after the onset of respiration, the F_O still remains partially leaky at 3 months in the membranes of heart mitochondria perhaps because it lacks an equivalent complement of F_1 . During the period from 3 to 12 months, the level of F_1 increases along with an increase in ATPase activity and this accompanies a decrease in proton leak consequent to binding of F_1 to F_O . In contrast, in aging heart in animals from 12 to 24 months, decreases of F_1 content with respect to that observed for F_O are detected, suggesting the presence of lone F_O leak channels and the propensity to undergo PT in these aging mitochondria (Guerrieri et al., 1992).

To determine if the membrane portion of the F_1F_O ATP synthase comprises a cell death regulatory moiety that could produce PT under cell stress, the Pinton group performed different measures of cell death and PTafter c-subunit expression levels were genetically manipulated by depletion or overexpression of c-subunit isomers in HeLa cells (Bonora et al., 2013). Proliferating cell lines rely on glycolysis for ATP production in normal glucose-containing medium, therefore depleting the c-subunit did not alter ATP levels in the cells. Depletion of the c-subunit, however, prevented CsA-sensitive PT measured by the calcein-cobalt quench technique and by mitochondrial morphological analysis. Cell death brought on by H_2O_2 was also attenuated by c-subunit depletion as was cell death in neurons under conditions of excitotoxicity.

Although the above study indicated that the F_1F_0 ATP synthase c-subunit was an important component of the mPTP (Bonora et al., 2013), this work did not directly determine what portion of ATP synthase could induce channel activity. Subsequent to that publication, work from the Bernardi group suggested that the mPT *pore* could only form from dimers of ATP synthase (Giorgio et al., 2013), demonstrating mPTP-like channel activity from purified dimers, and not monomers, of ATP synthase. However, the actual pore portion of the mPTP in this model remained to be determined.

Evidence that the c-subunit of ATP synthase creates the high conductance mPTP pore

More recent experiments have directly tested the hypothesis that the main membrane embedded portion of mammalian F_1F_0 ATP synthase, i.e. the c-subunit ring, forms the pore of the mPTP (Alavian et al., 2014; Azarashvili et al., 2014). Purified, reconstituted c-subunit has been shown previously to form a channel with a diameter of 2.3 nm which allows molecules up to 1.5 kDa to pass, similar to PT (McGeoch & Guidotti, 1997; McGeoch et al., 2000; McGeoch & McGeoch, 2008). In agreement, our own electrophysiologic recordings of the purified mitochondrial c-subunit yield a multi-conductance, voltage dependent channel with prominent subconductance states. Recordings contain a~100-pS conductance, which appears to be a subconductance state of a multiconductance activity rather than a separate conductance. Peak single channel conductances of \sim 1.5–2 nS are similar to activity described previously for the MCC (Kinnally et al., 1989). Also consistent with MCC, channel activity often but not always demonstrates negative rectification. At very positive patch pipette potentials of over 100 mV, single channel conductances of ~1.5 nS and ~2 nS are also consistently observed, presumably because the prolonged open states at negative potentials prevent observation of discrete single channel events that can therefore more easily be observed at positive potentials. This finding is in keeping with similar activity observed previously for mPTP (Petronilli et al., 1989).

Voltage dependence is an inherent property of the channel (Borjesson & Elinder, 2008) and is not dependent on the mitochondrial inner membrane potential or on the solutions used to record the currents. It is measured by varying the voltage across the membrane (the command or holding voltage). Published current-voltage (I-V) curves of mPTP (Petronilli et al., 1989; Kinnally et al., 1989) reveal that the channel shows both non-rectifying conductances and a rectification in the I-V either in the positive or negative voltage range, consistent with I-V plots of our recent recordings of the purified c-subunit (Alavian et al., 2014).

F₁ regulates biophysical characteristics of the purified c-subunit

Purified c-subunit protein reconstituted into liposomes clearly lacks extrinsic regulatory moieties that are important for mPTP opening. The effects of Ca^{2+} , a critical regulatory molecule, demonstrate this property. Ca^{2+} binding sites have not been detected in mitochondrial F_O , perhaps because mammalian c-subunits lack the formyl Met at the N-terminus to which Ca^{2+} binds to *E.coli* or chloroplast F_1F_O ATP synthase c-subunits (Zakharov et al., 1996). Although Ca^{2+} can bind to specific, low affinity and moderate capacity sites on the β -subunit of mitochondrial F_1 ATP synthase (Hubbard & McHugh, 1996), sites in other ATP synthase-interacting regulatory molecules may also be important for regulation by Ca^{2+} and other agents (Beutner et al., 1998; Beutner et al., 1996).

To determine the location of the c-subunit pore regulators, mitochondrial recordings were carried out using purified mitochondrial and F_1F_0 ATP synthase preparations. In these studies, the absence of an effect of a modulator was taken as an indication that the ligand or binding site for that modulator had been removed by the purification process. These studies

demonstrated that the c-subunit leak channel is regulated by the overlying F_1 and peripheral proteins (Alavian et al., 2014). In mitochondria or in inner membrane preparations lacking the outer membrane (such as submitochondrial vesicles, SMVs) (Chen et al., 2004) but containing the intact ATP synthase, Ca^{2+} activates the leak channel while CsA and ATP/ADP inhibit it, suggesting that the Ca^{2+} and CsA sensitive sites are present in these preparations. In contrast, removal of the F_1 and other peripheral membrane proteins by urea treatment of the inner membrane or removal of CypD by purification of ATP synthase monomers abrogates regulation of the c-subunit channel by CsA and Ca^{2+} and greatly diminishes sensitivity to ATP/ADP. These studies suggest that the CypD/Ca²⁺ binding site is contained within or associated with the F_1 portion of the ATP synthase and that a second, low-affinity ATP binding site of CypD and benzodiazepine 423, an ATP synthase-inhibitory and mPTP-sensitizing agent, on OSCP (Giorgio et al., 2009), and suggest that the assembly of F_1F_0 ATP synthase into monomers, dimers, and higher order oligomers may regulate the formation of the mPTP (Giorgio et al., 2013).

Channel activity of the purified c-subunit is inhibited by F_1 , suggesting a structural rearrangement whereby the stalk and F_1 of the ATP synthase inhibits opening of the c-subunit channel, aided by ADP/ATP/Bcl- x_L binding to the β -subunit and opposed by CypD/Ca²⁺ interaction with OSCP (Fig. 5). In order to demonstrate this further, mitochondria were treated with Ca²⁺ following which the F_1F_0 ATP synthase was immunoprecipitated using an antibody directed at the F_1 . These studies determined that Ca²⁺ exposure destabilizes the connection between the stalk and the c-subunit, disrupting protein/ protein interaction between the c-subunit ring itself upon reversible CypD and Ca²⁺– dependent movement of the stalk away from the c-subunit (Alavian et al., 2014).

Loss of protein/protein interaction between F_1 and F_0 requires only mild (60 µM) Ca²⁺ elevations in the bath which initiates what may indeed be reversible PT (Alavian et al., 2014). This concentration is well within the range of physiological Ca²⁺ concentrations found within the mitochondrial matrix (Csordas et al., 2001; Rizzuto et al., 2000; Rizzuto & Pozzan, 2006) or concentrations measured adjacent to the mitochondria in Ca²⁺ microdomains at the ER or plasma membrane (Rizzuto et al., 2009; Schneggenburger & Neher, 2005). That the loss of protein/protein interaction between F₁ and F₀ is likely to be reversible has been shown upon chelation of Ca²⁺ in mitoplasts (Beutner et al., 1998), intact mitochondria (Roestenberg et al., 2012), intact neurons (Jonas et al., 1999) as well as in reconstituted dimers of F-ATP synthase (Gomez et al., 2007), suggesting that the F₁ and the c-subunit can recombine to close the mPTP, reforming intact F₁F₀ ATP synthase and reinitiating enzymatic function (Pedersen & Hullihen, 1978). However, under certain conditions, this separation may become irreversible, forming pathophysiological PT (with MOMP).

Regulators of the mPTP may act directly on the F_1F_0 ATP synthase itself or may involve many known and undiscovered proteins that interact directly or indirectly with ATP synthase, as suggested in previous reports (Pasdois et al., 2013; Beutner et al., 1996; Chen et al., 2004) F_1 has binding sites that accommodate the effects of Ca^{2+} , Mg^{2+} , adenine

nucleotides and P_i ; and through CypD (un)binding those of H⁺, CsA and possibly of oxidants (Kruse et al., 2008; Giorgio et al., 2010). The new model of mPTP incorporates direct or indirect interaction with all known inducers, inhibitors and modulators of pore function.

Structural location of the pore within the c-subunit ring

The exact location of the pore within the c-subunit is becoming increasingly understood. We suggest that it is likely that the leak is located within the central portion of the c-subunit ring. We find that the c-subunit ring expands when it conducts ions, making it likely that the pore is formed within the expanding ring. Using fluorescent tetracysteine display with the placement of cysteine pairs on all c-subunit monomers within the ring, our studies show that Ca^{2+} influx into cells causes a decrease in fluorescence consistent with expansion of the ring, while CsA increases fluorescence consistent with a decrease in ring diameter (Alavian et al., 2014). Mutations targeted to four highly conserved glycines within the first (N terminus) alpha-helical region of the c-subunit (Norris et al., 1992) are known to increase the diameter of the ring and we find that these mutations increase average single-channel conductance compared with WTc-subunit rings (Alavian et al., 2014). When viewed from the inter-membrane space, the denuded c-subunit oligomer appears to have a central porelike structure that is normally obscured by the F₁ stalk components, suggesting that the mouth of the pore may be unmasked by removal of F1 (Pogoryelov et al., 2007). Although it has been suggested that phospholipids occupy the central cavity of the c-subunit ring in F_1F_0 ATP synthases from different species (Oberfeld et al., 2006; Meier et al., 2001; Matthies et al., 2009) other evidence provides for formation of a proteolipid or proteophospholipid channel structure within the central lipid region upon activation of PT (Abramov et al., 2007; Elustondo et al., 2013; Azarashvili et al., 2014; McGeoch & McGeoch, 2008; Pavlov et al., 2005). Polyhydroxybutyrate (PHB) is a polymer distinct from the lipids that may form an ion channel within the lipid milieu if mammalian c-subunit is indeed filled with PHB (Elustondo et al., 2013; Pavlov et al., 2005). Data suggest a working model whereby the c-subunit pore forms within the proteolipid milieu (for example by elevated matrix Ca^{2+}) whereupon the ring expands and F_1 shifts; the pore is closed by a decrease in diameter of the ring and inactivated by binding of the F₁ components to the ring (Fig. 5). The details of these changes and their regulation remain a work in progress.

How does physiological regulation of the mPTP alter synaptic plasticity? Conclusions and plans for the future

Closure of a leak within the inner mitochondrial membrane in the presence of $Bcl-x_L$ aids actively firing neurons to increase neurotransmitter release (Li et al., 2008; Li et al., 2013), consistent with a correlation between the increase in metabolic efficiency and the long-term higher efficacy of synaptic transmission found in $Bcl-x_L$ expressing neurons. In contrast, opening of a $Bcl-x_L$ -regulated inner membrane leak decreases metabolic efficiency, predisposes neurons to death and causes a decline in neurotransmitter release, consistent with a role for the c-subunit channel (putative mPTP) not only in neuronal death but in synaptic dysfunction. Neurons lacking $Bcl-x_L$ display a fluctuating mitochondrial inner

membrane potential and a marked depolarization in the presence of the ATP synthase inhibitor oligomycin (Chen et al., 2011). Current data also provide indirect support for regulation by Bcl- x_L of the F_1F_0 ATP synthase during healthy synaptic events, but direct observation of fluorescently labeled c-subunit and/or labeled F_1 will determine how the putative mPTP channel behaves during actual synaptic events and in synapses undergoing plasticity.

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plus plasma membrane Ca2+ influx increase vesicle fusion,

potentiating neurotransmission.



Fig. 1.

Mitochondrial Ca^{2+} buffering contributes to post-tetanic potentiation of neurotransmitter release. Images left to right show how Ca^{2+} uptake by and re-release from mitochondria enhance synaptic vesicle fusion and thereby increase neurotransmission



Fig. 2.

Mitochondrial Ca^{2+} is necessary for short term synaptic plasticity. Left panel demonstrates that mitochondrial Ca^{2+} contributes to the Ca^{2+} remaining in the synapse for about 1 min after a tetanus. After a tetanus, postsynaptic potentials initiated by neurotransmitter release are potentiated briefly. The right panel demonstrates that residual Ca^{2+} is necessary for these short term increases in neurotransmission. Both residual Ca^{2+} and posttetanic potentiation are dependent on mitochondrial Ca^{2+} release and are prevented by elimination of mitochondrial Ca^{2+} handling



Fig. 3.

Mitochondrial channel activity is necessary for short term plasticity. **a** Mitochondrial membrane recording obtained during and after brief high frequency stimulation (tetanus) given to the presynaptic nerve. Stimulation leads to delayed increases in mitochondrial membrane conductance that outlast the tetanus for up to 1 min. **b** Mitochondrial membrane recording obtained during and after brief high frequency stimulation (tetanus) given to the presynaptic nerve in the presence of the mitochondrial protonophore FCCP. FCCP prevents the change in mitochondrial membrane conductance after a tetanus. **c** FCCP prevents short term posttetanic potentiation of neurotransmitter release



Fig. 4.

Recovery of the readily releasable pool of neurotransmitter is regulated by Bcl-x_L. **a** Change in postsynaptic potential (PSP) amplitude over time in recordings from synapses undergoing repeated tetani. During the tetanus, depression of PSP amplitude occurs followed by rapid recovery in PSP amplitude after the tetanus. **b**, **c** Recovery time of PSP amplitude is prolonged by the Bcl-x_L inhibitor ABT-737, preventing recovery of the readily releasable pool of synaptic vesicles. **d** Diagram demonstrating three different synaptic vesicle pools. The readily releasable pool is defined as those vesicles that are docked at the presynaptic membrane and ready for release. Recovery of docked vesicles takes time and is dependent on Ca²⁺ and the Ca²⁺ binding protein calmodulin. **e** (left panel) During frequent stimulation at 2 Hz, there is no time for recovery of the readily releasable pool. Bcl-x_L injection into the presynaptic terminal does not influence recovery to the recycling pool that is releasing neurotransmitter at this frequency. (right panel) Bcl-x_L enhances the rate of recovery to the readily releasable pool that most slowly recovers after a tetanus. Therefore Bcl-x_L enhances the rate of recovery of this slowly recovering vesicle pool during stimulation at 0.03 Hz



Fig. 5.

The c-subunit of the ATP synthase forms the mPTP. **a** The c-subunit ring expands and the F_1 lifts away from the mouth of the pore when Ca^{2+} interacts with F_1 . **b** Bcl- x_L or ATP/ADP binding to the β subunit or CsA interacting with CypD on OSCP prevent F_1 removal from the mouth of the mPT pore. These mPTP inhibitors also decrease c-subunit ring diameter and channel conductance. The relative closure of the leak channel within the c-subunit ring provides enhanced coupling to the inner membrane, improving the efficiency of ATP production by the ATP synthase