

## Cell Death Pathways in Parkinson's Disease: Role of Mitochondria

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### Abstract

Parkinson's disease (PD) is a progressive neurodegenerative disease and is characterized pathologically by selective loss of nigrostriatal dopaminergic neurons and the formation of Lewy bodies. Although in the majority of cases the cause of PD is unknown, mitochondrial dysfunction, environmental toxins, oxidative stress, and abnormal protein accumulation may all be involved in disease pathogenesis. The discovery of genes causing rare familial forms of PD (including  $\alpha$ -synuclein, parkin, DJ-1, PINK1, and LRRK2) has shed light on our understanding of the molecular mechanisms of the development of the disease. Further studies from transgenic or toxin-induced experimental models have also provided insights into the etiology of human disease. Recently, accumulating evidence has suggested that mitochondrial dysfunction is one of the key players in molecular cell death pathways of PD. In this review, we provide an overview of the role of mitochondria in the pathogenesis of both sporadic and familial forms of PD. We also discuss the links between different pathways and highlight novel therapeutic opportunities which target mitochondria. *Antioxid. Redox Signal.* 11, 2135–2149.

### Introduction

**P**ARKINSON'S DISEASE (PD), first described by James Parkinson in 1817, is one of the most common progressive incurable neurodegenerative diseases. It affects ~1% of the population over 60 and up to 4% of those over 80 years old (31). Clinically, PD is characterized by motor impairments including resting tremor, bradykinesia, postural instability, rigidity, and some nonmotor symptoms such as cognitive and psychiatric problems. The pathological hallmarks of PD include: loss of dopaminergic (DAergic) neurons in the substantia nigra pars compacta (SNpc) and appearance of Lewy bodies in the surviving neurons. Substantia nigra DAergic neurons are a part of the interconnecting neuronal circuitry of the basal ganglia, which also involves other brain regions including the striatum, cortex, thalamus, and subthalamic nuclei.

Although the majority of PD cases are sporadic with unknown causes, a small proportion of PD cases are inherited, and mutations in several genes have been identified (Table 1). These genes include:  $\alpha$ -synuclein (120), parkin (70), DJ-1 (18), PTEN-induced kinase 1 (PINK1) (157), and leucine-rich repeat kinase 2 (LRRK2) (107, 179). A single mutation has been found in Omi/HtrA2 gene in sporadic PD cases (144). Mutations in UCHL-1 (81), POLG1 (5), and ATP13A2 (124) have also been

found in patients with parkinsonism, although there is still debate about whether these genes truly represent PD-causing genes.

The discovery of PD genes, together with the pathological and epidemiological investigation of sporadic PD cases, has provided us with insights into the principal pathways of PD pathogenesis (For reviews, see ref. 169). The identification of  $\alpha$ -synuclein-positive Lewy bodies in the brains of PD patients has suggested the importance of protein aggregation. The discovery of parkin mutations further confirmed the importance of Ubiquitin Proteasome System (UPS) dysfunction in PD pathogenesis. The identification of PINK1 and HtrA2, a mitochondrial kinase and protease respectively, has helped reignite interest in the pathophysiology of mitochondria and their potential role in PD. Finally, the identification of mutations in DJ-1, an oxidative stress sensor, and evidence from functional studies suggested the importance of oxidative stress. In this review, we will focus on the role of mitochondrial dysfunction in the pathogenesis of PD.

### Abnormal Mitochondria in PD Patients

An important piece of evidence linking mitochondrial dysfunction to PD came from the reports of complex I deficiency in the substantia nigra of patients with idiopathic

TABLE 1. PARKINSON'S DISEASE-ASSOCIATED GENES

Locus	Gene	Chromosome	Inheritance	Phenotype	Protein	Function
PARK1/4	SNCA	4q21	AD	Similar to IPD, early, rapid progression	$\alpha$ -synuclein	Implicated in synaptic vesicle formation
PARK2	Parkin	6q25.2-27	AR	Early-onset, slow progression, early dystonia, and dyskinesia	Parkin	Ubiquitin ligase E3
PARK5	UCHL-1	4p14	AD	Similar to IPD	UCHL-1	UPS component
PARK6	PINK1	1p35-36	AR	Early-onset, levodopa-responsive	PTEN-induced kinase 1	A protein kinase, may involved in mitochondria function
PARK7	DJ1	1p36	AR	Early-onset, levodopa-responsive	DJ-1	Protection against oxidative stress
PARK8	LRRK2	12p11.2-q13.1	AD	Similar to IPD	Dardarin	A protein kinase
PARK9	ATP13A2	1p36	–	–	ATPase type 13A2	Lysosomal type 5 P-type ATPase
PARK13	HTRA2	2p13	IPD	IPD	HtrA2/Omi	Mitochondrial serine protease

AD, autosomal dominant; AR, autosomal recessive; IPD, idiopathic Parkinson's disease; UPS, ubiquitin proteasome system.

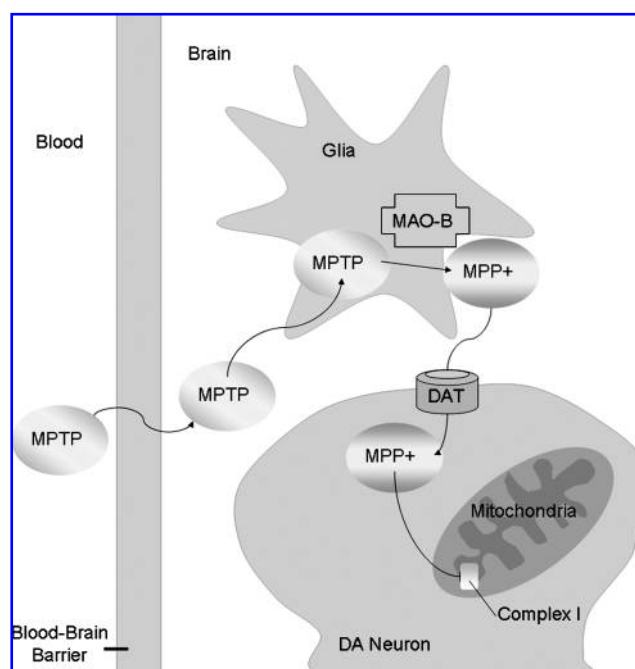
PD in 1989 (130). Recently Keeney *et al.* suggested that complex I is the only respiratory chain protein complex to be affected by endogenous oxidative damage and reduced structural stability (66), although defects in other complexes have also been reported by Bindoff *et al.* (16). The substantia nigra is not the only affected region in the body: reduced complex I activity has also been found in the frontal cortex, skeletal muscle, and platelets of patients with PD (17, 113, 114). Interestingly, deficiency in the substantia nigra and platelets has been consistently detected by several groups (77, 85, 131), whereas in the skeletal muscle the results are less definitive (85, 115, 152). The complex I deficiency in multiple regions suggests that this is a systemic defect, at least in some cases, but it does not help to differentiate acquired and genetic causes.

#### Environmental Toxins and PD: Mitochondrial Complex I Inhibition

The link between mitochondrial toxins and the pathogenesis of PD first emerged following the accidental exposure to 1-methyl-4-phenyl-1,2,3,4-tetrahydropyridine (MPTP), which led to an acute and irreversible parkinsonism (79). MPTP is converted to the active neurotoxic metabolite 1-methyl-4-phenylpyridinium ion ( $MPP^+$ ) by monoamine oxidase B in glial cells (139).  $MPP^+$  is a complex I inhibitor and a substrate for the dopamine transporter (Fig. 1). It therefore accumulates in DAergic neurons and causes cell death by complex I inhibition (99). In aged monkeys and baboons treated with MPTP,  $\alpha$ -synuclein-positive Lewy body-like intracellular inclusions are seen (39, 74). Paraquat, a complex I inhibitor with structural similarity to  $MPP^+$ , can also lead to selective DA neuron loss, as well as  $\alpha$ -synuclein aggregation and upregulation in mice (37, 86, 155).

Rotenone, another specific complex I inhibitor, is a commonly used pesticide. When infused into rodents at low doses over 1 month, rotenone leads to nigrostriatal neuronal loss, the formation of Lewy body-like inclusions and behavioral phenotypes reminiscent of PD (14). Furthermore, chronic exposure to rotenone can also lead to oxidation of DJ-1, accu-

mulation of  $\alpha$ -synuclein, and proteasomal impairment (13, 132, 154). However, the damage induced by rotenone is a multisystem degeneration and more widely spread than that seen in PD (58). This suggested that some of the toxin-induced animal models may not be the true representation of PD and



**FIG. 1. The MPTP metabolic pathway.** After administration, MPTP can freely cross the blood–brain barrier. Once MPTP has entered the brain, it will be metabolized to  $MPP^+$  by the enzyme monoamine oxidase B (MAO-B) in non-DAergic neurons.  $MPP^+$  is the active toxic compound and it will then be taken up by DA transporters. Once inside the DAergic neurons,  $MPP^+$  impairs mitochondrial respiration by inhibiting complex I activity, which will then causes mitochondrial dysfunction, oxidative stress, and cell death.

TABLE 2. MITOCHONDRIA TOXIN ANIMAL MODELS OF PD

Toxin	PD pathology
MPTP (acute)	20–50% DAergic neuron loss Reduced DA levels in the striatum
MPTP (chronic)	Up to 70–80% DAergic neuron loss Formation of $\alpha$ -synuclein positive inclusions
Paraquat	Small but significant loss of DAergic neurons Up-regulation and aggregation of $\alpha$ -synuclein
Rotenone (chronic)	Progressive loss of DAergic neurons Formation of $\alpha$ -synuclein and ubiquitin positive inclusions Oxidative damage Widespread cell loss were also seen in some cases

the disease is more complicated than just simple mitochondrial complex I inactivation (for a summary, see Table 2).

### Genetic Defects and PD: Impaired Mitochondrial DNA and Genomic DNA

#### Mitochondrial DNA mutation and deletion in PD

In the 1990s, Swerdlow *et al.* (147) and Gu *et al.* (53) reported that the complex I defect seen in PD patients can be transmitted to cybrid cells in which platelets from PD patients were fused with mitochondria-deficient cell lines. These cybrid cell lines have also shown increased reactive oxygen species (ROS) production and increased sensitivity to cell death induced by complex I inhibition (147). These findings suggest that the mitochondrial genome may contribute to the complex I deficiency in PD patients.

Mitochondrial DNA (mtDNA) encodes 13 subunits of the respiratory chain proteins, including seven complex I, one complex III, three complex IV, and two complex V subunits. The majority of the proteins are therefore encoded by the nuclear genome. mtDNA is in a hostile environment and is often the victim of mutations throughout the life of a cell. As well as point mutations, other larger scale abnormalities can be found, including deletion, duplication, and depletion. Increased levels of mtDNA deletion in the striatum of patients with PD were reported by Ikebe *et al.* in the early 1990s (60). Whether such deletions are a cause of PD or an age-related bystander phenomena remains unclear. In two studies using quantitative single cell techniques, high levels of mtDNA deletions were detected in the substantia nigra neurons in both aged controls and PD patients, with a slightly increased trend in PD individuals (12, 75). Interestingly, they have also shown that the mtDNA deletions were significantly higher in neurons with impaired cytochrome oxidase activity (75), suggesting that mtDNA deletions may account for the impairment of cellular respiration. Conversely, despite numerous studies, the role of single base pair mutations/polymorphisms and haplogroups in PD remains controversial (7, 24, 43, 59, 159), although it seems that a single nucleotide polymorphism in the DN3 gene (one of the complex I genes) had a protective effect in PD in certain age and gender groups (24, 43, 59). Overall, these findings suggested that al-

teration of the mitochondrial genome may be involved in the pathogenesis of PD but further genetic and functional studies are still needed.

### Nuclear Encoded Proteins and Familial PD

#### PINK1

Mutations in the PINK1 gene were first identified in three families with an autosomal recessive form of PD in 2004 (157). The PINK1 gene contains 8 exons and encodes a 581 amino acid (63 kDa) protein with an amino-terminal mitochondrial targeting sequence and a serine–threonine kinase catalytic domain (136). To date, PD-causing mutations of PINK1 have been described both within and outside the kinase domain with no obvious clustering within the gene. Some of the mutations have been reported to reduce the kinase activity of PINK1 *in vitro* (10, 137). Western blot analysis of PINK1 overexpressing cells suggested that the full length PINK1 protein could also be cleaved into a shorter form, which normally runs at 54 kDa (41, 122, 136). It has been shown that Rhomboid-7, a mitochondrial protease, is responsible for the cleavage of the precursor forms of PINK1 (168) in *Drosophila*. Further identification of the cleavage enzymes and cleavage sites of PINK1 in mammalian systems will help us gain more understanding of the processing of PINK1. In particular, it will be important to determine whether the active form is the full length or the cleaved form and which molecular steps are involved in its cleavage. PINK1 mRNA is ubiquitously expressed in human tissues and the highest expression is found in heart, muscle, and testes (156). In mammalian brains, PINK1 is uniformly expressed, with highest expression levels found in the cell bodies of neurons and glia (41, 153). Most reports have indicated that PINK1 localizes subcellularly in the inner membrane of mitochondria (41, 122, 136), the mitochondrial intermembrane space (122, 136), and/or the outer mitochondrial membrane (41, 178). However, the cytoplasmic localization of PINK1 has also been reported (10, 55, 166). To date, none of the known mutations affect the localization of PINK1, but some mutations can affect protein stability and cause increased degradation (10, 97). It is possible that some of the mutations may affect the cleavage of PINK1 and therefore affect its stability and functions. Further investigation in this area could increase our understanding the role of PINK1 in PD pathogenesis.

Knockdown of PINK1 using transient RNA interference has shown reduced mitochondrial membrane potential and increased rate of basal and stress-induced apoptosis (55, 118, 157). In contrast, overexpression of wild-type, but not mutant, PINK1 in tumor cell lines was shown to prevent activation of caspase-3 and release of cytochrome c from mitochondria to cytosol under stress conditions (118, 157, 165). More recently, stable knockdown of PINK1 by retrovirus showed reduced long-term neuronal viability, increased sensitivity to staurosporine-induced apoptosis, reduced mitochondria membrane potential, and increased basal free radical production in human DAergic neurons (170).

In *Drosophila* PINK1 knockout models, motor deficits including abnormal wing posture, rigidity, flight impairment, and reduced climbing ability have been reported and some of the motor phenotypes were progressive with age (26, 112, 164). The numbers of DAergic neurons in a certain key cluster of the fly brain also showed a small but significant decrease

(~10%) (26, 164, 173). In addition, cell loss was also found in the thoracic indirect flight muscles (173), and swollen mitochondria were seen in the muscle fibers as well as in surviving DAergic neurons (112). Those flies also display an increased sensitivity to paraquat and rotenone. This phenotype is similar to parkin knockout flies. Interestingly, the PINK1 knockout fly phenotypes can be rescued by overexpressing wild-type parkin (112, 149, 173).

Taken together, these studies suggest a chronic mitochondrial dysfunction in the absence of PINK1 in cell models and non-mammalian models, but further evidence in *in vivo* mammalian models is needed. To date, no motor impairments or DAergic neuron losses have been found in PINK1 loss-of-function mouse models (71, 178). Abnormalities have been observed in the nigrostriatal circuitry in PINK1 knockout mice. Kitada *et al.* reported a reduction in evoked dopamine release in striatal slices and in corticostriatal long-term potentiation and depression (71). These defects can be alleviated by D1 and D2 agonists, suggesting impaired release of synaptic DA. More recently, reduced mitochondrial complex activities, and increased sensitivity to oxidative stress have been detected in the same mice (42).

### Parkin

Mutations in the parkin gene were found in autosomal recessive early-onset PD (70), and parkin mutations are relatively common (accounting for ~50% of all autosomal recessive PD cases) (133). Parkin is a 465 amino acid protein with two RING fingers separated by an in-between RING domain at the carboxyl terminus; it functions as an E3 ubiquitin ligase (133). E3 ubiquitin ligases are one component of the UPS, a main pathway for removing misfolded or unwanted proteins from the cells (25). On the amino terminus of parkin, a ubiquitin-like domain binds to the RPN10 subunit of the 26S proteasome (127). Parkin can be phosphorylated by casein kinase-1, protein kinase A, and protein kinase C *in vitro*, and the phosphorylation is regulated by cellular stress, such as proteasomal dysfunction and endoplasmic reticulum stress (172).

Although usually described as an essentially cytosolic protein, parkin is mostly localized into the mitochondria in dividing neuroblastoma cells, and within the mitochondria parkin is mainly localized to the matrix and inner membrane (78). It has been suggested that parkin's mitochondrial translocation can be promoted by the phosphorylation of parkin by PINK1 (69). In neuronally differentiated PC12 cells, parkin was shown to associate with the outer membrane of mitochondria, where it plays an important role in preventing mitochondrial swelling, cytochrome c release, caspase activation, and the apoptosis induced by ceramide (29). This anti-apoptotic effect of parkin is abolished by PD-causing mutations and the proteasome inhibitor epoxomicin (29), suggesting that it is mediated by the E3 ubiquitin ligase activity of parkin. When cells are stressed with the complex I inhibitor rotenone, parkin is released from mitochondria into the cytosol (78).

In transgenic *Drosophila* models, swollen mitochondria with disintegrated cristae and apoptotic cell death were observed in the flight muscles of parkin knockout fly lines and flies overexpressing mutant parkin (51, 163). In mammalian models, parkin knockout mice showed a mild but significant decrease in mitochondrial respiratory capacity in the stri-

tum, as well as reduced expression of specific respiratory chain and antioxidant proteins, although the mitochondria morphology was not affected (108). Intriguingly, although a mild nonprogressive motor deficit, reduced synaptic excitability, and increased striatal extracellular dopamine concentrations were reported in young parkin knockout mice (49, 61); no loss of DAergic neurons or inclusion formations were described. These findings suggested that while parkin plays an important role in maintaining mitochondrial function, parkin deficiency alone may not be sufficient to cause PD, at least in mammalian transgenic models. This raised the hypothesis that neurodegeneration in these models may require further environmental or genetic stresses. For example, primary midbrain neurons from parkin knockout mice showed increased sensitivity to apoptotic cell death induced by mitochondria complex I inhibition induced by rotenone (21). Similar mechanisms might also apply in humans, since people with heterozygous parkin mutations have an increased risk of developing PD and progressive nigrostriatal dysfunction visualized by [<sup>18</sup>F]dopa positron emission tomography (PET) (67).

### DJ-1

A variety of missense, truncating, and deletion mutations have been identified in the DJ-1 gene, which causes an autosomal recessive form of PD (18). Similar to patients with parkin mutations, patients with DJ-1 mutations exhibit slow progressing young-onset PD with a good response to levodopa treatment and may have dystonia. However, unlike parkin, DJ-1 mutations are very rare, only accounting for ~1–2% of early-onset cases (18). The protein encoded by DJ-1 is a 23 kDa protein, which is expressed in both peripheral tissues and central nervous system. In the brain, DJ-1 is highly expressed in the cerebellum, hippocampus, and olfactory bulb, but has also been detected in striatum, substantia nigra pars compacta, and reticulate (8, 64, 125, 177). Subcellularly, the endogenous DJ-1 protein is predominately found in the cytoplasm, but a small proportion is also localized to the mitochondrial intermembrane space and the matrix (177). This mitochondrial localization suggests that DJ-1 might have a role in mitochondrial function, although no mitochondrial morphological changes have been reported in DJ-1 deficient models.

DJ-1 is a multifunctional protein. It can function as a modulator of androgen receptor-dependent transcription, an oncogene, and an oxidative stress sensor (98, 148). In terms of PD pathogenesis, the oxidative stress sensor function of DJ-1 is likely to be most crucial because it acts as an antioxidant protein or a redox sensor (20, 93). In cultured mammalian cells, knockdown of DJ-1 by siRNA leads to increased cell death induced by oxidative stress, ER stress, and proteasome inhibition (175). In terms of transgenic animal models, DJ-1 knockout mice showed motor abnormalities but no DAergic neuron loss was seen in the substantia nigra (50). Furthermore, increased sensitivity to mitochondrial complex I inhibition and oxidative stress has also been reported in DJ-1 knockout mice (68) and a physical interaction has been reported between DJ-1 and PINK1 (150). Interaction between DJ-1 and parkin has also been reported under oxidative conditions (96). However, both of these interactions have yet to be confirmed *in vivo*. In fly models, overexpression of DJ-1 failed to rescue the muscle phenotypes caused by PINK1 knockout

(173), suggesting that DJ-1 is either upstream of PINK1 or acts in a parallel pathway to PINK1.

#### *Omi/HtrA2*

Omi/HtrA2 is a mitochondrial serine protease and has also been associated with PD. The Omi/HtrA2 protein is localized to the mitochondrial intermembrane space and is released into the cytosol when cells are stimulated by pro-apoptotic stimuli (146). A G399S mutation in Omi/HtrA2 has been reported in four sporadic PD cases and an A141S polymorphism was also found to increase the risk of developing PD (144). Both mutations are suggested to affect the regulation of the proteolytic activity of Omi/HtrA2 and modulate cell death. However, genetically the role of this gene in PD pathogenesis remains unproven, as other reports have failed to identify a mutation or an association (126, 138). Interestingly, Omi/HtrA2 knockout mice have a strong parkinsonian phenotype, including rigidity, tremor, and striatal damage (89). Finally, HtrA2 phosphorylation has been shown to be PINK1 dependent (119). The phosphorylation of Omi/HtrA2 at Ser142 demonstrates increased protease activity and enhanced protective effect under stressed condition. In brains of patients with PD-associated PINK1 mutations, the phosphorylation of HtrA2 at Ser142 is decreased (119).

#### *$\alpha$ -Synuclein*

Mutations and multiplications in the  $\alpha$ -synuclein gene were found associated with an autosomal dominant form of PD (103, 120). Although mutations are extremely rare,  $\alpha$ -synuclein is regarded as central to disease pathogenesis, as it is a key component of Lewy bodies (143).  $\alpha$ -Synuclein protein is usually localized to the cytosol and synaptic terminals. However, it has recently been suggested that  $\alpha$ -synuclein may localize in or interact with the mitochondria. This has been observed in cells overexpressing wild-type or A53T mutant  $\alpha$ -synuclein and in isolated rat brain mitochondria. Evidence has suggested that this interaction can cause reduced mitochondrial complex I activity, increased ROS production, cytochrome c release, and increased mitochondrial calcium (34, 110). Overexpression of the G209A mutant or wild-type  $\alpha$ -synuclein can also increase the sensitivity of neurons to mitochondrial toxins such as rotenone in mammalian cells (105). In terms of transgenic models, mice overexpressing the human  $\alpha$ -synuclein gene are also more sensitive to complex I inhibition induced by MPTP and showed abnormal mitochondrial morphology (142), whereas  $\alpha$ -synuclein knockout mice are more resistant to the complex I inhibitor MPTP, and the complex II inhibitors malonate and 3-nitropropionic acid (30, 72). It is believed that this protective effect is mediated by the decreased free radical production. Moreover, transgenic mice overexpressing A53T or A30P mutant  $\alpha$ -synuclein developed a decreased complex IV activity in the spinal cord, neuronal loss, and accumulation of intraneuronal inclusions, which contain both  $\alpha$ -synuclein and degenerating mitochondria (88). Together, these findings suggest an important role of  $\alpha$ -synuclein in mitochondrial toxicity and cell death. Interestingly,  $\alpha$ -synuclein toxicity has also been shown in aging yeast models and this toxicity can be inhibited by abrogation of mitochondrial DNA (19), suggesting that functional mitochondria are important for  $\alpha$ -synuclein toxicity. Therefore the relation between  $\alpha$ -synuclein and mitochondrial function

may be complicated and the precise molecular pathways have yet to be characterized.

#### *LRRK2*

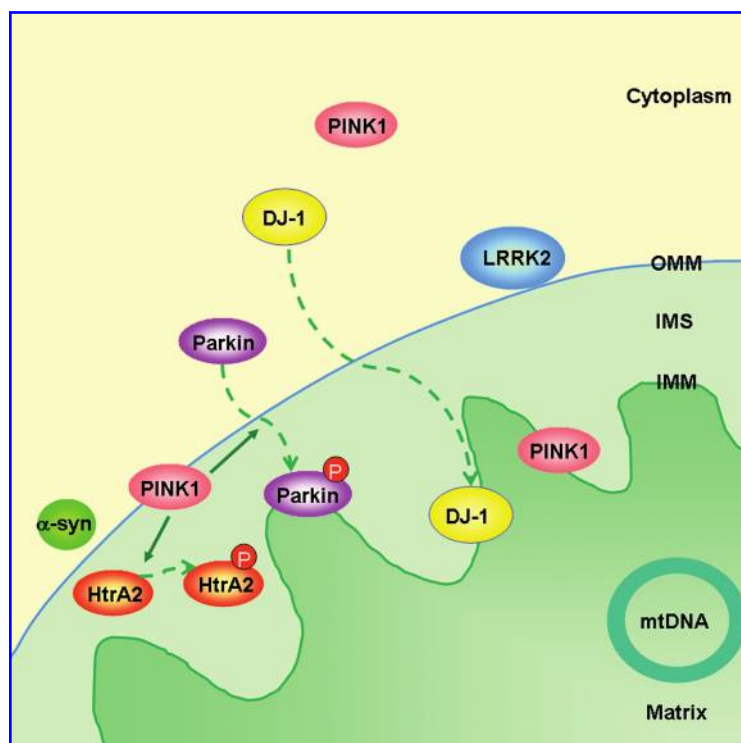
Mutations in the LRRK2 gene were first found in relatively late onset autosomal dominant PD (107, 179). LRRK2 mutations are found to account for 5–6% of familial PD cases and up to 1.6% of patients with sporadic PD (45). The protein encoded by LRRK2 is called dardarin (from the Basque word for tremor) (107). Dardarin is a large protein (2527 amino acids) with several predicted functional domains, including: the N-terminal leucine-rich repeats, the Ras/GTPase domain (Roc), the COR (C-terminal of Roc) domain, the serine/threonine protein kinase domain, and the carboxy terminal WD-40 like domain (52). Mutations have been reported in all the protein domains and there is no obvious correlation between the mutation sites and clinical phenotype. Although some mutations, such as G2019S, I2020T, and R1441G have been shown to increase the kinase activity of LRRK2, others seem to decrease or not affect the kinase activity (48, 52, 63, 83, 84). LRRK2 is widely expressed throughout the brain and peripheral tissues (44). Subcellularly, LRRK2 is mostly associated with the cytoplasmic membrane and has also been reported to be associated with mitochondrial outer membrane fractions (46, 141, 167), suggesting a role for LRRK2 in mitochondrial function. In primary cortical neuron cultures, overexpression of some LRRK2 mutants (R1441C, Y1699C, or G2019S) can lead to neuronal degeneration (52, 140, 141). Moreover, some LRRK2 mutations can also result in progressive reduction in neurite length and branching, both in primary neuronal cultures and in the intact rodent brain, where LRRK2 knockdown has the opposite effects (84). Interestingly, the LRRK2 GTPase domain has a significant sequence similarity with the Rho GTPase domain of Miro (54), which is essential for anterograde transport of mitochondria along microtubules (47).

Taken together, most of the PD-linked genes are found associated with mitochondria (Fig. 2) and mutations in those genes often lead to impaired mitochondrial function. However, the mechanisms for the mitochondrial dysfunction are yet not very clear. Studies of genetic and toxin models have suggested that impaired mitochondrial dynamics may contribute to the mitochondrial dysfunction in PD.

### **Mitochondrial Dynamics and PD: Possible Mechanisms for Mitochondrial Dysfunction?**

#### *Fission and fusion*

Mitochondria are extremely dynamic organelles and are undergoing continual fusion and fission (Fig. 3). The balance between fusion and fission not only determines the morphology of mitochondria in cells but also has a significant effect on mitochondrial function (23). Fusion and fission events lead to mixing of mitochondrial membranes and exchange of mitochondria contents. These events also contribute to the control of mitochondrial subcellular localization and dramatic mitochondrial morphology changes that occur during apoptosis. Mutations in some mitochondrial fusion and fission genes have been reported in neurodegenerative disease. For example, mutations in the optic atrophy 1 (OPA1) gene can cause a hereditary optic neuropathy leading to

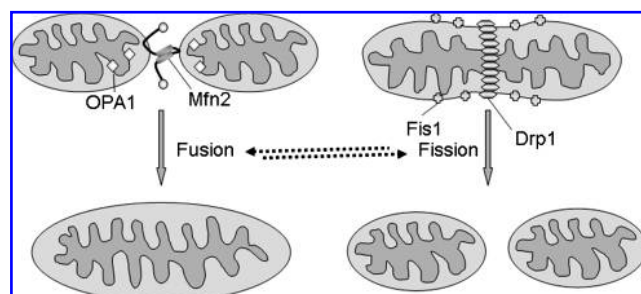


**FIG. 2. PD genes associated with mitochondria.** Among the PD-associated genes, both LRRK2 and  $\alpha$ -synuclein have been found associated with mitochondria outer membrane. Although known as a mitochondria kinase, PINK1 can localize to both the cytoplasm and the mitochondria, where it can affect HtrA2 phosphorylation. Parkin is a cytosolic protein, but can also be translocated to mitochondria, which may be promoted by phosphorylation by PINK1. DJ-1, another cytosolic protein, can also be translocated to mitochondria. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article at [www.liebertonline.com/ars](http://www.liebertonline.com/ars)).

blindness (32). OPA1, a GTPase, is a pro-fusion protein that is localized to the mitochondrial intermembrane space, and is tightly associated with the inner membrane (104). Another example is human mitofusion-2 (MFN2). Mutations in MFN2 cause Charcot-Marie-Tooth disease, a dominantly inherited neuropathy characterized by degeneration of peripheral sensory and motor axons (180). Mfn2 is a GTPase localized to the mitochondrial outer membrane and can promote mitochondrial fusion by forming complexes and tethering mitochondria together. It has been shown that MFN2 mutations can cause abnormal clustering of small fragmented mitochondria in both neuronal cell bodies and axons, and those clusters were unable to be transported down the axon (6). These

suggested that mitochondrial dynamics are critical for the integrity of the nervous system.

In terms of PD, no mutations in typical mitochondria fission and fusion genes have yet been found in PD patients. However, increased evidence from PINK1 and parkin studies has suggested potential involvement of mitochondrial dynamics in PD (111, 129, 164). As mentioned earlier, PINK1 or parkin deficiency can lead to abnormal mitochondrial morphology in the flight muscle and DAergic neurons of flies. Interestingly, these phenotypes can be suppressed by overexpressing the Drp1 gene, a mitochondrial fission-promoting component, or by downregulation of mitochondrial fusion promoting genes Opa1 and Marf, the *Drosophila* homologue of human Mfn gene (33, 111, 121, 174), suggesting that lack of PINK1 or Parkin can lead to increased mitochondrial fission in *Drosophila*. In mammalian cells, overexpression of PINK1 can lead to increased mitochondrial fission, where knockdown of PINK1 causes excessive fusion (173). Increased mitochondrial fusion has also been found in primary fibroblast cells from patients with PINK1 mutations (36). It is noteworthy that PINK1 deficiency led to opposite effects in *Drosophila* and mammalian systems. Further investigations are required to explain this discrepancy and also to gain more understanding of the role of mitochondrial fission and fusion in PD pathogenesis.



**FIG. 3. Mitochondrial fission and fusion.** During mitochondria fusion, mitofusin proteins link the outer mitochondrial membrane of two mitochondria, which lead to membrane fusion. Then Opa1, which is anchored on the inner mitochondrial membrane, regulates the fusion of the inner membrane. During fission, Fis1 circumscribes the outer mitochondrial membrane and interacts with Drp1, which leads to separation of the outer and inner membranes.

#### Maintaining calcium homeostasis

Apart from energy generation, another key function of mitochondria is to maintain the calcium ( $\text{Ca}^{2+}$ ) homeostasis within the cells. Mitochondria have a vast but finite capacity for buffering intracellular  $\text{Ca}^{2+}$ , by uptake and accumulation of  $\text{Ca}^{2+}$  into mitochondria. When mitochondrial  $\text{Ca}^{2+}$  is overloaded, the permeability transition pore (PTP) will be activated and therefore lead to permeabilization of mito-



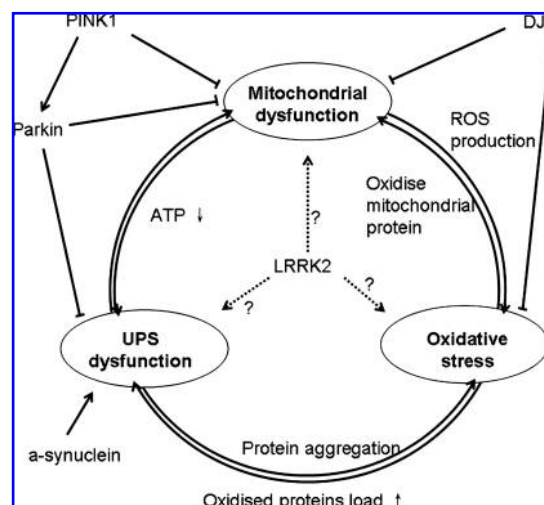
chondrial inner membrane, collapse of bioenergetics, and release of  $\text{Ca}^{2+}$ . In neurons, calcium homeostasis and calcium signaling can regulate numerous neuronal functions, such as synaptic transmission, neuronal plasticity, and cell survival, and therefore disruption in intracellular calcium homeostasis can have a major impact on neuronal health. Dysregulation of calcium homeostasis has been reported both in the physiological aging process and a range of neurodegenerative diseases, such as Alzheimer's disease, Huntington's disease, and amyotrophic lateral sclerosis (1, 2, 15, 109, 158). Recently, calcium homeostasis dysregulation has also been suggested to play a role in PD. In neuroblastoma cells expressing mutant  $\alpha$ -synuclein (A30P and A53T), Furukawa *et al.* have found higher plasma membrane ion permeability, an increase in both the basal level of intracellular  $\text{Ca}^{2+}$  concentrations and the  $\text{Ca}^{2+}$  response to membrane depolarization, as well as increased cell death, which can be inhibited by a  $\text{Ca}^{2+}$  chelator, BAPTA-AM (40). These findings suggest that mutant  $\alpha$ -synuclein can lead to perturbation in the  $\text{Ca}^{2+}$  homeostasis which contributes to the cell death. Although further investigations about whether mitochondria are involved in this process and its mechanisms are still needed, this is one piece of evidence indicating the involvement of impaired  $\text{Ca}^{2+}$  homeostasis in PD pathogenesis.

On the other hand, some studies using toxin models have implicated the involvement of  $\text{Ca}^{2+}$  homeostasis dysregulation, mitochondrial dysfunction, and PD-related cell death. In isolated brain mitochondria, the complex I inhibitors MPP<sup>+</sup> and rotenone can induce  $\text{Ca}^{2+}$  release into cytosol, membrane depolarization, and mitochondrial swelling, all of which can be inhibited by preventing the PTP opening (22, 106). It has also been shown that PTP inhibitors can reduce the cell death caused by MPP<sup>+</sup> in animal models (27). Whether the MPP<sup>+</sup> induced PTP opening and  $\text{Ca}^{2+}$  release is due to complex I inhibition has yet to be investigated. The mechanisms of calcium dysregulation in PD and its contributions to the pathogenesis of PD are still unclear and further studies in genetic and toxin PD models are required.

#### Mitochondrial Dysfunction, Oxidative Stress, and Protein Aggregation: A Network of Pathways

As mentioned earlier, mitochondrial dysfunction, oxidative stress and abnormal protein accumulation have all been implicated in the cell death pathways in PD. Accumulating evidence has suggested that these pathways are not functioning independently but rather as a network (Fig. 4).

Protein aggregation/proteasomal inhibition is another important pathway for PD pathogenesis. In PD patients, decreased 20S proteasomal enzymatic activities and reduced expression of the alpha-subunits of 26/20S proteasomes were detected, suggesting a possible failure of the UPS in PD brains (91). In toxin-induced animal models, proteasomal inhibition can lead to loss of nigral DAergic neurons (91, 92, 176), although there is still a debate as to whether these are good PD models because some reports failed to reproduce these observations (87). The UPS is an ATP-dependent protein degradation system (161). Therefore, deficiency in mitochondrial respiratory chain activity may lead to impaired ATP production, which can then result in limited proteasomal activity. In addition, mitochondrial dysfunction will also result in increased free radical generation, which can lead to an increase



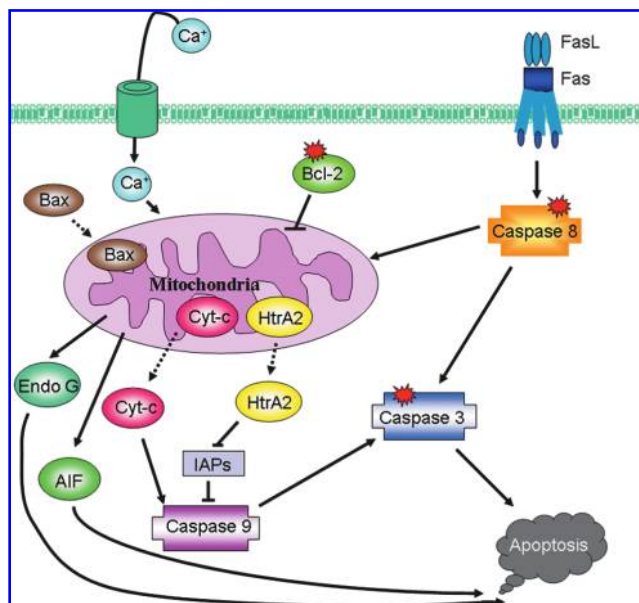
**FIG. 4. Network of PD pathways.** Interactions between the three major pathways and several PD associated genes.

in substrate load (oxidized proteins) for the proteasome (58). The proteasomal dysfunction will then lead to accumulation of damaged proteins, which have a potentially negative effect on cell function and survival. Conversely, proteasomal stress can also lead to mitochondrial dysfunction. For example, proteasome inhibition can lead to reduced mitochondrial complex I and complex II activities, increased mitochondrial ROS production, and reduced intramitochondrial protein translation (145).

Oxidative stress is another common underlying feature in PD pathogenesis and it is the result of unregulated production of ROS, which could originate from the mitochondria, cytoplasm, and also outside the cells. Mitochondria consume a great amount of oxygen via the electron transport chain and a small proportion of the oxygen is reduced to ROS, even under normal situations. In DAergic neurons, dopamine can generate ROS via monoamine oxidase (MAO) (82). Dopamine is synthesized in the cytosol and pumped into synaptic vesicles by vesicular monoamine transporter 2 (VMAT2). Defects in the secretory pathway can lead to synaptic vesicle shortage and reduced VMAT2 in the synapse, which will impede dopamine loading and cause increased cytosolic dopamine levels. This consequently leads to increased ROS production and oxidative stress. Furthermore, oxidative stress is not only generated in neurons. Glial cells are also a host of ROS when they are activated (76, 171). On PD brains, activation of glial cells has been reported in all affected regions, which may also contribute to the oxidative stress (123). In the other hand, oxidative stress can induce abnormal mitochondrial function, conversely inhibition of complex I by environmental toxins or mutations in complex I subunits leads to increased free-radical generation (128).

#### Cell Death Mechanisms in PD

There is now substantial evidence that mitochondrial dysfunction plays a crucial role in the pathogenesis of PD. However, the exact mechanism of cell death in PD is not very clear (Fig. 5). Extensive mitochondrial injury may impact the maintenance of sufficient cellular ATP, which can lead to necrotic cell death. Mild mitochondrial dysfunction can cause



**FIG. 5. Role of mitochondria in apoptosis.** Stars indicate molecules affected in PD brains. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article at [www.liebertonline.com/ars](http://www.liebertonline.com/ars)).

abnormal intracellular  $\text{Ca}^{2+}$  accumulation in neurons in response to excitotoxicity induced by neurotransmitters such as glutamate (38) and can also lead to excessive production of ROS and trigger apoptotic cell death. Mitochondria are also one of the key players in apoptosis (Fig. 5). Apoptotic stimuli lead to the release of small pro-apoptotic proteins, such as cytochrome c and apoptosis-inducing factor (AIF) that are normally localized in the mitochondrial intermembrane space, into cytosol. Upon entry into the cytosol, those pro-apoptotic proteins will trigger a caspase-dependent mechanism. Cytochrome c can bind to Apaf-1 (apoptotic protease-activating factor-1) and form the apoptosome. The apoptosome then activates caspase-9, which further cleaves and activates caspase-3. Caspase-3 then processes a variety of substrates such as PARP and ICAD (caspase-activated DNase) and leads to DNA fragmentation, cytoskeletal alterations, and cell death.

Apoptotic cell death has been suggested to play an important role in DA neuron loss. In postmortem brain tissue, a positive correlation was detected between the level of DA neuron loss and the percentage of caspase-3-positive neurons in the SN tissue (56). In addition, the percentage of active caspase-3-positive neurons among DA neurons was significantly higher in PD brains compared to controls (56). An increase in level of anti-apoptotic protein bcl-2 has also been reported in SN but not in the cerebral cortex of PD patients (95), although some other studies have shown conflicting results (162). Furthermore, a significantly higher percentage of activated caspase-8 positive DA neurons was detected in SN of PD patients (57). Surprisingly, inhibition of the caspase-8 pathway did not show neuroprotective effects against neurotoxin MPTP in primary DA neuron cultures, but seemed to trigger a switch from apoptotic cell death to necrosis (57). This suggested that necrosis might also play a role in DA neuron loss in PD.

In PD mouse models induced by chronic regimens of MPTP, inhibition of mitochondrial complex I led to transcriptional induction and translocation of a pro-apoptotic protein Bax, which in turn can cause cytochrome c release and activation of mitochondrial-dependent cell death pathways (116, 117). Caspase-3 activation and DNA fragmentation has also been reported in those models (151). Ablation of Bax or inhibition of Apaf-1 or the downstream substrate of caspase-3, poly (ADP-ribose) polymerase (PARP), can protect against MPTP-induced neurotoxicity (28, 94, 160). In cultured cells, MPP<sup>+</sup> induces cell death via increased Bax expression, release of cytochrome c and caspase-9/-3 activation (65, 80). More recently, it has been suggested that deficiency of a PD-associated gene (PINK1) can lead to cell death via the mitochondrial mediated apoptosis (Bax translocation to mitochondria, activation of caspase-9/-3 and PARP) in long-term culture of human DAergic neurons (170). All these findings suggest that although necrosis might also play a role in neurodegeneration in PD, the mitochondrial-mediated apoptosis pathway is the key player of neuronal loss in PD. Of course, other cell death pathways may also contribute to the neuronal loss in PD. For example, acute high doses of MPTP can lead to nonapoptotic cell death (62, 73, 100).

### Therapeutic Opportunities

It is hypothesized that drugs which can improve mitochondrial function might slow the progression of PD. Co-enzyme Q10 was one of the first to be investigated. Co-enzyme Q10 is a component of the respiratory chain that shuttles electrons between complexes I/II and III and it also functions as an antioxidant (35). In aged mice, administration of co-enzyme Q10 attenuates the reduction of striatal dopamine concentration and dopaminergic axons induced by MPTP (9). A pilot study in PD patients showed that oral administration of co-enzyme Q10 produced a trend towards increased complex I activity (134). A later study from Shults and colleagues showed that co-enzyme Q10 supplementation could slow the motor functional decline in patients with early PD (135). In 2007, a randomized, double blind, futility clinical trial run by the NINDS NET-PD Investigators could not reject co-enzyme Q10 as futile and suggested that this compound is worth future studies (101).

Creatine, another potential treatment, is a substrate for cytosolic and mitochondrial creatine kinases. It can be converted to phosphocreatine, which will then transfer its phosphoryl group to ADP to synthesise ATP and produce energy (4). Creatine showed neuroprotective effects against MPP<sup>+</sup> in primary neuronal cultures (3). In MPTP mouse models, oral supplementation with creatine reduced dopaminergic neuron loss (90). In a double-blind placebo-controlled study, oral creatine supplementation failed to show a significant treatment effect on UPDRS scores (11). However, in patients with creatine treatment there was a lower requirement for dopamine therapy, which suggested a potential neuroprotective effect of creatine. Another randomized, double blind, futility clinical trial in early PD patients also could not reject creatine as futile (102).

Despite these relatively disappointing results, the recent strengthening evidence of the role of mitochondria in PD does motivate the search for more molecules that can address the deficiencies in the pathways.



## Conclusions

The important question for understanding the cell death pathways of PD and for finding potential therapies is to determine the common pathogenesis pathway of not only Mendelian genetic forms of PD but also sporadic PD. Mitochondrial dysfunction may be the key player in the PD pathogenesis pathway. Mitochondrial dysfunction has been detected in both sporadic PD patients and patients with familial forms of PD. Abnormal mitochondrial function has also been reported in various transgenic animal models with either overexpression or knockout of PD associated genes. Moreover, mitochondrial toxin-induced animal models have displayed some typical PD symptoms, including loss of DA neurons, aggresome formation, and movement problems. However, many questions still need to be addressed in this field: how does mitochondria dysfunction occur in PD; is it the primary event or a secondary consequence; is restoring the mitochondria function sufficient to rescue the neuronal cell death in PD? Further investigation into the mechanism of mitochondria dysfunction in PD may provide answers to some of these questions.

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#### Abbreviations Used

AIF = apoptosis-inducing factor  
 Apaf-1 = apoptotic protease-activating factor-1  
 DAergic = dopaminergic  
 LRRK2 = leucine-rich repeat kinase 2  
 MAO = monoamine oxidase MFN2, human mitofusion-2  
 MPP<sup>+</sup> = 1-methyl-4-phenylpyridinium ion mtDNA, mitochondrial DNA  
 MPTP = 1-methyl-4-phenyl-1,2,3,4-tetrahydropyridine  
 OPA1 = optic atrophy 1  
 PARP = poly (ADP-ribose) polymerase  
 PD = Parkinson's disease  
 PINK1 = PTEN-induced kinase 1  
 PTP = permeability transition pore  
 ROS = reactive oxygen species  
 SNpc = substantia nigra pars compacta  
 UPS = Ubiquitin Proteasome System  
 VMAT2 = vesicular monoamine transporter 2



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