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Downstream mechanisms triggered by mitochondrial dysfunction in the basal ganglia: from experimental models to neurodegenerative diseases

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3-nitropropionic acid; dopamine; Huntington's chorea; huntingtin; long-term potentiation; parkin; Parkinson's disease; PINK1; rotenone; striatum

Abstract

Mitochondrial dysfunctions have been implicated in the cellular processes underlying several neurodegenerative disorders affecting the basal ganglia. These include Huntington's chorea and Parkinson's disease, two highly debilitating motor disorders for which recent research has also involved gene mutation linked to mitochondrial deficits. Experimental models of basal ganglia diseases have been developed by using toxins able to disrupt mitochondrial function: these molecules act by selectively inhibiting mitochondrial respiratory complexes, uncoupling cellular respiration. This in turn leads to oxidative stress and energy deficit that trigger critical downstream mechanisms, ultimately resulting in neuronal vulnerability and loss. Here we review the molecular and cellular downstream effects triggered by mitochondrial dysfunction, and the different experimental models that are obtained by the administration of selective mitochondrial toxins or by the expression of mutant genes.

1. Introduction

The basal ganglia (BG) are a richly interconnected group of brain nuclei communicating with elements of the sensory, motor, cognitive, and motivational apparatuses of the brain. In particular, BG play a key role in the subtle regulation of voluntary and purposive movements and are involved in motor learning and memory [188]. The observation of humans suffering from neurodegenerative diseases affecting the BG, such as Parkinson's disease (PD) and Huntington's disease (HD), has provided the most widely accepted view of the function of these structures, which has been further confirmed experimentally [2,55,74]. Notably, their pathophysiology includes oxidative stress and impairment of mitochondrial energy metabolism, in particular a specific dysfunction of complex I in PD and of complex II in HD [26,159,160,170]. Mitochondria provide the bulk of energy supply to the cell in the form of adenosine triphosphate (ATP). Neurons are extremely sensitive to ATP depletion due to their high energy demand and for this reason they are strongly affected by impairments of energy supply, which lead to necrotic or apoptotic cellular death [76,129]. Interestingly, although mitochondrial dysfunction is involved in both PD and HD, the pattern of neuronal loss observed in these two pathologies is different: the hallmark of PD is the loss of substantia nigra pars compacta (SNc) dopaminergic neurons [100,101], whereas HD is characterized by the selective degeneration of striatal medium-sized spiny neurons using γ aminobutyric acid (GABA) as neurotransmitter and the relative sparing of cholinergic interneurons [151]. Experimental and clinical data suggest that some of the molecular mechanisms for such differential vulnerability originate from the selective mitochondrial impairment underlying PD and HD. Accordingly, chemical inhibition of either complex I or II have led to useful and relevant experimental models of, respectively, PD and HD. It should be mentioned, however, that although none of these models fully reproduces the features of the human diseases, they contributed to improve our knowledge on some of their molecular, cellular and pathophysiological mechanisms. Such mechanisms include, beside the disruption of mitochondrial energy metabolism [8], common and specific molecular cascades that ultimately lead to neuronal death. Here we will review these

models in the context of neurological diseases affecting the BG, with a particular regard to the downstream mechanisms triggered by mitochondrial dysfunction.

2. Basal ganglia in physiological and pathological condition

As mentioned above, the BG are a network of interconnected subcortical structures involved in the control of motor function and in reward and cognitive processes [2,55,74]. The striatum (caudate and putamen nuclei) is classically considered the main input nucleus of the BG, receiving abundant glutamatergic afferences from the cortex and in turn projecting to the output BG nuclei, i.e. the internal *globus pallidus* (GPi) and *substantia nigra pars reticulata* (SNr). Such projections are both direct and indirect via the external *globus pallidus* (GPe) and the subthalamic nucleus (STN). A more recent view of BG organization (Figure 1) now places both the striatum and STN as the two major input stations, the latter belonging to the "hyperdirect" cortex-STN-GPi/SNr pathway [107]. The balance between excitatory (glutamatergic) and inhibitory (GABAergic) synaptic activy within the BG is crucial for their physiological functioning and, accordingly, disruptions of this balance are believed to underlie several hypo- or hyper kinetic movement disorders, such as PD and HD [2,56,186,187]. It is thus of primary importance to further characterize their molecular and cellular pathophysiological mechanisms, in order to develop new therapeutic strategies able to slow disease progression and neuronal loss.

Parkinson's disease - PD is a debilitating neurodegenerative movement disorder with a long course and a high prevalence (1.6 over 100 individuals aged >65 years in the European Union) that increases with demographic ageing [54]. The progressive loss of dopaminergic neurons of the SNc characterizing PD leads to the disruption of the excitation/inhibition balance in the BG and to the manifestation of the main PD symptoms: postural instability, muscle rigidity, tremor and bradykinesia/akinesia. SNc neuron loss results in an excessive activity of glutamatergic pathways of

the BG, including the corticostriatal afferent pathway [86,173] and STN efferent neurons [95], both playing a key role in the expression of PD symptoms [35,79,161]. PD is also anatomopathologically characterized by cytoplasmic inclusions in dopaminergic neurons called Lewy bodies, constituted by α-synuclein-ubiquitin complexes [133]. Besides these evidences, the etiology of the disease remains largely unknown and the available treatments, such as administration of the dopamine precursor 3,4-dihydroxy-L-phenylalanine (L-DOPA) or deep-brain stimulation of BG structures, are only symptomatic. Furthermore, motor fluctuations and dyskinesia complicate L-DOPA therapy in most patients within 5-10 years of treatment initiation. The large majority of PD cases are idiopathic, but a number of specific genetic mutations and exogenous factors responsible for sporadic PD have been identified. Interestingly, current evidence suggests that dysfunction of mitochondrial complex I [52], as well as a possible aberrant interplay between dopamine and αsynuclein [190], may play a major role in PD. In this context, dysfunction of α -synuclein has been shown to indirectly but significantly impact on neuronal mitochondrial function, and there is accumulating evidence for a close relationship between α -synuclein and oxidative damage: overexpression of mutant α-synuclein sensitizes neurons to oxidative stress and damage by dopamine and complex I inhibitors, resulting in increased protein carbonylation and lipid peroxidation in vitro and in vivo [1]. However, since the function of α -synuclein is still unclear, further work is needed to understand the molecular mechanisms involving this protein and dopamine leading to the selective loss of SNc neurons characterizing PD.

Huntington's disease - HD is an autosomal dominant neurological disorder with a prevalence of 4-8 people in 100,000 in Western Europe [94]. It is characterized by the progressive loss of GABAergic medium-sized spiny neurons of the striatum, while cholinergic interneurons are spared [63]. HD symptoms include abnormal "dance-like" movements (chorea), dystonia, cognitive deficits and psychiatric disorders. Treatments that can actually prevent the physical and mental decline associated with HD are lacking, and available antichoreic drugs offer patients only a limited

respite from constant involuntary movements and have long-term side effects [18,184]. Neuronal transplantation provides some years of improvement and stability but not a permanent cure for the disease [5]. The mutated gene responsible for HD was identified in 1993 as the HD gene (IT15) by the HD Collaborative Research Group [114]. Its protein product is huntingtin (Htt) and, since its discovery, researchers are still elucidating the function of both normal and mutant Htt (mHtt). The mutation causing HD is an increased length of a CAG triplet repeat (>36) resulting in a polyglutamine (polyQ) expanded mHtt. The expression of Htt, and mHtt, is widespread in both the central and peripheral nervous systems, and the mechanisms by which mHtt induces the selective loss of striatal projection neurons are still poorly understood. In the pathophysiology of HD, excitotoxic processes linked to N-methyl-D-aspartate (NMDA) receptor activation [62], abnormal activity of corticostriatal glutamatergic pathway [81,83], and mitochondrial complex II dysfunction [24,84,112] have been hypothesized.

3. Biochemistry and physiology of the mitochondrion

Mitochondria generate most of the eukaryotic cell's supply of ATP through the process known as oxidative phosphorylation, a biochemical pathway first characterized by Mitchell and Moyle in 1967 that utilizes energy released by the catabolism of nutrients to synthesize ATP [123]. Mitochondria participate in catabolic processes by several biochemical pathways, including Krebs cycle (also known as the citric acid or tricarboxylic acid cycle), and oxidation of fatty acids and amino acids. The end result of these pathways is the production of two kinds of energy-rich electron donors: reduced nicotinamide adenine dinucleotide (NADH) and succinate. Electrons from NADH and succinate are passed to oxygen that is reduced to water through oxidative phosphorylation, a multi-step redox process occurring on the mitochondrial inner membrane through the mitochondrial electron transport chain. This chain is constituted by a set of five large monomeric (I, II and V) or dimeric (III and IV) enzyme complexes that are associated to a variety of cofactors and electron-

transferring proteins (Figure 2). Complex I or NADH-coenzyme Q oxidoreductase (also known as NADH dehydrogenase) is the first element in the electron transport chain [105]. The reaction catalyzed by complex I consists in the reduction of coenzyme Q10 (or ubiquinone) by NADH and the donation of two electrons. As the electrons pass through complex I, four protons (H⁺) are pumped from the matrix into the intermembrane space. Complex II or succinate-Q oxidoreductase (also known as succinate dehydrogenase), which is also a part of the Krebs cycle, oxidizes succinate to fumarate and reduces coenzyme Q10 [36]. Complex III or Q-cytochrome c oxidoreductase (also known as cytochrome c reductase or cytochrome bc_1 complex) catalyzes the oxidation of one molecule of ubiquinol and the reduction of two molecules of cytochrome c through a complex reaction called O cycle, which pumps four more H⁺ in the intermembrane space [48]. Complex IV (also known as cytochrome c oxidase) is the last element of the electron transport chain and mediates the final reaction, consisting in the transfer of the electrons to O₂ (that is reduced to 2 H₂O accepting 4 electrons) while pumping two H⁺ in the intermembrane space every two electrons transported [33]. The final step in the oxidative phosphorylation pathway is ATP synthesis. catalyzed by complex V or ATP synthase [21]. Interestingly, this mushroom-shaped giant protein complex is found in all forms of life and functions in the same way in both prokaryotes and eukaryotes [21]: it utilizes the energy stored in the form of the H⁺ gradient (Δp) across the mitochondrial inner membrane, generated by the electron transport chain, to synthesize ATP from adenosine diphosphate (ADP) and phosphate (P_i).

Besides energy production through Krebs cycle and oxidative phosphorylation, mitochondria have some other important roles for the physiological functioning of the cell. For example, they participate to Ca²⁺ homeostasis [90,127] in association with the endoplasmic reticulum [147], contain circular DNA molecules (mitochondrial genome) encoding for tRNAs, rRNAs, and complexes I, III, IV and V [40], and participate to cellular metabolism and proliferation [115].

4. Mitochondrial downstream mechanisms in cell death

Mitochondria are essential to cell life. Accordingly, the loss of mitochondrial ATP production leading to energy metabolism deficit can kill a cell by necrosis, and lack of ATP is particularly critical for excitable cells such as neurons, in which the Na⁺/K⁺-ATPase uses more than 40% of the available ATP to keep resting membrane potential at physiological values [81]. However, mitochondria also play an active role in cellular death by participating in complex phenomena leading to apoptotic processes [77]. Indeed, these organelles are involved in a number of key events in apoptosis [75,77], the most critical of which is mitochondrial outer membrane permeabilization (MOMP) occurring early during this programmed death process [76]. MOMP consists in the release of proteins that normally are found in the space between inner and outer mitochondrial membranes, such as cytochrome c and pro-apoptotic factors. The mechanisms responsible for MOMP may involve the opening of the mitochondrial permeability transition pore (mtPTP), leading to collapse of Δp , loss of mitochondrial membrane potential ($\Delta \Psi_m$) and matrix swelling [130], which can ultimately result in outer membrane breaking [132]. The mtPTP putatively consists of the voltagedependent anion channel in the outer membrane, the adenine nucleotide transporter translocator in the inner membrane, cyclophilin D, and other molecules [174,175]. Other mechanisms do not involve mtPTP and seem to be mediated by apoptosis-regulating proteins of the Bcl-2 family (Bax and Bak) acting directly on the outer membrane [76]. The consequences of MOMP are dramatic: as the outer mitochondrial membrane breaks, a number of molecules are released into the cytoplasm triggering downstream processes that lead to apoptotic cell death (Figure 3). These molecules include, in particular: i) cytochrome c, which binds to the cytosolic protein Apaf-1 (apoptotic peptidase-activating factor 1) and to the nucleotide dATP, and then recruits and activates procaspase-9 into caspase-9 [108]; ii) several pro-caspases (2, 3, 8 and 9) [76] as well as apoptosisinducing factor (AIF) [167]; iii) caspase regulators such as Smac (second mitochondria-derived activator of caspases), or its murine equivalent DIABLO (direct IAP-binding protein with low pI),

which removes IAPs (inhibitor of apoptosis proteins) from caspase-IAP complexes, abrogating caspase inhibition [64].

Another important factor contributing to mitochondrial downstream processes leading to cell death is the release of reactive oxygen species (ROS) and free radicals (Figure 3). Mitochondria are the major source of ROS, in particular superoxide anion $(\cdot O_2)$ as a byproduct the abovementioned Q cycle at complex III level [65,93]. Other ROS include hydrogen peroxide (H₂O₂) produced from ·O₂ by superoxide dismutase (SOD). Uncoupling electron transfer increases ROS production, and the release of cytochrome c due to MOMP contributes to electron transfer uncoupling, which can result in a feedback mechanism further increasing ROS production [77]. Besides being harmful by directly damaging DNA, oxidizing fatty acids and amino acids, and inactivating enzymes by oxidation, ROS can also trigger several signaling pathways. Indeed, some of them exert a prosurvival action, such as those mediated by ERK (extracellular regulated protein), PI(3)K/Akt (phosphoinositide 3-kinase/Akt) and NF-κB (nuclear factor κB), whereas some others can activate p53 tumor suppressor protein transcription factor, JNK (c-Jun N-terminal kinase) and p38 protein kinases that are linked to apoptosis, contributing to the abovementioned pro-apoptotic events occurring during MOMP [65]. Moreover, glutamate transporters [50] are also vulnerable to ROS, resulting in reduced uptake function and build-up of extracellular glutamate levels that can be toxic to neurons and astrocytes [172]. Prolonged exposure to glutamate leads to hyperactivation of ionotropic glutamate receptors [13,111] and to the concomitant influx of ions and water into the cell [43]. In particular, excessive activation of NMDA receptors increases intracellular Ca²⁺ levels, which is known to promote a great number of processes contributing to cell death [60,81,88,121,128]. These processes include excitotoxicity, stimulation of phospholipase A2 and Ca²⁺-dependent protein kinases, and production of ROS and free radicals that may trigger a vicious cycle worsening mitochondrial dysfunction that in turn predisposes neurons to excitotoxic damage (Figure 3).

But how these mitochondrial downstream mechanisms leading to cell death are triggered? Which of them are relevant to neurodegenerative diseases? A multitude of factors have been implicated in these processes. The following sections will review the currently utilized experimental models of mitochondrial impairment that attempt to address the molecular, cellular and physiological mechanisms of BG neurodegenerative diseases.

5. Mitochondrial complex I dysfunction and Parkinson's disease

Dysfunction of mitochondrial complex I has been associated to sporadic forms of PD [52] and parkinsonism, the latter term referring to a syndrome of tremor, rigidity, bradykinesia and postural instability that, beside PD or "primary parkinsonism", includes rare secondary cases that may result from toxicity, head trauma or other medical disorders [44,52]. Complex I derangement results in an enhanced production of ROS that, in turn, further impairs mitochondrial function in a vicious cycle [170], triggering the above described downstream mechanisms leading to neuronal death. Accordingly, neuroscientists took advantage of several selective complex I inhibitors to develop experimental models relevant to PD [97].

6-hydroxydopamine (**6-OHDA**) - The neurotoxin 6-OHDA is a structural analog of catecholamines and has played a fundamental role in research on PD since the late 1960s [155,177], after the discovery of its lethal proprieties on catecholaminergic neurons [148]. Neurotoxic effects of 6-OHDA occur through a two-step mechanism involving accumulation of the toxin into catecholaminergic neurons by the dopamine and noradrenaline membrane transporters, followed by mitochondrial complex I inhibition [17]. The action mechanism by which 6-OHDA reversibly inhibits complex I still needs to be better characterized. However, it seems that this toxin does not compete with NADH for its binding site on the enzyme, but rather it binds to the enzyme-substrate

complex and the resulting enzyme-substrate-inhibitor complex has a reduced catalytic activity [72]. 6-OHDA is toxic at both central and peripheral level. However, since this molecule is unable to cross the blood-brain barrier, it is toxic only when directly injected into the brain by stereotaxic procedures. The selectivity of 6-OHDA for SNc dopaminergic neurons is thus achieved by directly targeting this structure, in association or not with a treatment blocking noradrenalin uptake such as desipramine. 6-OHDA injection in the SNc or in the medial forebrain bundle produces a massive (>90%) degeneration of dopaminergic neurons and specific motor deficits, some of which mimicking those of PD. 6-OHDA is classically utilized in rats, but an increasingly number of papers now reports this technique also in mice. However, 6-OHDA dopaminergic denervation in rodents lacks key neuropathological and clinical features of PD: Lewy bodies do not appear in neurons and tremor is absent. Usually, 6-OHDA is injected unilaterally, and this is for two main reasons: first, the massive bilateral dopamine depletion provoked by 6-OHDA is easily lethal in rodents, which moreover need to be force-fed; second, animals with unilateral 6-OHDA lesion have unilateral motor impairments that can be efficiently detected and measured, such as ipsilateral akinesia and contralateral rotations following administration of dopaminergic agents [37,86,178]. Some scientists perform partial bilateral lesions (~60% of dopaminergic loss) by injecting 6-OHDA in the dorsal striatum to target dopaminergic terminals, thus representing an "early stage" model of PD that can also allow to study more complex behavioral changes such as reaction time [3], a parameter also measured in humans [70]. The 6-OHDA PD model has provided a considerable amount of information at cellular and molecular level. For example, glutamatergic transmission in the BG is significantly affected in rats with massive dopamine denervation [162]: in vitro electrophysiological studies show an enhanced glutamatergic activity of striatal medium-sized spiny neurons [31,87] that is supported by in vivo data [173]. Moreover, the two forms of synaptic plasticity described at corticostriatal synapse, long-term depression (LTD) and long-term potentiation (LTP), are lost in parkinsonian rats [28], as well as depotentiation of LTP [28,142]. Another interesting feature of the 6-OHDA model of PD is that it can be associated to

antiparkinsonian therapies, such as L-DOPA and chronic high-frequency stimulation of the STN [89], with some interesting outcomes [29]. For example, L-DOPA treatment has been shown to either ameliorate hypokinetic motor deficits [113] or to induce dyskinesia in hemiparkinsonian rats [143] depending on the administration mode. Moreover, L-DOPA treatment is also capable to reverse some cellular and molecular changes observed at striatal level after unilateral 6-OHDA lesion in rats, in particular glutamatergic hyperactivity at corticostriatal synapses [113], hypersensitization of striatal D2-like dopamine receptors [4,144] and of group II metabotropic glutamate receptors [146], as well as endocannabinoid system abnormalities [87,113]. Similarly, STN stimulation is also effective in progressively reducing akinesia and reversing glutamatergic hyperactivity at corticostriatal synapses [86].

1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) - This neurotoxin was discovered when drug-addicted Californians accidentally injected with "synthetic heroin" (1-methyl-4-phenyl-4-propionoxypiperidine, MPPP or desmethylprodine) contaminated with MPTP and suddenly developed parkinsonian symptoms [7,102]. MPTP is a highly lipophilic mitochondrial complex I inhibitor that easily crosses the blood-brain barrier and can thus be administrated systemically to obtain experimental PD models [149]. It becomes toxic through its transformation to 1-methyl-4-phenyl-2,3-dihydropyridinium (MPDP⁺) by the enzyme monoamine oxidase B (MAO-B) expressed by glia and serotoninergic neurons [99], and its subsequent spontaneous oxidation to 1-methyl-4-phenylpyridinium (MPP⁺) [165,171]. The dopamine transporter (DAT) then carries MPP⁺ into dopaminergic neurons, where it is accumulated into synaptic vesicles by the vesicular monoamine transporter (VMAT). Once in the cell, it can enter mitochondria using $\Delta \Psi_m$ driving force where it blocks complex I [131,152,164,166]. Various protocols of MPTP administration in mice (acute vs. chronic; repeated injections of low doses vs. a single high dose, etc.) exist in the literature [120], while the rat appears to be refractory to this toxin. Chronic intoxication with low doses of MPTP is also used in monkeys, in which it mimics at best the motor symptoms of PD including tremor,

bradykinesia, muscle rigidity and postural instability, as well as some neuropathological features including the massive loss of SNc neurons. [97,124,166]. On the other hand, degeneration of nigrostriatal dopamine neurons is not accompanied by the more general loss of monoaminergic cells and the presence of Lewy bodies observed in PD, at least in non-chronic models [67]. The MPTP model has been particularly useful for studying the functional changes occurring in the primate BG after dopamine depletion, providing insights into the pathophysiology of PD. For example, STN neurons recorded from awake monkeys showed an increased rate of spontaneous firing activity with periodic oscillations at low β-frequency, which in humans is highly correlated with tremor [12,15,117], confirming that this structure becomes hyperactive in PD and contributes to the disruption of BG functioning. Moreover, the rationale for targeting STN by deep-brain stimulation arose from the primate MPTP model. Recently, some studies using chronic MPTP intoxication in mice showed inhibition of the ubiquitin-proteasome system paralleled by the apparition of neuronal inclusions containing ubiquitin and α-synuclein [66,119]. Interestingly, such alterations were reduced in mice lacking α -synuclein [66], further supporting the involvement of this protein in the pathophysiological processes of PD [190]. In MPTP-treated mice some interesting motor impairments relevant to PD can be detected by a number of behavioral tests that are sensitive to subtle changes in dopamine levels [118].

Concerning the mechanisms of MPTP toxicity, NMDA receptor and inducible nitric oxyde synthase (iNOS) have also been implicated in MPTP-mediated loss of SNc neurons, because such neurodegeneration was reduced by NMDA receptor antagonists [176], in mice lacking iNOS [109] or by an anti-inflammatory compound (of the diindolylmethane class) suppressing NF-κB-dependent expression of iNOS [34]. Other reports have suggested a neurodegenerative mechanism based on mitochondrial downstream apoptotic processes [17], which involve up-regulation of JNK [157] and Bax [180], release of cytochrome *c* and activation of caspase-3 and -9 [183]. Accordingly, systemic pharmacological blockade of JNK or p53 (which regulates Bax) resulted in reduced damage to nigrostriatal neurons after MPTP intoxication [59,157].

Rotenone - Rotenone is a complex I inhibitor used in broad spectrum insecticides, piscicides and pesticides. It can naturally be found in the roots and stems of several tropical plants such as the jícama vine plant (*Pachyrhizus erosus*). Rotenone is highly lipophilic and, unlike MMP⁺, it does not need to be actively transported. Thus, it can quickly and easily accumulate in tissues and then reach the brain [78]. Systemic (intravenous) administration of rotenone in rats induces a highly selective degeneration of SNc neurons paralleled with hypokinesia and rigidity, and cytoplasmatic inclusions containing ubiquitin and α-synuclein [14,27]. The administration route of this inhibitor seems essential for the set up of experimental PD models, since chronic intranasal inoculation failed to induce dopamine neuron degeneration [154]. The action mechanisms of rotenone are still poorly characterized, but evidence from experimental in vitro and in vivo PD models by chronic intoxication suggest that this toxin causes a delayed depletion of glutathione, which is accompanied by oxidative damage to proteins and DNA [78]. Electrophysiological data show that rotenone acute application on corticostriatal slices induces an early hyperpolarization of striatal cholinergic interneurons, followed by a late depolarizing response that seems linked, respectively, to activation of ATP-sensitive K⁺ channels and decreased Na⁺/K⁺-ATPase function [19]. More recent electrophysiological studies targeted striatal spiny neurons, which respond by a marked membrane depolarization resulting in the loss of field potential, coupled to an increased release of excitatory amino acids and dopamine. Interestingly, these effects were not attenuated by acting on glutamatergic synaptic transmission [39,47] but they were reduced by antagonists of dopamine D2like [47] or adenosine A2A receptors [11], suggesting that monoaminergic and purinergic systems may play a role in the selective toxicity of rotenone.

Paraquat - Paraquat is the trade name for 1,1'-dimethyl-4,4'-bipyridinium dichloride, a structural analog of MPP⁺ and one of the most widely used pesticides and herbicides in the world. It is lipophilic and enters easily into the cell where is taken up across the mitochondrial inner membrane

by a carrier-mediated and $\Delta \Psi_m$ -dependent process, and once in the matrix it is reduced by complex I. The reduced form of paraquat then reacts with oxygen to form ROS (in particular O_2) and cause mitochondrial oxidative stress leading to neuronal death [45]. Accordingly, synthetic SOD/catalase mimetics can protect dopaminergic neurons both in cell lines and in mice treated with this toxin [140]. An epidemiological association has been found between the use of paraquat in agriculture and the incidence of parkinsonism [57], and this toxin is now used to model PD. Some mechanisms underlying acute paraquat neurotoxicity begin now to be elucidated. At molecular level, they seem to involve sequential phosphorylation of JNK and c-Jun, and the activation of caspase-3, leading to apoptosis [139]. At the cellular level, paraquat inhibits AMPA receptors on dopaminergic neurons, suggesting that a decreased excitability and function of these cells in the SNc may contribute to the pathogenesis of PD [104]. Long-term paraquat administration (up to 24 weeks) has been shown to produce a slowly progressing degeneration of dopaminergic neurons of the SNc [135] and the ventral tegmental area (a source of the mesocortical dopaminergic projection) [134], leading to delayed deficits in dopaminergic transmission that resemble early presymptomatic stages of PD. However, another study with chronic exposure to paraquat (intranasal inoculation) in mice did not report dopaminergic loss, but this toxin induced severe hypokinesia and vestibular damage [154],

Manganese - Although manganese intoxication is not properly an experimental model of PD, its action mechanisms are relevant to this disease because they involve mitochondrial complex I inhibition. Manganese (Mn) is an essential trace element and is required for several physiological enzymatic reactions. Exposure to excessive levels of this metal through inhalation of manganese-containing dust can evoke a syndrome with psychiatric disturbances and severe extrapyramidal motor dysfunctions closely resembling those of PD, called manganism. Clinical manifestations of manganism arise from focal injury to the BG due to the fact that these nuclei accumulate most of the excess manganese compared with other brain regions. The mechanisms of the cellular damage caused by this element have been attributed to its capacity to produce toxic levels of free radicals

and induce mitochondrial dysfunction, thus enhancing ROS production [58,91]. Manganese is sequestered by brain and liver mitochondria via the mitochondrial Ca²⁺ uniporter [71], and its toxicity seems to result from a direct and/or indirect inhibitory effect of Mn(III) and Mn(II) on complex I leading to oxidative stress [42,68]. Moreover, Mn(II) catalyzes the auto oxidation of dopamine to dihydrobenzothiazine (DHBT) and then to 7-(2-aminoethyl)-3,4-dihydro-5-hydroxy-2H-1,4-benzothiazine-3-carboxylic acid (DHBT-1), which is a complex I inhibitor [163]. We have shown that chronic manganese intoxication in rats (MnCl₂ dissolved in drinking water) induces a hyperactivation of corticostriatal glutamatergic afferences [38], reminding that observed after 6-OHDA lesion, paralleled by an enhanced sensitivity of presynaptic D2-like dopamine receptors [32].

6. Gene mutation, mitochondria and Parkinson's disease

Around 5% of PD cases are familial forms that have an earlier onset (~45 years) [53] and that arise from the mutation of several identified genes, in particular *parkin* and *PINK1* [phosphatase and tensin homologue (PTEN)-induced putative kinase 1] [1,192]. *Parkin* and *PINK1* are involved in autosomal recessive PD (ARPD), and they are particularly interesting here because both clinical and experimental evidence have associated their mutation with mitochondrial dysfunction.

Parkin - Parkin is a 465 amino acid E2-dependent E3 ubiquitin ligase involved in protein ubiquitination and removal of damaged proteins. A large variety of homozygous and heterozygous mutations of parkin gene have been reported, all of them abolishing or reducing parkin activity and representing ~50% of ARPD cases [1]. Severe mitochondrial pathology and increased vulnerability to oxidative stress have been shown in *Drosophila* null mutants [80]. In mice, deletion of *parkin* exon 3 resulted in reduced excitability of striatal medium-sized spiny neurons and behavioral deficits sensitive to nigrostriatal pathway dysfunction [73]. Moreover, these animas had an impaired

mitochondrial function paralleled by a decreased expression of complex I and IV subunits [136]. On the other hand, deletion of either exon 2 or 3 did not cause dopaminergic neuron degeneration [73,96], thus questioning the validity of *parkin* mutant mice as a PD model [141].

The mechanisms by which parkin is linked to mitochondrial function are not yet completely elucidated. In ceramide-mediated apoptosis, parkin seems to promote the degradation of protein substrates localized in or around mitochondria, delaying MOMP and subsequent cytochrome c release and caspase-3 activation [51]. Other indirect actions of parkin on mitochondria have been hypothesized, all linked to its role in protein ubiquitination and degradation [1]. Recently, it has been shown that a wide array of complex I inhibitors, including 6-OHDA, MPP⁺, paraquat, NO and iron, as well as dopamine, all altered parkin solubility, leading to parkin aggregation and thus compromising its neuroprotective function [185]. Overall, parkin seems to play an important role in cell protection against oxidative stress, and its mutation disrupts this function as well as its role as ubiquitin ligase, leading to an impaired removal of mitochondrion-associated damaged proteins and thus to mitochondrial damage [192]. Interestingly, dopamine convalently modifies parkin, which results in the loss of its activity [103] and suggests a possible mechanisms for the selective loss of dopaminergic neurons in ARPD as well as in idiopatic PD. Furthermore, it has been shown that overexpression of Pael-R (parkin associated-endothelin-receptor-like receptor, an endoplasmic reticulum-associated substrate of parkin) leads to Pael-R aggregation, which in turn results in endoplasmic reticulum stress and dopaminergic neuron death. This effect was alleviated by parkin overexpression as well as dopamine synthesis inhibition, implicating dopamine in such toxic aggregation process [192].

PINK1 - Mutations in *PINK1* have been identified in three large consanguineous families, two Italian and one Spanish, in which several cases of ARPD were reported [179]. PINK1 is a 581 amino acid protein expressed ubiquitously, whose transcription is activated by PTEN and whose N-terminal kinase domain targets mitochondria. *PINK1* mutations have been reported to be distributed

mostly in the region coding for this domain. In particular, the $G\rightarrow A$ amino acid substitution in exon 4 (G309D) found in the Spanish family, when overexpressed in a neuroblastoma cell line, impaired PINK1 kinase activity, its interaction with mitochondria and its import inside these organelles, resulting in the reduction of $\Delta \Psi_m$. Accordingly, overexpression of wild-type PINK1 decreased the release of cytochrome c from mitochondria both in control conditions and in staurosporine-induced stress [179]. However, the direct link between PINK1 and mitochondria still needs to be elucidated. Interestingly, data arising from *Drosophila* suggest that PINK1 and parkin may act in a common pathway in the pathogenesis of PD, because PINK1 loss of function mutation could be rescued by using transgenic expression of parkin [168,191]. Moreover, recent evidence in *Drosophila* and mammalian cell culture showed that parkin phosphorylation by PINK1 promotes its mitochondrial translocation, further suggesting a possible pathological mechanism for PD associating these two proteins [98].

7. Mitochondrial complex II dysfunction and Huntington's disease

Complex II or succinate dehydrogenase (succinate-Q oxidoreductase) participates not only to oxidative phosphorylation, but also to the Krebs cycle. Its experimental or accidental blockade thus results in a dramatic ATP depletion and, interestingly, in a neurodegenerative pattern and motor symptoms closely resembling those of HD. Several toxins have been discovered being able to selectively block this enzyme, and scientists took advantage of this for developing models relevant to HD. In particular, 3-nitropropionic acid (3-NP), which was identified in the 1950s in a toxic tropical flowering plant belonging to the *Fabaceae* family, but is also present in other plants and fungi. It has been suggested that 3-NP is dehydrogenated by complex II to 3-nitroacrylate, which then irreversibly inhibits the enzyme [46]. Accidental exposure to 3-NP mimics the pathophysiology of HD in humans and, accordingly, chronic 3-NP administration has long been used as an experimental HD model both in rodents and monkeys [22-25,112,137,189]. 3-NP

produces brain lesions that are mostly confined to the striatum, with selective loss of medium-sized spiny neurons and relative sparing of interneurons [10,137]. Other complex II blockers also used in research include malonic acid (MA) [82] and the more cell-permeable methylmalonic acid (MMA) [116], two synthetic dicarboxylic acids. They compete with succinate but do not react with the enzyme, thus their inhibitory effect is reversible, and chronic MA treatment produces lesions similar to those observed with 3-NP [9,82].

At functional level, rats with systemic subacute 3-NP administration develop motor symptoms resembling striatal-induced dystonia [10,92], impaired responses in the cross-maze task and perseverative behavior [145]. Motor troubles relevant to HD have been observed in tufted capuchin monkeys (*Cebus apella*), which showed spontaneous and apomorphine-induced dystonia and dyskinesia after two months of chronic 3-NP treatment [153]. Spontaneous and apomorphine-induced dystonias of foot and leg, and some dyskinesias of the hindlimb were also reported in baboons, which also showed significant impairments in a test designed to assess the functional integrity of the frontostriatal pathway in both humans and nonhuman primates [137].

The mechanisms of action underlying the selective toxicity of 3-NP, MA and MMA have been in part elucidated. The strong impairment in energy metabolism due to succinate dehydrogenase inhibition depletes ATP levels, leading to to Na⁺/K⁺-ATPase dysfunction and subsequent neuronal membrane depolarization, followed by de-inactivation of NMDA receptors by relieving voltage-dependent Mg²⁺ block [81,83]. In line with these findings, it has been shown that acute slice application of 3-NP or MMA on brain slices induces a potentiation of NMDA receptor-mediated synaptic excitation, resulting in a LTP of corticostriatal synaptic transmission [30], as well as other alterations of striatal synaptic plasticity [145]. Interestingly, NMDA receptor-mediated potentiation is observed in medium-sized spiny neurons but not in cholinergic interneurons [30], is promoted by NR2B containing NMDA receptors [39], is induced by the activation of the metabotropic glutamate subtype 1 (mGlu1) receptor/protein kinase C pathway as well as dopamine D2-like receptors, and is negatively regulated by D1-like receptors [85]. Accordingly, acute 3-NP

treatment modulates the expression of several genes involved in glutamatergic and dopaminergic signaling [125]. These evidences suggest that NMDA receptor-dependent mechanisms may underlie the vulnerability of striatal medium-sized spiny neurons to complex II dysfunction, and that the selective loss might be attributed to the high contents of dopamine in the striatum. Another striking difference in the reactivity to complex II blockade between striatal medium-sized spiny neurons and cholinergic interneurons is that the former respond to the toxin by a depolarization, while the latter by a hyperpolarization that might represent a neuroprotective mechanism [158]. The excitotoxic dopamine-mediated hyperactivation of NMDA receptors confined to striatal spiny neurons, combined with energy failure, could converge into a common downstream mechanism leading to the selective neuronal loss observed during HD. Such neurodegeneration seems also to involve acute inflammatory processes, as suggested by the activation of NF-κB by in vitro 3-NP application [126]. Moreover, an apoptotic mechanism might also participate, as suggested by the progressive activation of p53 and JNK, followed by c-Jun activation and expression, induced in the striatum of 3-NP intoxicated rats and in cultured neurons treated with this toxin [69]. Moreover, enhanced expression of the apoptosis markers Bcl-2 and caspase-3 has also been detected in the caudate nucleus of HD patients [181], as well as in the striatum of rats intoxicated with 3-NP [182].

The 3-NP model of HD has also been successfully used to test neuroprotective strategies that might be helpful in slowing the progression of the disease. For example, it has been shown that the uncompetitive NMDA receptor antagonist memantine, which is currently used for Alzheimer's disease treatment, can reduce the irreversible loss of corticostriatal field potential caused by acute 3-NP application [169]. Another study showed that striatal *in situ* continuous delivery of CNTF (ciliary neurotrophic factor), an endogenous astrocyte activator, could reduce striatal neurodegeneration, cognitive impairment and motor symptoms in primates chronically treated with 3-NP [16]. Interestingly, CNTF-mediated neuroprotection seems to occur by improving glutamate handling [61], in particular by enhancing the function of glutamate transporters (unpublished

observation), further suggesting a role of glutamate-mediated toxicity in the progressive loss of striatal medium-sized spiny neurons in HD.

8. Mutant huntingtin, mitochondria and Huntington's disease

There is increasing evidence suggesting that mitochondrial dysfunction characterizing HD is associated to the expression of mHtt [20]. For example, it has been shown that mitochondrial impairment occurs even in asymptomatic carriers expressing mHtt with 41-47 CAG repeats [156], and mitochondria isolated from early HD patients and YAC72 transgenic mice have reduced Ca²⁺ buffering capacity [138]. Furthermore, culture cells expressing mHtt showed impairment of mitochondrial respiration and ATP synthesis [122]. But which is the molecular link between mHtt and mitochondria leading to the dysfunction of these organelles? One candidate is p53: mHtt has been shown to bind to p53, up-regulating its transcriptional activity and increasing its levels in PC12 cells, primary neuronal cultures, mHtt-Tg mice and post-mortem brains of HD patients [6]. This, in turn, increases the expression of PUMA (p53 up-regulated modulator of apoptosis) and BAX (Bcl-2-associated X protein), two pro-apoptotic members of the Bcl-2 family, leading to mitochondrial damage and cell death [6]. Another possible molecular link between mHtt and mitochondrial dysfunction is PGC-1α [peroxisome proliferator-activated receptor (PPAR)-γ coactivator 1α). PGC-1α is a key element that co-regulates the transcription of some cellular programs modulating mitochondrial respiration, oxidative stress defense and adaptive thermogenesis. In particular, PGC-1α binds to nuclear transcription factors regulating nuclearencoded mitochondrial genes such as cytochrome c, mitochiondrial transcription factor A and complex I-V components [150]. At molecular level, mHtt interferes with the PGC-1α promoter leading to reduced PGC-1α transcription [49]. Interestingly, PGC-1α knock-out mice showed microvacuolation of neuropil and neurons in the striatum, as well as an abnormal energy metabolic phenotype [106,110]. Furthermore, PGC-1α is a potent suppressor of ROS production, suggesting

that reduced expression or loss of this transcriptional co-regulator might sensitize neurons to oxidative stress [20]. Accordingly, PGC-1 α is decreased in striatal medium-sized spiny neurons, but not in interneurons, of R6/2 HD mice, suggesting a possible mechanism for the selective neuronal loss characterizing HD [49]. Finally, beside these indirect molecular links, mHtt binds directly to the mitochondrial outer membrane, forming large clusters that can impair mitochondrial function, change their morphology and interfere with their intracellular movement [20,41].

9. Conclusions

The experimental use of selective mitochondrial toxins allowed the development of animal models of neurodegenerative diseases involving the BG. Uncoupling complex I or II leads to physiological, behavioral and anatomopathological alterations in rodents and primates that mimic those observed, respectively, in PD and HD. The major contribute of these experimental models, however, is that they provided precious insights to understand the mechanisms underlying PD and HD onset and progression. In particular, elucidation of the events occurring at the cellular level leading to neuronal death offered us several clues on possible new treatments for PD and HD targeting specific molecules that participate to the pathogenic cascade triggered by mitochondrial dysfunction.

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Figure legends

Figure 1. Schematic representation of the basal ganglia circuit. The structures and circuitry of the BG are represented here, along with their connections to the cerebral cortex, the thalamus and the brain stem/spinal cord. Note the three projection pathways to the output BG structures (GPi/SNr): the "direct" one from the striatum, the "indirect" from the striatum through GPe and STN, and the "hyperdirect" from the cortex through the STN. The neurotransmitters utilized in the described projections are illustrated in different colors. Abbreviations: GABA, γ-aminobutyric acid; GPe/i, *globus pallidus pars externa/interna*; SNc/r, *substantia nigra pars compacta/reticulata*; STN, subthalamic nucleus.

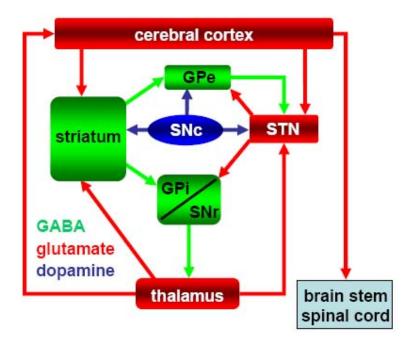


Figure 2. The mitochondrial respiratory chain and the targets of mitochondrial toxins.

Complex I to IV of the mitochondrial respiratory chain catalyzing oxidative phosphorylation are in green. The two electrons (2 e⁻) donated during the reduction of ubiquinone (Q) by NADH are transported through complexes I, II, III and cytochrome c (Cyt c) to complex IV, which transfers them to O_2 to generate water. During this process ten protons (H⁺) for each 2 e⁻ are pumped from the matrix to the intermembrane space by complexes I, II and IV, generating a H⁺ gradient (Δp) across the inner membrane contributing to mitochondrial membrane potential ($\Delta \Psi_m$). This gradient is utilized by ATP synthase (in red), also called complex V, to synthesize ATP from ADP and P_i. The toxins utilized in experimental models of BG diseases target either complex I (for PD) or II (for HD). Note that complex II blockade also affects Krebs cycle, having a greater impact on cellular energy production.

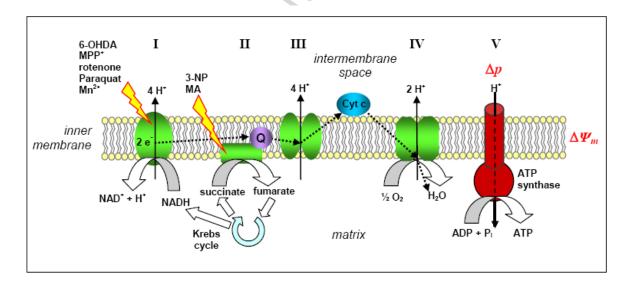


Figure 3. Downstream mechanisms triggered by mitochondrial dysfunction: converging towards neuronal death. Mitochondrial damage and respiratory chain uncoupling by mitochondrial toxins results in the decrease of ATP synthesis and in the increase in ROS production, the former leading to energy failure promoting cell death, the latter further contributing to cellular and mitochondrial damage. This can result in an impaired Ca^{2+} buffering that, together with excessive Ca^{2+} entering through NMDA receptors, leads to increased Ca^{2+} levels both in the cytoplasm and in the mitochondria. Elevated mitochondrial Ca^{2+} concentration triggers mitochondrial outer membrane permeabilization (MOMP) by opening of the mitochondrial permeability transition pore (mtPTP), resulting in the collapse of Δp and $\Delta \Psi_m$, release of cytochrome c and other apoptosis-promoting factors, and increased ROS production and Ca^{2+} accumulation. This downstream effects, in turn, will further contribute to cellular and mitochondrial damage in a deadly feedback cycle. Impaired ATP synthesis, excessive ROS production, Ca^{2+} mediated excitotoxic processes, and release of pro-apoptotic factors all converge towards neuronal death.

